MICROBIAL COMPOSITIONS AND METHODS

REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of and priority to U.S. Provisional Patent Application No. 63/426,025, filed November 16, 2022 and U.S. Provisional Patent Application No. 63/547,326, filed November 3, 2023, the disclosure of which is hereby incorporated by reference in its entirety for all purposes.

BACKGROUND

[0002] Many microbes having beneficial effects on plant growth and properties are known; in addition these microbes may have beneficial effects on soil characteristics. Although compositions and methods utilizing such microbes have been described, there remains a need for improvement.

INCORPORATION BY REFERENCE

[0003] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0004] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0005] Figure 1a shows a method of preparation of a microbial composition from individual microbial stocks.

[0006] Figure 1b shows a method of growth and treatment of a microbial stock.

[0007] Figure 1c shows a method of preparation of a microbial composition.

[0008] Figure 1d shows a method of combining one or more microbes and one or more heterologous components.

[0009] Figure 2 shows the topography of a Maximum-Likelihood phylogentic tree displaying 195 ribotype gene signatures representing the OSL probiotic culture collection.

[0010] Figure 3 shows water holding capacity of soil samples.

[0011] Figure 4 shows turf resulting from treated (right) and untreated (left) seeds.

[0012] Figure 5 shows a box and whiskers chart of increased biomass in treated plants.

DETAILED DESCRIPTION

I. Compositions and methods

A. Microbes

[0013] Provided herein are compositions and methods including and/or utilizing one or more microbes, or that result from utilizing one or more microbes, in plant germination, growth, maintenance, and/or use, and other uses as described herein. The one or more microbes may be used in conjunction with any suitable plant or plants and the soil or other growth medium in which the plant or plants grow. As used herein, "microbe" or "microorganism" are used interchangeably and include the two prokaryotic domains, Bacteria and Archaea, as well as eukaryotic fungi and protists. When a specific strain, deposit, or the like, of a microbe is described, this includes progeny and/or mutants thereof. The terms “plurality of microbes,” “plurality of microorganisms,” “consortium of microbes,” “consortium of microorganisms,” are used interchangeably herein, and include groups of two or more different microbes. Unless indicated otherwise, and as used herein, the term “different microbe,” includes a microbe that is taxonomically different from another microbe, e.g., different class, order, family, genus, species, or strain. Unless indicated otherwise, and as used herein, the term “different microbes,” includes two or more microbes, each of which is taxonomically different from the other microbes, e.g., different class, order, family, genus, species, or strain.

[0014] The term "plant," as used herein, includes a whole plant, any reproductive or developmental form or stage thereof, or to a part or fragment of a plant. The term "plant" may therefore be used to encompass plant propagules, seedlings, germinants, tube stock and mature plants or any parts or fragments thereof, including but not limited to hypocotyls, leaves, branches, stems, roots, heads/kernels, crown, tissue samples, seeds, fruits, nuts, flowers or cones.

[0015] Any suitable microbe can be used, such as a bacteria, an archaea, a protozoa, an algae, a fungus, for example a mycorrhizae, a virus, or a combination thereof. Preferably, the microbe is, at some point in its lifecycle, a unicellular organism; however, the microbe can exist in a multicellular state. In preferred embodiments, the compositions and/or methods comprise one or more bacteria.

[0016] In certain embodiments, the one or more microbes are bacteria. In certain embodiments, the one or more microbes are rhizobacteria. In certain embodiments, the one or more microbes are saprophytic. In certain embodiments, the one or more microbes belong to the genus of *Streptomyces*. The microbe can be any suitable strain of *Streptomyces*, including but not

limited to *Streptomyces janthinus*, *Steptomyces cinerochromogenes*, *Streptomyces chromofuscus*, *Streptomyces atratus*, *Streptomyces aurantiogriseus*, *Streptomyces rimosus*, *Streptomyces venezuelae*, *Streptomyces violaceus*, *Streptomyces violascens*, *Streptomyces viridodiasticus*, *Streptomyces griseus*. In certain embodiments, one or more microbes are of *Streptomyces* genus and one or more microbes are of non-*Streptomyces* genus. In certain embodiments, the non-*Streptomyces* genera are one or more of *Pseudomonas*, *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis*, or a combination therof. In certain embodiments, the non-*Streptomyces* genera are one or more of *Pseudomonas*, *Microvirga*, *Micrococcus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis*, or a combination therof. In certain embodiments, the non-*Streptomyces* genera are one or more of *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis*, or a combination therof. In certain embodiments, the non-*Streptomyces* genera are one or more of, *Micrococcus*, *Bradyrhizobium*, or *Pseudomonas*, or a combination therof. In certain embodiments, the non-*Streptomyces* genera are *Bradyrhizobium*, *Pseudomonas*, or a combination thereof. In certain embodiments, the non-*Streptomyces* genus includes *Bradyrhizobium*. In certain embodiments, the non-*Streptomyces* genus includes *Pseudomonas*,

[0017] Certain of the microbes described in this Application were deposited with the American Type Culture Collection (ATCC, Manassas, Va.) on November 15, 2022 and assigned the deposit numbers shown in Table 2. The deposits were made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microbes for the Purposes of Patent Procedure.

[0018] In certain embodiments, one or more microbes comprising one or more genetic sequences for 16S rRNA(s) are used. Sequences are as shown in Table 1.

[0019]

TABLE 1

SEQ ID NO	Genus/Species	Strain #	Sequence
1	Lysinibacillus capsica	162	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCTTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCCTTTACTTCATGGTGAAGGACTGAAA GACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT AAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGG CTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAA GAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTT GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACG CTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGC CCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA CGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC CAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCT TCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTG TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATC TTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGC CAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCGG ATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAG GTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGG TG
2	Lysinibacillus capsici	161	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCTTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCCTTTACTTCATGGTGAAGGACTGAAA GACGGTTTCGGCTGTTGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT AAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGG CTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAA GAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTT GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACG CTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGC CCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA CGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC CAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCT TCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTG TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATC TTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGC CAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCGG ATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGGTG
3	Lysinibacillus capsici	159	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGAAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTACCTTGTAGTTTGGGATAACTCCGGGAAACCGGGGCTAATACCGAATAATCTCCTTTACTTCATGGTGAAGGACTGAAAGACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCTTGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTTGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCTTCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGCCAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGGTG
4	Lysinibacillus capsici	150	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGAAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGGGAAACCGGGGCTAATACCGAATAATCTCCTTTACTTCATGGTGAAGGACTGAAAGACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCTGATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCTTGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTTGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC

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5	Lysinibacillus capsici	155	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAACCTCTTTTACTTCATGGTGAAAGACTGAAA GACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT AAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGG CTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAA GAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTT GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACG CTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGC CCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA CGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC CAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCT TCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTG TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATC TTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGC CAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCGG ATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAG GTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGG TG
6	Lysinibacillus capsici	174	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCTCTTGCTTCATGGCGAGAGACTGAAA GACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC

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7	Lysinibacillus capsici	166	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCTCTTGCTTCATGGCGAGAGACTGAAA GACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT AAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGG CTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAA GAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTT GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACG CTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGC CCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA CGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC CAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCT TCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTG TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATC TTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGC CAACTCGCGAGAGGGAGCTAATCCGATAAATTCGTTCTCAGTTCGG ATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAG GTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGG TG

SEQ ID NO	Genus/Species	Strain #	Sequence
8	Lysinibacillus capsici	160	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCTTGTAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCTCTTGCTTCATGGCGAGAGACTGAAA GACGGTTTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCT AGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACC TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTC CTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCT GATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACCT TGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGC CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT AAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGG CTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGAA GAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTT GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACG CTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGC CCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA CGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTAC CAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCT TCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTG TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATC TTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTGC CAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCGG ATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAG GTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGG TG
9	Lysinibacillus capsici	163	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAG AAAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAAC ACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGGGAAACCGG GGCTAATACCGAATAATCTCTTTTACTTCATGGTGAAAGACTGAAA GACGGCATCTCGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGC TAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGAC CTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT CCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCC TGATGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAA ACTCTGTTGTAAGGGAAGAACAAGTACAGTAGTAACTGGCTGTACC TTGACGGTACCTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAG CCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCG TAAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACG GCTCAACCGTGGAGGGTCATTGGAAACTGGGGGACTTGAGTGCAGA AGAGGAAAGTGGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATT TGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCG CCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACA AGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCC TTCGGGGGCAACGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGAT CTTAGTTGCCATCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTG ACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTT ATGACCTGGGCTACACACGTGCTACAATGGACGATACAAACGGTTG CCAACTCGCGAGAGGGAGCTAATCCGATAAAGTCGTTCTCAGTTCG GATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACA CACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGA GGTAACCTTTTGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGG GTG
10	*Paenibacillus* cellulositrophicus A	56	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GATGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGAGGGAATGATGA AAGACGGAGCAATCTGTCACTTGCGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGGTAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGACCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
11	*Paenibacillus* cellulositrophicus A	59	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GAAGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGAGGGAATGATGA AAGACGGAGCAATCTGTCACTTGCGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGATAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGACCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
12	*Paenibacillus* cellulositrophicus A	62	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GAAGGAGAGCTTGCTCTCCTGATAGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGAGGGGATGATGA AAGACGGAGCAATCTGTCACTTGCGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGGTAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGGCCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
13	*Paenibacillus* cellulositrophicus A	41	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GATGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG

SEQ ID NO	Genus/Species	Strain #	Sequence
			TGAGCTAATACCGGATATCTCATTTTCTCTCCTGAGGGGATGATGA AAGATGGAGCAATCTGTCACTTGCGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGATAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGACCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
14	*Paenibacillus* cellulositrophicus A	67	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GATGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGGGGGAATGATGA AAGACGGAGCAATCTGTCACTTGCGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGGTAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTACAGAGATGTACCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
15	*Paenibacillus* cellulositrophicus A	49	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GAAGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGGGGGAATGATGA AAGACGGAGCAATCTGTCACTTGTGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGATAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGGCCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTTGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
16	*Paenibacillus* cellulositrophicus A	65	GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGGACTT GATGGAGAGCTTGCTCTCCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCTGCAAGACCGGGATAACCCACGGAAACG TGAGCTAATACCGGATATCTCATTTCCTCTCCTGAGGGAATGATGA AAGACGGAGCAATCTGTCACTTGTGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCGGTAGAGTAACTGCTATCGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAAGGCCAA GGCTCAACCTTGGTTCGCACTGGAAACTGGGTGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGATATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGGCCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATTT TAGTTGCCAGCACTTCGGGTGGGCACTCTAGAATGACTGCCGGTGA CAAACCGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCAGTACAACGGGAAGC GAAGCCGCGAGGTGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG GATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAA TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACA CACCGCCCGTCACACCACGAGAGTTTACAACACCCGAAGTCGGTGA GGTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGGTAGATGATTGGG GTG
17	*Paenibacillus* illinoisensis	206	GACGAACGCTGGCGGCATGCCTAATACATGCAAGTCGAGCGGACTT GAAGAGAAGCTTGCTTCTCTGATGGTTAGCGGCGGACGGGTGAGTA ACACGTAGGCAACCTGCCCTCAAGCTTGGGACAACTACCGGAAACG GTAGCTAATACCGAATACTTGCTTCTTTCGCCTGAAGGAAGCTGGA AAGACGGAGCGATCTGTCACTTGAGGATGGGCCTGCGGCGCATTAG CTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGA CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGAC TCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGC CTGACGGAGCAATGCCGCGTGAGTGATGAGGGTCTTCGGATCGTAA AGCTCTGTTGCCAGGGAAGAACGTCCTTGAGAGTAACTGCTCAAGG AGTGACGGTACCTGAGAAGAAAGCCCCGGCTAACTACGTGCCAGCA GCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGC GTAAAGCGCGCGCAGGCGGTCATTTAAGTCTGGTGTTTAATCCCGG GGCTCAACCCCGGATCGCACTGGAAACTGGATGACTTGAGTGCAGA AGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATG TGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACTGAC GCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG TAGTCCACGCCGTAAACGATGAATGCTAGGTGTTAGGGGTTTCGAT ACCCTTGGTGCCGAAGTTAACACATTAAGCATTCCGCCTGGGGAGT ACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACA AGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTA CCAGGTCTTGACATCCCTCTGACCGTCCTAGAGATAGGGCTTTCCT TCGGGACAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAGCCCTTGATCT TAGTTGCCAGCACTTCGGGTGGGCACTCTAAGGTGACTGTCGGTGA CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA TGACCTGGGCTACACACGTACTACAATGGCCGGTACAACGGGCTGT GAAGCCGCGAGGTGGAACGAATCCTAAAAAGCCGGTCTCAGTTCGG ATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATTGCTAGTAAT CGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACAC ACCGCCCGTCACACCACGAGAGTTTATAACACCCGAAGTCGGTGGG GTAACCGCAAGGAGCCAGCCGCCGAAGGTGGGATAGATGATTGGGG TG
18	*Aureimonas* A sp001425485	199	GATGAACGCTGGCGGCATGCTTAACACATGCAAGTCGGACGGGAAG TGGTGCTTCCAGTGGCGGACGGGTGAGTAACGCGTAAGAACCTGCC CTTGGGAGGGGAACAACAACTGGAAACGGTTGCTAATACCCCGTAG GCTGAGGAGCAAAAGGAGGAATCCGCCCGAGGAGGGGCTCGCGTCT GATTAGCTAGTTGGTGAGGCAATAGCTTACCAAGGCGATGATCAGT AGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGC GAAAGCCTGACGGAGCAATGCCGCGTGGAGGTAGAAGGCCCACGGG TCGTGAACTTCTTTTCTCGGAGAAGAAGCAATGACGGTATCTGAGG AATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGTAAGACAGAG GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGT GGCTTTTCAAGTCCGCCGTCAAATCCCAGGGCTCAACCCTGGACAG GCGGTGGAAACTACCAAGCTGGAGTACGGTAGGGGCAGGGGGAATT TCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAACG GCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGC TAGGGGAGCAAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAC GATGGATACTAGGCGCTGTGCGTATCGACCCGTGCAGTGCTGTAGC TAACGCGTTAAGTATCCCGCCTGGGGAGTACGTTCGCAAGAATGAA ACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGG TTTAATTCGATGCAAAGCGAAGAACCTTACCGGGGCTTGACATGCC GCGAATCCTCTTGAAAGAGAGGGGTGCCTTCGGGAACGCGGACACA GGTGGTGCATGGCTGTCGTCAGCTCGTGCCGTAAGGTGTTGGGTTA AGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCACCGTTGAG TTTGGAACCCTGAACAGACTGCCGGTGATAAGCCGGAGGAAGGTGA GGATGACGTCAAGTCATCATGCCCCTTATGCCCTGGGCGACACACG TGCTACAATGGCCGGGACAAAGGGTCGCGATCCCGCGAGGGTGAGC TAACTCCAAAAACCCGTCCTCAGTTCGGATCGCAGGCTGCAACTCG CCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCAGCCATACGG CGGTGAATTCGTTCCCGGGCCTTGTACACACCGCCCGTCACACTAT GGGAGCTGGCCATGCCCGAAGTCGTTACCTTAACCGCAAGGAGGGG GATGCCGAAGGCGGGGCTAGTGACTGGAGTG
19	*Aureimonas* A sp001425485	112	GATGAACGCTGGCGGCATGCTTAACACATGCAAGTCGAACGGGAAG TGGTGTTTCCAGTGGCGAACGGGTGAGTAACGCGTAAGAACCTGCC CTTGGGAGGGGAACAACAACTGGAAACGGTTGCTAATACCCCGTAG GCTGAGGAGCAAAAGGAGAAATCCGCCCAAGGAGGGGCTCGCGTCT GATTAGCTAGTTGGTGAGGCAATAGCTTACCAAGGCGATGATCAGT AGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGC GAAAGCCTGACGGAGCAATGCCGCGTGGAGGTGGAAGGCCCACGGG TCGTCAACTTCTTTTCTCGGAGAAGAAACAATGACGGTATCTGAGG AATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGTAAGACAGAG GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGT GGCTTTTCAAGTCCGCCGTCAAATCCCAGGGCTCAACCCTGGACAG GCGGTGGAAACTACCAAGCTGGAGTACGGTAGGGGCAGAGGGAATT TCCGGTGGAGCGGTGAAATGCATTGAGATCGGAAAGAACACCAACG GCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGC TAGGGGAGCAAATGGGATTAGAGACCCCAGTAGTCCTAGCCGTAAA CGATGGATACTAGGTGCTGTGCGACTCGACCCGTGCAGTGCTGTAG CTAACGCGTTAAGTATCCCGCCTGGGGAGTACGTTCGCAAGAATGA AACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGC CGCGAATCCTCTTGAAAGAGAGGGGTGCCCTCGGGAACGCGGACAC AGGTGGTGCATGGCTGTCGTCAGCTCGTGCCGTAAGGTGTTGGGTT AAGTCTCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCACTATGAG TTTGGAACCCTGAACAGACCGCCGGTGTTAAGCCGGAGGAAGGAGA GGATGAGGCCAAGTCATCATGCCCCTTATGCCCTGGGCGACACACG TGCTACAATGGGCGGGACAAAGGGTCGCGATCTCGCGAGGGTGAGC TAACTCCAAAAACCCGTCCTCAGTTCGGATTGCAGGCTGCAACTCG CCTGCATGAAGCAGGAATCGCTAGTAATCGCCGGTCAGCCATACGG CGGTGAATCCGTTCCCGGGCCTTGTACACACCGCCCGTCACACTAT AGGAGCTGGCCATGTTTGAAGTCATTACCCTTAACCGTAAGGAGGG GGATGCCTAAGGCTAGGCTTGCGACTGGAGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
20	*Aureimonas* A sp001425485	86	GATGAACGCTGGCGGCATGCTTAACACATGCAAGTCGGACGGGAAG TGGTGTTTCCAGTGGCGGACGGGTGAGTAACGCGTAAGAACCTGCC CTTGGGAGGGGAACAACAGCTGGAAACGGCTGCTAATACCCCGTAG GCTGAGGAGTAAAAGGAGGAATCCGCCCGAGGAGGGGCTCGCGTCT GATTAGCTAGTTGGTGAGGCAATAGCTTACCAAGGCGATGATCAGT AGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGC GAAAGCCTGACGGAGCAATGCCGCGTGGAGGTAGAAGGCCCACGGG TCGTGAACTTCTTTTCCCGGAGAAGAAGCAATGACGGTATCTGGGG AATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAG GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGT GGCTTTTTAAGTCCGCCGTCAAATCCCAGGGCTCAACCCTGGACAG GCGGTGGAAACTACCAAGCTGGAGTACGGTAGGGGCAGAGGGAATT TCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAACG GCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGC TAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAA CGATGGATACTAGGCGCTGTGCGTATCGACCCGTGCAGTGCTGTAG CTAACGCGTTAAGTATCCCGCCTGGGGAGTACGTTCGCAAGAATGA AACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGC CGCGAATCCTCTTGAAAGAGAGGGGTGCCTTCGGGAACGCGGACAC AGGTGGTGCATGGCTGTCGTCAGCTCGTGCCGTAAGGTGTTGGGTT AAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCATCGTTAA ATTTGGAACCCTGAACAGACTGCCGGTGATAAGCCGGAGGAAGGTG AGGATGACGTCAAGTCATCATGCCCCTTATGCCCTGGGCGACACAC GTGCTACAATGGCCGGGACAAAGGGTCGCGATCCCGCGAGGGTGAG CTAACTCCAAAAACCCGTCCTCAGTTCGGATTGCAGGCTGCAACTC GCCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCAGCCATACG GCGGTGAATTCGTTCCCGGGCCTTGTACACACCGCCCGTCACACTA TGGGAGCTGGCCATGCCCGAAGTCGTTACCTTAACCGCAAGGAGGG GGATGCCGAAGGCAGGGCTAGTGACTGGAGTG
21	*Aureimonas* A sp001425485	87	GATGAACGCTGGCGGCATGCTTAACACATGCAAGTCGGACGGGAAG TGGTGTTTCCAGTGGCGGACGGGTGAGTAACGCGTAAGAACCTGCC CTTGGGAGGGGAACAACAGCTGGAAACGGCTGCTAATACCCCGTAG GCTGAGGAGCAAAAGGAGGAATCCGCCCGAGGAGGGGCTCGCGTCT GATTAGCTAGTTGGTGAGGCAATAGCTTACCAAGGCGATGATCAGT AGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGC GAAAGCCTGACGGAGCAATGCCGCGTGGAGGTAGAAGGCCTACGGG TCGTGAACTTCTTTTCCCGGAGAAGAAGCAATGACGGTATCTGGGG AATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAG GATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGT GGCTTTTTAAGTCCGCCGTCAAATCCCAGGGCTCAACCCTGGACAG GCGGTGGAAACTGCCAAGCTGGAGTACGGTAGGGGCAGAGGGAATT TCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAACG GCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGC TAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAA CGATGGATACTGGGCGCTGTGCGTATCGACCCGTGCAGTGCTGTAG CTAACGCGTTAAGTATCCCGCCTGGGGAGTACGTTCGCAAGAATGA AACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGC CGCGAATCCTCTTGAAAGAGAGGGGTGCCTTCGGGAACGCGGACAC AGGTGGTGCATGGCTGTCGTCAGCTCGTGCCGTAAGGTGTTGGGTT AAGTCCCGCAACGAGCGCAACCCTCGTGTTTAGTTGCCACTGTTGA GTTTGGAACCCTGAGCAGACTGCCGGTGATAAGCCGGAGGAAGGTG AGGATGACGTCAAGTCATCATGCCCCTTATGCCCTGGGCGACACAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GTGCTACAATGGCCGGGACAAAGGGTCGCGATCCCGCGAGGGTGAG CTAACTCCAAAAACCCGTCCTCAGTTCGGATTGCAGGCTGCAACTC GCCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCAGCCATACG GCGGTGAATTCGTTCCCGGGCCTTGTACACACCGCCCGTCACACTA TGGGAGCTGGCCATGCCCGAAGTCGTTACCTTAACCGCAAGGAGGG GGATGCCGAAGGCAGGGCTAGTGACTGGAGTG
22	*Bradyrhizobium* elkanii	209	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCAGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAAGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCTCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTGCAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
23	*Bradyrhizobium* elkanii	191	AGCGAACGCTGGCGGCAGGCTTAACACACGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTTGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT

SEQ ID NO	Genus/Species	Strain #	Sequence
			AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACGATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
24	*Bradyrhizobium* elkanii	136	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACGTTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGGCAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGTACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGC GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGCCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
25	*Bradyrhizobium* elkanii	182	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAACGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAGGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
26	*Bradyrhizobium* elkanii	188	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGTTTACTCACTAGTGGCGCAGCTAAC GCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAATTC AAAGGAATTGACGGGGGCCCGCACGAGCGGTGGAGCATGTGGTTTA ATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGTC GCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGACA GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTA AGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAG TTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTG GGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACAC GTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTCG CAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCG AGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCAC GGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATG GGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCAG CCGGCCACGGTAGGGTCAGCGACTGGGGTG
27	*Bradyrhizobium* elkanii	145	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
28	*Bradyrhizobium elkanii*	121	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGGGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGCTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
29	*Bradyrhizobium elkanii*	144	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAGGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA CGTGCTACAATGGCGGTAACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGTGCGCTAACCGAAAGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
30	*Bradyrhizobium elkanii*	115	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCAT AGCAATATGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGT CGCGGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTA GTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGT GGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACA

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGTGCTACAATGGCGGTGACAATGGGATGCTAAGGGGCGACCCTTC GCAAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTC GAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCA CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT GGGAGTTGGTTTTACCTGAAGACGGCGCGCTAACCGAAGGGGGGCA GCCGGCCACGGTAGGGTCAGCGACTGGGGTG
31	*Bradyrhizobium* denitrificans	133	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG GCAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACC CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGG GACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAG GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA GTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGT CGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGG GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACG TGCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGC AAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGA GCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACT GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGG GAGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCA GCCGACCACGGTAGGGTCAGCGACTGGGGTG
32	*Bradyrhizobium* denitrificans	122	AGCGAACGCTGGCGGCAGGCTTAACACGTGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG GCAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCTAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATAAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT

SEQ ID NO	Genus/Species	Strain #	Sequence
			AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGG GACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAG GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA GTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGT TGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGG GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGAGCTACACACG TGCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGC AAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGA GCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACG GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGG GAGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCA GCCGACCACGGTAGGGTCAGCGACTGGGGTG
33	*Bradyrhizobium* denitrificans	130	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG GCAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACAGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTA ATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGGG ACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAGG TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG TCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGTT GAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGGG GATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACGT GCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGCA AATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGAG CCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACGG TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG AGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCAG CCGACCACGGTAGGGTCAGCGACTGGGGTG
34	*Bradyrhizobium* denitrificans	193	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG GCAACCCTGATCCAGCCATGCCGCGTGAGTGAGGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAAATGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGG GACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAG GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA GTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGT TGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGG GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACG TGCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGC AAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGA GCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACG GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGG GAGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCA GCCGACCACGGTAGGGTCAGCGACTGGGGTG
35	*Bradyrhizobium* denitrificans	97	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG GCAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTT AATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGG GACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAG GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA GTCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGT TGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGG GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACG TGCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGC AAATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGA GCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACG GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGG GAGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCA GCCGACCACGGTAGGGTCAGCGACTGGGGTG
36	*Bradyrhizobium* denitrificans	181	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATA AGCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCT GATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGT AGCCGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGC CCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGG TTGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAA TAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG GGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGG GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGC CTTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGC GAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGC GAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGT GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG ATGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAA CGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGGGAGCATGTGGTTTA ATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGGG ACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAGG TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG TCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGTT GAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGGG GATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACGT GCTACAATGGCGATGACAGTGGGAAGCTAAGGGGTGACCCTTCGCA AATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGAG CCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACGG TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG AGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGAGGCAG CCGACCACGGTAGGGTCAGCGACTGGGGTG
37	*Bradyrhizobium* denitrificans	186	AGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAGCGGGCGT AGCAATACGTCAGCGGCAGACGGGTGAGTAACGCGTGGGAACGTAC CTTTTGGTCGGAACAACACAGGGAAACTTGTGCTAATACCGGATAA GCCCTTACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCTG ATTAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCGACGATCAGTA GCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCC CAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGG CAACCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGGT TGTAAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAAT AAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGG GCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGGG TCTTTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGCC TTTGATACTGAAGATCTTGAGTTCGGGAGAGGTGAGTGGAACTGCG AGTGTAGAGGCGAAATTCGTAGATATTCGCAAGAACACCAGTGGCG AAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGTG GGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGA TGAATGCCAGCCGTTGGTGGGTTTACTCACCAGTGGCGCAGCTAAC GCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTC AAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTA ATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATGTTTGGG ACCGGTCGCAGAGACGTGACCTTCTCTTCGGAGCCCGAAACACAGG TGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG TCCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGTT GAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGGG GATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACGT GCTACAATGGCGGTGACAGTGGGAAGCTAAGGGGTGACCCTTCGCA AATCTCAAAAAGCCGTCTCAGTTCGGATTGGGCTCTGCAACTCGAG CCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCACGCCACGG TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG AGTTGGCTTTACCTGAAGGCGGTGCGCTAACCAGCAATGGGGGCAG CCGACCACGGTAGGGTCAGCGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
38	*Microvirga* sp OATH 1	21	AACGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAACGCATCC TTCGGGGTGAGTGGCAGACGGGTGAGTAACGCGTGGGAACGTGCCC TTCAGTTCGGGATAACCCAGGGAAACTTGGGCTAATACCGGATACG TGCGAGAGCAGAAAGATTTATCGCTGAAGGATCGGCCCGCGTCTGA TTAGCTAGTTGGTGGGGTAATGGCCCACCAAGGCGACGATCAGTAG CTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCCC AAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGC AAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCTTAGGGTT GTAAAGCTCTTTCGTCCGGGACGATAATGACGGTACCGGAAGAAGA AGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGG CTAGCGTTGTTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGCT TTGTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATTGCCT TCGATACTGCATGGCTTGAGACCGGAAGAGGTAAGTGGAACTGCGA GTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGCGA AGGCGGCTTACTGGTCCGGTTCTGACGCTGAGGCGCGAAAGCGTGG GGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGAT GAATGCCAGCCGTTGGCGAGCTTGCTCGTCAGTGGCGCAGCTAACG CTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA AAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAA TTCGAAGCAACGCGCAGAACCTTACCAGCCTTTGACATGTCCCGTA TGGATCCTGGAGACAGGTTCCTTCAGTTCGGCTGGCGGGAACACAG GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA GTCCCGCAACGAGCGCAACCCTCGCCCTTAGTTGCCATCATTCAGT TGGGCACTCTAAGGGGACTGCCGGTGATAAGCCGAGAGGAAGGTGG GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGGCTACACACG TGCTACAATGGCGGTGACAAAGGGCAGCGAACCCGCGAGGGGGAGC TAATCCTTAAAAGCCGTCTCAGTTCAGATTGCACTCTGCAACTCGA GTGCATGAAGGCGGAATCGCTAGTAATCGTGGATCAGAACGCCACG GTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGG GAGTTGGTCTTACCCGACGGCGCTGCGCCAACCGCAAGGAGGCAGG CGACCACGGTAGGGTCAGCGACTGGGGTG
39	*Pseudomonas* poae	14	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTTACCTAATACGTGATTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
40	*Pseudomonas* sp OATH 2	30	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCATTAACCTAATACGTTAGTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
41	*Pseudomonas* sp OATH 3	33	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTTACCTAATACGTGATTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
42	*Pseudomonas* sp OATH6	44	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTTACCTAATACGTGATTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAGC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
43	*Pseudomonas* poae	76	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			AGGAAGGGCAGTTACCTAATACGTGATTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAGC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
44	*Pseudomonas* sp OATH 16	77	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCATTAACCTAATACGTTAGTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTATAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAACCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
45	*Pseudomonas* sp OATH 14	69	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGGAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCATTAACCTAATACGTTAGTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTATAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAACCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
46	*Pseudomonas* azotoformans	158	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGGACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTTGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
47	*Pseudomonas* azotoformans	180	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGGACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTTGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
48	*Pseudomonas* azotoformans	167	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGGACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGCCCTTAGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
49	*Pseudomonas* azotoformans	156	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGGACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
50	*Pseudomonas* azotoformans	24	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGA GAGAAGCTTGCTTCTCTTGAGAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGGACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
51	*Pseudomonas* fluorescens	82	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTAAATTAATACTTTGCTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
52	*Pseudomonas* fluorescens	80	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGGCAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTTACCTAATACGTGATTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATTCAAAACTGACTGACTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTAATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
53	*Pseudomonas* E sp002836515	42	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGGCAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTAAATTAATACTTTGCTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAGCATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
54	*Pseudomonas* sp OATH 53	147	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA CGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
55	*Pseudomonas* sp OATH 56	165	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA GGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
56	*Pseudomonas* E sp003253735	200	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA CGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTCGAGTACGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGGTACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTCACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
57	*Pseudomonas* E sp003253735	207	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA CGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGGGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGGCTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAAC TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
58	*Pseudomonas* straminea	152	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA GGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
59	*Pseudomonas* sp OATH 55	164	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGTTGA CGGGAGCTTGCTCCCTGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTAATAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAA AGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGTTCCTTGAGAACTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGCCTTGACATGC TGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCAGACAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTT ATGGTGGGAACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGT CACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
60	*Pseudomonas* koreensis	52	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
61	*Pseudomonas* koreensis	70	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
62	*Pseudomonas* sp OATH 45	134	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAGGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
63	*Pseudomonas* sp OATH 51	142	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCGGAAGTAGCTAGTCTAACCTTCGGGGGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
64	*Pseudomonas* koreensis	28	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
65	*Pseudomonas koreensis*	61	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
66	*Pseudomonas* sp OATH 15	71	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTAAATTAATACTTTGCTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTA ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
67	*Pseudomonas* sp OATH 4	39	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA AAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCC GCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGG AGGAAGGGCAGTAAATTAATACTTTGCTGTTTTGACGTTACCGACA GAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGA GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGG TGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAAC TGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAAT TTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGT GGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAG CGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA ACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAG CTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAA AACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTG GTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCC AATGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACATTGAGAC AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT AAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCGCGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACAC ACGTGCTACAATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGG AGCTAATCCCATAAAACCGATCGTAGTCCGGATCGCAGTCTGCAAC TCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAATGT CGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACC ATGGGAGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGG ACGGTTACCACGGTGTGATTCATGACTGGGGTG
68	*Streptomyces* violaceorectus	114	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGACCTGGGAAGGCATCTTCTCGGGTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGGG AGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCC TGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAA GAACCTTACCAGGCCTTGACATCCAATGAACTTTCCAGAGATGGAT TGGTGCCTTCGGGAGCATTGAGACAGGTGCTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACC CTTGTCCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGAC TGCCAGTGACAAACCGGAGGAAGGCGGGGATGACGTCAAGTCATCA TGGCCCTTACGGCCTGGGCTACACACGTGCTACAATGGTCGGTACA AAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAACCGATC GTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATC GCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCACCAGAA GTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGATTCA TGACTGGGGTG
69	*Streptomyces* sp OATH 38	110	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGACCTGGGAAGGCATCTTCTCGGGTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGAGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCG AAGAACCTTACCAGGCCTTGACATCCAATGAACTTTCCAGAGATGG ATTGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAA CCCTTGTCCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAG ACTGCCGGTGACAAACCGGAGGAGGGTGGGGATGACGTCAAGTCAT CATGGCCCTTACGGCCTGGGCTACACACGTGCTACAATGGTCGGTA CAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAACCGA TCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAA TCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGG GCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCACCAG AAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGATT CATGACTGGGGTG
70	*Streptomyces* sp OATH 40	116	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGAATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAGAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAAC GCGAAGAACCTTACCTGGTCTTGACATGTCGAGAACTTTCCAGAGA TGGATTGGTGCCTTCGGGAACTCGAACACAGGTGCTGCATGGCTGT CGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG CAACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGAACTCTAAG GAGACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGT CATCATGGCCCTTACGACCAGGGCTACACACGTACTACAATGGTAG GGACAGAGGGCTGCAAACCCGCGAGGGCAAGCCAATCCCAGAAACC CTATCTCAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCG GAATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAGTACGTTC CCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCA CCAGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGTGT GGCCGATGACTGGGGTG
71	*Streptomyces* rochei	123	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCCGGAAACGGGGTCTAATA CCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCGGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTAACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCTGGTCTTGACATGTCGAGAACTTTCCAGAGATG GATTGGTGCCTTCGGGAACTCGAACACAGGTGCTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGAACTCTAAGGA GACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCA TCATGGCCCTTACGACCAGGGCTACACACGTACTACAATGGTAGGG ACAGAGGGCTGCAAACCCGCGAGGGCAAGCCAATCCCAGAAACCCT ATCTCAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGA ATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCACC AGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGTGTGG CCAATGGCTGGGGTG
72	*Streptomyces* labedae	113	GACGAACGTTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTAGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGGGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCAAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGAACTCTAAGGA GACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCA TCATGGCCCTTACGACCAGGGCTACACACGTACTACAATGGTAGGG ACAGAGGGCTGCAAACCCGCGAGGGCAAGCCAATCCCAGAAACCCT ATCTCAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGA ATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCACC AGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGTGTGG CCGATGACTGGGGTG

SEQ ID NO	Genus/Species	Strain #	Sequence
73	*Streptomyces* rochei	189	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAGAC AGGGTCCCCCTAGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGACAAACCGGAGGAAGGTGGGGATGACGTCAA GTCATCATGGCCCTTACGACCAGGGCTACACACGTACTACAATGGT AGGGACAGAGGGCTGCAAACCCGCGAGGGCAAGCCAATCCCAGAAA CCCTATCTCAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGT CGGAATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTG CACCAGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGT GTGGCCGATGACTGGGGTG
74	*Streptomyces* griseoincarnatus	102	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAATCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGAGTCTGCAACTCGACTCCATGAA GTCGGAATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGT TGCACCAGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACG GTGTGGCCGATGACTGGGGTG
75	*Streptomyces* griseoincarnatus	23	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
76	*Streptomyces* griseoincarnatus	202	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTATAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCAGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT

SEQ ID NO	Genus/Species	Strain #	Sequence
			TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
77	*Streptomyces griseoincarnatus*	75	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGCGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
78	*Streptomyces griseoincarnatus*	74	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCGCTTGGGCATCCAAGCGGGTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATCAGAG ATGGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
79	*Streptomyces* nigra	73	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCGCTTGGGCATCCAAGTGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCCAGAGAT GGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG

SEQ ID NO	Genus/Species	Strain #	Sequence
80	*Streptomyces* sp OATH 8	48	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCTACTTGGGCATCCAAGTGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
81	*Streptomyces* sp OATH 12	60	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCTACTTGGGCATCCAAGTGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
82	*Streptomyces* sp OATH 22	90	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCTACTTGGGCATCCAAGTGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCCTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCCGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAGC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCAAGTCATGAAAGTCGGTGA CACCTGAAGCCGGTGGCCTAACCTTTTTGGAGGGAGCCGTCGAAGG TGGGATCGGTAATTAGGACT
83			
84	*Streptomyces* sp001509795	72	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCGCTTGGGCATCCAAGTGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
85	*Streptomyces* flavoviridis	81	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACCTTCGGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCCCGCAGGCATCTGCGGGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTAGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAG ACAGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
86	*Streptomyces* sp OATH 41	117	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACCTTCGGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCCCGCAGGCATCTGCGGGGTTCGAAAGCTCC GGCGGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAGGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAG ACAGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
87	*Streptomyces* flavoviridis	27	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACCTTCGGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACTGACCCCCGCAGGCATCTGCGGGGTTCGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAG ACAGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
88	*Streptomyces* fimbriatus	11	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCGCCTTCGGGCGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACAACCACTTCGGGCATCCGATGGTGGTGGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTA ACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAG ACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCCGTGTTGCCAGCAAGCCCCTTCGGGGGTGTTGGGGA CTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGAC GTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACA ATGGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTC AAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCAT GAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAA TACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTC GGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTG TCGAAGGTGGGACTGGCGATTGGGACG
89	*Streptomyces* rochei	16	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAGAC AGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC

SEQ ID NO	Genus/Species	Strain #	Sequence
			AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
90	*Streptomyces* rochei	19	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAGAC AGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
91	*Streptomyces* rochei	125	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCCCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCT GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAGAC AGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
92	*Streptomyces* misionensis	127	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GATACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
93	*Streptomyces* misionensis	129	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAGCGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGCGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATTGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
94	*Streptomyces* misionensis	128	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAGGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGTGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCGAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
95	*Streptomyces* misionensis	55	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCTTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
96	*Streptomyces* misionensis	37	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGTGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
97	*Streptomyces* misionensis	35	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGT AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
98	*Streptomyces* misionensis	131	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGGA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCATGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGGTCGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCCGCGATACCGTGGGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACGCACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
99	*Streptomyces* misionensis	3	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
100	*Streptomyces* misionensis	36	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
101	*Streptomyces* misionensis	47	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTCGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
102	*Streptomyces* griseoviridis A	184	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGACGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACCGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGGGCTGCGATACCGTGAGGTGGAGCGAACCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
103	*Streptomyces* griseoviridis A	50	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCGTCTTGGGCATCCTTGACGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
104	*Streptomyces* griseoviridis A	66	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCAGATATGACCGTCTTGGGCATCCTTGACGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
105	*Streptomyces* griseofuscus	2	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCATCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCTCGGGGCTTAACCCCGAGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACCAGCGATTGGGACG
106	*Streptomyces* sp OATH 10	54	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCATCTTGGGCATCCTTGATGATGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCTCGGGGCTTAACCCCGAGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACCAGCGATTGGGACG
107	*Streptomyces* griseofuscus	135	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCATCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGG AAGCTCGGGGCTTAACCCCGAGTCTGCAGTCGATACGGGCTAGCTA GAGTATGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGCCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCGGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACCAGCGATTGGGACG
108	*Streptomyces* misionensis	17	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCATCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
109	*Streptomyces* misionensis	53	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATGACCATCTTGGGCATCCTTGATGGTGTAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC AACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
110	*Amycolatopsis* lurida	149	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTTCCGCGGGCATCCGTGGTGGTGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCCATGGCCCAACTCTTCGGAGAGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
111	*Amycolatopsis* OATH 54	153	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTTCCGCGGGCATCCGTGGTGGTGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCCATGGCCCAACCCGCAAGGGGGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
112	*Amycolatopsis* lurida	194	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTTCCGCGGGCATCCGTGGTGGCGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAGGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGG AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCCATGGCCCAACTCTTCGGAGAGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
113	*Amycolatopsis* lurida	151	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTTCTGCGGGCATCCGTGGTGGTGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCCATGGCCCAACTCTTCGGAGAGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
114	*Amycolatopsis* lurida	168	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTGCTGATCGCATGGTTGGTGGTGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCCATGGCCCAACTCTTCGGAGAGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
115	*Amycolatopsis* lurida	154	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCTTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGTACTTTGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACTGCTGATCGCATGGTTGGTGGTGGAAAGCTCCGGC GGTACAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCGCCAGGGAC GAAGCGCAAGTGACGGTACCTGGATAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCGTTCGTGA AAACTCCACGCTTAACGTGGAGCGTGCGGGCGATACGGGCAGACTT GAGTTCGGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCTGTAAACGTTGGGCGCTAGGTGTGGGC GACATCCACGTTGTCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGCTTGACATGCGCCAGACATCCCTAGAGATAG GGCTTCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTATCCTACGTTGCCAGCGCGTTATGGCGGGGACTCGTGGGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCTGGTACAG AGGGCTGCGATACCGCGAGGTGGAGCGAATCCCTTAAAGCCGGTCT CAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCCCATGGCCCAACCCGCAAGGGGGGGAGTGGTCGAAGGTGGGACT GGCGATTGGGACG
116	*Rhodococcus* qingshengii	187	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGTGAG GCCTTTCGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGT GATCTGCCCTGCACTTCGGGATAAGCCTGGGAAACTGGGTCTAATA CTGGATATGACCTCCTATCGCATGGTGGGTGGTGGAAAGATTTATC GGTGCAGGATGGGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGACCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAC GAAGCGCAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTGCCCGGAAT TACTGGGCGTAAAGAGTTCGTAGGCGGTTTGTCGCGTCGTTTGTGA AAACCAGCAGCTCAACTGCTGGCTTGCAGGCGATGCGGGCAGACTT GAGTACTGCAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCA GTAACTGACGCTGAGGAACGAAAGCGTGGGTAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCGCTAGGTGTGGGT TCCTTCCACGGAATCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGTTTGACATATACCGGAAAGCTGCAGAGATGT GGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGTCAG CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC CTATCTTACGTTGCCAGCACGTTATGGTGGGGACTCGTAAGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCCAGTACAG AGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAGCTGGTCT CAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCGGTGGCTTAACCCCTTGTGGGAGGGAGCCGTCGAAGGTGGGAT CGGCGATTGGGACG
117	*Rhodococcus* erythropolis	146	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGTAAG GCCTTTCGGGGTACACGAGCGGCGAACGGGTGAGTAACACGTGGGT GATCTGCCCTGCACTTCGGGATAAGCCTGGGAAACTGGGTCTAATA CCGGATATGACCTCCTATCGCATGGTGGGTGGTGGAAAGATTTATC GGTGCAGGATGGGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGACCTGAGAGGGTGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAC GAAGCGCAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTGTCCGGAAT TACTGGGCGTAAAGAGTTCGTAGGCGGTTTGTCGCGTCGTTTGTGA AAACCAGCAGCTCAACTGCTGGCTTGCAGGCGATACGGGCAGACTT GAGTACTGCAGGGGAGACTGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCA GTAACTGACGCTGAGGAACGAAAGCGTGGGTAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCGCTAGGTGTGGGT TCCTTCCACGGAATCCGTGCCGTAGCTAACGCATTAAGCGCCCCGC CTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGG GCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGA AGAACCTTACCTGGGTTTGACATATACCGGAAAGCTGCAGAGATGT GGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGTCAG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC CTATCTTATGTTGCCAGCACGTTATGGTGGGGACTCGTAAGAGACT GCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCAT GCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCCAGTACAG AGGGCTGCGAGACCGTGAGGTGGAGCGAATCCCTTAAAGCTGGTCT CAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTCGGAGTCG CTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGC CTTGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAA GCCGGTGGCTTAACCCCTTGTGGGAGGGAGCCGTCGAAGGTGGGAT CGGCGATTGGGACG
118	*Micrococcus* luteus	32	GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGTAACACGT GAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCT AATACCGGATAGGAGCGTCCACCGCATGGTGGGTGTTGGAAAGATT TATCGGTTTTGGATGGACTCGCGGCCTATCAGCTTGTTGGTGAGGT AATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGAC CGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA GCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACG CCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGTAG GGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAAC TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCCG GAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTC GTGAAAGTCCGGGGCTTAACCCCGGATCTGCGGTGGGTACGGGCAG ACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGGA ATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTCTG GGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGA TTAGATACCCTGGTAGTCCATGCCGTAAACGTTGGGCACTAGGTGT GGGGACCATTCCACGGTTTCCGCGCCGCAGCTAACGCATTAAGTGC CCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGA CGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAA CGCGAAGAACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGA GATACGGTTTCCCCTTTGGGGCGGGTTCACAGGTGGTGCATGGTTG TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC GCAACCCTCGTTCCATGTTGCCAGCACGTAATGGTGGGGACTCATG GGAGACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAA TCATCATGCCCCTTATGTCTTGGGCTTCACGCATGCTACAATGGCC GGTACAATGGGTTGCGATACTGTGAGGTGGAGCTAATCCCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCAAGTCACGAAAGTTGGTAAC ACCCGAAGCCGGTGGCCTAACCCTTGTGGGGGGAGCCGTCGAAGGT GGGACCAGCGATTGGGACT
119	*Micrococcus* luteus	43	GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGTAACACGT GAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCT AATACCGGATAGGAGCGTCCACCGCATGGTGGGTGTTGGAAAGATT TATCGGTTTTGGATGGACTCGCGGCCTATCAGCTTGTTGGTGAGGT AATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGAC CGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA GCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACG CCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGTAG GGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAAC TACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCCG GAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTC GTGAAAGTCCGGGGCTTAACCCCGGATCTGCGGTGGGTACGGGCAG ACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTGTAGCGGTGGA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTCTG GGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGA TTAGATACCCTGGTAGTCCATGCCGTAAACGTTGGGCACTAGGTGT GGGGACCATTCCACGGTTTCCGCGCCGCAGTTAACGCATTAAGTGC CCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGA CGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAA CGCGAAGAACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGA GATACGGTTTCCCCTTTGGGGCGGGTTCACAGGTGGTGCATGGTTG TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC GCAACCCTCGTTCCATGTTGCCAGCACGTCGTGGTGGGGACTCATG GGAGACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAA TCATCATGCCCCTTATGTCTTGGGCTTCACGCATGCTACAATGGCC GGTACAATGGGTTGCGATACTGTGAGGTGGAGCTAATCCCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCAAGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCTAACCCTTGTGGGGGGAGCCGTCGAAGGT GGGACCAGCGATTGGGACT
120	*Streptomyces* sp OATH 44	126	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAGACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA TTTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCGAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
121	*Streptomyces* sp OATh 66	210	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACGATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATCCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTTTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
122	*Streptomyces* sp OATH 63	204	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACCGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAGGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCGCGTCACGAAAGTCGGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
123	*Streptomyces* sp OATH 52	143	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCGCACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGTATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
124	*Streptomyces* sp OATH B	5	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
125	*Streptomyces* sp OATH 57	170	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGAGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
126	*Streptomyces* sp OATH 49	140	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACTGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCCTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
127	*Streptomyces* sp OATH G	34	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCACCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACTGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
128	*Streptomyces* sp OATH 7	46	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGCCTCCATCGCATGGTGGAGGTTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
129	*Streptomyces* sp OATH 5	40	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGTCTCCATGGCATCTTGGGGACTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA

SEQ ID NO	Genus/Species	Strain #	Sequence
			ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
130	*Streptomyces* sp OATH 9	51	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGTCTCCACGGCATCTTGGGGACTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
131	*Streptomyces* sp OATH 13	68	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGTCTCCATGGCATCTTGGCGACTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
132	*Streptomyces* sp OATH 46	137	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGTCTCCATGGCATCTTGGAGACTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT GGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGCTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
133	*Streptomyces* sp OATH 12	63	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGAGTCTCCATGGCATCTTGGAGACTGGAAAGCTCCG GCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAA CGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGC TAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGG GCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCA CGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
134	*Streptomyces* lydicus	45	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACCACCGACCGCATGGTCTGGTGGTGGAAAGCTCC GGCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTG ATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTTCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAG ACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACT CACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGT CAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAAT GGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAA AAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGA AGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATA CGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGG TAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAATCGTC GAAGGTGGGACTGGCGATTGGGACG
135	*Streptomyces* lydicus	203	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACCACCGACCGCATGGTCTGGTGGTGGAAAGCTCC GGCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTG ATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATATCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTTCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAG ACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACT CACAGGAGACTGCCGGGGTCAGCTCGGAGGAAGGTGGGGACGACGT CAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAAT GGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAA AAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGA AGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATA CGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGG TAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGAGGGAATCGTCG AAGGTGGGACTGGCGATTGGGACG
136	*Streptomyces* lydicus	78	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACCACCGACCGCATGGTCTGGTGGTGGAAAGCTCC GGCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTG ATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTG GGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTTCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAG ACAGGGTCCCCCTTGTGGTCGGTTTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACT CACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGT CAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAAT GGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAA AAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGA AGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATA CGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			TAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAATCGTC GAAGGTGGGACTGGCGATTGGGACG
137	*Streptomyces* sp OATH 17	79	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCGGTTTCGGCCGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATATGACGCGCTCCCGCATGGGATGCGTGTGGAAAGCTCC GGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTG ATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACC GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG CAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGG GAAGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACT ACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGG AATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGATG TGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCAGG CTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAA TGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGG GCCGACACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGAT TAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTG GGCGACATTCCACGTTGTCCGCGCCGCAGCTAACGCATTAAGTTCC CCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAAC GCGAAGAACCTTACCAAGGCTTGACATACACCGGAAACCTCTGGAG ACAGGGGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCG TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA ACCCTTGTCCTGTGTTGCCAGCGGGTTATGCCGGGGACTCACAGGA GACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCA TCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGT ACAATGAGCTGCGAAGCCGTGAGGTGGAGCGAATCTCAAAAAGCCG GTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGA GTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTTCCC GGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACC CGAAGCCGGTGGCCCAACCCTTGTGGGGGGAGCCGTCGAAGGTGGG ACTGGCGATTGGGACG
138	*Streptomyces* sp OATH D	7	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTG AAAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCT AGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGG CGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC

SEQ ID NO	Genus/Species	Strain #	Sequence
			AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCA CAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
139	*Streptomyces* sp OATH 50	141	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGCCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTG AAAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCT AGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGG CGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCA CAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
140	*Streptomyces* sp OATH 26	94	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGGGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTAGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTTCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCTCCCTTGTGGTCGGTGTACAGGCGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCA CAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGCCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
141	*Streptomyces* griseoaurantiacus	26	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAACTCTTCGGAGGTTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCCGTGGCCCAACCCGCAAGGGAGGGAGCGGTCGAAGG TGGGACTGGCGATTGGGACG
142	*Streptomyces* griseoaurantiacus	18	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAGT GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGAT AGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAACTCTTCGGAGGTTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCCGTGGCCCAACCCGCAAGGGAGGGAGCGGTCGAAGG TGGGACTGGCGATTGGGACG
143	*Streptomyces* sp OATH 65	208	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCTTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCCGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
144	*Streptomyces* sp OATH 27	57	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCTTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
145	*Streptomyces* sp OATH 61	197	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTGGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC

SEQ ID NO	Genus/Species	Strain #	Sequence
			AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
146	*Streptomyces* sp AOTH 58	173	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAGCCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
147	*Streptomyces* sp OATH A	4	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
148	*Streptomyces* sp OATH E	10	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
149	*Streptomyces* sp OATH 62	201	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACAACCACTGACCGCATGGTCGGGTGGTGGAAAGCTCCGG CGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAAC GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCG CGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA AGAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAA TTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTG AAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCT AGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG CGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGC CGATACTGACGCCGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA GATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGG CGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCC GCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGG GGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGC GAAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGAC AGGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCAC GGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACGATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAACACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
150	*Streptomyces* sp OATH 20	85	GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTGAA CACGGAGCTTGCTCTGTGGGATCAGTGGCGAACGGGTGAGTAACAC GTGAGCAACCTGCCCCTGACTCTGGGATAAGCGCTGGAAACGGCGT CTAATACTGGATATGTGACGTGACCGCATGGTCTGCGTCTGGAAAG AATTTCGGTTGGGGATGGGCTCGCGGCCTATCAGCTTGTTGGTGAG GTAATGGCTCACCAAGGCGTCGACGGGTAGCCGGCCTGAGAGGGTG ACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGG CAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCAA CGCCGCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTTAGC AGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTA ACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTC CGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGG TTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGC AGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTG AAATGCGCAGATGTCAGGAGGAACACCGGTGGCGAAGGCGGATCTC TGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAAACAG GATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGT GTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGT GCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATT GACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGC AACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTA GAGATAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTG TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC GCAACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGA CTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGAC GTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACA ATGGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTC AAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCAT GAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAA TACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTG TCGAAGGTGGGACTGGCGATTGGGACG
151	*Streptomyces* sp OATH 30	99	GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTGAA CACGGAGCTTGCTCTGTGGGATCAGTGGCGAACGGGTGAGTAACAC GTGAGCAACCTGCCCCTGACTCTGGGATAAGCGCTGGAAACGGCGT CTAATACTGGATATGTGACGTGACCGCATGGTCTGCGTCTGGAAAG AATTTCGGTTGGGGATGGGCTCGCGGCCTATCAGCTTGTTGGTGAG GTAATGGCTCACCAAGGCGTCGACGGGTAGCCGGCCTGAGAGGGTG ACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGG CAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCCGATGCAGCAA CGCCGCGTGAGGGACGACGGCCTTCGGGTTGTAAACCTCTTTTAGC AGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAAAAGCGCCGGCTA ACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTATC CGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTG CTGTGAAATCCGGAGGCTCAACCTCCGGCCTGCAGTGGGTACGGGC AGACTAGAGCGCGGTAGGGGAGATTGGAATTCCTGGTGTAGCGGTG GAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGATCTC TGGGCCGTAACTGACGCTGAGGAGCGAAAGGGTGGGGAGCAAACAG GCTTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGT GTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGT GCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACCCAAAGGAATT GACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGC AACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTA GAGATAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTG TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC GCAACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGA CTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGGC GTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACA ATGGCCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTC AAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCAT GAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAA TACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTC GGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTG TCGAAGGTGGGACTGGCGATTGGGACG
152	*Streptomyces* OATH 28	96	GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTGAA GCAGGAGCTTGCTCTTGTGGATCAGTGGCGAACGGGTGAGTAACAC GTGAGCAACCTGCCCCTGACTCTGGGATAAGCGCTGGAAACGGCGT CTAATACTGGATATGTGACGTGACCGCATGGTCTGCGTTTGGAAAG ATTTTTCGGTTGGGGATGGGCTCGCGGCCTATCAGCTTGTTGGTGA GGTAATGGCTCACCAAGGCGTCGACGGGTAGCCGGCCTGAGAGGGT GACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG GCAGCAGTGGGAAATATTGCACAATGGGCGGAAGCCTGATGCAGCA ACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTTAG CAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCT AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGT CCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCG GTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGG CAGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGT GAGATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCT CTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACA GGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGG TGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAG TGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAAT TGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACG CAACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATT AGAGATAGTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG CGCAACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGG ACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGA CGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTAC AATGGCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCT CAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCA TGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGA ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGT CGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCT GTCGAAGGTGGGACTGGCGATTGGGACG
153	*Streptomyces* sp OATH 64	205	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTTCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAACG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC GACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGGGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGCGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
154	*Streptomyces* sp OATH F	13	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTTCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAACG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC GACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
155	*Streptomyces* sp OATH 22	89	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGAATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCCTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC GACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCGTGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
156	*Streptomyces* sp OATH 44	132	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGTGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGCAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGGCTAATA CCGGATACGAGCCTTCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAACG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTATG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGACTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGCGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC GTTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC GACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
157	*Streptomyces* sp OATH 43	124	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTTCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAACG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACTCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTA GAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCACAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACCCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCGTTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
158	*Streptomyces* sp OATH 59	179	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAGGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGC GACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATGCACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTTGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTTAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
159	*Streptomyces* sp900105755	25	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGTCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
160	*Streptomyces* sp900105755	20	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
161	*Streptomyces* sp900105755	196	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAAGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACG GGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAG TCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGCC GGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAAG CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC GGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTT CCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAAC ACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAG GTGGGACTGGCGATTGGGACG
162	*Streptomyces* sp OATH 11	58	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
163	*Streptomyces* sp OATH 19	84	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATCTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTC AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC CCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCA CAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCA AGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG CCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAA AGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAG TCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG TTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTA ACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGA AGGTGGGACTGGCGATTGGGACG
164	*Streptomyces* sp OATH 36	108	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGAGCCTCCAAGGCATTTTGGAGGCTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCAGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCAGATGCAGCGACGCCGT GTGAGGGATGACGGCCTTCGGGTCGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGATTGTGA AAGCCCGAGGCTTAACCTCGGGTCTGCAGTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAGGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAAGCATTAGAGATA GTGCCCCCCTTGTGGTCGGTGTACAGGCGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
165	*Streptomyces* sp OATH 47	138	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATAACACCTCCACTCTCCTGGGTGGAGGTTAAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGC AAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGCACACACCGCCCGTCACGTCACGAAAGTTGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTAGCGATTGGGACG
166	*Streptomyces* sp OATH 48	139	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATAACACCTCCACTCTCCTGGGTGGAGGTTAAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCGGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGCCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTTGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTAGCGATTGGGACG
167	*Streptomyces* sp OATH C	6	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATAACACCTCCACTCTCCTGGGTGGAGGTTAAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACA GGCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTTGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTAGCGATTGGGACG
168	*Streptomyces* antibioticus B	22	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATCACTCTTGCAGGCATCTGTGAGGGTCGAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGGCCAGAGATG GTCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGTCCTTCGGGATGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAAAGAGCAGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
169	*Streptomyces* antibioticus B	185	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATATCACTCCTGCAGGCATCTGTGAGGGTCGAAAGCTCCGGC GGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATG GCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC CACACTGGGACTGAGACGCGGCCCAGACTCCTACGGGAGGCTGCAG TGGGGAATATTGCACAATGGGCGAAAGCCCGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAACCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCCTAACCCCGGGTCTGCATTCGATACGGGCTAGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ACACCCTGGTAGTCCACGCCGTAAACGGTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATACACCGGAAACGGCCAGGGATG GTCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTTCTGTGTTGCCAGCATGTCCTTCGGGATGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATTATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAAAGAGCAGCGATACCGTGAGGTGGAGCGAATCTCAAAAA GCCGGCCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
170	*Streptomyces* globosus	120	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAGAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAGGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCCCGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
171	*Streptomyces* globosus	198	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTAGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGTGACCG GCCACACTGGGACTGAGACACAGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			AACACCCGGAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
172	*Streptomyces* globosus	119	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATACAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
173	*Streptomyces* globosus	31	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTTTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
174	*Streptomyces* globosus	1	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
175	*Streptomyces* globosus	183	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCCAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GGAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGCGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
176	*Streptomyces* globosus	157	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAACATCCAGAGA TGGGTGCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
177	*Streptomyces* globosus	176	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CTTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAACATCCAGAGA TGGGTGCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
178	*Streptomyces* globosus	178	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAACATCCAGAGA TGGGTGCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			AACACCCGAAGCCGGTGGCCTAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
179	*Streptomyces* globosus	175	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA CGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAACATCCAGAGA TGGGTGCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
180	*Streptomyces* globosus	177	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGTGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAACATCCAGAGA TGGGTGCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
181	*Streptomyces* globosus	172	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCTTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGTGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACAGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
182	*Streptomyces* globosus	171	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGCGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACAGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGTCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
183	*Streptomyces* globosus	169	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATACGACTGCGGAAGGCATCTTCCGTGGTGGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCCAGTCACGTCGGATGT GAAAGCCCGAGGCTTAACCTCGGGTCTGCATTCGATACGGGCTGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATTAGAGA TAGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATACCGTGAGGTGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCTTGTGGAGGGAGCCGTCGAA GGTGGGACTGGCGATTGGGACG
184	*Streptomyces* bikiniensis	12	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA GCCCTTCGGGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGC AATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATA CCGGATACGACCTGGGAAGGCATCTTCTCGGGTGGAAAGCTCCGGC GGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATG GCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGC GTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA GAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAAT TATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGTGA AAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGCTA GAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGC GCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCC ATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAG ATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTGGC GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCG CCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCG AAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGATG GTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGTCA GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC CTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTCAC AGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAA GTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGGC CGGTACAAAGAGCTGCGATGCCGCGAGGCGGAGCGAATCTCAAAAA GCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGT CGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGT TCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAA CACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAA GGTGGGACTGGCGATTGGGACG
185	*Streptomyces* sp OATH 32	101	AGTGAACGCTGGCGGTAGGCCTAACACATGCAAGTCGAACGGCAGC ACAGTAAGAGCTTGCTCTTATGGGTGGCGAGTGGCGGACGGGTGAG GAATACATCGGAATCTACCTTTTCGTGGGGGATAACGTAGGGAAAC TTACGCTAATACCGCATACGACCTCCGGGTGAAAGCAGGGGACCTT CGGGCCTTGCGCGGATAGATGAGCCGATGTCGGATTAGCTAGTTGG CGGGGTAAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAG GATGATCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGG GAGGCAGCAATGGGGAATATTGGACAATGGGCGCAAGCCTGATCCA GCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTT TGTTGGGAAAGAAAAGCAGTCGATTAATACTCGGTTGTCCTGACGG TACCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGT AATACGTAGGGCGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAG CTCGTAGGCGGTTTGTCGCGTCTGCTGTGAAATCCGGAGGCTCAAC CTCCGGCCTGCAGTGGGTACGGGCAGACTAGAGTGCGGTAGGGGAG ATTGGAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGA ACACCGATGGCGAAGGCAGATCTCTGGGCCGTAACTGACGCTGAGG AGCGAAAGGGTGGGGAGCAAACAGGCTTAGATACCCTGGTAGTCCA CCCCGTAAACGTTGGGAACTAGTTGTGGGGTCCATTCCACGGATTC CGTGACGCAGCTAACGCATTAAGTTCCCCGCCTGGGGAGTACGGCC GCAAGGCTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGC GGAGCATGCGGATTAATTCGATGCAACGCGAAGAACCTTACCAAGG CTTGACATATACGAGAACGGGCCAGAAATGGTCAACTCTTTGGACA CTCGTAAACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGA TGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTCTATGTTGC CAGCACGTAATGGTGGGAACTCATGGGATACTGCCGGGGTCAACTC GGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGTCTT GGGCTTCACGCATGCTACAATGGCCGGTACAAAGGGCTGCAATACC GCGAGGTGGAGCGAATCCCAAAAAGCCGGTCCCAGTTCGGATTGAG GTCTGCAACTCGACCTCATGAAGTCGGAGTCGCTAGTAATCGCGGA TCAGCAACGCTGCGGTGAATACGTTCCCGGGTCTTGTACACACCGC

SEQ ID NO	Genus/Species	Strain #	Sequence
			CCGTCAAGTCATGAAAGTCGGTAACACCTGAAGCCGGTGGCCTAAC CTTTTTGGAGGGAGCCGTCGAAGGTGGGATCGGTAATTAGGACT
186	*Streptomyces* sp OATH 39	111	AGTGAACGCTGGCGGTAGGCCTAACACATGCAAGTCGAACGGCAGC ACAGAGGAGCTTGCTCCTTGGGTGGCGAGTGGCGGACGGGTGAGGA ATACATCGGAATCTACTCTGTCGTGGGGGATAACGTAGGGAAACTT ACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGACCTTCG GGCCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGTG GGGTAAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGA TGATCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGA GGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTTTG TTGGGAAAGAAATCCAGCTGGCTAATACCCGGTTGGGATGACGGTA CCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAA TACGAAGGGTGCAAGCGTTACTCGGAATTACTGGGCGTAAAGCGTG CGTAGGTGGTCGTTTAAGTCCGTTGTGAAAGCCCTGGGCTCAACCT GGGAACTGCAGTGGATACTGGGCGACTAGAGTGTGGTAGAGGGTAG CGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAAC ACCGGTGGCGAAGGCGGATCTCTGGGCCATTACTGACGCTGAGGAG CGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCGTAAACGTTGGGAACTAGGTGTTGGCGACATTCCACGTCGTCGG TGCCGCAGCTAACGCATTAAGTTCCCCGCCTGGGGAGTACGGCCGC AAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGCGG AGCATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCT TGACATATACCGGAAAGCATCAGAGATGGTGCCCCCCTTGTGGTCG GTATACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGT TGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTTCTGTGTTGCCAG CATGCCTTTCGGGGTGATGGGGACTCACAGGAGACTGCCGGGGTCA ACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCCTTGTG TCTTGGGCTGCACACGTGCTACAATGGCCGGTACAATGAGCTGCGA TGCCGTGAGGCGGAGCGAATCTCAAAAAGCCGGTCTCAGTTCGGAT TGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAATCG CAGATCAGCATCGCTGCGGTGAATACGTTCCCGGGCCTTGTACACA CCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCC CAACCCCTTGTGGGAGGGAGCTGTCGAAGGTGGGACTGGCGATTGG GACG
187	*Streptomyces* sp OAT 37	109	AGTGAACGCTGGCGGTAGGCCTAACACATGCAAGTCGAACGGCAGC ACAGTAAGAGCTTGCTCTTACGGGTGGCGAGTGGCGGACGGGTGAG GAACACATCGGAATCTACTCTGTCGTGGGGGATAACGTAGGGAAAC TTACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGACCTT CGGGCCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGA TGGGGTAAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAG GATGATCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGG GAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGACCCA GCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTT TGTTGGGAAAGAAATCCAGCTGGCTAATACCCGGTTGGGATGACGG TACCCAAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGT AATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGAG CTCGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAAC CCCGGGTCTGCATTCGATACGGGCTAGCTAGAGTGTGGTAGGGGAG ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGA ACACCGGTGGCGAAGGCGGATCTCTGGGCCATTACTGACGCTGAGG AGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAAACGTTGGGAACTAGGTGTTGGCGACATTCCACGTCGTC GGTGCCGCAGCTAACGCATTAAGTTCCCCGCCTGGGGAGTACGGCC GCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGC GGAGCATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CTTGACATATACCGGAAAGCATCAGAGATGGTGCCCCCCTTGTGGT CGGTATACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGTGAGAT GTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTTCTGTGTTGCC AGCATGCCTTTCGGGGTGATGGGGACTCACAGGAGACTGCCGGGGT CAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCCTTA TGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAATGAGCTGC GATGCCGTGAGGCGGAGCGAATCTCAAAAAGCCGGTCTCAGTTCGG ATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTTGCTAGTAAT CGCAGATCAGCATTGCTGCGGTGAATACGTTCCCGGGCCTTGTACA CACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGCCGGTGG CCCAACCCCTTGTGGGAGGGAGCTGTCGAAGGTGGGACTGGCGATT GGGACG
188	*Streptomyces* sp OATH 31	100	AGTGAACGCTGGCGGTAGGCCTAACACATGCAAGTCGAACGGCAGC ACAGAGGAGCTTGCTCCTTGGGTGGCGAGTGGCGGACGGGTGAGGA ATACATCGGAATCTACTCTGTCGTGGGGGATAACGTAGGGAAACTT ACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGACCTTCG GGCCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGCG GGGTAAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGA TGATCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGA GGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATGCAGC GACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCA GCAGGGAAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGC TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTG TCCGGAGTTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTC GGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGG GCTAGCTAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGG TGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATC TCTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC AGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAG GTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAA GTTCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAA TTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGAC GCAACGCGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCAT CAGAGATGGTGCCCCCCTTGTGGTCGGTATACAGGTGATGCATGGC TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA GCGCAACCCTTGTCCTGTGTTGCCAGCATGCCTTTCGGGGTGATGG GGACTCACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGAC GACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCT ACAATGGCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAAT CTCAAAAAGCCGGTCACAGTTCGGATTGGGGTCTGCAACTCGACCC CATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGT GAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAA GTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAG CTGTCGAAGGTGGGACTGGCGATTGGGACG
189	*Streptomyces* sp OATH 60	190	AGTGAACGCTGGCGGTAGGCCTAACACATGCAAGTCGAACGGCAGC ACAGTAAGAGCTTGCTCTTATGGGTGGCGAGTGGCGGACGGGTGAG GAATACATCGGAATCTACCTTTTCGTGGAGGATAACGTAGGGAAAC TTACGCTAATACCGCATACGACCTTCGGGTGAAAGCAGGGGACCTT CGGGCCTTGCGCGGATAGATGAGCCGATGTCGGATTAGCTAGTTGG CGGGGTAAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAG GACGATCAGCCACACTGGAACTGAGACACGGCCCAGACTCCTACGG GAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA GCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTT CAGCAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCG GCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGT TGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACG

SEQ ID NO	Genus/Species	Strain #	Sequence
			TCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATAC GGGCAGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGC GGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGA TCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGA ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACT AGGTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATT AAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGG AATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCG ACGCAACGCGAAGAACCTTACCAAGGCTTGACATACATCGGAAAAC CCTGGAGACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATG GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAAC GAGCGCAACCCTTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTG GGGACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGA CGACGTCAAGTCATCATGTCCCTTATGTCTTGGGCTGCACACGTGC TACAATGGCCGGTACAATGAGCTGCGACACCGCGAGGTGGAGCGAA TCTCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACC CCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGG TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAA AGTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGA GCTGTCGAAGGTGGGACTGGCGATTGGGACG
190	*Streptomyces* sp OATH 42	118	ATTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAGCGGATGA GAGGAGCTTGCTCCTGGATTCAGCGGCGGACGGGTGAGTAATGCCT AGGAATCTGCCTGGTAGTGGGGGGCAACGTTTCGAAAGGAACGCTA ATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTT GCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAA TGGCTCACCAAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCA GTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAACGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGGTGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATCCGATACGGGCAGGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTCCTGTGTTGCCAGCATGCCCTTCGGGGTGATGGGGACTC ACAGGAGACCGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAAAGAGCTGCGATGCCGCGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
191	*Streptomyces* cavourensis	64	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAACACTCCTGCCTGCATGGGTGGGGGTTGAAAGCTCCG

SEQ ID NO	Genus/Species	Strain #	Sequence
			GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
192	*Streptomyces* bacillaris	15	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAATACTCCTGCCTGCATGGGTGGGGGTTGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA

SEQ ID NO	Genus/Species	Strain #	Sequence
			GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
193	*Streptomyces* sp OATH 23	91	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAATACTCTGTTCCGCATGGGACGGGGTTGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGT TGCACCAGAAGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACG GTGTGGCCGATGACTGGGGTG
194	*Streptomyces* bacillaris	29	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAATACTCTGTTCCGCATGGGACGGGGTTGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG

SEQ ID NO	Genus/Species	Strain #	Sequence
			CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
195	*Streptomyces* cavourensis	38	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAACACTCTGTTCCGCATGGGACGGGGTTGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG
196	*Streptomyces* bacillaris	211	GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGATGAA ACCGCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGG GCAATCTGCCCTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAA TACCGGATAATACTCTGTTCCGCATGGGACGGGGTTGAAAGCTCCG GCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAA TGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCG GCCGCACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCC GCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGG AAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAGGAGCTCGTAGGCGGCTTGTCACGTCGGATGT

SEQ ID NO	Genus/Species	Strain #	Sequence
			GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAGC TAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAAT GCGCAGATATCAGGAGGGACACCGGTGGCGAAGGCGGATCTCTGGG CCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT AGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTG GCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCC CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACG GGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCGACGCAACG CGAAGAACCTTACCAAGGCTTGACATATACCGGAAAGCATCAGAGA TGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCATGGCTGTCGT CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA CCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGGTGATGGGGACTC ACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTC AAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGCGCTACAATG GCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAA AAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAA GTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATAC GTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGT AACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCG AAGGTGGGACTGGCGATTGGGACG

[0020] In certain embodiments provided herein, a composition or method utilizes one or more microbes. Any suitable microbes may be used.

[0021]

Table 2: ATCC deposits

Designation	ATCC No.
1	PTA-127367
2	PTA-127368
3	PTA-127369
4	PTA-127370
5	PTA-127371
6	PTA-127372
7	PTA-127373
8	PTA-127374
9	PTA-127375
10	PTA-127376

Designation	ATCC No.
11	PTA-127377
12	PTA-127378
13	PTA-127379
14	PTA-127380
15	PTA-127381
16	PTA-127382
17	PTA-127383
18	PTA-127384
19	PTA-127385
20	PTA-127386
21	PTA-127387
22	PTA-127388
23	PTA-127389
24	PTA-127390
25	PTA-127391
26	PTA-127392
27	PTA-127393
28	PTA-127394
29	PTA-127395
30	PTA-127396
31	PTA-127397
32	PTA-127398
33	PTA-127399
34	PTA-127400
35	PTA-127401
36	PTA-127402
37	PTA-127403
38	PTA-127404
39	PTA-127405
40	PTA-127406
41	PTA-127407
42	PTA-127408
43	PTA-127409

Designation	ATCC No.
44	PTA-127410
45	PTA-127411
46	PTA-127412
47	PTA-127413

[0022] Deposits of each of O-46 through O140 is and has been maintained by Oath, Inc., or its predecessors or agents, at either 568 Duncan Farms Rd., Steele AL 35987, 4136 E Bujia Segunda, Tucson, AZ, 85718 or 505 Coastal South Blvd., La Jolla, CA. 92307, since prior to the filing date of this application. Access to these deposits will be available during the pendency of the application to the Commissioner of Patents and Trademarks and persons determined by the Commissioner to be entitled thereto upon request, as well as to equivalent bodies and persons outside the United States. Upon allowance of any claims in the application, the Applicant(s) will make available to the public without restriction deposits of each of O-46 through O140 with the American Type Culture Collection (ATCC, Manassas, Va.) or other depository that conforms to the Budapest Treaty. The bacteria deposited with the ATCC will be taken from the same deposits maintained at the locations described above. Additionally, Applicant will meet all the requirements of 37 C.F.R. § 1.801-1.809, including providing an indication of the viability of the sample when the deposit is made.

[0023] This deposit of the aforementioned bacteria will be maintained in the ATCC or other depository that conforms to the Budapest Treaty, which are a public depositories, for a period of 30 years, or 5 years after the most recent request, or for the enforceable life of the patent, whichever is longer, and will be replaced if it ever becomes nonviable during that period. Applicant will impose no restrictions on the availability of the deposited material; however, Applicant has no authority to waive any restrictions imposed by law on the transfer of biological material or its transportation in commerce.

[0024] In certain embodiments, one or more mycorrhiza, for example one or more mycorrhizal fungus, are used in addition to the *Streptomyces* bacteria. The term "mycorrhiza" or "mycorrhizal fungus or fungi," as used herein includes a fungal cell associated with a root of a plant. The mycorrhiza can be an endomycorrhiza or an ectomycorrhiza. The mycorrhiza can be an Arbuscular endomycorrhiza, Ericoid endomycorrhiza, Arbutoid endomycorrhiza, Monotropoid endomycorrhiza, orchidaceous endomycorrhiza, or ectendomycorrhiza. In certain embodiments, the mycorrhiza comprises any one of the mycorrhiza identified in the FungalRoot database (Soudzilovskaia et al. (2020) NEW PHYTOLOGIST;

<https://www.gbif.org/dataset/744edc21-8dd2-474e-8a0b-b8c3d56a3c2d>). In certain embodiments endomycorrhizal fungi belonging to the phylum Glomeromycota are used.

B. Compositions comprising one or more microbes

1. Microbial compositions

[0025] Provided herein are microbial compositions.

[0026] In certain embodiments provided is a composition comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, even still more preferably 10-40, further preferably 10-30, different Streptomyces microbes. Any suitable microbe microbes, such as those described herein, may be used. In certain embodiments the composition further comprises cells of one or more non-*Streptomyces* microbes. Any suitable non-*Streptomyces* microbes, such as those described herein, may be used. In certain embodiments, two or more of the microbes are heterologous to each other. In certain embodiments, the microbes of one or more non-*Streptomyces* microbe comprises microbes of *Pseudomonas*, *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination therof. In certain embodiments the one or more microbes of non-*Streptomyces* microbe comprises *Pseudomonas*, *Microvirga*, *Micrococcus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination therof. In certain embodiments the one or more microbes of non-*Streptomyces* microbe comprises *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination therof.

[0027] In certain embodiments, provided herein is a composition comprising one or more Streptomyces microbes, wherein the one or more Streptomyces microbes comprise a 16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5 identical, or 100% identical, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to a nucleic acid sequence to one or more of SEQ ID NOs:68-109 and 120-196.

[0028] In certain embodiments provided is composition comprising *Streptomyces* spp. microbes and at least one, two, three, four, five, 6, or 7 and/or not more than one, two, three, four, five, 6, 7, or 8, preferably 2-8, more preferably 2-6, yet more preferably 3-8, such as 2, 3, 4, 5, 6, 7, 8, or 8 additional microbes selected from the group consisting of *Pseudomonas* spp.,

Microvirga spp., *Paenibacillus* spp., *Aureimonas* spp., *Bradyrhizobium* spp., *Rhodococcus* spp., *Amycolatopsis* spp., and *Lysinibacillis* spp.. In certain embodiments the composition comprises microbes of *Pseudomonas* spp. In certain embodiments the composition comprises microbs of *Microvirga* spp. In certain embodiments the composition comprises microbs of *Micrococcus* spp. In certain embodiments the composition comprises microbs of *Paenibacillus* spp. In certain embodiments the composition comprises microbs of *Aureimonas* spp. In certain embodiments the composition comprises microbs of *Bradyrhizobium* spp. In certain embodiments the composition comprises microbs of *Rhodococcus* spp. In certain embodiments the composition comprises microbs of *Lysinibacillis* spp.

[0029] In certain embodiments, provided is a composition comprising microbs of one or more *Streptomyces* strains and microbs of at least one non-*Streptomyces* species, wherein the non-*Streptomyces* species is a nitrogen-fixing species. In certain embodiments the nitrogen-fixing non-*Streptomyces* species comprise microbs of *Pseudomonas* spp., *Microvirga* spp., Bradyrhyizobium spp., *Aureimonas* spp., *Paenibacillus* spp., and/or Lysinibacillus spp. In certain embodiments the composition comprises microbs of e spp . In certain embodiments the composition comprises microbs of *Microvirga* spp. . In certain embodiments the composition comprises microbs of *Aureimonas* spp . In certain embodiments the composition comprises microbs of *Paenibacillus* spp. In certain embodiments the composition comprises microbs of *Bradyrhizobium* spp . In certain embodiments the composition comprises microbs of *Lysinibacillis* spp .

[0030] In certain embodiments provided herein is a composition comprising one or more microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2 and/or one or more microbes of OATH-46-OATH-140.

[0031] In embodiments including one or more *Streptomyces* microbes, any suitable *Streptomyces* microbes may be used. The microbes may be of one or more *Streptomyces* species and/or one or more *Streptomyces* strains. In certain embodiments, microbes are microbes of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60, for example at least 5, or at least 10, or at least 15, or at least 20, and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60 yet even more preferably 10-30 different *Streptomyces* strains. In certain embodiments, *Streptomyces* microbes comprise comprise microbes of one or more of *Streptomyces* antibioticus B, *Streptomyces* bacillaris,*Streptomyces* bikiniensis,*Streptomyces* cavourensis,*Streptomyces* fimbriatus,*Streptomyces* flavoviridis,*Streptomyces* globosus,*Streptomyces*

griseoaurantiacus,*Streptomyces* griseofuscus,*Streptomyces* griseoincarnatus, *Streptomyces* griseoviridis A.*Streptomyces* labedae,*Streptomyces* lydicus,*Streptomyces* misionensis,*Streptomyces* nigra,*Streptomyces* rochei,*Streptomyces* sp. OATH_5,*Streptomyces* sp. OATH_7,*Streptomyces* sp. OATH_8,*Streptomyces* sp. OATH_9,*Streptomyces* sp. OATH_10,*Streptomyces* sp. OATH_11,*Streptomyces* sp. OATH_12,*Streptomyces* sp. OATH_13,*Streptomyces* sp. OATH_17,*Streptomyces* sp. OATH_19,*Streptomyces* sp. OATH_20,*Streptomyces* sp. OATH_22A,*Streptomyces* sp. OATH_22B,*Streptomyces* sp. OATH_23,*Streptomyces* sp. OATH_26,*Streptomyces* sp. OATH_27,*Streptomyces* sp. OATH_28,*Streptomyces* sp. OATH_30,*Streptomyces* sp. OATH_31,*Streptomyces* sp. OATH_34,*Streptomyces* sp. OATH_36,*Streptomyces* sp. OATH_37,*Streptomyces* sp. OATH_38,*Streptomyces* sp. OATH_39,*Streptomyces* sp. OATH_40,*Streptomyces* sp. OATH_41,*Streptomyces* sp. OATH_42,*Streptomyces* sp. OATH_43,*Streptomyces* sp. OATH_44,*Streptomyces* sp. OATH_46,*Streptomyces* sp. OATH_47,*Streptomyces* sp. OATH_48,*Streptomyces* sp. OATH_49,*Streptomyces* sp. OATH_50,*Streptomyces* sp. OATH_52,*Streptomyces* sp. OATH_57,*Streptomyces* sp. OATH_58,*Streptomyces* sp. OATH_59,*Streptomyces* sp. OATH_60,*Streptomyces* sp. OATH_61,*Streptomyces* sp. OATH_62,*Streptomyces* sp. OATH_63,*Streptomyces* sp. OATH_64,*Streptomyces* sp. OATH_65,*Streptomyces* sp. OATH_66,*Streptomyces* sp. OATH_A,*Streptomyces* sp. OATH_B,*Streptomyces* sp. OATH_C,*Streptomyces* sp. OATH_D,*Streptomyces* sp. OATH_E,*Streptomyces* sp. OATH_F,*Streptomyces* sp. OATH_G,*Streptomyces* sp001509795,*Streptomyces* sp900105755, and/or *Streptomyces* violaceorectus. In certain embodiments, , *Streptomyces* microbes comprise one or more of microbes of OATH_5,*Streptomyces* sp. OATH_7,*Streptomyces* sp. OATH_8,*Streptomyces* sp. OATH_9,*Streptomyces* sp. OATH_10,*Streptomyces* sp. OATH_11,*Streptomyces* sp. OATH_12,*Streptomyces* sp. OATH_13,*Streptomyces* sp. OATH_17,*Streptomyces* sp. OATH_19,*Streptomyces* sp. OATH_20,*Streptomyces* sp. OATH_22A,*Streptomyces* sp. OATH_22B,*Streptomyces* sp. OATH_23,*Streptomyces* sp. OATH_26,*Streptomyces* sp. OATH_27,*Streptomyces* sp. OATH_28,*Streptomyces* sp. OATH_30,*Streptomyces* sp. OATH_31,*Streptomyces* sp. OATH_34,*Streptomyces* sp. OATH_36,*Streptomyces* sp. OATH_37,*Streptomyces* sp. OATH_38,*Streptomyces* sp. OATH_39,*Streptomyces* sp. OATH_40,*Streptomyces* sp. OATH_41,*Streptomyces* sp. OATH_42,*Streptomyces* sp. OATH_43,*Streptomyces* sp. OATH_44,*Streptomyces* sp. OATH_46,*Streptomyces* sp. OATH_47,*Streptomyces* sp. OATH_48,*Streptomyces* sp. OATH_49,*Streptomyces* sp. OATH_50,*Streptomyces* sp. OATH_52,*Streptomyces* sp. OATH_57,*Streptomyces* sp. OATH_58,*Streptomyces* sp. OATH_59,*Streptomyces* sp. OATH_60,*Streptomyces* sp.

OATH_61,*Streptomyces* sp. OATH_62,*Streptomyces* sp. OATH_63,*Streptomyces* sp. OATH_64,*Streptomyces* sp. OATH_65,*Streptomyces* sp. OATH_66,*Streptomyces* sp. OATH_A,*Streptomyces* sp. OATH_B,*Streptomyces* sp. OATH_C,*Streptomyces* sp. OATH_D,*Streptomyces* sp. OATH_E,*Streptomyces* sp. OATH_F,*Streptomyces* sp. OATH_G. In certain embodiments, *Streptomyces* microbes *Streptomyces* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 68-109 and 120-196.

[0032] In embodiments including one or more non-*Streptomyces* microbes, any suitable non-*Streptomyces* microbes may be used. In certain embodiments, microbes of one or more non-*Streptomyces* strain comprise microbes of *Pseudomonas*, *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* strain, or a combination therof. In certain embodiments, the one or more microbes of non-*Streptomyces* strain comprises *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* strain, or a combination therof.

[0033] In embodiments including microbes of one or more *Pseudomonas* strains, any suitable strain(s) of *Pseudomonas* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Pseudomonas* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Pseudomonas* strains are used. In certain embodiments, one or more *Pseudomonas* microbes comprise a first microbe of a first *Pseudomonas* strain. In certain embodiments, one or more *Pseudomonas* microbes comprise a second microbe of a second *Pseudomonas* strain, different from the first strain. In certain embodiments, one or more *Pseudomonas* microbes comprise a third microbe of a third *Pseudomonas* strain, different from the first and second strains. In certain embodiments, one or more *Pseudomonas* microbes comprise a fourth microbe of a fourth *Pseudomonas* strain, different from the first, second, and third strains. In certain embodiments, one or more *Pseudomonas* microbes comprise a fifth microbe of a fifth *Pseudomonas* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Pseudomonas* strains comprise microbes of one or more of *Pseudomonas* E sp003253735, *Pseudomonas* fluorescens, *Pseudomonas* koreensis, *Pseudomonas* poae *Pseudomonas* sp. OATH_2, *Pseudomonas* sp. OATH_3, *Pseudomonas* sp. OATH_4, *Pseudomonas* sp. OATH_6, *Pseudomonas* sp. OATH_14, *Pseudomonas* sp. OATH_15, *Pseudomonas* sp. OATH_16, *Pseudomonas* sp. OATH_45 *Pseudomonas* sp. OATH_51 *Pseudomonas* sp. OATH_53, *Pseudomonas* sp. OATH_55, *Pseudomonas* sp. OATH_56, *Pseudomonas* sp.002836515, and/or *Pseudomonas* straminea are used. In certain

embodiments, microbe or microbes of *Pseudomonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 39-67.

[0034] In embodiments including microbes of one or more *Microvirga* strains, any suitable strain(s) of *Microvirga* may be used. In certain embodiments, the *Microvirga* strain comprises *Microvirga* sp. OATH1. In certain embodiments, microbe(s) of the *Microvirga* strain have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NO: 38.

[0035] In embodiments including microbes of one or more *Micrococcus* strains, any suitable strain(s) of *Micrococcus* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Micrococcus* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Micrococcus* strains are used. In certain embodiments, one or more *Micrococcus* microbes comprise a first microbe of a first *Micrococcus* strain. In certain embodiments, one or more *Micrococcus* microbes comprise a second microbe of a second *Micrococcus* strain, different from the first strain. In certain embodiments, microbes of *Micrococcus* strains comprise microbes of *Micrococcus* luteus. In certain embodiments, the microbe or microbes of *Micrococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 118-119.

[0036] In embodiments including microbes of one or more *Paenibacillus* strains, any suitable strain(s) of *Paenibacillus* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Paenibacillus* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Paenibacillus* strains are used. In certain embodiments, one or more *Paenibacillus* microbes comprise a first microbe of a first *Paenibacillus* strain. In certain embodiments, one or more *Paenibacillus* microbes comprise a second microbe of a second *Paenibacillus* strain, different from the first strain. In certain embodiments, one or more *Paenibacillus* microbes comprise a third microbe of a third *Paenibacillus* strain, different from the first and second strains. In certain embodiments, one or more *Paenibacillus* microbes comprise a fourth microbe of a fourth *Paenibacillus* strain, different from the first, second, and

third strains. In certain embodiments, one or more *Paenibacillus* microbes comprise a fifth microbe of a fifth *Paenibacillus* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Paenibacillus* strains comprise microbes of one or more of *Paenibacillus* cellulositrophicus A and/or *Paenibacillus* illinoisensis.. In certain embodiments, microbe or microbes of *Paenibacillus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 10-17.

[0037] In embodiments including microbes of one or more *Aureimonas* strains, any suitable strain(s) of *Aureimonas* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Aureimonas* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Aureimonas* strains are used. In certain embodiments, one or more *Aureimonas* microbes comprise a first microbe of a first *Aureimonas* strain. In certain embodiments, one or more *Aureimonas* microbes comprise a second microbe of a second *Aureimonas* strain, different from the first strain. In certain embodiments, one or more *Aureimonas* microbes comprise a third microbe of a third *Aureimonas* strain, different from the first and second strains. In certain embodiments, one or more *Aureimonas* microbes comprise a fourth microbe of a fourth *Aureimonas* strain, different from the first, second, and third strains. In certain embodiments, microbes of *Aureimonas* strains comprise microbes of *Aureimonas* A sp001425485. In certain embodiments, microbe or microbes of *Aureimonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 18-21.

[0038] In embodiments including microbes of one or more *Bradyrhizobium* strains, any suitable strain(s) of *Bradyrhizobium* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Bradyrhizobium* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Bradyrhizobium* strains are used. In certain embodiments, one or more *Bradyrhizobium* microbes comprise a first microbe of a first *Bradyrhizobium* strain. In certain embodiments, one or more *Bradyrhizobium* microbes comprise a second microbe of a second *Bradyrhizobium* strain, different from the first strain. In certain embodiments, one or more *Bradyrhizobium* microbes comprise a third microbe of a third *Bradyrhizobium* strain, different from the first and second strains. In certain embodiments, one or more *Bradyrhizobium* microbes comprise a fourth microbe of a fourth *Bradyrhizobium* strain,

different from the first, second, and third strains. In certain embodiments, one or more *Bradyrhizobium* microbes comprise a fifth microbe of a fifth *Bradyrhizobium* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Bradyrhizobium* strains comprise microbes of one or more of *Bradyrhizobium* denitrificans and/or *Bradyrhizobium* elkanii. In certain embodiments, microbe or microbes of Bradyrhyzobium strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 22-37.

[0039] In embodiments including microbes of one or more *Rhodococcus* strains, any suitable strain(s) of *Rhodococcus* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Rhodococcus* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Rhodococcus* strains are used. In certain embodiments, one or more *Rhodococcus* microbes comprise a first microbe of a first *Rhodococcus* strain. In certain embodiments, one or more *Rhodococcus* microbes comprise a second microbe of a second *Rhodococcus* strain, different from the first strain. In certain embodiments, one or more *Rhodococcus* microbes comprise a third microbe of a third *Rhodococcus* strain, different from the first and second strains. In certain embodiments, one or more *Rhodococcus* microbes comprise a fourth microbe of a fourth *Rhodococcus* strain, different from the first, second, and third strains. In certain embodiments, one or more *Rhodococcus* microbes comprise a fifth microbe of a fifth *Rhodococcus* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Rhodococcus* strains comprise microbes of one or more of *Rhodococcus* erythropoli and/or *Rhodococcus* qingshengii. In certain embodiments, microbe or microbes of *Rhodococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 116-117.

[0040] In embodiments including microbes of one or more *Amycolatopsis* strains, any suitable strain(s) of *Amycolatopsis* may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 *Amycolatopsis* strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 *Amycolatopsis* strains are used. In certain embodiments, one or more *Amycolatopsis* microbes comprise a first microbe of a first *Amycolatopsis* strain. In certain embodiments, one or more *Amycolatopsis* microbes comprise a second microbe of a second *Amycolatopsis* strain, different from the first strain. In certain embodiments, one or more *Amycolatopsis* microbes comprise a third microbe of a third *Amycolatopsis* strain, different

from the first and second strains. In certain embodiments, one or more *Amycolatopsis* microbes comprise a fourth microbe of a fourth *Amycolatopsis* strain, different from the first, second, and third strains. In certain embodiments, one or more *Amycolatopsis* microbes comprise a first microbe of fifth *Amycolatopsis* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Amycolatopsis* strains comprise microbes of one or more of *Amycolatopsis* lurida and/or *Amycolatopsis*_OATH_54. In certain embodiments, microbe or microbes of *Amycolatopsis* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NOs: 110-115.

[0041] In embodiments incoluding microbes of one or more Lysinibacillus strains, any suitable strain(s) of Lysinibacillus may be used. In certain embodiments, cells (microbes) of at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 Lysinibacillus strains and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 Lysinibacillus strains are used. In certain embodiments, one or more Lysinibacillusmicrobes comprise a first microbe of a first Lysinibacillus strain. In certain embodiments, one or more Lysinibacillus microbes comprise a second microbe of a second Lysinibacillus strain, different from the first strain. In certain embodiments, one or more Lysinibacillus microbes comprise a third microbe of a third Lysinibacillus strain, different from the first and second strains. In certain embodiments, one or more Lysinibacillus microbes comprise a fourth microbe of a fourth Lysinibacillus strain, different from the first, second, and third strains. In certain embodiments, one or more Lysinibacillus microbes comprise a fifth microbe of a fifth Lysinibacillus strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of Lysinibacillusstrains comprise microbes of Lysinibacillus capsici. In certain embodiments, microbe or microbes of Lysinibacillus strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity identity to SEQ ID NOs: 1-9.

[0042] In certain embodiments, compositions and/or methods include one or more microbes deposited as ATCC Nos. PTA-127367 to PTA-127411, also referred to as one or more microbes of Designation 1-45, respectively, as shown in Table 1, and/or one or more microbes of deposits designation OATH-1 to OATH-140. Deposits may be referred to herein by ATCC number, by numerical designation (e.g., ATCC-1, corresponding to Designation 1, PTA-127367, etc). Unless indicated otherwise, a composition said to comprises an ATCC or OATH designation, includes one or more microbes of the ATCC or OATH deposit, and progeny and/or mutants

thereof. Any suitable combination of the one or more microbes deposited as ATCC Nos. PTA-127367 to PTA-127411, also referred to as Designation 1-45, respectively, as shown in Table 1, may be used. In certain embodiments, the composition one or more microbes of Designation 1 (ATCC No. PTA-127367) and/or one or more microbes of Designation 2 (ATCC No. PTA-127368) and/or one or more microbes of Designation 3 (ATCC No. PTA-127369) and/or one or more microbes of Designation 4 (ATCC No. PTA-127370) and/or one or more microbes of Designation 5 (ATCC No. PTA-127371) and/or one or more microbes of Designation 6 (ATCC No. PTA-127372) and/or one or more microbes of Designation 7 (ATCC No. PTA-127373) and/or one or more microbes of Designation 8 (ATCC No. PTA-127374) and/or one or more microbes of Designation 9 (ATCC No. PTA-127375) and/or one or more microbes of Designation 10 (ATCC No. PTA-127376) and/or one or more microbes of Designation 11 (ATCC No. PTA-127377) and/or one or more microbes of Designation 12 (ATCC No. PTA-127378) and/or one or more microbes of Designation 13 (ATCC No. PTA-127379) and/or one or more microbes of Designation 14 (ATCC No. PTA-127380) and/or one or more microbes of Designation 15 (ATCC No. PTA-127381) and/or one or more microbes of Designation 16 (ATCC No. PTA-127382) and/or one or more microbes of Designation 17 (ATCC No. PTA-127383) and/or one or more microbes of Designation 18 (ATCC No. PTA-127384) and/or one or more microbes of Designation 19 (ATCC No. PTA-127385) and/or one or more microbes of Designation 20 (ATCC No. PTA-127386) and/or one or more microbes of Designation 21 (ATCC No. PTA-127387) and/or one or more microbes of Designation 22 (ATCC No. PTA-127388) and/or one or more microbes of Designation 23 (ATCC No. PTA-127389) and/or one or more microbes of Designation 24 (ATCC No. PTA-127390) and/or one or more microbes of Designation 25 (ATCC No. PTA-127391) and/or one or more microbes of Designation 26 (ATCC No. PTA-127392) and/or one or more microbes of Designation 27 (ATCC No. PTA-127393) and/or one or more microbes of Designation 28 (ATCC No. PTA-127394) and/or one or more microbes of Designation 29 (ATCC No. PTA-127395) and/or one or more microbes of Designation 30 (ATCC No. PTA-127396) and/or one or more microbes of Designation 31 (ATCC No. PTA-127397) and/or one or more microbes of Designation 32 (ATCC No. PTA-127398) and/or one or more microbes of Designation 33 (ATCC No. PTA-127399) and/or one or more microbes of Designation 34 (ATCC No. PTA-127400) and/or one or more microbes of Designation 35 (ATCC No. PTA-127401) and/or one or more microbes of Designation 36 (ATCC No. PTA-127402) and/or one or more microbes of Designation 37 (ATCC No. PTA-127403) and/or one or more microbes of Designation 38 (ATCC No. PTA-127404) and/or one or more microbes of Designation 39 (ATCC No. PTA-127405) and/or one or more microbes of Designation 40 (ATCC No. PTA-127406) and/or one or more microbes of Designation 41

(ATCC No. PTA-127407) and/or one or more microbes of Designation 42 (ATCC No. PTA-127408) and/or one or more microbes of Designation 43 (ATCC No. PTA-127409) and/or one or more microbes of Designation 44 (ATCC No. PTA-127410) and/or one or more microbes of Designation 45 (ATCC No. PTA-127411). In certain embodiments, a composition can include one or more microbes from one or more microbes of Designation 46 (ATCC No. PTA-127412), also designated individually as O-46 to O-140 herein. In certain embodiments, the composition comprises one or more microbes of Designation O-46 and/or one or more microbes of Designation O-47 and/or one or more microbes of Designation O-48 and/or one or more microbes of Designation O-49 and/or one or more microbes of Designation O-50 and/or one or more microbes of Designation O-51 and/or one or more microbes of Designation O-52 and/or one or more microbes of Designation O-53 and/or one or more microbes of Designation O-54 and/or one or more microbes of Designation O-55 and/or one or more microbes of Designation O-56 and/or one or more microbes of Designation O-57 and/or one or more microbes of Designation O-58 and/or one or more microbes of Designation O-59 and/or one or more microbes of Designation O-60 and/or one or more microbes of Designation O-61 and/or one or more microbes of Designation O-62 and/or one or more microbes of Designation O-63 and/or one or more microbes of Designation O-64 and/or one or more microbes of Designation O-65 and/or one or more microbes of Designation O-66 and/or one or more microbes of Designation O-67 and/or one or more microbes of Designation O-68 and/or one or more microbes of Designation O-69 and/or one or more microbes of Designation O-70 and/or one or more microbes of Designation O-71 and/or one or more microbes of Designation O-72 and/or one or more microbes of Designation O-73 and/or one or more microbes of Designation O-74 and/or one or more microbes of Designation O-75 and/or one or more microbes of Designation O-76 and/or one or more microbes of Designation O-77 and/or one or more microbes of Designation O-78 and/or one or more microbes of Designation O-79 and/or one or more microbes of Designation O-80 and/or one or more microbes of Designation O-81 and/or one or more microbes of Designation O-82 and/or one or more microbes of Designation O-83 and/or one or more microbes of Designation O-84 and/or one or more microbes of Designation O-85 and/or one or more microbes of Designation O-86 and/or one or more microbes of Designation O-87 and/or one or more microbes of Designation O-88 and/or one or more microbes of Designation O-89 and/or one or more microbes of Designation O-90 and/or one or more microbes of Designation O-91 and/or one or more microbes of Designation O-92 and/or one or more microbes of Designation O-93 and/or one or more microbes of Designation O-94 and/or one or more microbes of Designation O-95 and/or one or more microbes of Designation O-96 and/or one or more microbes of Designation O-97 and/or one or more microbes of Designation O-98

and/or one or more microbes of Designation O-99 and/or one or more microbes of Designation O-100 and/or one or more microbes of Designation O-101 and/or one or more microbes of Designation O-102 and/or one or more microbes of Designation O-103 and/or one or more microbes of Designation O-104 and/or one or more microbes of Designation O-105 and/or one or more microbes of Designation O-106 and/or one or more microbes of Designation O-107 and/or one or more microbes of Designation O-108 and/or one or more microbes of Designation O-109 and/or one or more microbes of Designation O-110 and/or one or more microbes of Designation O-111 and/or one or more microbes of Designation O-112 and/or one or more microbes of Designation O-113 and/or one or more microbes of Designation O-114 and/or one or more microbes of Designation O-115 and/or one or more microbes of Designation O-116 and/or one or more microbes of Designation O-117 and/or one or more microbes of Designation O-118 and/or one or more microbes of Designation O-119 and/or one or more microbes of Designation O-120 and/or one or more microbes of Designation O-121 and/or one or more microbes of Designation O-122 and/or one or more microbes of Designation O-123 and/or one or more microbes of Designation O-124 and/or one or more microbes of Designation O-125 and/or one or more microbes of Designation O-126 and/or one or more microbes of Designation O-127 and/or one or more microbes of Designation O-128 and/or one or more microbes of Designation O-129 and/or one or more microbes of Designation O-130 and/or one or more microbes of Designation O-131 and/or one or more microbes of Designation O-132 and/or one or more microbes of Designation O-133 and/or one or more microbes of Designation O-134 and/or one or more microbes of Designation O-135 and/or one or more microbes of Designation O-136 and/or one or more microbes of Designation O-137 and/or one or more microbes of Designation O-138 and/or one or more microbes of Designation O-139 and/or one or more microbes of Designation O-140. In certain embodiments, a composition comprises at least 5, 10, 15, 20, 25, 30, 35, or 40 of one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or not more than 5, 10, 15, 20, 25, 30, 35, or 40 of one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411), preferably 5-45, more preferably 10-45, even more preferably 20-45, yet more preferably 35-45. In certain embodiments, a composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 of one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or one or more microbes of Designation O-46 to O-140, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[0043] In certain embodiments, microbes included in a composition herein are biologically pure. As used herein, a "pure" or "biologically pure" organism or population of organisms, such as microbe or microbial population, or the like, includes a population of organisms in the absence of other species or types. A "substantially pure culture" includes a culture which contains substantially no other microbes than the desired strain or strains, e.g., other microbes may be present but not in quantities and/or forms that interfere with the intended use of the culture. A substantially pure culture includes a culture that is substantially free of other contaminants, which can include microbial contaminants as well as undesirable chemical contaminants.

[0044] In certain embodiments, microbes included in a composition herein are isolated. As used herein, "isolate," "isolated," "isolated microbe," "isolated microorganism" and like terms, include the meaning that the one or more microbes has been separated from at least one of the materials with which it is associated in a particular environment (for example soil, water, plant tissue). Thus, an "isolated microbe" does not exist in its naturally occurring environment; rather, the microbe has been removed from its natural setting and placed into a non-naturally occurring state of existence.

[0045] In certain embodiments, microbes of a composition or method are heterologous to each other, and/or heterologous to a soil, plant, plant part, seed, seedling, plant propagule, or other substance in association with the microbes; in certain embodiments at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 30, 40, 50, 60, 70, 80, 90 or 100 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 30, 40, 50, 60, 70, 80, 90 100, 120, or 140, preferably 2-140, more preferably 2-100, even more preferably 2-80, still more preferably 2-60, yet more preferably 2-40 for example at least 2, preferably at least 3, more preferably at least 4, even more preferably at least 5, yet more preferably at least 7, still more preferably at least 10 microbes of a composition or method are heterologous to each other, or heterologous to a soil, plant, plant part, seed, seedling, plant propagule, or other substance in association with the microbes. As used herein, the terms "heterologous," "exogenous," and the like, when referring to one material related to a second material, include a material that is not naturally associated with the second material. Thus, a microbe is considered heterologous to a plant or a plant part, such as a root, or a seed, or the like, if the microbe is not found in nature associated with the particular plant, plant part (e.g., root), seed, or the like, or is not found in the number indicated; in some cases, a population of microbes may contain some microbes that are heterologous to the material, and some that are not heterologous (i.e., normally found with the material) to the material. A microbe can also be heterologous to another microbe if the two are not naturally found together, or are not found in the numbers and/or ratios indicated.

[0046] In certain embodiments, total colony forming units (CFUs) per gram of a microbial composition is at least 10^4, 10^5,10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^5,10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16}, preferably 10^4 to 10^{11}, more preferably 10^4 to 10^9 even more preferably 10^5 to 10^9, yet more preferably 10^5 to 10^8, still more preferably 10^5 to 10^8. In certain embodiments a composition comprises at least 10^8 CFU. In certain embodiments a composition comprises at least 10^9 CFU. In certain embodiments a composition comprises at least 10^9 CFU. In certain embodiments, each of the different microbes (e.g., microbes of a specific strain) is present at at least 10^4, 10^5,10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^5,10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition. In certain embodiments at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, preferably at least 10%, more preferably at least 20%, even more preferably at least 30%, still more preferably at least 40%, yet more preferably at least 50% of different strains of microbes in composition are present in a ratio to each other (CFU to CFU) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25. In certain embodiments at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, preferably at least 10%, more preferably at least 20%, even more preferably at least 30%, still more preferably at least 40%, yet more preferably at least 50% of different strains of microbes in composition are present in a weight ratio to each other of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25. A "colony forming unit," or "CFU," as those terms are used herein, includes a microbial cell that is viable, that is, able to multiply via binary fission under suitable conditions. Methods for determining a number of CFUs in a sample are well-known in the art.

[0047] In certain embodiments, a composition comprises a liquid medium in which the one or more microbes, e.g., as described above, are distributed. In certain embodiments the liquid medium is heterologous to microrganisms in the composition. In certain embodiments, the liquid medium comprises an aqueous medium. In certain embodiments, the aqueous medium comprises a combination of mediums in which one or more of the one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or one or more microbes of Designation O-46 to O-140 has been growing.

2. Dry compositions

[0048] In certain embodiments a composition is a dry composition. Generally, a dry composition comprises 10 wt% or less water. In certain embodiments a composition comprises less than 5, 4, 3, 2, 1, 0.5, 0.2, 0.1%, 0.05%, 0.01%, 0.005%, 0.001%, 0.0005%, or 0.0001% wt% water, for example less than 0.1%, preferably less than 0.05%, more preferably less than 0.01%, even more preferably less than 0.005%, yet more preferably less than 0.001%, still more preferably less than 0.0005%. In certain embodiments, a composition comprises less than 5, such as less than 4, or less than 3, or less than 2% water. In certain embodiments, a composition comprises less than 1% water. In certain embodiments, a composition comprises less than 0.5% water.In certain such embodiments, a composition consists essentially of the one or more microbes, e.g., a composition produced from a combination of different liquid media comprising the microbes, in some cases, media in which the microbes have been grown, that is then treated to obtain the desired dryness, and which may include one or more components from the media, and/or other components, that do not materially affect the basic and novel characteristics the composition.

3. Particulate compositions.

[0049] _In certain embodiments, provided herein are compositions comprising particles, such as particles comprising one of the microbial compositions provided herein. As used herein a "particle," or "particles" include discrete objects larger than atoms or molecules; a particle can be large enough to be seen with the naked eye, or microscopic. "Particle size" includes size as determined by methods used in the art, in particular, sieving.

[0050] In certain embodiments, provided herein are compositions comprising a plurality of particles wherein each particle comprises a composition comprising one or more microbes. The particles of the composition may be any suitable size; in some cases particles are all within a certain size range, in other cases particles may be present in two or more populations, each of which is within a different size range. In certain embodiments the particles have a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um. In certain embodiments, at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, or 99% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, 99, 99.5, or 100%, or 100%, for example 10-100%, preferably 20-100%, more preferably 50-100%, even more preferably 80-100%, still more preferably 90-100% of the particles have a mean particle

size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[0051] In certain embodiments, such as embodiments where the composition comprises at least 60, 70, 80, 90, 92, 95, 97, 98, 99, or 99.5%, or 100%, microbes (wt%), particles may have a mean or median particle size of at least 0.1, 0.2, 0.5, 0.7, 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, or 20 um and/or not more 0.2, 0.5, 0.7, 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 30, or 40 um, preferably 0.2-40 um, more preferably 0.5-20 um, even more preferably 1-20 um, still more preferably 1-15 um, yet more preferably 2-15 um, even still more preferably 2-12 um.

[0052] In certain embodiments, larger particles may be used, e.g., in compositions for aerial application and/or some delayed release compositions larger particles may be used, for example, with a mean size, or a median size, of at least 100, 150, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 3000, 4000, 5000, or 7000 um and/or no more than 150, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 3000, 4000, 5000, 7000, or 10,000 um, or even larger, such as 200-10,000, preferably 500-5000, more preferably 1000-10,000 um. Such larger particulate compositions can be useful, for example to allow for release of microbes in two or more batches as the particles are subject to conditions that allow release of microbes from the surface of the particles but others are retained in the particle until the conditions occur again (e.g., rainfall, irrigation, or the like, see below). It will be understood that for any composition in which a plurality of populations of particles is used, with different particle sizes, any suitable sizes may be used for the composition.

[0053] Certain particulate compositions are dry compositions. Certain particulate compositions consist essentially of a microbial composition. Certain particulate compositions comprise a microbial composition that includes one or more agricultural adjuvants.

4. Delayed release compositions

[0054] In certain embodiments, delayed release compositions are provided. A "delayed release" composition, as that term is used herein, includes a composition that does not release at least a portion of its active ingredients, e.g., microbes, on first exposure to the environment, or to an environmental trigger in the environment in which it will be used; in certain embodiments, a delayed release composition can release a portion of its active ingredients, e.g., microbes, on first exposure, so long as an additional portion is not released, while in other embodiments none of the active ingredients, e.g., microbes, is released on first exposure. Any suitable materials and

configuration may be used, so long as not all of the microbes are released on first exposure to the environment of use or environmental trigger. Materials useful in providing delayed release compositions are well-known in the art; while many of these are useful in pharmaceutical preparations, suitable modifications, if necessary, will be readily apparent. In general materials and/or configurations of such compositions are such that microbes are confined to the composition during normal conditions of manufacture and transport, but that release at least a portion of the microbes on exposure to one or more environmental triggers, that is, one or more conditions found in the environment of use. Any suitable trigger may be used, such as water, electromagnetic radiation (e.g., sunlight, or certain wavelengths of sunlight), temperature, or even air (e.g., if particles are relatively unexposed to air during transport and storage, for example in an airtight bag, then start to degrade on exposure to air, e.g., when placed in their environment of use), or a combination thereof. In certain embodiments, an environmental trigger is water, which can come from, e.g., rainfall, irrigation, or the like. In general, "exposure to" the environmental trigger or trigger includes sufficient exposure of the composition that the process that occurs to release microbes can occur.

[0055] In certain embodiments, provided is a delayed release composition comprising a plurality of particles, each of which comprises a composition comprising microbes, wherein the plurality of particles comprises a first population of particles wherein each particle of the first population comprises one or more first components configured to confine at least a portion of the microbes to the particles, and wherein the one or more first components are such that the one or more first components lose sufficient integrity upon exposure to one or more environmental triggers that at least a portion of the confined microbes are released from the particles. In certain embodiments, the composition comprises a microbial composition as provided herein. In certain embodiments the first components are configured to confine at least 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99% of the microbes, for example at least 60%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%. Any suitable configuration of the first components may be used. In certain embodiments the first components form a shell wherein the microbes are confined within, and/or embedded in, and/or associated with a surface of, the shell. In certain embodiments the one or more first components form a matrix in which the microbes are embedded or otherwise associated. In certain embodiments the one or more first components form a plurality of lamellae, wherein the particles are confined between, and/or embedded in, and/or associate with a surface of, the lamellae. It will be appreciated that any or all of these may be combined in particles. In certain embodiments the environmental trigger comprises water, air, temperature, electromagnetic radiation, or a combination thereof. In certain embodiments the environmental trigger is water, for example, water from rainfall, irrigation, or

even humidity of the air. In certain embodiments, exposure to the trigger is sufficient to release all the microbes; in other embodiments, repeated exposures and/or duration of exposure is required. Thus, for example, a composition may be formulated so that it remains intact until a first rainfall, when most or all of the particles in the composition are exposed to water. Components and configuration can be such that all microbe are released at the first rainfall; alternatively, components and configuration can be such that repeated rainfalls, or rainfall of sufficient duration to keep exposing the compositions to water for a prolonged period, is required to release all the microbes. In certain embodiments one or more first components and/or structure of the particles are such that exposure to the trigger causes sufficient loss of integrity that at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, or 99% and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, 99, or 100% of the microbes are released. In certain embodiments 30-100% of the microbes are released. In certain embodiments 50-100% of the microbes are released. In certain embodiments n 80-100% of the microbes are released. In certain embodiments 90-100% of the microbes are released. In certain embodiments 5-80% of the microbes are released. In certain embodiments 5-60% of the microbes are released. In certain embodiments 5-40% of the microbes are released. In certain embodiments 10-40% of the microbes are released. In certain embodiments 5-30% of the microbes are released. In certain embodiments 10-30% of the microbes are released. In certain embodiments 5-25% of the microbes are released. In certain embodiments 10-25% of the microbes are released. In certain embodiments a composition further comprises a second population of particles wherein each particle of the second population comprises one or more second components configured to confine at least a portion of the microbes to the particles, and wherein the one or more second components are such that the one or more second components withstand exposure to the one or more environmental triggers that cause the first components of the first population to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the second population. In certain embodiments an additional 5-80% of the microbes are released. In certain embodiments an additional 5-60% of the microbes are released. In certain embodiments an additional 5-40% of the microbes are released. In certain embodiments an additional 10-40% of the microbes are released. In certain embodiments an additional 5-30% of the microbes are released. In certain embodiments an additional 10-30% of the microbes are released. In certain embodiments an additional 5-25% of the microbes are released. In certain embodiments an additional 10-25% of the microbes are released. In certain embodiments a composition comprises a third population of particles wherein each particle of the third population comprises one or more third components configured to confine at least a portion

of the microbes to the particles, and wherein the one or more third components are such that the one or more third components withstand exposure to the one or more environmental triggers that cause the first and second components of the first population and second populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the third population. In certain embodiments an additional 5-80% of the microbes are released. In certain embodiments an additional 5-60% of the microbes are released. In certain embodiments an additional 5-40% of the microbes are released. In certain embodiments an additional 10-40% of the microbes are released. In certain embodiments an additional 5-30% of the microbes are released. In certain embodiments an additional 10-30% of the microbes are released. In certain embodiments an additional 5-25% of the microbes are released. In certain embodiments an additional 10-25% of the microbes are released. In certain embodiments a composition further comprises a fourth population of particles wherein each particle of the fourth population comprises one or more fourth components configured to confine at least a portion of the microbes to the particles, and wherein the one or more fourth components are such that the one or more fourth components withstand exposure to the one or more environmental triggers that cause the first, second and third components of the first population, second and third populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the fourth population. In certain embodiments an additional 5-80% of the microbes are released. In certain embodiments an additional 5-60% of the microbes are released. In certain embodiments an additional 5-40% of the microbes are released. In certain embodiments an additional 10-40% of the microbes are released. In certain embodiments an additional 5-30% of the microbes are released. In certain embodiments an additional 10-30% of the microbes are released. In certain embodiments an additional 5-25% of the microbes are released. In certain embodiments an additional 10-25% of the microbes are released.

5. Compositions comprising one or more agriculturally acceptable adjuvants.

[0056] Provided herein are compositions comprising microbes, such as a composition as described above, and one or more agriculturally acceptable adjuvants. An "agriculturally acceptable adjuvant," as that term is used herein, includes a natural or synthetic, organic or inorganic material with which the active compounds (e.g. the one or more microbes as disclosed herein) are combined, e.g., to facilitate their manufacture, storage, use, or the like, where the substance can be used under the desired conditions, e.g., conditions in which plants grow or are maintained, or are to be grown or maintained. Thus, in certain embodiments provided herein is a

composition comprising any one of the compositions comprising one or more microbes as described above and further comprising one or more agriculturally acceptable adjuvants. It will be appreciated that in certain cases, such as delayed release compositions comprising one or more components to confine microbes and to release them on exposure to one or more environmental triggers, certain of the components may already be considered as agriculturally acceptable adjuvants; in such cases, one or more additional components, also considered agriculturally acceptable adjuvants, may be used.

[0057] Any suitable adjuvant may be used. In certain embodiments at least one of the agriculturally acceptable adjuvants is heterologous to the one or more microbes of the composition. In certain embodiments the one or more agriculturally acceptable adjuvants comprise one or more liquid carriers, solid carriers, surfactants, viscosity modifiers, thickeners, rheology additives, structuring agents, preservatives, biocides or biostatic agents, antifreezes, crystallization inhibitors, suspending agents, dyes, anti-oxidants, foaming agents, light absorbers, light blockers, mixing auxiliaries, antifoams, complexing agents, neutralizing or pH-modifying substances and buffers, corrosion inhibitors, fragrances, wetting agents, take-up enhancers, micronutrients, plasticizers, glidants, lubricants, and dispersants.an emulsifier, a carrier, a stabilizer, or a combination thereof. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise one or more surfactants. Any suitable surfactant may be used. Generally, it is desired that a surfactant facilitates dissolution of a component or formation of an emulsion with a component, and a suitable surfactant will do so, while not affecting viability of the one or more microbes, or not affect viability to a sufficient degree to interfere with the intended use of the composition. Surfactants belong to different classes such as cationic surfactants, anionic surfactants, non-ionic surfactants, ionic surfactants, and amphoteric surfactants. A surfactant can be any surfactant or a combination of two or more surfactants useful to disperse the microbes and/or other components in the composition or tank mix for application. Any suitable concentration of surfactant can be used, such as at least 0.1, 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, or 15% and/or not more than 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, or 20% w/w, for example 0.5 to 20%, preferably 1 to 10%, more preferably 2 to 8%, even more preferably 3 to 8%, yet more preferably 5 to 7%. Non-ionic surfactants suitable for this invention include ethoxylated linear alcohols, ethoxylated alkyl phenol, alkyl EO/PO copolymer, polyalkylene glycol monobutyl ether ethoxylated fatty acids/oils, sorbitan laurate, polysorbate, sorbitan oleate, ethoxylated fatty acid alcohols, or alkyl phenols, alkanolamides or alkyloamides (such as diethanolamide, lauric acid monoisopropanolamide, and ethoxylated myristamide), xyethylene fatty acid esters, polyoxyethylene fatty alcohol ethers (such as alkylaryl polyglycol ethers), alkylphenol/alkylene oxide addition products, such as nonylphenol ethoxylate; alcohol/alkylene

oxide addition products, such as tridecylalcohol ethoxylate. Anionic surfactants include alkyl-, alkylaryl- and arylsulfonates or salts thereof (such as sodium, potassium or calcium salts of lauryl sarcosinate, alkylbenzenesulfonate, dodecylbenzenesulfonate, alkylnaphthalenesulfonates such as dibutylnaphthalenesulfonate, or C.sub.14-16 olefin sulfonates), alkyl-, alkylaryl- and arylsulfates or salts thereof (such as sodium, potassium or calcium salts of tridedeth sulfate, lauryl sulfate, decyl sulfate, and diethanolammonium lauryl sulfate) protein hydrolysates, derivatives of polycarboxylic acid (such as ammonium lauryl ether carboxylate), olefin sulfonates (such as sodium alpha olefin sulfonate), sarcosinates (such as ammonium cyclohexyl palmitoyl taurinate), succinates (such as disodium N-octadecyl sulfosuccinamate), phosphorus derivatives (such as phosphoric acid esters and their equivalent salts). Cationic surfactants include alkylbenzyltrimethylammonium chloride, ammonium lauryl sulfate and lauramine oxide. Further examples of surfactants include nitrogen-surfactant blends such as Prefer 28 (Cenex), Surf-N (US), Inhance (Brandt), P-28 (Wilfarm) and Patrol (Helena); esterified seed oils including Sun-It II (AmCy), MSO (UAP), Scoil (Agsco), Hasten (Wilfarm) and Mes-100 (Drexel); and organo-silicone surfactants include Silwet L77 (UAP), Silikin (Terra), Dyne-Amic (Helena), Kinetic (Helena), Sylgard 309 (Wilbur-Ellis) and Century (Precision), polysorbate 20, polysorbate 80, Tween 20, Tween 80, Scattics, Alktest TW20, Canarcel, Peogabsorb 80, Triton X-100, Conco NI, Dowfax 9N, Igebapl CO, Makon, Neutronyx 600, Nonipol NO, Plytergent B, Renex 600, Solar NO, Sterox, Serfonic N, T-DET-N, Tergitol NP, Triton N, IGEPAL CA-630, Nonident P-40, Pluronic.

[0058] In certain embodiments the one or more surfactants comprise a non-ionic, cationic, or anionic surfactant, or a combination thereof. In certain embodiments the one or more surfactants comprise Tween 20 or Tween 80. In certain embodiments the one or more surfactants comprise soy lecithin or yucca powder or a derivative thereof, or a combination thereof. In certain embodiments the one or more surfactants are organic. In certain embodiments the one or more surfactants are at a total concentration of at least 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, or 9 wt% and/or no more than 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, 9, or 10 wt%, for example 0.5-10 wt%, preferably 1-3 wt%, more preferably 1.8-2.2 wt%.

[0059] In certain embodiments, a composition comprising one or more agriculturally acceptable adjuvants is a solid composition. In certain embodiments, a composition comprising one or more agriculturally acceptable adjuvants is a liquid composition

[0060] In certain embodiments, a composition the one or more adjuvants comprise one or more carriers. As used herein, the term "carrier" includes a substance with which the one or more microbes associate in such a way that the one or more microbes are carried with the substance;

the association may be merely physical, e.g., a physical combination of microbes with carrier; alternatively or additionally, the association may be chemical, e.g., noncovalent, such as adsorption, or covalent. In certain embodiments in which the composition is a solid composition, one or more solid carriers may be used. Any suitable solid carrier may be used. Exemplary solid carriers include, carbohydrates including mono or disaccharides, such as glucose, mannose, lactose, sucrose; oligo or poly-saccharides such as maltodextrin or pectin, or oligo- or polysaccharides derived from one or more plant substances; talc, titanium dioxide, pyrophyllite clay, attapulgite clay, kieselguhr, silica (silicon dioxide), limestone, bentonite, calcium montmorillonite water soluble salts such as sodium, potassium, magnesium, calcium or ammonium salts of acetate, carbonate, chloride, citrate, phosphate, or sulfate such as calcium carbonate; plant parts such as cottonseed husks, wheat flour, soybean flour, wood flour, ground walnut shells, lignin and similar substances, yeast extracts, fish meal, pumice, or mixtures thereof. In certain embodiments, the carrier comprises an alcohol and/or a saccharide, e.g., inulin, glycerol and/or a monosaccharide, disaccharide, trisaccharide, or polysaccharide. In certain embodiments, the carrier comprises glucose, sucrose, lactose, maltose, and/or galactose. In certain embodiments, the carrier comprises glucose. In certain embodiments, the carrier is at a concentration in the composition of at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 wt% and/or no more than 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 wt%, for example 50-100 wt%, preferably 70-100 wt%, more preferably 80-100 wt%, even more preferably 90-100 wt%, still more preferably 95-100 wt%.

[0061] In certain embodiments, a composition comprises a monosaccharide, e.g., glucose, an emulsifier (surfactant), e.g., soy lecithin, and microbes. In certain embodiments, the monosaccharide is present at at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5% and or not more than 85, 90, 95, 96, 97, 98, 99, 99.5, or 99.9%, such as 90-99%, preferably 85-99%, more preferably 90-99%, even more preferably 90-98%, yet more preferably 90-96%, still more preferably 90-94%; In certain embodiments, the emulsifier is present at at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 1, 1.2, 1.5, 2, 3, 4, or 5% and/or not more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 1, 1.2, 1.5, 2, 3, 4, 5, or 7%, such as 0.1-5%, preferably 0.1-4%, more preferably 0.1-3%, still more preferably 0.5-3%. In certain embodiments, the microbes are present at at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 1, 1.2, 1.5, 2, 3, 5, 6, 7, 8, 9, or 10% and/or not more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 1, 1.2, 1.5, 2 3, 5, 6, 7, 8, 9, 10, 12, or 15%, such as 0.1-15%, preferably 0.5-12%, more preferably 0.5-10%, still more preferably 1-12%, yet more preferably 1-10%, still yet more preferably 2-10%, even yet more preferably 4-8%.

[0062] In certain embodiments the one or more agriculturally acceptable adjuvants comprise one or more materials that protect the microbes from one or more aspects of an environment in

which the microbes will be stored and/or used. In certain embodiments the one or more agriculturally acceptable adjuvants comprise a light absorber or light blocker, or a combination thereof. In certain embodiments the light absorber or light blocker protects the microbes of the composition from ultraviolet (UV) light. In certain of these embodiments, the microbes are enclosed in the material, e.g., the material forms an opaque or translucent shell. Alternatively or additionally, the material can be a UV absorber, either in a shell or as a matrix or similar in which the microbes are situated. In certain embodiments the one or more materials are such that they release some or all of the microbes upon exposure to one or more environmental triggers, such as one or more environmental triggers described herein. In certain embodiments the one or more environmental triggers comprises water.

[0063] In certain embodiments, a composition comprising one or more agriculturally acceptable adjuvants is stable at temperatures between 4 °C. and 37 °C for at least 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3 or 4 weeks, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months, or 1, 2, 3, 4, or 5 years, for example, stable at between 4 °C. and 37 °C for at least one week, preferably at least one month, more preferably at least 6 months, even more preferably at least 12 months, yet more preferably at least 2 years. "Stable," as that term is used herein in relation to a composition, includes that the composition retains sufficient viability to be used for its intended purpose.

[0064] In certain embodiments, a composition includes an antifreeze agent for cold storage, e.g., at temperature less than -5, -10, -15, -20, -25, -30, -40, -50, -60, -70, -80 °C, for example less than -5, preferably less than -10, more preferably less than -15, even more preferably less than -20 °C. Such an agent can be considered an "agriculturally acceptable adjuvant," as that term is used herein, in that it maintains the one or more microbes in a form where they are viable for their intended use, though generally after steps to grow the microbes and further treat them. In certain embodiments the antifreeze agent comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride and ammonium sulfate. In certain embodiments the antifreeze agent comprises glycerol. In certain embodiments the glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50%, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22% wt%. In certain of these embodiments the composition comprises microbes of only one strain.

[0065] Certain embodiments provide a plurality of particles comprising a composition comprising one or more agriculturally acceptable adjuvants, as described herein, and a composition comprising microbes, such as one of the microbial compositions herein.

[0066]

6. Compositions comprising additional microbes.

[0067] In certain embodiments provided are methods and compositions utilizing any one of the compositions described above, and further including additional microbes. In certain embodiments provided is a composition comprising one or more microbes as described above and further comprising cells of one or more additional microbial species or strains different from those of one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or one or more microbes of Designations O-46 to O-140. In certain embodiments the additional microbial species comprise fungi, bacteria, or a combination thereof. In certain embodiments the additional microbial species comprise fungi. In certain embodiments the fungi comprise mycorrhizal fungi.

7. Seeds, seedlings, or other plant propagules and one or more microbes

[0068] In certain embodiments, provided are seeds, seedlings, or other plant propagules comprising microbes, for example of one of the microbial compositions described herein, including but not limited to in sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6. A "plant propagule," as that term is used herein, includes any plant material used for the purpose of plant propagation, including but not limited to seeds, seedlings, and stem cuttings. In certain embodiments provided is a population of seeds, seedlings, or other plant propagules comprising a composition comprising a plurality of microbes, such as described above, including but not limited to in sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6, wherein at least a portion of the microbes of the composition are associated with the seeds, seedlings, or other plant propagules. It will be appreciated that in certain cases, e.g., where a large number of different microbes are used, individual seeds, seedlings, or plant propagules may not necessarily comprise every one of the different microbes; this is acceptable so long as the overall population comprises a sufficient number of the different microbes, preferably all of them, for the microbes to operate for the desired purpose. Thus, in certain embodiments at least 50, 60, 70, 80, 85, 90, 95, 97, or 99%, or 100%, of the seeds, seedlings, or other plant propagules of the population, for example at least 50%, preferably at least 60%, more preferably at least 80%, yet more preferably at least 85%, and even yet more preferably at least 90%, each has at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or one or more microbes of Designations O-46 to O-140 associated with it, for example at least 10, preferably at least 20, more preferably at least 30, even more preferably at least 40, yet more preferably at least 50%. In certain

embodiments the microbes are present on each seed, seedling, or other plant propagule in an average total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, or 50,000 and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, or 1M CFU per seed, seedling, or other plant propagule, for example, 10-1M, preferably 100-500,000, more preferably 500-500,000, even more preferably 1000-500,000, yet more preferably 5000-500,000, yet more preferably 5000-1M. In certain embodiments the population of seeds, seedlings, or other plant propagules comprises one or more microbes of Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or one or more microbes of Designations O-46 to O-140. In certain embodiments the microbes of the composition are disposed on surfaces, in pores, or a combination thereof, of the seeds, seedlings, or other plant propagules. In certain embodiments a composition comprises at least 100, 500, 1000, 5000, 10,000, 50,000, 100,000, or 1M seeds, seedlings, other plant propagules, for example at least 1000, preferably at least 10,000, more preferably at least 100,000. In certain embodiments the composition is configured to be suitable for aerial deposition, e.g., aerial deposition of seeds, seedlings, or other plant propagules comprising microbes as described herein, so that a desired proportion of the deposited seeds, seedlings, or other plant propagules are situated so that they can germinate and grow under suitable conditions. In certain embodiments a composition comprises seeds, wherein the seeds are contained in a bag or container suitable for commercial sale. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the seed, seedling, or other plant propagule. In certain embodiments the seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of a particular plant or class of plants. Any suitable plant or class of plants may be used, such as any one of the plants or classes of plants of section I.B.10, below. In certain embodiments, the seeds, seedlings, or other plant propagules comprise those of grass or trees. In certain embodiments the seeds, seedlings, or other plant propagules comprise grass seeds. A "grass," as that term is used herein, includes monocotyledonous plants used for lawns, turf, or animal feed, such as pasture, fodder and rangeland grasses, and also includes monocotyledonous plants found in grasslands and in wetlands, forests, and tundra. "Grass," as that term is used herein, does not include domesticated cereal crops. "Turf," as that term is used herein, includes grass used for planted surfaces, such as playing surfaces, for example in fields, courses, e.g., golf courses, and pitches, for sports or other recreation. A "grassland," includes a grass-dominated biome, such as a temperate or a tropical grassland, including but not limited to savannas, pampas, steppes, and

prairies. In certain embodiments the grass seeds comprise turf seeds. In certain embodiments the seeds, seedlings, or other plant propagules of trees. In certain embodiments the composition comprises tree seeds. In certain embodiments the composition comprises tree seedlings. In certain embodiments the composition comprises seeds, seedlings, or other plant propagules of a commercial crop. A "commercial crop," as that term is used herein, includes a plant where the plant or one or more parts of the plant are directly or indirectly sold in a market or otherwise used in a commercial endeavor, e.g., grains (cereals), vegetables, and the like, described in more detail below. In certain cases, the commercial crop is for animal consumption, e.g., by domesticated animals, or by humans. As used herein, the term "domesticated animal" includes commercially reared avian and mammalian animals, including but not limited to poultry such as chickens, game birds, geese, turkeys and ducks, goats, sheep, alpacas, cattle, bison, horses, and pigs. In certain embodiments the commercial crop comprises a cereal crop. In certain embodiments the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments the commercial crop comprises a berry. In certain embodiments the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments the commercial crop comprises an oilseed plant. In certain embodiments the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments the commercial crop comprises a tree nut. In certain embodiments the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments the commercial crop comprises a brassica vegetable. In certain embodiments the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments the commercial crop comprises a cucurbit vegetable. In certain embodiments the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments the commercial crop comprises a bulb vegetable. In certain embodiments the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments the commercial crop comprises citrus. In certain embodiments the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments the commercial crop comprises a fruiting vegetable. In certain embodiments the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments the commercial crop comprises legume or vegetable such as beans. In certain embodiments the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments the commercial crop comprises a pome fruit. In

certain embodiments the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments the commercial crop comprises a root, tuber or corm vegetable. In certain embodiments the root, tuber or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments the commercial crop comprises a stone fruit. In certain embodiments the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments the commercial crop comprises a grass. In certain embodiments the grass comprises grass for livestock feed. In certain embodiments the grass comprises turf grass. In certain embodiments the commercial crop comprises a tree. In certain embodiments the tree comprises an evergreen tree. In certain embodiments the tree comprises a deciduous tree. In certain embodiments the commercial crop comprises an herb or spice. In certain embodiments the commercial crop comprises cannabis. In certain embodiments the commercial crop comprises an ornamental plant. In certain embodiments the ornamental plant comprises a flowering plant, a bush or a shrub. In certain embodiments the commercial crop comprises an energy or raw material plant. In certain embodiments the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax. In certain cases the energy or raw material plant is for use in producing a biofuel.

8. Plants or plant parts and one or more microbes (optionally with soil).

[0069] In certain embodiments, provided are compositions that comprise a plant or plant part and one or more microbes of the microbial compositions described herein, including but not limited to, in sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6. The plant part may be, e.g., roots of the plant. The microbes can be disposed on or in the roots, e.g., as rhizobacteria.

[0070] In certain embodiments provided is a plant or plant part comprising one or more of the microbes of the composition of any one the microbial compositions disclosed herein, including but not limited to of sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6, disposed on or in the plant or plant part. In certain embodiments the one or more microbes are disposed on or in a plant part comprising a root of the plant. In certain embodiments at least 1, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the plant or plant part. In certain embodiments the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000,

100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, e.g., 10-10^{16}, preferably 100-10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}. In certain embodiments the composition further comprises mycorrhizal fungi. The plant may be any suitable plant, such as a plant described in Section B.10. In certain embodiments the plant is a grass. In certain embodiments the grass is a grassland grass. In certain embodiments the grass is a turf grass. In certain embodiments the plant is a tree. In certain embodiments the tree is a deciduous tree. In certain embodiments the tree is an evergreen tree. In certain embodiments the tree is a forest tree. In certain embodiments the plant is a commercial crop. In certain embodiments the commercial crop comprises a cereal crop. In certain embodiments the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments the commercial crop comprises a berry. In certain embodiments the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments the commercial crop comprises an oilseed plant. In certain embodiments the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments the commercial crop comprises a tree nut. In certain embodiments the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments the commercial crop comprises a brassica vegetable. In certain embodiments the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments the commercial crop comprises a cucurbit vegetable. In certain embodiments the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments the commercial crop comprises a bulb vegetable. In certain embodiments the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments the commercial crop comprises citrus. In certain embodiments the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments the commercial crop comprises a fruiting vegetable. In certain embodiments the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments the commercial crop comprises legume or vegetable such as beans. In certain embodiments the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments the commercial crop comprises a pome fruit. In certain embodiments the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments the commercial crop comprises a root, tuber or corm vegetable. In certain

embodiments the root, tuber or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments the commercial crop comprises a stone fruit. In certain embodiments the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments the commercial crop comprises a grass. In certain embodiments the grass comprises grass for livestock feed. In certain embodiments the grass comprises turf grass. In certain embodiments the commercial crop comprises a tree. In certain embodiments the commercial crop comprises an evergreen tree. In certain embodiments the commercial crop comprises a deciduous tree. In certain embodiments the commercial crop comprises an herb or spice. In certain embodiments the commercial crop comprises cannabis. In certain embodiments the commercial crop comprises an ornamental plant. In certain embodiments the ornamental plant comprises a flowering plant, a bush or a shrub. In certain embodiments the commercial crop comprises an energy or raw material plant. In certain embodiments the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax. In certain cases the energy or raw material plant is for use in producing a biofuel. In any of the above embodiments, the composition may comprise roots of the plant and further comprise soil in which the plant is growing or has grown. In certain embodiments the soil is within 0.1 cm of roots of the plant. In certain embodiments the soil is within 0.5 cm of roots of the plant. In certain embodiments the soil is within 1 cm of roots of the plant. In certain embodiments the soil is within 2 cm of roots of the plant. In certain embodiments the soil is within 3 cm of roots of the plant. In certain embodiments the soil is within 5 cm of roots of the plant. In certain embodiments the soil is within 7 cm of roots of the plant. In certain embodiments the soil is within 10 cm of roots of the plant. In certain embodiments the soil is within 15 cm of roots of the plant. In certain embodiments the soil is within 20 cm of roots of the plant. In certain embodiments the soil is within 50 cm of roots of the plant. In certain embodiments the soil is within 100 cm of roots of the plant. In certain embodiments the microbes of the composition comprise at least 0.01, 0.05, 0.1, 0.5, 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 0.01%, at least 0.05% at least 01%, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%. In certain embodiments the composition further comprises mycorrhizal fungi. In certain embodiments the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%. In certain embodiments

beneficial microbes other than the microbes of the composition comprising microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight. In certain embodiments the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil. In certain embodiments the soil has an average water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%. As used herein, "water holding capacity" or "WHC" of soil includes weight percent of a soil or soil sample that is water when the soil or soil sample is saturated with water. Water holding capacity can be determined by any suitable method, e.g., exposing soil or a soil sample to sufficient water to saturate the soil, weighing the soil, then drying the sample. Initial weight – dry weight/initial weight x 100 = % WHC. Other methods may be used in certain instances, such as a neutron probe or moisture meter. In certain embodiments the soil has an average carbon content of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20% and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, or 40% (w/w), for example, 5-30%, preferably 7-30%, more preferably 10-30%, yet more preferably 10-25%. in certain embodiments the soil has a soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil. In certain embodiments the soil does not comprise a significant amount or concentration of synthetic fertilizer, or a detectable amount. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of synthetic fertilizer. In certain embodiments the soil does not comprise a significant amount or concentration of herbicide, e.g., synthetic herbicide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of herbicide, e.g.,

synthetic herbicide. In certain embodiments the soil does not comprise a significant amount or concentration of pesticide, e.g., synthetic pesticide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of pesticide, e.g., synthetic pesticide. In certain embodiments the soil does not comprise a significant amount or concentration of insecticide, e.g., synthetic insecticide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of insecticide, e.g., synthetic insecticide. In certain embodiments the soil does not comprise a significant amount or concentration of fungicide, e.g., synthetic fungicide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of fungicide, e.g., synthetic fungicide. In certain embodiments the soil does not comprise a significant amount or concentration of bactericide, e.g., synthetic bactericide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of bactericide, e.g., synthetic bactericide. In certain embodiments the soil does not comprise a significant amount or concentration of nematicide, e.g., synthetic nematicide. The amount can be, e.g., less than that allowed by organic farming criteria for the area; such criteria are well-known. In certain embodiments the soil does not comprise a detectable amount or concentration of nematicide, e.g., synthetic nematicide.

[0071] In certain embodiments provided herein is a composition comprising a plant, e.g. wherein the plant or part of the plant is for animal consumption, and soil in which the plant is growing, wherein (i) the soil and/or roots of the plant in the soil comprise one or more microbes heterologous to the soil and/or plant; and (ii) the plant or plant part comprises a density of one or more nutrients, e.g., one or more nutrients for the animal, that is greater than reference plant or plant part. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100 that are heterologous to the plant and/or soil. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably

at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*. In certain embodiments the composition comprises one or more different microbes of a microbial composition disclosed herein, including but not limited to in e.g., in sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6. In certain embodiments the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 one or more different microbesfor example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95. In certain embodiments nutrient density of the one or more animal nutrients is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%. In certain embodiments the one or more nutrients is increased in density by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%. In certain embodiments the animals comprise humans or domesticated animals. In certain embodiments the animals comprise humans. In certain embodiments the animals comprise domesticated animals. In certain embodiments the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses. In certain embodiments the animals are cattle. In certain embodiments the increased nutrient density comprises increased protein density, increased mineral density, increased vitamin density, or a combination thereof. In certain embodiments the increased nutrient density comprises increased protein density. In certain embodiments the increased nutrient density comprises increased

vitamin density. In certain embodiments the increased vitamin density comprises increased vitamin A density. In certain embodiments the increased vitamin density comprises increased vitamin B_1 (thiamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B_2 (riboflavin) density. In certain embodiments the increased vitamin density comprises increased vitamin B_3 (niacin, nicotinic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_5 (pantothenic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_6 (pyridoxal, pyridoxine, or pyidoxamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B_7 (biotin) density. In certain embodiments the increased vitamin density comprises increased vitamin B_9 (folic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_{12} density. In certain embodiments the increased vitamin density comprises increased vitamin C density. In certain embodiments the increased vitamin density comprises increased choline density. In certain embodiments the increased vitamin density comprises increased vitamin D density. In certain embodiments the increased vitamin density comprises increased vitamin E density. In certain embodiments the increased vitamin density comprises increased vitamin K1 density. In certain embodiments the increased vitamin density comprises increased vitamin K2 density. In certain embodiments the increased nutrient density comprises increased mineral density. In certain embodiments the increased mineral density comprises increased calcium density. In certain embodiments the increased mineral density comprises increased magnesium density. In certain embodiments the increased mineral density comprises increased sodium density. In certain embodiments the increased mineral density comprises increased potassium density. In certain embodiments the increased mineral density comprises increased iron density. In certain embodiments the increased mineral density comprises increased copper density. In certain embodiments the increased mineral density comprises increased manganese density. In certain embodiments the increased mineral density comprises increased zinc density. In certain embodiments the increased mineral density comprises increased iodine density. In certain embodiments the increased mineral density comprises increased chromium density. In certain embodiments the increased mineral density comprises increased molybdenum density. In certain embodiments the increased mineral density comprises increased phosphorus density. In certain embodiments the increased mineral density comprises increased molybdenum density. In certain embodiments the increased mineral density comprises increased selenium density. The plant may be any suitable plant, such as a plant as disclosed herein, e.g., Section 1.B.10.

9. Populations of plants and microbes (optionally with soil)

[0072] In certain embodiments, provided are compositions comprising populations of plants comprising microbes of a microbial composition as described herein, including but not limited to those of sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6, in certain cases also including soil the plants grow or have grown in. Thus, in certain embodiments provided is a population of plants wherein the plants or part of the plants comprises the microbe or microbes of the composition of sections I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6, disposed on or in the plant or plant part. In certain embodiments the population at least 100, 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 3M, 5M, 10M, 50M, 100M, 500M, 1B, 2B, 5B, 10B, 50B, 100B, 1T, 10T, 100T plants and/or not more than 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 3M, 5M, 10M, 50M, 100M, 500M, 1B, 2B, 5B, 10B, 50B, 100B, 1T, 10T, 100T, or 500T plants, for example 100 to 500T, preferably 1000 to 500T, more preferably 100,000 to 500T, even more preferably 1M to 500T, yet more preferably 1B to 500T, still more preferably 10B to 500T; in some cases more than 1M, for example more than 10M, preferably more than 100M, more preferably more than 1B, even more preferably more than 10B, yet more preferably more than 100B, still more preferably more than 1T or even more than 10T, or more than 100T, or even more than 500T. Larger populations can be found in, e.g., large agricultural lands, or pasture lands, grasslands, forests, and the like. In certain embodiments, described elsewhere herein, compositions as described herein can be deposited in very large areas, such as areas of grasslands, forests, or the like, e.g., wild or undomesticated grasslands, forests, or the like; such areas may exceed hundreds, thousands, or tens of thousands of square miles; it will be appreciated that, especially in the case of grasslands, such areas can contain billions or even trillions of individual plants. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition are heterologous to the plant or plant part. In certain embodiments the one or more microbes are disposed on or in a plant part comprising a root of the plant. In certain embodiments the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, e.g., 10-10^{16}, preferably 100- 10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}. In certain embodiments the composition further comprises mycorrhizal fungi. In certain embodiments the plants are grass. In certain

embodiments the grass is a grassland grass. In certain embodiments the grass is a turf grass. In certain embodiments the plants are trees. In certain embodiments the trees are deciduous trees. In certain embodiments the trees are evergreen trees. In certain embodiments the trees are forest trees. In certain embodiments the plants are a commercial crop. In certain embodiments the commercial crop comprises a cereal crop. In certain embodiments the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments the commercial crop comprises a berry. In certain embodiments the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments the commercial crop comprises an oilseed plant. In certain embodiments the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments the commercial crop comprises a tree nut. In certain embodiments the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments the commercial crop comprises a brassica vegetable. In certain embodiments the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments the commercial crop comprises a cucurbit vegetable. In certain embodiments the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments the commercial crop comprises a bulb vegetable. In certain embodiments the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments the commercial crop comprises citrus. In certain embodiments the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments the commercial crop comprises a fruiting vegetable. In certain embodiments the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments the commercial crop comprises legume or vegetable such as beans. In certain embodiments the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments the commercial crop comprises a pome fruit. In certain embodiments the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments the commercial crop comprises a root, tuber or corm vegetable. In certain embodiments the root, tuber or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments the commercial crop comprises a stone fruit. In certain embodiments the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments the commercial crop comprises a grass. In certain embodiments the grass comprises grass for livestock feed. In certain embodiments the grass comprises turf grass. In certain embodiments the

commercial crop comprises a tree. In certain embodiments the commercial crop comprises an evergreen tree. In certain embodiments the commercial crop comprises a deciduous tree. In certain embodiments the commercial crop comprises an herb or spice. In certain embodiments the commercial crop comprises cannabis. In certain embodiments the commercial crop comprises an ornamental plant. In certain embodiments the ornamental plant comprises a flowering plant, a bush or a shrub. In certain embodiments the commercial crop comprises an energy or raw material plant. In certain embodiments the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax. In certain cases the energy or raw material plant is for use in producing a biofuel. In certain embodiments, the population of plants is distributed over an area of at least 0.1, 0.5, 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, or 100,000 square miles and/or not more than 0.5, 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000 50,000, 100,000, 500,000, 1M, 2M, 10M, or 50M square miles, for example, 0.1 to 50M square miles, preferably 0.1 to 10M square miles, more preferably 1 to 10M square miles, yet more preferably 10 to 10M square miles, still more preferably 100 to 10M square miles, yet still more preferably 1000 to 1M square miles. As described above, this can be, e.g., grassland, forest, or the like that have had compositions of microbes as described herein applied. In certain embodiments, a composition further includes soil in which the plants grow or have grown. Unless indicated otherwise, the soil can be considered to be the soil extending to the depth, or average depth, of roots of the plants. In certain embodiments the soil is within 0.1 cm of roots of the plant. In certain embodiments the soil is within 0.5 cm of roots of the plant. In certain embodiments the soil is within 1 cm of roots of the plant. In certain embodiments the soil is within 2 cm of roots of the plant. In certain embodiments the soil is within 3 cm of roots of the plant. In certain embodiments the soil is within 5 cm of roots of the plant. In certain embodiments the soil is within 7 cm of roots of the plant. In certain embodiments the soil is within 10 cm of roots of the plant. In certain embodiments the soil is within 15 cm of roots of the plant. In certain embodiments the soil is within 20 cm of roots of the plant. In certain embodiments the soil is within 50 cm of roots of the plant. In certain embodiments the soil is within 100 cm of roots of the plant. Thus, provided herein are compositions comprising a population of plants and microbes, as described herein, and soil in which the plants grow or have grown, the microbes comprise at least 0.01, 0.05, 0.1, 0.51, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 0.01%, or at least 0.1%, or 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%. In certain embodiments the composition further comprises mycorrhizal fungi. In certain embodiments the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80,

or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%. In certain embodiments the composition comprises beneficial microbes other than the microbes of the composition comprising microbes; these can be present, e.g., at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight. In certain embodiments the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil. In certain embodiments the soil has an average water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%. In certain embodiments the soil and plant parts in the soil have an average carbon content of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20% and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, or 40% (w/w), for example, 5-30%, preferably 7-30%, more preferably 10-30%, yet more preferably 10-25%. In certain embodiments the soil has a soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil. In certain embodiments the soil is to a depth of not more than 20, 30, 40, 50, 60, 70, 80, 90, or 100 cm, for example not more than 100 cm, preferably not more than 80 cm, more preferably not more than 60 cm, even more preferably not more than 40 cm, yet more preferably not more than 30 cm, still more preferably not more than 20 cm. In certain embodiments the soil and plant parts in the soil have an average carbon content of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 35, 37, 40, 42, 45, 50, 55, or 60 and/or not more than 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 35, 37, 40, 42, 45, 50, 55, 60, or 70 metric ton per hectare, for example 10-70, preferably 10-60, more preferably 15-60, yet more preferably 15-50, still more preferably 18-60, even still more preferably 18-55 metric ton per

hectare. In certain embodiments, the soil is to a depth of at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, or 150 cm and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, or 200 cm, for example not more than 100 cm, preferably not more than 80 cm, more preferably not more than 60 cm, even more preferably not more than 40 cm, yet more preferably not more than 30 cm, still more preferably not more than 20 cm, or to the depth of roots of the plants. In certain cases, for example as indicated herein, soil is less than average depth of roots, e.g., typically though not necessarily in the case of a forest.

10. Plants

[0073] In certain embodiments herein, methods or compositions include one or more plants or plant parts, or seeds, seedlings, or other plant propagules of plants, or land in which plants grow, have grown, or will grow, or other methods and compositions as described herein that comprise plants or plant parts. In certain embodiments the plants are grass. In certain embodiments the grass is a grassland grass. Grassland grasses include but are not limited to Rhodes grass, red oat grass, lemon grass, purple needlegrass, blue grama, buffalo grass, and galleta. In certain embodiments the grass is a turf grass. Turf grasses include but are not limited to annual ryegrass, bahiagrass, bermudagrass, buffalograss, carpetgrass, centipedegrass, creeping bentgrass, fine fescue, Kentucky bluegrass, perennial ryegrass, rough bluegrass, St. Augustinegrass, tall fescue, zoysiagrass, Kikuyugrass (*Pennisetum clandestinum*) Annual bluegrass (*Poa annua*), or a combination thereof. In certain embodiments the plants are trees. In certain embodiments the trees are deciduous trees. In certain embodiments the trees are evergreen trees. In certain embodiments the trees are forest trees. In certain embodiments the plants are a commercial crop. In certain embodiments the commercial crop comprises a cereal crop. In certain embodiments the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments the commercial crop comprises a berry. In certain embodiments the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments the commercial crop comprises an oilseed plant. In certain embodiments the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments the commercial crop comprises a tree nut. In certain embodiments the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments the commercial crop comprises a brassica vegetable. In certain embodiments the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments the commercial crop comprises a cucurbit vegetable.

In certain embodiments the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments the commercial crop comprises a bulb vegetable. In certain embodiments the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments the commercial crop comprises citrus. In certain embodiments the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments the commercial crop comprises a fruiting vegetable. In certain embodiments the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments the commercial crop comprises legume or vegetable such as beans. In certain embodiments the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments the commercial crop comprises a pome fruit. In certain embodiments the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments the commercial crop comprises a root, tuber or corm vegetable. In certain embodiments the root, tuber or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments the commercial crop comprises a stone fruit. In certain embodiments the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments the commercial crop comprises a grass. In certain embodiments the grass comprises grass for livestock feed. In certain embodiments the grass comprises turf grass. In certain embodiments the commercial crop comprises a tree. In certain embodiments the commercial crop comprises an evergreen tree. In certain embodiments the commercial crop comprises a deciduous tree. In certain embodiments the commercial crop comprises an herb or spice. In certain embodiments the commercial crop comprises cannabis. In certain embodiments the commercial crop comprises an ornamental plant. In certain embodiments the ornamental plant comprises a flowering plant, a bush or a shrub. In certain embodiments the commercial crop comprises an energy or raw material plant. In certain embodiments the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax. In certain cases the energy or raw material plant is for use in producing a biofuel. In certain embodiments a plant is a hemp plant.

11. **Compositions comprising soil.**

[0074] In certain embodiments, provided herein are compositions comprising soil, such as soil in which plants are growing or have grown, wherein the soil comprises one or more microbes, such as one or more microbes or combinations of microbes heterologous to the soil. In certain embodiments, microbes are those of one of the microbial compositions provided herein.

[0075] In certain embodiments provided is a composition comprising soil in which plants are growing or have grown wherein the soil comprises at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, or 100 and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40, or 1-150, preferably 1-100, more preferably 2-80, even more preferably 2.

[0076] In certain embodiments composition comprising soil in which plants are growing or have grown wherein the soil comprises one or more microbes of a microbial composition as provided herein, at least 1, 2, 5, 10, 15, 20, 30, 35, 40, or 45 different microbes of a microbial composition as described herein,.

[0077] In certain embodiments, the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[0078] Alternatively or additionally, in certain embodiments the soil has a water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[0079] Alternatively or additionally, in certain embodiments the soil has a concentration of beneficial microbes of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[0080] Alternaively or additionally, in certain embodiments the soil has a soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil. In certain embodiments the soil has an average carbon content of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20% and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,

13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, or 40% (w/w), for example, 5-30%, preferably 7-30%, more preferably 10-30%, yet more preferably 10-25%.

[0081] Alternatively or additionally, in certain embodiments the soil does not contain a significant amount (concentration) of synthetic fertilizer, or, in certain embodiments, does not contain a detectable amount. Alternatively or additionally, in certain embodiments the soil does not contain a significant amount (concentration) of synthetic pesticide, or, in certain embodiments, does not contain a detectable amount. Alternatively or additionally, in certain embodiments the soil does not contain a significant amount (concentration) of synthetic herbicide, or, in certain embodiments, does not contain a detectable amount.

[0082] Alternatively or additionally, the soil may comprise the plants or parts of the plants. Any suitable plant or plant part may be part of the composition, such as those described herein, e.g. in Section B.10. In certain embodiments, the part of the plants comprises roots of the plants. In certain embodiments, the microbes are disposed on or in the roots. In certain of these embodiments, the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, *e.g.*, 10-10^{16}, preferably 100-10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}. In certain embodiments, the composition further comprises mycorrhizal fungi.

[0083] All weights are dry weights, unless otherwise indicated. Values for density, water holding capacity, beneficial microbes, soil carbon content, concentration of synthetic fertilizer, herbicide, and/or fungicide, or other relevant soil characteristics, may be determined by any suitable method. In certain embodiments, some or all of the values are determined on a soil sample. In certain embodiments, at least a portion of the values are determined by use of a probe. In certain embodiments, at least some of the values are determined by above-ground techniques, such as satellite imaging, lidar, or the like. See further description of carbon in soil provided herein, for further description of sampling and analytic techniques. As used herein, a "significant" amount of a synthetic fertilizer, herbicide, or pesticide includes an amount that is above established standards for organic farming in the area in which soil and/or plants are situated.

12. Systems

[0084] In certain embodiments provided herein is a system comprising (i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more other entities; (ii) a second entity, or a third entity controlled directly or indirectly, at least in part, by the second entity, that obtains, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, are achieved for the second entity; (iii) an agreement between the first and second entities that delineates an apportionment of the economic benefits between the first and second entities; and (iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines the apportionment between the first and second entities, and communicates information comprising the apportionment to the first and/or second entities. In certain embodiments the second entity is (i) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts; (ii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold; (iii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration; or (iv) an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold. In certain embodiments the land comprises pastureland. In certain embodiments the land comprises rangeland. In certain embodiments the land comprises land on which grass is grown for feed for the animals. In certain embodiments the land comprises land on which grain is grown for feed for the animals. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration. In certain embodiments the use of the land comprises a sport, game, or other recreation or entertainment, e.g., a golf course. In certain embodiments the second entity is an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions. In certain embodiments the land is grassland, forest, or rangeland. In certain embodiments the second entity is a governmental entity. In certain embodiments the

second entity is a private entity. In certain embodiments the one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, comprises(i) reduced costs due to decreased water use for the plants and/or (ii) reduced costs due to decreased use of fertilizer for the plants; and/or (iii) reduced costs due to decreased use of herbicides for the plants; and/or (iv) reduced costs due to decreased use of pesticides for the plants; and/or (v) increased biomass of the plants and/or (vi) increased price per plant or plant product or unit thereof and/or (vii) ability to use a greater area of land to grow or maintain the plants and/or (viii) ability to grow plants in a wider range of environmental conditions and/or (ix) a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants;and/or (x) a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; and/or (xi) a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; and/or (xii) a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants; In certain embodiments the one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, comprises a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants, or a combination thereof. In certain embodiments the one or more economic benefits comprise reduced costs due to decreased water use for the plants. In certain embodiments the one or more economic benefits comprise increased price per plant or plant product or unit thereof. In certain embodiments the one or more economic benefits comprise a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants. In certain embodiments the animals are cattle. In certain embodiments the animals are dairy animals, *e.g.*, cows, goats, or sheep. In certain embodiments the animals are poultry. In certain embodiments the poultry are raised for slaughter. In certain embodiments the poultry are egg layers. In certain embodiments the system comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 500, or 1000 other entities, different from the first entity, that obtain, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for each of the entities; agreements between the first entity and each other entity that delineates an apportionment of the economic benefits between the first entity and each of the other entities;

and one or more processors that receives information regarding each of the agreements and information regarding the one or more economic benefits for each of the other entities, determines the apportionment between the first entity and each of the other entities, and communicates information comprising the apportionment to the first entity and/or each of the other entities.

[0085] Any suitable microbial composition may be used in the systems of this section, such as a composition comprising a plurality of different microbes. In certain embodiments a microbial composition as described herein is used.

C. Methods

1. Application to plants, plant parts, soil or other growth medium

[0086] In certain embodiments, provided herein is a method comprising applying a microbial composition, such as a microbial composition as disclosed herein, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a first application. Unless indicated otherwise, or clear from context, the phrase "apply a microbial composition," or similar phrase, as used herein, when used in terms of application to soil or plants in soil, also includes planting or otherwise contacting soil with seeds, seedlings, or other plant propagules that comprise microbes, such as seeds, seedlings, or other plant propagules described herein. In certain embodiments, at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes in the composition are at a concentration that is at least 2, 5, 10, 50, 100, 500, or 1000x the concentration of the same microbe found or detected in an untreated control plant, or a part thereof, and/or soil or other growth medium in which the plant grows or will grow, preferably at 2x, more preferably at least 5x, even more preferably at least 10x, yet more preferably at least 50x, still more preferably at least 500x. In certain embodiments, at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes in the composition are undetectable in an untreated control plant, or a part thereof, and/or to soil in which the plant grows or will grow. In certain embodiments, the derivative composition is an aqueous composition. The composition or derivative can be applied in any suitable manner. In certain embodiments, a composition comprising microbes is aqueous, or is combined with an aqueous medium, and the aqueous material is applied to soil or other growth medium in which the plant grows or will grow, by any suitable means, e.g., as part of

irrigation water. In certain embodiments, the microbial composition or derivative thereof is a solid composition, e.g., particles or the like, as described herein, and is applied as a solid. For solid or liquid application, in certain embodiments application comprises aerial application, e.g., by manned and/or unmanned aerial vehicle. As used herein, "control" or "reference" or similar words, when used in connection with plants, plant parts, soil, and/or other growth medium, or other aspects as described herein, includes plants, plant parts, soil, and/or other growth medium, or other aspects as described herein, to which a microbial composition as described herein has not been applied. In certain embodiments it includes but is not limited to plants, plant parts, soil, and/or other growth medium before application of a microbial composition. It can include information gathered for one or more growing seasons or years, for example, information gathered for the previous 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 years, for example, 10 years. Typically such information will be an average. In certain embodiments it includes but is not limited to plants, plant parts, soil, or other growth medium the same as the plants, plant parts, soil, or other growth medium to which the microbial composition is applied, e.g., the same soil, the same plants, etc, for example, an adjacent or nearby field that comprises the same crops or other plants, which are typically treated similarly or the same as the treated soil and plants. Any suitable number of application of the composition, or a derivative produced from the composition can be applied, for example at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 applications, and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 applications, for example 1-20 applications. In certain embodiments, the method further comprises applying the composition, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a second application. In certain embodiments, the method further comprises applying the composition, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a third application. In certain embodiments, the method further comprises applying the composition, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a fourth application. In certain embodiments, the method further comprises applying the composition, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a fifth application. In certain embodiments, the method further comprises applying the composition, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a sixth application. In certain embodiments, the applications are separated by at least 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3, or 4 weeks, or 1, 2, 3, 4, 5, 6, 8, or 10 months, or 1, 2, 3, 4, or 5 years and/or

not more than 2, 3, 4, 5, or 6 days, or 1, 2, 3, or 4 weeks, or 1, 2, 3, 4, 5, 6, 8, or 10 months, or 1, 2, 3, 4, 5 or 10 years. In certain embodiments an application comprises at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, or 400 and/or not more than 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400, or 500 g microbes/acre, for example 5-5-500 or 5-200 or 5-100 or 5-50 g/acre, preferably 50-200 g microbes/acre, more preferably 75-125 g/acre, even more preferably 100 g/acre. In certain embodiments, each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre. In certain embodiments, soil and/or plants or parts or products of plants are tested for mineral and/or other nutrient content before one or more applications, and, in some cases, the amount of one or more minerals and/or other nutrients in the soil is modulated based, at least in parts, on the results of the testing. An amount of a mineral or other nutrient may be increased, or decreased. Further description of testing of soil and/or plants or components of plants, and addition of macronutrients, micronutrients, and/or carbon sources, may be as disclosed herein. In certain embodiments, the application of the composition leads to a concentration of at least 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 0.5%, or at least 1%, preferably at least 2%, more preferably at least 5%, even more preferably at least 10%, yet more preferably at least 20%, still more preferably at least 40% of the microbes that is at least 2, 5, 10, 50, 100, 500, 1000, 10,000, 50,000, or 100,000x higher than the concentration of the same microbe found or detected in an untreated control plant or soil or other growth medium in which the plant grows or will grow, for example at least 2x, or at least 10x, or at least 100x, preferably at least 500x, more preferably at least 1000x, yet more preferably at least 5000, still more preferably at least 50,000x. In certain embodiments, the method further comprises applying one or more soil amendments to the soil. In certain embodiments, the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes. In certain embodiments, a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow and/or the plants or parts of the plants. Such analysis may be performed before the first application. It may additionally or alternatively be performed at one or more times after the first application. In certain embodiments, the method further comprises growing the plant in the soil. In certain embodiments, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 1%, or at least 2%, or at least 5%, or at least 10%, preferably at least 20%, more

preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition colonize roots of the plants, for example at least 1%, or at least 2%, or at least 5%, or at least 10%, preferably at least 20, more preferably at least 40, yet more preferably at least 60, still more preferably at least 80%. In certain embodiments, the composition or derivative is applied to a plurality of plants, or a parts thereof, and/or to soil or other growth medium in which the plurality of plants grow or will grow. In certain embodiments, the plurality comprises at least 10, 20, 50, 100, 500, 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 5M, 10M, 50M, 100M, 500M, 1B, 5B, 10B, 50B, or 100B of the plants, for example at least 100, preferably at least 1000, more preferably at least 100,000, even more preferably at least 10M, yet more preferably at least 100M, still more preferably at least 1B. In certain embodiments, the plants are grasses. In certain embodiments, the grasses are turf grasses. In certain embodiments, the plants are grassland grasses. In certain embodiments, the plants are trees. In certain embodiments, the trees are deciduous trees. In certain embodiments, the trees are evergreen trees. In certain embodiments, the trees are forest trees. In certain embodiments, the plant is a commercial crop. In certain embodiments, the commercial crop comprises a cereal crop. In certain embodiments, the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments, the commercial crop comprises a berry. In certain embodiments, the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments, the commercial crop comprises an oilseed plant. In certain embodiments, the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments, the commercial crop comprises a tree nut. In certain embodiments, the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments, the commercial crop comprises a brassica vegetable. In certain embodiments, the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments, the commercial crop comprises a cucurbit vegetable. In certain embodiments, the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments, the commercial crop comprises a bulb vegetable. In certain embodiments, the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments, the commercial crop comprises citrus. In certain embodiments, the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments, the commercial crop comprises a fruiting vegetable. In certain embodiments, the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments, the commercial crop comprises

legume or vegetable such as beans. In certain embodiments, the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments, the commercial crop comprises a pome fruit. In certain embodiments, the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments, the commercial crop comprises a root, tuber, or corm vegetable. In certain embodiments, the root, tuber, or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments, the commercial crop comprises a stone fruit. In certain embodiments, the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments, the commercial crop comprises a grass. In certain embodiments, the grass comprises grass for livestock feed. In certain embodiments, the grass comprises turf grass. In certain embodiments, the commercial crop comprises a tree. In certain embodiments, the commercial crop comprises an evergreen tree. In certain embodiments, the commercial crop comprises a deciduous tree. In certain embodiments, the commercial crop comprises an herb or spice. In certain embodiments, the commercial crop comprises cannabis. In certain embodiments, the commercial crop comprises an ornamental plant. In certain embodiments, the ornamental plant comprises a flowering plant, a bush, or a shrub. In certain embodiments, the commercial crop comprises an energy or raw material plant. In certain embodiments, the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax.

[0087] In certain embodiments, provided herein are methods comprising testing a growth medium, such as soil, and/or plants or one or more components of plants, e.g., one or more plants growing in the growth medium, to determine one or more characteristics of the growth medium, e.g., soil, and/or plants or components of plants, and, if results of the testing indicate, adjusting the growth medium and/or plants or plant components, for example, adjusting growth medium such as soil, to modulate one or more of the characteristics determined in the tests, generally to provide improved conditions for plant growth, growth and colonization of microbes applied, etc, in conjunction with one or more applications of a microbial composition, e.g., as described herein. In certain embodiments, the makeup and/or application amount of the microbial composition may be determined, at least in part, by results of the tests. The testing may be performed at any suitable time, e.g., before plants or their seeds or other propagules are introduced to the growth medium, and/or at intervals during a growing season for the plants, and/or at the end of the growing season. After each such test, or after some portion of such tests, the growth medium and/or plants or plant parts, such as growth medium, e.g., soil, and/or microbial composition may be adjusted to modulate one or more of the characteristics

determined in the tests; thus, for a given growing season any suitable number of tests and adjustments may be performed, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, preferably at least 1, more preferably at least 2, even more preferably at least 3, yet more preferably least 4, still more preferably at least 5. The test or tests may be any suitable test, depending on the characteristic or characteristics to be determined. In certain embodiments, content of one or more macronutrients is determined, e.g., content in growth medium, e.g., soil and/or plant or component of a plant. In certain embodiments, content of one or more micronutrients is determined, e.g., content in growth medium, e.g., soil and/or plant or component of a plant. In certain embodiments, content of one or more carbon sources is determined, e.g., content in growth medium, e.g., soil and/or plant or or component of a plant. Additionally or alternatively, pH may be determined. In certain embodiments, one or more macronutrients and/or one or more micronutrients and/or carbon sources are applied to the growth medium, e.g., soil, and/or to plants at least in part on the results of one or more tests for micronutrients, micronutrients, and/or carbon sources, respectively. Method of determining macronutrient and micronutrient and carbon source characteristics are well-known in the art, and any suitable test or tests may be used. Thus, in certain embodiments, provided herein is a method comprising applying to a plant growth medium (a) a plurality of microbes; (b) one or more macronutrients and/or (c) one or more micronutrients and/or (d) one or more carbon sources, wherein a composition and/or effective amount of (a), (b), (c) and/or (d) is determined at least in part by one or more results of a first test on one or more samples comprising growth medium to which the plurality of microbes is to be applied or has been applied and/or a component of a plant or plants growing in the growth medium. In certain embodiments the plants are not cannabis. The plants may be any suitable plants or class of plants, such as described in Section B.10. In certain embodiments, the growth medium comprises soil. In certain embodiments, the composition and/or effective amount of (a), (b), (c) and/or (d) is further determined, at least in part, by a type of plant or plants in the growth medium. In certain embodiments, composition and/or effective amount of (b) and/or (c) and/or (d) is determined; in certain of these embodiments the composition and/or effective amount of (a) is not determined by test results and/or type of plants in growth medium. In certain embodiments the plurality of microbes is applied to the plant growth medium at an amount of at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, or 400 and/or not more than 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400, or 500 g microbes/acre, for example 5-5-500 or 5-200 or 5-100 or 5-50 g/acre, preferably 50-200 g microbes/acre, more preferably 75-125 g/acre, even more preferably 100 g/acre. In certain embodiments, the plurality of microbes is present at a concentration of at least 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, or 10^{12} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, or 10^{13} cfu/g, for

example 10^5-10^{13} cfu/g, preferably 10^7-10^{11} cfu/g, more preferably 10^8-10^{10} cfu/g. In certain embodiments, the plurality of microbes applied to the plant growth medium at an amount of at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} and/or not more than 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} cfu/acre, for example 10^6-10^{16} cfu/acre, preferably 10^8-10^{14} cfu/acre, more preferably 10^9-10^{13} cfu/acre, even more preferably 10^{10}-10^{12} cfu/acre. In certain embodiments, the plurality of microbes is applied 2, 3, 4, 5, 6, 7, 8, 9, or 10 times during a growing season, for example 1-10 times, preferably 3-8 times. In certain embodiments, the time between applications is 1 week to 1 year. In certain embodiments, the plurality of microbes is applied via irrigation and/or aerial delivery vehicle, for example via irrigation or for example via aerial delivery. In certain embodiments, macronutrients comprise ammonium, nitrate, phosphate, potassium, sodium, calcium, magnesium, or a combination thereof. In certain embodiments, an amount of nitrate in the growth medium is determined and compared to a preferred range of nitrate in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of nitrate within the preferred range or closer to the preferred range after treatment. In certain embodiments the preferred range of nitrate comprises at least 10, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, or 140 and/or not more than 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 35-90 lbs/acre. In certain embodiments, an amount of phosphate in the growth medium is determined and compared to a preferred range of phosphate in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of phosphate within the preferred range or closer to the preferred range after treatment. In certain embodiments the preferred range of phosphate comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 50-100 lbs/acre. In certain embodiments, an amount of potassium in the growth medium is determined and compared to a preferred range of potassium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of potassium within the preferred range or closer to the preferred range after treatment. In certain embodiments the preferred range of potassium comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 75-100 lbs/acre. In certain embodiments, an amount of calcium in the growth medium is determined and compared to a preferred range of calcium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of calcium within the preferred range or closer to the preferred range after treatment. In certain

embodiments, the preferred range of calcium comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 60-120 lbs/acre. In certain embodiments, an amount of magnesium in the growth medium is determined and compared to a preferred range of magnesium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of magnesium within the preferred range or closer to the preferred range after treatment. In certain embodiments the preferred range of magnesium comprises at least 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, or 40 and/or not more than 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50 lbs/acre, preferably 13-20 lbs/acre. In certain embodiments, an amount of sodium in the growth medium is determined and compared to a preferred range of sodium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of sodium within the preferred range or closer to the preferred range after treatment. In certain embodiments, the preferred range of sodium comprises no more than 500, 400, 300, 200, 150, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 lbs/acre, preferably no more than 100 lbs/acre. In certain embodiments micronutrients comprise zinc, iron, manganese, copper, cobalt, molybdenum, selenium, nickel, boron, silicon, aluminum, chloride, or a combination thereof. In certain embodiments the plant growth medium is treated to adjust the amount of one or more of the micronutrients. In certain embodiments, the plant growth medium is treated with a composition comprising sea minerals. The method may comprise testing the growth medium for amount and/or type of carbon source. In certain embodiments the growth medium is treated to provide one or more carbon sources, in certain cases based, at least in part, on results of the test. In certain embodiments, the carbon source comprises humates or humic acid. Additionally or alternatively the carbon source comprises fulvic acid. The method may comprise applying fertilizer, compost, or the like to the plant growth medium. In certain embodiments the method further comprisies performing a second test on the plant growth medium to provide a second result comprising an amount of one or more microbes in the plurality of microbe after application to the plant growth medium. In certain embodiments the test comprises determining whether or not, or to what extent, the microbes have grown in the soil and/or on the plants. In certain embodiments the method comprises performing a third test on a sample comprising a plant component to provide a third result. In certain embodiments the plant component comprises sap, a leaf, a petiole, a root, a flower, or a fruit, for example, a petiole. Fin certain embodiments, the method comprisers applying an effective composition and/or amount of one or more amendments to the plant growth medium and/or plant, wherein the effective composition and/or amount of one or more amendments is determined at least in part by the third result. In certain

embodiments, the effective composition and/or amount of one or more amendments is applied to the plant growth medium and/or plant via a foliar spray or irrigation. In certain embodiments the method comprises performing a fourth test for carbon content of soil to provide a fourth result. In certain embodiments a fifth test on the plant growth medium to provide a fifth result, for example, at the end of the growing season or other suitable time. In certain embodiments, the fifth comprises a carbon content test. In certain embodiments the method further comprisies performing a pathogen analysis, a toxin analysis, a water analysis, a soil bulk density test, a soil water content test, or a combination thereof. In certain embodiments a plant in the plant growth medium and/or the growth medium, e.g., soil, exhibits one or more improved properties as compared to reference plant and/or growth medium, e.g., soil, wherein the improved properties comprise:(i) reduced water consumption;(ii) increased soil water holding capacity;(iii) improved soil density;(iv) increased soil carbon content;(v) increased rate of soil carbon content increase;(vi) increased density of beneficial microbes in soil;(vii) increased yield; or(viii) increased nutrient density. In certain embodiments the composition and/or effective amount is further determined at least in part by one or more desired results, a duration for to achieve the desired results, and/or a type of cultivation practice to be used to cultivate one or more plant in the plant growth medium. In certain embodiments, at least 20, 40, 50, 60, 70, 80, 90, 95, 97 98, 99 or 100% of the microbes in the plurality of microbes are *Streptomyces*. In certain embodiments, the plurality of microbes comprises one or more strains of mycorrhizae. In certain embodiments the plurality of microbes comprises a microbial composition as provided herein. In certain embodiments, one or more compositions comprising one or more macronutrients or substance effective to change soil content and/or plant content of one or more macronutrients, and/or one or more micronutrients or substance effective to change soil content and/or plant content of one or more micronutrients, and/or one or more carbon sources, is provided based, at least in part, on the testing described herein, and used to treat the growth medium and/or plants. In certain embodiments the composition comprises sea minerals. In certain embodiments the composition comprises humates, humic acid, or fulvic acid.

2. Contacting with seed, seedling, or other plant propagule

[0088] In certain embodiments, provided herein is a method comprising contacting a surface of a seed, seedling, or other plant propagule with a microbial composition, such as a microbial composition as disclosed herein or a derivative produced from the composition. The method results in one or more microbes of the microbial composition associated with the seed, seedling, or other plant propagule, e.g., to produce seeds, seedlings, or other plant propagules associated with one or more microbes as described herein, for example, with microbes on the surface and/or

within pores of the seed, seedling, or other plant propagule, or otherwise associated in such a way as to maintain contact or proximity to the seed, seedling, or other plant propagule until use of same, e.g., planting of same. Any suitable method for associating one or more microbes with seeds, seedlings, or other plant propagules may be used, such as one or more methods known in the art. Methods include, but are not limited to, spraying, immersing, coating, encapsulating, or dusting the seed, seedling, or other plant propagule, or portion thereof, with the composition or derivative of the composition. In certain embodiments, a derivative of a microbial composition is used that both associates microbes with the seeds, seedlings, or other plant propagules and protects microbes that associate with the seeds, seedlings, or other plant propagules from the environment, e.g., to enhance stability until such time as seeds are used. Any suitable derivative may be used, such as a derivative that comprises clay. In certain embodiments, the seed, seedling, or other plant propagule is coated with and/or comprises within pores of the seed, seedling, or other plant propagule at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of different microbes of the composition. In certain embodiments, the method comprises contacting the surface of a seed with the composition. In certain embodiments, at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the microbes are heterologous to the seed, seedling, or other plant propagule and/or to each other. In certain embodiments, the method comprises contacting the surface of the seed, seedling, or other plant propagule with at least 10, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 2000, 5000, 10,000, 50,000, or 100,000 CFUS of the microbes of the composition or derivative, for example at least 10, preferably at least 50, more preferably at least 100, even more preferably at least 200, yet more preferably at least 500, still more preferably at least 1000. In certain embodiments, the method further comprises placing the treated seeds, seedlings, or other plant propagules in soil and exposing it to suitable conditions for growth. In certain embodiments, the method further comprises applying one or more soil amendments to the soil. In certain embodiments, the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes. In certain embodiments, a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plant grows or will grow. Suitable analyses and amendment may be by methods described herein. In certain embodiments, the method further comprises growing the plant in the soil. The seeds, seedlings, or plant propagules may be of any suitable plant or class of plants, such as those described in section B.10. In certain embodiments, the

seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of grass or trees. In certain embodiments, the seeds, seedling, or other plant propagules comprise grass seeds. In certain embodiments, the grass seeds comprise turf seeds. In certain embodiments, the grass seeds comprise grassland seeds. In certain embodiments, the seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of trees. In certain embodiments, the seeds, seedlings, or other plant propagules of trees comprise tree seeds. In certain embodiments, the seeds, seedlings, or other plant propagules of trees comprise tree seedlings. In certain embodiments, the seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of commercial crops. In certain embodiments, the commercial crop comprises a cereal crop. In certain embodiments, the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments, the commercial crop comprises a berry. In certain embodiments, the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments, the commercial crop comprises an oilseed plant. In certain embodiments, the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments, the commercial crop comprises a tree nut. In certain embodiments, the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments, the commercial crop comprises a brassica vegetable. In certain embodiments, the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments, the commercial crop comprises a cucurbit vegetable. In certain embodiments, the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments, the commercial crop comprises a bulb vegetable. In certain embodiments, the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments, the commercial crop comprises citrus. In certain embodiments, the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments, the commercial crop comprises a fruiting vegetable. In certain embodiments, the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments, the commercial crop comprises legume or vegetable such as beans. In certain embodiments, the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments, the commercial crop comprises a pome fruit. In certain embodiments, the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments, the commercial crop comprises a root, tuber, or corm vegetable. In certain embodiments, the root, tuber, or corm vegetable comprises carrot,

potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments, the commercial crop comprises a stone fruit. In certain embodiments, the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments, the commercial crop comprises a grass. In certain embodiments, the grass comprises grass for livestock feed. In certain embodiments, the grass comprises turf grass. In certain embodiments, the commercial crop comprises a tree. In certain embodiments, the commercial crop comprises an evergreen tree. In certain embodiments, the commercial crop comprises a deciduous tree. In certain embodiments, the commercial crop comprises an herb or spice. In certain embodiments, the commercial crop comprises cannabis. In certain embodiments, the commercial crop comprises an ornamental plant. In certain embodiments, the ornamental plant comprises a flowering plant, a bush, or a shrub. In certain embodiments, the commercial crop comprises an energy or raw material plant. In certain embodiments, the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax.

3. Contacting with a population of seeds, seedlings, or other plant propagules

[0089] In certain embodiments, provided herein is a method comprising contacting surfaces of a populations of seeds, seedlings, or other plant propagules with a microbial composition as disclosed herein, or a derivative produced from the composition. The method results in one or more microbes of the microbial composition associated with the seeds, seedlings, or other plant propagules, e.g., to produce a population seeds, seedlings, or other plant propagules associated with one or more microbes as described herein, for example, with microbes on the surface and/or within pores of the seeds, seedlings, or other plant propagules, or otherwise associated in such a way as to maintain contact or proximity to the seeds, seedlings, or other plant propagules until use of same, e.g., planting of same. Any suitable method for associating one or more microbes with seeds, seedlings, or other plant propagules may be used, such as one or more methods known in the art. Methods include, but are not limited to, spraying, immersing, coating, encapsulating, or dusting the seeds, seedlings, or other plant propagules, or portion thereof, with the composition or derivative of the composition. In certain embodiments, a derivative of a microbial composition is used that both associates microbes with the seeds, seedlings, or other plant propagules and protects microbes that associate with the seeds, seedlings, or other plant propagules from the environment, e.g., to enhance stability until such time as seeds are used. Any suitable derivative may be used, such as a derivative that comprises clay. In certain embodiments, individual seeds, seedlings, or other plant propagules of the population are coated with and/or comprise within pores of the seeds, seedlings, or other plant propagules at least 10,

15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition. In certain embodiments, at least 50, 60, 70, 80, 90, 95, or 99%, or 100%, of the different microbes in the composition are present in the population of seeds, seedlings, or other plant propagules of the population, for example at least 50, preferably at least 60, more preferably at least 80, even more preferably at least 90, yet more preferably at least 95, still more preferably at least 99, and even still more preferably 100%. In certain embodiments, at least at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition is heterologous to the seeds, seedlings, or other plant propagule preferably at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 40. In certain embodiments, the population comprises at least 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 200,000, 500,000, or 1M seeds, seedlings, or other plant propagules. In certain embodiments, the method comprises contacting the population of seeds, seedlings, or other plant propagules with a sufficient quantity of the composition or derivative so that each seed, seedling, or other plant propagule is contacted with at least 10, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 2000, 5000, 10,000, 50,000, or 100,000 CFUS of the microbes of the composition or derivative, for example at least 10, preferably at least 50, more preferably at least 100, even more preferably at least 200, yet more preferably at least 500, still more preferably at least 1000. In certain embodiments, the method further comprises placing the seeds, seedlings, or other plant propagules in soil and exposing them to suitable conditions for growth. In certain embodiments, the method further comprises applying one or more soil amendments to the soil. Suitable analyses and amendment may be by methods described herein. In certain embodiments, the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes. In certain embodiments, a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow. In certain embodiments, the method further comprises growing the plant in the soil. In certain embodiments, at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, or 99%, or 100%, of the microbes of the composition colonize roots of the plants, for example at least 10, preferably at least 20, more preferably at least 40, yet more preferably at least 60, still more preferably at least 80%. The seeds, seedlings, or other plant propagules may be of any suitable plant or class of plant, such as those described in Section B.10. In certain embodiments, the seeds, seedling, or other plant propagules comprise seeds,

seedlings, or other plant propagules of grass or trees. In certain embodiments, the seeds, seedling, or other plant propagules comprise grass seeds. In certain embodiments, the grass seeds comprise turf seeds. In certain embodiments, the seeds, seedlings, or other plant propagules comprise seeds, seedlings, or other plant propagules of trees. In certain embodiments, the seeds, seedlings, or other plant propagules comprise tree seeds. In embodiment 578 provided herein is the method of embodiment 576 comprising tree seedlings. In certain embodiments, the seeds, seedlings, or other plant propagules comprise seeds, seedlings, or other plant propagules of commercial crops. In certain embodiments, the commercial crop comprises a cereal crop. In certain embodiments, the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum. In certain embodiments, the commercial crop comprises a berry. In certain embodiments, the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry. In certain embodiments, the commercial crop comprises an oilseed plant. In certain embodiments, the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean. In certain embodiments, the commercial crop comprises a tree nut. In certain embodiments, the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia. In certain embodiments, the commercial crop comprises a brassica vegetable. In certain embodiments, the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi. In certain embodiments, the commercial crop comprises a cucurbit vegetable. In certain embodiments, the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant. In certain embodiments, the commercial crop comprises a bulb vegetable. In certain embodiments, the bulb vegetable comprises onion, garlic, or shallots. In certain embodiments, the commercial crop comprises citrus. In certain embodiments, the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo. In certain embodiments, the commercial crop comprises a fruiting vegetable. In certain embodiments, the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape. In certain embodiments, the commercial crop comprises legume or vegetable such as beans. In certain embodiments, the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts. In certain embodiments, the commercial crop comprises a pome fruit. In certain embodiments, the pome fruit comprises apple, crabapple, pear, quince, or mayhaw. In certain embodiments, the commercial crop comprises a root, tuber, or corm vegetable. In certain embodiments, the root, tuber, or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip. In certain embodiments, the commercial

crop comprises a stone fruit. In certain embodiments, the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry. In certain embodiments, the commercial crop comprises a grass. In certain embodiments, the grass comprises grass for livestock feed. In certain embodiments, the grass comprises turf grass. In certain embodiments, the commercial crop comprises a tree. In certain embodiments, the commercial crop comprises an evergreen tree. In certain embodiments, the commercial crop comprises a deciduous tree. In certain embodiments, the commercial crop comprises an herb or spice. In certain embodiments, the commercial crop comprises cannabis. In certain embodiments, the commercial crop comprises an ornamental plant. In certain embodiments, the ornamental plant comprises a flowering plant, a bush, or a shrub. In certain embodiments, the commercial crop comprises an energy or raw material plant. In certain embodiments, the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax.

4. Aerial application

[0090] In certain embodiments, provided herein is a method comprising applying a composition comprising a plurality of microbes to an area comprising soil by aerial application. Such methods are especially useful when a composition is applied to large areas of land, e.g., grasslands or forests, or any application where aerial application is desired or advantageous. The composition comprising a plurality of microbes may be any suitable composition. In certain embodiments, the composition comprising a plurality of microbes is a composition comprising a plurality of microbes disclosed herein, or a derivative produced from the composition, to an area comprising soil by aerial application. In certain embodiments, the composition comprises a delayed release composition. In certain embodiments, the area further comprises plants growing in the soil. In certain embodiments, the plants comprise grasses or trees. In certain embodiments, the plants comprise grasses. In certain embodiments, the plants comprise trees. In certain embodiments, the area is a grassland. In certain embodiments, the area is a forest. In certain embodiments, the area comprising soil is a degraded soil ecosystem. In certain embodiments, the area comprising soil is a deforested area. In certain embodiments, the area comprising soil is a forested area. In certain embodiments, the area comprising soil is a rangeland for livestock grazing. In certain embodiments, the area comprising soil is an agricultural land. In certain embodiments, the aerial application is by unmanned aerial delivery vehicle. In certain embodiments, the aerial application comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 separate applications by the unmanned aerial delivery vehicle, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet

more preferably at least 100, still more preferably at least 500. In certain embodiments, each of the separate applications is to a part of the area at least a portion of which is different from a part of the area of the other applications. In certain embodiments, the application is by a plurality of unmanned aerial delivery devices. In certain embodiments, the plurality comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 unmanned aerial delivery vehicles, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500. In certain embodiments, the unmanned aerial vehicles are drones. In certain embodiments, manned aerial vehicles are used, e.g., in the same numbers as for unmanned. In certain embodiments, a combination of manned and unmanned aerial vehicles is used, which can be any suitable combination. In certain embodiments, the composition or derivative produced from the composition is applied over an area of at least 10, 100, 1000, 10,000, 100,000, 1M, 10M, 100M, or 1B hectares, for example at least 10, preferably at least 100, more preferably at least 10,000, even more preferably at least 1M, yet more preferably at least 10M, still more preferably at least 100M. In certain embodiments, the method further comprises applying one or more soil amendments to the soil. In certain embodiments, the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes. In certain embodiments, the method further comprises determining a carbon content of soil of the area before the application or applications. In certain embodiments, the method further comprises determining a carbon content of soil of the area after the application or applications.

5. Carbon

[0091] Provided herein are methods and compositions associated with increasing carbon content of soil and/or plants growing in soil by a method that includes applying a microbial composition or derivative thereof to the soil. The microbial composition or derivative may be applied directly to the soil, e.g., as part of a liquid or solid composition. In certain cases, a microbial composition is considered "applied to" the soil if seeds, seedlings, or other plant propagules comprising the microbial composition are applied to soil and allowed to grow. Such treatment can alter the characteristics of the soil and plants growing in the soil so that more carbon is moved from the atmosphere into the soil and/or plants than would occur without application of the microbial composition or derivative thereof. In most cases, no other changes, or minimal changes, to soil or plants need be used, e.g., it is not necessary to alter plant type, agricultural practices, or the like, to increase the carbon content. The methods can reduce or even eliminate a carbon footprint for an agricultural operation, such as cultivation of the commercial or other crops, or raising domesticated animals, or even create a carbon-negative

operation. Thus, for example, domesticated animal production, such as livestock production, can be converted from an activity that is a significant contributor to global carbon emissions to one that contributes significantly less carbon, or is even carbon negative. In certain cases, microbial composition or derivative thereof is applied to areas that are largely or completely uncultivated. In certain cases microbial composition or derivative thereof is applied to one or more grasslands, such as one or more grasslands that are largely or completely uncultivated. In certain cases microbial composition or derivative thereof, is applied to one or more forests, such as one or more forests that are largely or completely uncultivated. In certain cases, some or all of the land to which microbial composition or derivative thereof comprises damaged soil and/or plant ecosystem, such as a deforested area. In certain cases, application of microbial composition or derivative thereof is conducted on a large scale, such as treating hundreds, thousands, tens of thousands, hundreds of thousands, millions, or even tens of millions, of square miles. In such cases, enormous amounts of carbon may be removed from the atmosphere and converted to carbon in the soil and/or plants.

[0092] The use of microbial compositions or derivatives thereof can confer additional benefits in addition to increasing removal of carbon from atmosphere to soil and/or plants. These can include one or more of reduced water use to grow the plants, increased biomass of plants, increased bioavailability of plant nutrients in soil, increased uptake of nutrients by the plants, increased nutrient content of the plants, improvements in soil characteristics, such as density, water holding capacity, and/or content of beneficial microbes, compared to without use of the microbial composition or derivative thereof. Thus, it is possible for a user to enjoy one or more economic benefits, including a financial benefit related to the increased conversion of atmospheric carbon to carbon in soil and/or plants.

[0093] Thus, in certain embodiments, a method comprises enhancing a rate at which atmospheric carbon is converted to carbon products in soil in which plants are grown and/or in the plants comprising applying a composition comprising one or more microbes to the plants and/or soil in a first application, wherein the rate is greater than that for reference soil and/or plants wherein the plants are grown without the composition. In certain embodiments the rate of conversion of atmospheric carbon to carbon products in soil in which the plants are grown and/or the plants is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300%. In certain

embodiments the enhancement of rate of conversion results in an increase in soil carbon content of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare/year and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare/year for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare/year, compared to reference soil. In certain embodiments, the enhancement of rate of conversion results in an increase in soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3/year, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3/year compared to reference soil.

[0094] In certain embodiments, a method comprises increasing soil carbon content comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, and/or the plants, a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby increasing soil carbon content. In certain embodiments the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[0095] In certain embodiments, a method comprises reducing an overall carbon footprint of an agricultural operation, wherein the method comprises allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, and/or the plants, a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time, and/or using such plants in the operation, thus reducing the carbon footprint of the operation. In certain embodiments, the agricultural operation comprises raising a commercial crop, such as a commercial crop described herein, for example in Section II.B.10. In certain embodiments, the carbon footprint is reduced by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 98, or 99%, or 100%, preferably at least 5%, more preferably at least 10%, still more preferably at least 20%. In certain embodiments, the operation

becomes carbon negative, for example, such that more carbon is removed from the atmosphere by the operation than is produced. In certain embodiments, the agricultural operation comprises raising domesticated animals. In certain embodiments, provided is a method of reducing an overall carbon footprint for raising domesticated animals comprising feeding the animals, and/or allowing the animals to feed on, plants or parts of plants, wherein the plants have been or are growing in soil to which has been applied a composition comprising a plurality of different microbes, wherein the composition (i) increases carbon dioxide transfer from atmosphere to soil thus increasing carbon content of the soil, compared to without the composition; (ii) increases biomass of the plants in a given area, compared to without the composition, so that carbon produced per unit biomass of plants is decreased; and/or (iii) increases nutrient density of the plants, compared to without the composition, so that less biomass of plants is used to produce a given amount of increase in economically valuable attribute of the domesticated animals or a combination thereof, thus decreasing overall carbon footprint for raising the domesticated animals. In certain embodiments, the carbon footprint is reduced by at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 98, or 99%, or 100%, preferably at least 5%, more preferably at least 10%, still more preferably at least 20%. In certain embodiments, the operation becomes carbon negative, for example, such that more carbon is removed from the atmosphere by the operation than is produced. In certain embodiments, the economically valuable attribute comprises weight of the animal. In certain embodiments the economically valuable attribute comprises nutritional value of a material supplied by the animal. In certain embodiments the economically valuable attribute comprises an amount of a product produced by the animal. The method of claim 153 wherein the economically valuable attribute comprises increased nutrient density of a material or material from the animal that is consumed by humans, such as meat, organs, milk, or eggs. In certain embodiments, he increased nutrient density comprises increased protein content, increased mineral content, increased vitamin content, or a combination thereof. In certain embodiments the increased nutrient density comprises increased mineral content, wherein mineral content comprises calcium, magnesium, iron, or a combination thereof. In certain embodiments the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses. In certain embodiments the animals are cattle. In certain embodiments the plants or parts of plants that the cattle are feed or feed on, for at least part of their growth, comprise grasses. In certain embodiments the grasses comprise pasture or range grasses. In certain embodiments the plants or parts of plants that the cattle are feed or feed on, for at least part of their growth comprise grain. In certain embodiments at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99%, or 100%, of the plants or plant parts which the animals are fed and/or allowed to feed on are plants or plant parts from plants have been or are

growing in soil to which has been applied the composition comprising a plurality of microbes. In certain embodiments methane production from the soil in which the plants have been grown or are growing is reduced. In certain embodiments the carbon footprint is reduced at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, for example, at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 50%, yet more preferably at least 80%, still more preferably at least 90%.In certain embodiments the raising of the domesticated animals is overall carbon negative.

[0096] In certain embodiments provided is a method of reducing soil methane production comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing conditions for the plants to grow in the soil;thereby increasing decreasing soil methane production.

[0097] In certain embodiments provided is a method of obtaining a financial benefit, such as a carbon credit and/or other credit, comprising allowing plants to grow in an area of soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing conditions for the plants to grow in the soil; (iii) determining the increase in soil carbon content over the period of time in the area of soil and/or other characteristic for which a financial benfit may be obtained; and (iv) based at least in part on (iii), obtaining a financial benefit, such as a carbon credit and/or other credit.

[0098] In certain embodiments provided is system comprising (i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more second entities(ii) the second entity, or a plurality of second entities, that (a) owns, controls, or otherwise has rights to land in an area of land on which plants grow and (b) uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities, wherein the area of land at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares;(iii) an agreement between the first and second entities or between

the first entity and each of the plurality of second entities that delineates an apportionment of the economic benefits between the first and second entities or between the first entity and each of the plurality of second entities; and (iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines an apportionment between the first and second entities or between the first entity and each of the plurality of second entities and communicates information comprising the apportionment to the first and/or second entities. In certain embodiments the second entity comprises a governmental entity. In certain embodiments the second entity comprises a private entity. In certain embodiments the system comprises a plurality of second entities wherein the plurality of second entities comprises at least 5, 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, or 50,000 entities and/or not more than 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, 50,000, or 100,000 entities. In certain embodiments at least 10, 20, 30, 50, 70, 80, 90, 95, or 99% of the second entities are private farming entities. In certain embodiments the economic benefit comprises a carbon credit based, at least in part, on an increase of carbon in the soil. In certain embodiments the economic benefit comprises a financial benefit attributable to the plants. In certain embodiments the financial benefit comprises payment for the plants or parts of the plants. In certain embodiments the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants. In certain embodiments he plants are trees. In certain embodiments the financial benefit comprises a financial benefit realized from animals that eat the plants.

[0099] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00100] Any suitable area of land may be used. In certain embodimants, an area is at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares.

[00101] In certain embodiments, a method comprises increasing total soil carbon. Additionally or alternatively in certain embodiments, a method comprises increasing total soil organic carbon. Additionally or alternatively, in certain embodiments, a method comprises increasing total soil inorganic carbon. Additionally or alternatively, in certain embodiments, a

method comprises increasing mineral-associated organic material (matter) (MAOM). Additionally or alternatively, in certain embodiments, a method comprises increasing particulate organic material (matter) (POM). Additionally or alternatively, in certain embodiments, a method comprises increasing microbial necromass. Additionally or alternatively, in certain embodiments, a method comprises increasing soil aggregates. Additionally or alternatively, in certain embodiments, a method comprises increasing root biomass, or a component of root biomass.

[00102] The method may also include increasing carbon content of the plants, i.e., above-ground portions of the plants. Plants of the methods may include any suitable plants, such as one or more of those described in Section I.B.10.

[00103] In certain embodiments, the method further comprises improving one or more soil characteristics and/or characteristics of plant cultivation. In certain embodiments, the method further comprises improving soil density. Alternatively or additionally, in certain embodiments, the method further comprises increasing plant biomass. Alternatively or additionally, in certain embodiments, the method further comprises decreasing water use to grow the plants. Alternatively or additionally, in certain embodiments, the method further comprises increasing water holding capacity of the soil. Alternatively or additionally, in certain embodiments, the method further comprises increasing nutrient uptake of the plants from the soil. Alternatively or additionally, in certain embodiments, the method further comprises increasing nutrient content of the plants or parts of the plants. Alternatively or additionally, in certain embodiments, the method further comprises increasing content of beneficial microbes in the soil and/or on the plants or plant parts. Alternatively or additionally, in certain embodiments, the method further comprises decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants. Alternatively or additionally, in certain embodiments, the method further comprises reducing nitrous oxide, by reduction and/or omission. Alternatively or additionally, in certain embodiments, the method further comprises increasing community biodiversity, e.g., increasing microbial biodiversity.

[00104] In certain embodiments, the method further comprises realizing a financial benefit from increasing soil carbon or increasing a component of soil carbon. Alternatively or additionally, in certain embodiments, the method further comprises realizing a financial benefit from reducing water use. Alternatively or additionally, in certain embodiments, the method further comprises realizing a financial benefit from reducing nitrous oxide, by reduction and/or omission. Alternatively or additionally, in certain embodiments, the method further comprises realizing a financial benefit from increasing community biodiversity, e.g., increasing microbial

biodiversity. The financial benefit may comprise, e.g. a credit, such as a carbon credit, or other credit associated with non-carbon aspects, such as as described above.

[00105] Various carbon measurements may be used, alone or in combination with measurements of other characteristics of soil or carbon pools in soil. If it desired to obtain a carbon credit or other financial benefit based, at least in part, on an increase of soil carbon content, measurements that conform to those required by the issuing body or other associated body, or that have been suitably validated against required measurements, are used. Characteristics measured or calculated from measurements can include one or more of total soil carbon, total organic carbon, total inorganic carbon, plant organic matter (POM), mineral-associated organic matter (MAOM), root biomass, live microbial mass, microbial necromass, plant root exudate, and/or soil aggregates. In embodiments in which a value for a characteristic for soil and/or plants treated with a microbial composition is compared with a value for reference (untreated) soil and/or plants, typically the same measurement and analytical techniques are used for treated and reference soil. For certain measurements, one or more soil samples are analyzed, such as one or more core samples, usually taken to a specific depth of soil. Any suitable depth may be used. In certain embodiments depth is at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, or 100 cm and/or not more than 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100 or 150 cm, preferably 5-150, more preferably 10-100, still more preferably 20-100 cm, such as 10-100 cm. In certain embodiments, a sample is taken to the depth of roots of plants growing in the soil. The soil sample is then analyzed for one or more characteristics. In certain embodiments, one or more measurements are performed that do not require a soil sample; any suitable technique may be used, for example, measurement by a probe inserted into the soil, satellite imaging, and/or lidar. For characteristics measured on soil samples or by probe, any suitable number of samples or measurements may be used; this number may vary according to reporting and validation requirements or other requirements.

[00106] Total soil carbon may be measured by any suitable technique. In certain embodiments, total soil carbon is measured from a soil sample, such as a core sample. Techniques to measure total soil carbon in a soil sample are known in the art. In certain embodiments, total soil carbon is measured by a method that does not require a soil sample, such as by a probe inserted into soil, and/or by a measurement taken above ground, such as satellite imaging and/or lidar. In certain embodiments a probe is used. Any suitable probe may be used so long as it provides the level of accuracy and precision required for the measurement and/or is approved by a carbon-credit issuing body or other associated body. Probes may measure other soil characteristics in addition to total carbon, such as one or more of pH, bulk density, soil organic matter, soil inorganic matter, carbonous soil minerals, nitrate, ammonia, soil moisture,

microbial biomass, basal respiration rate, fungal/bacterial ratio, water holding capacity, and/or soil texture. Exemplary probes include those available from Soil in Formation (SIF), 9666 Olive Blvd., Suite 625, Saint Louis, Missouri 63132, USA or PES Technologies, Diss, East Anglia, UK. Plant organic matter (POM), mineral-associated organic matter (MAOM), live microbial mass, microbial necromass, plant root exudate, and/or soil aggregates may be measured by any suitable technique, such as those known in the art. In certain embodiments, one or more of the measurements is taken on a soil sample. In certain embodiments, one or more measurements is taken without requiring a soil sample, e.g., using a probe. One or more soil characteristics that can affect stability of carbon in soil, such as stability of one or more carbon pools in soil, may also be measured. These can include bulk density, soil moisture, soil texture, and/or soil temperature. Additionally or alternatively, stability of soil aggregates can be measured. In certain embodiments, one or more of the measurements is taken on a soil sample. In certain embodiments, one or more measurements is taken without requiring a soil sample, e.g., using a probe, for example, one or more of bulk density, soil moisture, soil texture and/or soil temperature; in certain embodiments, all of these characteristics are measured without requiring a soil sample, e.g., by use of a probe. In addition, soil respiration may be measured, either in a soil sample or without requiring a soil sample, e.g., by probe. In certain embodiments, one or more of the above characteristics are combined to obtain one or more values for carbon in the soil, for example, one or more values for carbon of a certain stability, or certain minimal stability, e.g., to conform with requirements of a carbon-credit issuing body or associated body.

6. Uses

[00107] In certain embodiments, provided herein is use of the composition a composition as disclosed herein in increasing carbon content of soil in which plants grow compared to before use of the composition. In certain embodiments, the soil comprises an area of at least 1000, 10,000, 100,000, 1M, 10M, or 100M hectares. In certain embodiments, carbon content is increased by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton/hectare, wherein the soil carbon content is measured to a depth of 20 cm soil. In certain embodiments, the soil is soil in which grasses grow.

[00108] In certain embodiments, provided herein is use of the composition as disclosed herein in reducing methane production in soil in which plants grow compared to before use of the composition.

[00109] In certain embodiments, provided herein is use of the composition as disclosed herein in coating a surface of seeds, seedlings, or other plant propagules with one or more microbes of the composition.

[00110] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing beneficial organisms in soil in which plants grow and to which composition applied, compared to without.

[00111] In certain embodiments, provided herein is use of the composition as disclosed herein in transitioning to organic farming in 3 years or less, or 2 years or less, or 1.5 years or less.

[00112] In certain embodiments, provided herein is use of the composition as disclosed herein in improving soil density, soil water holding capacity, soil water retention capacity, in soil in which plants grow, compared to without.

[00113] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing mycorrhizal fungi on or in roots of plant, compared to a reference plant.

[00114] In certain embodiments, provided herein is use of the composition as disclosed herein in preventing or reducing flooding.

[00115] In certain embodiments, provided herein is use of the composition as disclosed herein in decreasing use of synthetic fertilizer, herbicide, and/or pesticide on plants or soil in which plants grow, compared to without.

[00116] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing nutrient uptake by a plant grown in soil to which composition applied compared to without.

[00117] In certain embodiments, provided herein is use of the composition as disclosed herein in decreasing uptake of one or more toxins, e.g., heavy metals, by plants grown in soil comprising composition.

[00118] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing plant nutrient density of a plant grown in soil to which composition applied compared to without.

[00119] In certain embodiments, provided herein is use of the composition as disclosed herein in reducing carbon footprint for raising livestock.

[00120] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing oil production of a plant not cannabis.

[00121] In certain embodiments, provided herein is use of the composition as disclosed herein in regenerating degraded soil.

7. Modulating soil characteristics

[00122] In certain embodiments provided herein are methods of modulating one or more characteristics of soil. Generally, the modulation will improve the one or more soil characteristics. An "improved" soil characteristic, as that term is used herein, includes a characteristic that has been modulated by the method in such a way as to advantageously affect germination, growth, quality, or other desired property of plants grown and/or maintained in the soil, and/or typically, increased the soil's resistance to drought, flooding, pests, and the like. Soil characteristics that can be modulated, e.g., improved, include soil density, soil water holding capacity (WHC), density of beneficial microbes in the soil, water retention of the soil, bioavailability of one or more plant nutrients in the soil, and/or carbon content of the soil.

[00123] In certain embodiments provided is a method of modulating, e.g., improving, one or more characteristics of soil in which plants grow and/or are maintained, comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time thereby modulating, e.g,, improving the one or more characteristics compared to reference soil and plants.

[00124] In certain embodiments provided is a method of increasing water holding capacity of soil in which plants are grown comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes or a derivative thereof; and (ii) providing suitable conditions for the plants to grow in the soil for a period of time; thereby increasing the water holding capacity of the soil, for example, WHC compared to reference soil and plants. In certain embodiments, WHC is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time. In certain embodiments, WHC is increased to at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55% in the period of time.

[00125] In certain embodiments provided is a method for converting one or more plant nutrients in soil in which plants are grown from non-bioavailable to bioavailable form (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/orthe plants; and (ii) providing conditions suitable for

growth of the plants and proliferation and/or other actions of the microbes for a duration sufficient for the one or more plant nutrients in the soil to convert from non-bioavailable to bioavailable form; whereby the one or more plant nutrients are converted from non-bioavailable to bioavailable form. In certain embodiments bioavailable form of the plant nutrient is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%. In certain embodiments the plant nutrient is nitrogen, phosphorus, potassium, or a combination thereof. In certain embodiments the plant nutrient is nitrogen. In certain embodiments the plant nutrient is phosphorus. In certain embodiments the plant nutrient is potassium. In certain embodiments the plant nutrient is calcium (Ca), magnesium (Mg), sulfur (S), sodium (Na), iron (Fe), manganese (Mn), zinc (Zn), copper (Cu), nickel (Ni), boron (B), molybdenum (Mo), silicon (Si), cobalt (Co), selenium (Se), or chloride (Cl), or a combination thereof. In certain embodiments the plant nutrient is calcium (Ca). In certain embodiments the nutrient is magnesium (Mg). In certain embodiments the nutrient is sulfur (S). In certain embodiments the nutrient is sodium (Na). In certain embodiments the nutrient is iron (Fe). In certain embodiments the nutrient is manganese (Mn). In certain embodiments the nutrient is zinc (Zn). In certain embodiments the nutrient is copper (Cu). In certain embodiments the nutrient is nickel (Ni). In certain embodiments the nutrient is boron (B). In certain embodiments the nutrient is molybdenum (Mo). In certain embodiments the nutrient is silicon (Si). In certain embodiments the nutrient is cobalt (Co). In certain embodiments the nutrient is selenium (Se). In certain embodiments the nutrient is chloride (Cl). In certain embodiments the method further comprises reducing or eliminating toxin uptake by the plants.

[00126] The one or more characteristics can comprise density of the soil, e.g., wherein density of the soil is improved. In certain embodiments, soil density before the first application is outside of an optimal range. In certain embodiments, soil density after the period of time is within an optimal range. In certain embodiments the density is modulated to at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm^3 dry weight of soil. In certain embodiments the one or more characteristics comprises

water holding capacity (WHC) of the soil, wherein WHC of the soil is increased. In certain embodiments WHC is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time. In certain embodiments WHC is increased to at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55% in the period of time. In certain embodiments the one or more characteristics comprises water retention of the soil, wherein the water retention of the soil is increased. In certain embodiments water retention is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time. In certain embodiments the one or more characteristics comprise a density of beneficial microbes in the soil, wherein the density is increased. In certain embodiments the density of beneficial microbes is increased at least 20, 50, 100, 200, 500, 1,000, or 10,000% and/or not more than 50, 100, 200, 500, 1,000, 10,000, or 100,000%, for example, at least 100%, preferably at least 500%, more preferably at least 1000%. In certain embodiments the one or more characteristics comprises bioavailability of one or more plant nutrients in the soil, wherein bioavailability of the one or more nutrients is increased. In certain embodiments the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months. In certain embodiments the method further comprises increasing carbon content of the soil compared to reference in the period of time. In certain embodiments carbon content in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300% in the period of time compared to reference. In certain embodiments the increase in soil carbon content is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton

carbon/hectare, such as wherein the soil carbon content is measured to a depth as described herein, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare, compared to reference. In certain embodiments the increase in soil carbon content after the period of time is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil. In certain embodiments soil carbon content is measured to a depth of at least 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, or 90 cm and/or not more than 15, 20, 25, 30, 40, 50, 60, 70, 80, 90 or 100 cm, for example, 10-100 cm, preferably 10-80 cm, more preferably 15-75 cm, even more preferably 15-60 cm, yet more preferably 15-50 cm, still more preferably 15-30 cm; in some cases 20 cm.

[00127] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant and/or soil. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least

95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*.

[00128] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00129] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

8. Reducing water use

[00130] Water is becoming a scarce commodity, and droughts and other extreme weather events are becoming more common, thus it is desirable to reduce the amount of water needed to germinate, grow, and/or maintain plants. Provided herein are methods and compositions for reducing water use for plants, e.g., reducing the amount of water necessary to germinate, grow and/or maintain plants, using a composition comprising one or more microorganisms, e.g., a plurality of microorganisms; reduction of water use is generally as compared to water use before the use of the composition. It will be appreciated that reduced water use in an operation where water is provided to plants for growth will considerably reduce the costs associated with the operation. A reduced need for water, and improvements to soil, e.g., as described herein, can also provide increased drought resistance, both for commercially raised plants as well as plants that are uncultivated, e.g., plants in grazing lands, grasslands, forests, and the like. It can also reduce the frequency and/or severity of environmental insults, such as fires, e.g., wildfires and/or floods, due to a variety of factors which can include greater water content of the plants and/or soil, improved plant and soil health, increased production of plant substances that confer resistance to fire, and/or greater plant density. Larger areas of land may also become available for plants, e.g., for agriculture as water requirements are reduced. Grasslands, rangelands, forests, and other non-irrigated areas can also see an increase in areas in which plants grow. Other concomitant effects can occur, such increases in plant biomass, community biodiversity, e.g., microbial community biodiversity, nutritional components of plants, soil and/or plant carbon, and/or other beneficial effects, such as effects described herein.

[00131] In certain embodiments provided herein is a method of reducing water use for growth and/or maintenance of plants in soil comprising allowing the plants to grow and/or be maintained in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil, the plants, a first application of a composition comprising a plurality of different

microbes or a derivative thereof; and (ii) providing suitable conditions for the plants to grow and/or be maintained in the soil for a period of time, thereby decreasing the amount of water necessary to produce a given amount of biomass from the plants and/or to maintain the plants in a desired state, compared to the amount of water necessary to produce the biomass and/or maintain the plants in a desired state for reference soil and plants, for the period of time.

[00132] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant and/or soil. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*.

[00133] In certain embodiments a microbial composition as described herein is used, , or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00134] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

9. Obtaining economic benefit

[00135] In certain embodiments provided is a method of obtaining an economic benefit from land on which plants are grown, wherein the land comprises at least 10, 100, 1000, 10,000, 100,000, 1M, or 10M, hectacres, comprising (i) obtaining and using one or more compositions comprising a microbial consortium, wherein (a) the one or more compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity, or plurality of second entities that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity (b) the second entity or plurality of second entities uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities ; (ii) determining a quantity of the one or more economic benefits; and (iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities. In certain embodiments the apportioning is done according to an agreement or agreements between the first and second entities or between the first entity and each of the plurality of second entities. In certain embodiments the apportioning is done by a processor that receives information regarding the one or more economic benefits and the agreement, processes the information to determine a quantitative value or values for economic benefits for apportionment between the first and second entities, or between the first entity and each of the plurality of second entities, and communicates the quantitative value or values to the first and/or second entities. In certain embodiments the second entity comprises a governmental entity. In certain embodiments the second entity comprises a private entity. In certain embodiments further comprises a plurality of second entities wherein the plurality of second entities comprises at least 5, 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, or 50,000 entities and/or not more than 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, 50,000, or 100,000 entities. In certain embodiments at least 10, 20, 30, 50, 70, 80, 90, 95, or 99% of the second entities are private farming entities. In certain embodiments the economic benefit comprises a carbon credit based, at least in part, on an increase of carbon in the soil. In certain embodiments the economic benefit comprises a financial benefit attributable to the plants. In certain embodiments the economic benefit comprises payment for the plants or parts of the plants. In certain embodiments the economic benefit comprises obtaining a further carbon credit for carbon stored in the plants. In certain embodiments the plants are trees.In

certain embodiments the financial benefit comprises a financial benefit realized from animals that eat the plants. The plants may be any suitable plants, such as those described herein.

10. Repair and regneration

[00136] Microbial compositions, such as those disclosed herein, can be used to restore or repair land that has been damaged or degraded, e.g., by human activity, so that the land is not capable of growth and/or maintenance of plants that previously grew, or capable only of decreased growth and/or maintenance of plants that previously grew. Each year 10 million hectares are abandoned due to soil erosion and/or diminished productivity, and another 10 million hectares due to salinization. It is projected that globally, almost one-third of agricultural land has been lost since 1960 and those that remain are losing topsoil at rates considered 6-10 times greater than the rate of soil formation. To compensate, this lost cropland is being replaced by clearing substantial portions of the world's rain forests promoting land area losses representing more than 60% of the deforestation now occurring worldwide. Use of microbial compositions, such as those described herein, can partially or completely repair such land and regenerate one or more plants of the land. Vegetation can also be restored in soil where it has been partially or completely depleted. Such land is subject to, e.g., drought, flooding, or other environmental insults that undamaged or undegraded land is not, or not to the degree of the damaged or degraded land. A variety of factors may be at play in such degradation or damage, many, most, or all of which may be partially or completely reversed by use of one or more microbial compositions, such as those disclosed herein.

[00137] In certain embodiments provided herein is a method of regenerating vegetation in a soil that has been partially or completely depleted of one or more types of vegetation and/or has reduced capacity to grow and/or maintain new vegetation, comprising (i) applying to the soil, plants growing or to be grown in the soil, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and(ii) providing suitable conditions for the plants to grow in the soil for a period of time. In certain embodiments the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months. In certain embodiments the method further comprises placing seeds, seedlings, or other plant propagules of the plants on or in the soil. In certain embodiments the vegetation comprises one or more grasses and has been partially or completely depleted by overgrazing. In certain embodiments the vegetation comprises one or more trees and has been partially or completely depleted by tree clearing. In certain embodiments the vegetation

comprises one or more commercial crops and has been partially or completely depleted by poor management practice.

[00138] In certain embodiments provided is a method of repairing damaged or degraded soil comprising (i) applying to the soil a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for plants to grow in the soil for the period of time. In certain embodiments the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months.

[00139] In certain embodiments provided herein is method for decreasing or eliminating flooding on land that has experienced or is likely to experience flooding, wherein soil of the land has grown, is growing, or will grow plants, comprising (i) applying to the soil, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby decreasing or eliminating flooding on the land. In certain embodiments the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months.

[00140] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant and/or soil. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more

preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*.

[00141] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00142] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

11. Nutrients

[00143] Microbial compositions, such as those disclosed herein, can be used to increase nutrient uptake and/or nutrient content in plants. Such increases can, for example, be in nutrients useful to the plant in growth, repair, maintenance and the like, and/or in nutrients for an animal that consumes the plants or parts of the plants, e.g., domesticated animals that consume the plants as at least part of their feed, or humans who consume the plants. Increasing nutrient availability to plants, e.g., by converting non- or low-bioavailable substances to more bioavailable forms can provide numerous benefits; it will be appreciated that one major benefit can be a reduced or even eliminated need for one or more synthetic fertilizers, as one or more of nitrogen, phosphate, potassium, and/or other plant nutrients may be more readily available from natural sources in the soil, thus reducing or eliminating the need for synthetic versions.

[00144] In certain embodiments provided herein is a method for increasing density of one or more nutrients in plants or plant parts, e.g., plants or plant parts to be consumed by animals, comprising (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/orthe plants, ; and (ii) providing conditions suitable for growth of the plants for a period of time, e.g., a period of time sufficient for the plants or plant parts to be suitable for consumption by the animals; thereby increasing density of the one or nutrients in the plants or plant parts compared to reference plants or plant parts. In certain embodiments the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or

not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year. In certain embodiments the one or more nutrients is increased in density by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%. In certain embodiments the animals comprise humans or domesticated animals. In certain embodiments the animals comprise humans. In certain embodiments the animals comprise domesticated animals. In certain embodiments the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses. In certain embodiments In certain embodiments the animals are cattle. In certain embodiments the increased nutrient density comprises increased protein density, increased mineral density, increased vitamin density, or a combination thereof. In certain embodiments the increased nutrient density comprises increased protein density. In certain embodiments the increased nutrient density comprises increased vitamin density. In certain embodiments the increased vitamin density comprises increased vitamin A density. In certain embodiments vitamin density comprises increased vitamin B_1 (thiamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B_2 (riboflavin) density. In certain embodiments the increased vitamin density comprises increased vitamin B_3 (niacin, nicotinic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_5 (pantothenic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_6 (pyridoxal, pyridoxine, or pyidoxamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B_7 (biotin) density. In certain embodiments the increased vitamin density comprises increased vitamin B_9 (folic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B_{12} density. In certain embodiments the increased vitamin density comprises increased vitamin C density. In certain embodiments the increased vitamin density comprises increased choline density. In certain embodiments the increased vitamin density comprises increased vitamin D density. In certain embodiments the increased vitamin density comprises increased vitamin E density. In certain embodiments the increased vitamin density comprises increased vitamin K1 density. In certain embodiments the increased vitamin density comprises increased

vitamin K2 density. In certain embodiments the increased nutrient density comprises increased mineral density. In certain embodiments the increased mineral density comprises increased calcium density. In certain embodiments the increased mineral density comprises increased magnesium density. In certain embodiments the increased mineral density comprises increased sodium density. In certain embodiments the increased mineral density comprises increased potassium density. In certain embodiments the increased mineral density comprises increased iron density. In certain embodiments the increased mineral density comprises increased copper density. In certain embodiments the increased mineral density comprises increased manganese density. In certain embodiments the increased mineral density comprises increased zinc density. In certain embodiments the increased mineral density comprises increased iodine density. In certain embodiments the increased mineral density comprises increased chromium density. In certain embodiments the increased mineral density comprises increased molybdenum density. In certain embodiments the increased mineral density comprises increased phosphorus density. In certain embodiments the increased mineral density comprises increased molybdenum density. In certain embodiments the increased mineral density comprises increased selenium density. In certain embodiments the method further comprises increasing biomass of the plants or plant parts.

[00145] In certain embodiments provided is a method for increasing uptake of one or more plant nutrients by plants grown in soil comprising (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/or the plants; and (ii) providing conditions suitable for growth of the plants and proliferation and/or other actions of the microbes for a suitable duration for plant nutrient uptake to increase; whereby plant nutrient uptake by the plants is increased. In certain embodiments the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year. In certain embodiments uptake of the one or more plant nutrients by the plants is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-

700, still more preferably 10-500, yet more preferably 20-500%. In certain embodiments the nutrient is nitrogen, phosphorus, potassium, or a combination thereof. In certain embodiments the nutrient is nitrogen. In certain embodiments the nutrient is phosphorus. In certain embodiments the nutrient is potassium. In certain embodiments n the nutrient is calcium (Ca), magnesium (Mg), sulfur (S), sodium (Na), iron (Fe), manganese (Mn), zinc (Zn), copper (Cu), nickel (Ni), boron (B), molybdenum (Mo), silicon (Si), cobalt (Co), selenium (Se), or chloride (Cl), or a combination thereof. In certain embodiments the nutrient is calcium (Ca). In certain embodiments the nutrient is magnesium (Mg). In certain embodiments the nutrient is sulfur (S). In certain embodiments the nutrient is sodium (Na). In certain embodiments the nutrient is iron (Fe). In certain embodiments the nutrient is manganese (Mn). In certain embodiments the nutrient is zinc (Zn). In certain embodiments the nutrient is copper (Cu). In certain embodiments the nutrient is nickel (Ni). In certain embodiments the nutrient is boron (B). In certain embodiments the nutrient is molybdenum (Mo). In certain embodiments the nutrient is silicon (Si). In certain embodiments the nutrient is cobalt (Co). In certain embodiments the nutrient is selenium (Se). In certain embodiments the nutrient is chloride (Cl).

[00146] The method may further comprise reducing or eliminating toxin uptake by the plants. The method may further comprise reducing water use by the plants. The method may further comprise increasing water holding capacity of the soil. The method may further comprise increasing uptake of atmospheric carbon by the plants and conversion of atmospheric carbon to soil carbon.

[00147] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant and/or soil. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably

at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*.

[00148] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00149] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

12. Conversion to organic farming

[00150] An agricultural practice can be converted from a non-organic practice to an organic practice in a surprisingly short time if a microbial composition, such as a composition as disclosed herein, is applied to the land and/or plants, e.g., as described herein. An "organic" agricultural practice, as that term is used herein, is a practice that conforms to applicable requirements for organic farming in the area in which the practice is situated. Although requirements may vary, depending on the locality, in general an organic agricultural operation is one in which little or no synthetic fertilizer, pesticide, or herbicide is used and, typically, where soil levels of certain substances, e.g., toxins or other deleterious substances, are below a certain level. Additional or alternative criteria may exist for a given locality. Microbial compositions, such as those disclosed herein, when applied to land and/or plants, e.g., as disclosed herein, restore soil health and vitality and can enable greater nutrient bioavailability and uptake by plants, and can reduce toxin levels in soil, all of which can accelerate the changes necessary to conform to local organic agricultural requirements. Depending on the starting point of the agricultural practice, the changes can occur in as little as three years, two years, or even a year, even if the practice is a conventional farming practice, e.g., a practice reliant or even heavily reliant on use of synthetic fertilizer, pesticide, and herbicide. Additional benefits may also be realized, e.g., as described herein, such as increased plant biomass, increased plant nutrient density, increased soil carbon, and/or reduced water use.

[00151] Thus provided herein is a method to convert non-organic agricultural practice, e.g. a conventional agricultural practice, to organic agricultural practice comprising (i) applying a composition comprising a plurality of microbes to plants, and/or to soil in which the plants grow or will grow, in a first application at a first time, wherein up to the first time the plants and soil were subject to non-organic farming practice; (ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time wherein after the period of time the non-organic agricultural practice has been converted to an organic agricultural practice. In certain embodiments the period of time is not more than 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, or 5 years, for example not more than 5, preferably not more than 4, more preferably not more than 3.5, even more preferably not more than 3, yet more preferably not more than 2.5, still more preferably not more than 2, yet still more preferably not more than 1.5 years.

[00152] In certain embodiments provided herein is a method for reducing concentration of a toxin in a soil, reducing uptake of the toxin by plants growing in the soil, and/or reducing a concentration of the toxin in the plants or plant parts, comprising (i) applying a composition comprising a plurality of microbes to the plants, or parts thereof, and/or to the soil, in a first application;(ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time wherein after the period of time concentration of the toxin in the soil, uptake of the toxin by plants growing in the soil, and/or concentration of the toxin in the plants or plant parts is reduced compared to before the first application. As used herein, a "toxin" includes a substance that, directly or indirectly, has a deleterious effect on an animal, e.g., a human that is exposed to the toxin, e.g., ingests it. In certain embodiments the period of time is at least 1, 2, 5, 7, 10, 12, 18, or 24 months and/or 2, 5, 7, 10, 12, 18, 24, or 36 months for example 1-36 months, preferably 2-25 months, more preferably 5-18 months. In certain embodiments the reduction is at least 5, 10, 20, 30, 40, 50, 60, 70, 80, 85, 90, 92, 95, 96, 97, 98, or 99%, or 100%. In certain embodiments the toxin comprises a synthetic pesticide, such as a synthetic pesticide, or impurity thereof, or an herbicide, such as a synthetic herbicide, or impurity thereof. In certain embodiments the toxin comprises a hydrocarbon. In certain embodiments the hydrocarbon comprises a petroleum hydrocarbon. In certain embodiments the hydrocarbon comprises a polynuclear aromatic hydrocarbon. In certain embodiments the toxin comprises a heavy metal. In certain embodiments the heavy metal comprises lead, arsenic, cadmium, chromium, or mercury.

[00153] In certain embodiments, the method further comprises, after the period of time, reducing water use to grow the plants and/or increasing nutrient density of the plants or plant parts and/or increasing biomass of the plants and/or increasing soil carbon content.

[00154] Any suitable microbial composition may be used in the methods of this section, such as a composition comprising a plurality of different microbes. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant and/or soil. In certain embodiments the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria. In certain embodiments at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic. In certain embodiments the different microbes are *Streptomyces*.

[00155] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00156] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

13. Economic benefit

[00157] In certain embodiments provided herein is a method of obtaining an economic benefit from land on which plants are grown comprising (i) obtaining and using one or more compositions comprising a plurality of different microbes, wherein (a) the one or more

compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity, and (b) the second entity uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity;(ii) determining a quantity of the one or more economic benefits; and (iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities. In certain embodiments the apportioning is done according to an agreement or agreements between the first and second entities.In certain embodiments the apportioning is done by a processor that receives information regarding the one or more economic benefits and the agreement, processes the information to determine a quantitative value or values for economic benefits for apportionment between the first and second entities, and communicates the quantitative value or values to the first and/or second entities. In certain embodiments the second entity is (i) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts; (ii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold; (iii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration; or (iv) an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold. In certain embodiments the land comprises pastureland. In certain embodiments the land comprises rangeland. In certain embodiments the land comprises land on which grass is grown for feed for the animals. In certain embodiments the land comprises land on which grain is grown for feed for the animals. In certain embodiments the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration. In certain embodiments the use of the land comprises a sport, game, or other recreation or entertainment, e.g., a golf course. In certain embodiments the second entity is an entity that owns, controls, manages or otherwise has rights to land in which plants are grown

with no or minimal alteration to plant or soil conditions. In certain embodiments the land is grassland, forest, or rangeland. In certain embodiments the second entity is a governmental entity. In certain embodiments the second entity is a private entity. In certain embodiments the one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, comprises(i) reduced costs due to decreased water use for the plants and/or (ii) reduced costs due to decreased use of fertilizer for the plants; and/or (iii) reduced costs due to decreased use of herbicides for the plants; and/or (iv) reduced costs due to decreased use of pesticides for the plants; and/or (v) increased biomass of the plants and/or (vi) increased price per plant or plant product or unit thereof and/or (vii) ability to use a greater area of land to grow or maintain the plants and/or (viii) ability to grow plants in a wider range of environmental conditions and/or (ix) a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants;and/or (x) a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; and/or (xi) a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; and/or (xii) a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants; In certain embodiments the one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, comprises a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants, or a combination thereof. In certain embodiments the one or more economic benefits comprise reduced costs due to decreased water use for the plants. In certain embodiments the one or more economic benefits comprise increased price per plant or plant product or unit thereof. In certain embodiments the one or more economic benefits comprise a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants. In certain embodiments the animals are cattle. In certain embodiments the animals are dairy animals, *e.g.*, cows, goats, or sheep. In certain embodiments the animals are poultry. In certain embodiments the poultry are raised for slaughter. In certain embodiments the poultry are egg layers. In certain embodiments the one or more compositions are supplied by the first entity that produces, distributes, or otherwise supplies the one or more compositions to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 500, or 1000 other entities, different from the first entity, that obtain, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants

grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for each of the entities; wherein the apportioning is done according to an agreement or agreements between the first entity and each other entity that delineates an apportionment of the economic benefits between the first entity and each of the other entities; and wherein the apportioning is done by one or more processors that receives information regarding each of the agreements and information regarding the one or more economic benefits for each of the other entities, determines the apportionment between the first entity and each of the other entities, and communicates information comprising the apportionment to the first entity and/or each of the other entities.

[00158] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00159] The plants in the soil may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

14. Trees

[00160] Microbial compositions, e.g., microbial compositions described herein, can be used to improve one or more characteristics of trees. Typically, microbial compositions are supplied to a user along with a second composition comprising one or more macronutrients, micronutrients, or carbon sources for the trees; either or both of the microbial composition and the nutrient composition may be tailored according to the type of tree, type of land, condition of the tree, and the like. Instructions for use may also be supplied, e.g., as written material, oral material, or material presented in audiovisual form. Tree growth can be increased, e.g., as compared to reference tree growth, e.g, growth of the same tree in a certain previous time period, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 years, or a similar tree in the same environment. Additionally or alternatively, there can be an increase in sap production and/or various compounds found in sap, e.g., an increase in sugars, terpenes, minerals, nutrients, carbon compounds, hormones, various organic carbon compounds, acids and proteins. Additionally or alternatively there can be an increase in carbon-rich materials excreted from tree leaf exudate. Other benefits include and increase in root exudate production and/or enhancement of a tree's ability to tap into new sources of groundwater and/or an increase in macronutrients and/or micronutrients deposited in leaves and tree canopy and/or an increase in tree canopy and/or an improvement in tree photosynthetic capacity and/or enzymatically signaling tree roots to search for water and key nutrients and/or

reduction in evapotranspiration rates and/or increased retention of stomatal conductance of tree foliage and/or an increase in tree primary and secondary growth and/or increases in epicormic growth and/or an increase in tree seed germination rates and/or reduction in tree seed germination time and/or Increases in plant growth rates in the stages of conception (seed), birth (sprout), adult (mature), and elder (decline) and/or Improved tree immune responses to stresses such as drought and soil degradation and/or Increased soil and root Mycorrhization and/or faster wound healing, e.g., after a pruning session. Effects may be seen in a very short time, e.g., less than 6, 5, 4, 3, 2, or 1 month, such as new epicormic growth thought to be dead or in slow growing areas and/or dramatic increases in leaf macro/micronutrient density and/or mproved leaf color and/or improved shoot elongation and bud development on all parts of mature and juvenile trees and/or root biomass increases and/or increases in soil water holding capacity and/or revitalization of mature trees. The various characteristics may be determined by any suitable methods, such as methods known in the art. Tree growth may be measured by tree ring growth, which can be measured by, e.g., core samples. An exemplary protocol is provided in Example 29. In certain embodiments, in addition to a microbial composition and a nutrient composition, a user may be supplied with a kit for measuring tree ring growth. In certain embodiments, provided is a kit comprising a microbial composition and a nutrient composition wherein the compositions comprise sufficient material for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 treatments, for example, 1 treatment, or two treatments of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 trees, for example, 1 tree, or two trees. The tree can be a healthy tree, but in many cases a tree that is dormant or even a tree thought to be dead.

[00161] In certain embodiments provided is a method of improving one or more characteristics of a tree rooted in soil comprising (i) providing one or more nutrients to the soil in which the tree is rooted; and (ii) providing a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil and/or the tree in a first application. Both the microbes and the nutrients may be supplied in separate containers to a user. The improved characteristic may be one or more of those described above. In certain embodiments, the improved characteristic is an increase in tree rings, such as at least a 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, or 400% increase. In certain embodiments, the improved characteristic is an increase in diameter at breast height, such as at least a 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, or 400% increase Improvements in one or more characteristics may occur in a time after first application of the microbes and nutrients of less than 6 months, 8 months, 10 months, 1, 1.2, 1.5, 1.7, or two years.

[00162] In certain embodiments provided is a method of revitalizing a dormant tree comprising applying to the soil in which the tree is rooted and/or the tree a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil in wherein the microbial composition the tree is rooted in a first application and allowing the tree to grow for a duration of time, such as less than 6 months, 8 months, 10 months, 1, 1.2, 1.5, 1.7, or two years.

[00163] In certain embodiments provided is a kit comprising (i) a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes in a first package; and (ii) a composition comprising at least 1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, or 200 and/or not more than 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, 200 or 500 nutrients in a second package, different from the first

[00164] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used.

[00165] A tree may be any suitable tree, such as a tree as disclosed herein, for example in Section I.B.10

[00166] In certain embodiments provided is a kit comprising (i) a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes in a first package; and (ii) a composition comprising at least 1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, or 200 and/or not more than 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, 200 or 500 nutrients in a second package, different from the first.

15. Increased biomass

[00167] Microbial compositions, such as microbial compositions described herein, can be used to increase biomass of one or more plants grown in a growth medium where the growth medium and/or the plants have been treated with the microbial composition, e.g., a microbial composition as described herein.

[00168] In certain embodiments provided herein is a method for increasing biomass of plants or plant parts, e.g., plants or plant parts to be consumed by animals, comprising (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/orthe plants, ; and (ii) providing conditions suitable for growth of the plants

for a period of time; thereby increasing biomass of the plants or plant parts compared to reference plants or plant parts. In certain embodiments the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year. In certain embodiments the biomass is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[00169] In certain embodiments a microbial composition as described herein is used, or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned vehicles is used, for example as described herein.

[00170] The plants may be any suitable plants, such as plants described herein, e.g. one or more of those described in Section I.B.10.

16. Production methods

[00171] Microbial compositions as disclosed herein can be produced using any suitable method. In certain embodiments, provided herein are methods for preparing, *e.g.*, propagating, one or more microbes from a stock, *e.g.*, a seed, comprising the one or more microbes. Stocks of the microbes can be propagated for use in the compositions of the present application using techniques known in the art. The stock may comprise any suitable number of microbes. In certain cases, it may be beneficial that the stocks are isolated and/or pure. In other cases, it may be beneficial that the stocks comprise a plurality of different microbes. The stock can be any suitable stock as described herein, such as a cryostock, for example a glycerol stock, a solid medium comprising one or more microbe, e.g., an agar plate, and/or a liquid medium comprising one or more microbe. Typically, the stock is brought to a working form, for example thawed in the case of a cryostock. The stock is then inoculated into a heterologous medium. The medium is typically chosen based on the nutritional requirements of the microbes. After inoculation, growth

is commonly effected in a culture vessel, such as a flask or a bioreactor. The culture vessel can be any appropriate shape or size for propagating the microbes. The culture vessel can range in size and scale from 10s of mLs to liters to 1000s of liters. The culture vessel can be made of any suitable material known and used in the art, for example glass and/or stainless steel. After inoculated, the culture is incubated at an optimal growth temperature for the microbe such that the microbes replicate to a suitable level. The growth medium can be incubated at (*e.g.*, the microbes are grown at) a temperature of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 26, or 38 °C and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 °C, for example 10-40 °C, preferably 20-30 °C, more preferably 26-30 °C for a suitable period of time, such as at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 days and/or not more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days, for example 0.1-15 days, preferably 5-12 days, more preferably 7-10 days. Cultures can be propagated in batch, fed-batch, *e.g.*, nutrients are added intermittently to the culture to maintain optimal conditions without diluting the culture, or continuously, *e.g.*, a continuous stirred reactor, for example a turbidostat or a chemostat. The microbes can be sub-cultured any number of times as needed to scale-up to produce the desired amount of microbes for the for use in the compositions as disclosed herein. Once the desired amount of microbes have been produced, the microbes can then be processed into a composition as described herein. In certain embodiments, at least a portion of the growth medium is removed. The growth medium can be removed using any suitable technique, such as filtration, centrifugation, spray drying, or the like. The microbes can be further dried after removing at least a portion of the growth medium. The microbes from each propagated stock may be processed, for example into a powder, individually and later combined, for example as a powder, with microbes from one or more stocks and/or one or more agriculturally acceptable adjuvants. Additionally or alternatively, the microbes from one or more propagated stock may combined and then processed, for example into a powder, and later combined, for example as a powder, with microbes from one or more processed batches and/or one or more agriculturally acceptable adjuvants.

[00172] In preferred embodiments, the methods as disclosed herein are performed aseptically.

[00173] The methods as disclosed herein can be used to grow any suitable number of microbe stocks simultaneously and/or sequentially. In certain embodiments, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 microbe stocks are separately grown using the method as disclosed herein.

[00174] In certain embodiments, a growth medium (*e.g.*, solid or liquid medium) is inoculated with a stock of microbes. The stock can comprise any suitable stock, such as a cryostock, *e.g.*, a glycerol stock, a solid medium comprising one or more of the first microbe, *e.g.*, an agar plate,

and/or a liquid medium comprising one or more of the first microbe. In certain embodiments, the stock comprises a glycerol stock comprising a glycerol concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50%, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22%.

[00175] In certain embodiments, at least a portion of the microbe stock is transferred to a solid medium and distributed onto the solid medium, *e.g.*, streaked or spread, and then grown at a suitable temperature and time whereby the microbes are propagated. The solid medium can be any suitable solid medium. In preferred embodiments, the solid medium comprises one or more starches, for example an oat starch, and a gelling agent, for example agar. In more preferred embodiments, the solid medium comprises one or more starches, a gelling agent, and a plurality of vitamins. In certain embodiments the solid medium comprises ISP-3 or ISP-4 medium. The gelling agent can be any suitable gelling agent, for example agar, pectin, gelatin, and the like, preferably at a concentration of at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, or 4 wt% and/or no more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, or 5 wt%, for example 0.1-5 wt%, preferably 0.2-2 wt%, more preferably 0.4-1 wt%. In certain embodiments, the solid medium has been sufficiently dried prior to transfer of the at least portion of the stock such that there are not visible droplets on the surface of the solid medium.

[00176] In certain embodiments, at least a portion of the stock of microbes and/or microbes propagated on solid medium is transferred to a liquid medium, and then grown at a suitable temperature and time whereby the microbes are propagated. The liquid medium can be any suitable liquid medium. In preferred embodiments, the liquid medium comprises one or more starches, for example an oat starch. In more preferred embodiments, the liquid medium comprises one or more starches and a plurality of vitamins. In certain embodiments, the liquid medium comprises oat medium, for example ISP-3 or ISP-4 without the agar.

[00177] After inoculating the growth medium, the growth medium is incubated at a suitable temperature for a suitable period of time such that the microbes replicate to a suitable level. In certain embodiments, the growth medium is incubated at (*e.g.*, the microbes are grown at) a temperature of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 26, or 38 °C and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 °C, for example 10-40 °C, preferably 20-30 °C, more preferably 26-30 °C. In certain embodiments, the growth medium is incubated for (*e.g.*, the microbes are grown for) at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 days and/or not more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days, for example 0.1-15 days, preferably 5-12 days, more preferably 7-10 days. In certain embodiments, for example when the growth

medium comprises a solid medium, the suitable level to which the first microbe grows comprises a confluency of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95% and/or no more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100%, for example 5-100%, preferably 50-100%, more preferably 70-100%. In certain embodiments, for example when the growth medium comprises a liquid medium, the suitable level to which the first microbe grows comprises a microbe concentration, *e.g.*, turbidity, as measured by optical density, for example at 600 nM (OD_{600}), of at least 0.2, 0.4, 0.6, 0.8, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 20 and/or no more than 0.4, 0.6, 0.8, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 50, for example 0.2-50, preferably 0.5-10, more preferably 1-5. Any suitable method can be used to measure the concentration of microbes in the culture, for example optical density, cell counting, cytometry, dry cell weight, colony forming units, and/or nucleic acid quantification.

[00178] In certain embodiments, after the microbes have grown to a suitable level, at least a portion of the heterologous medium is removed. Where the heterologous medium comprises a solid medium, the population of microbes can be removed from the solid medium, *e.g.*, harvested, using any suitable technique, such as scraping. Where the heterologous medium comprises a liquid medium, the population of microbes can be removed from the liquid medium using any suitable technique, such as filtration, centrifugation, spray drying, or the like. Any suitable number of propagations may be performed to scale-up to generate the desired amount of microbes. In certain embodiments, the population of microbes is then further concentrated/dried.

[00179] The propagated microbes can be concentrated by, for example, removing at least a portion of the first and/or second heterologous medium. Any suitable amount of the heterologous medium can be removed, such as at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100% of the heterologous medium. The heterologous medium can be removed using any suitable method, for example filtering and/or drying in a sterile environment.

[00180] In certain embodiments, the at least portion of the growth medium is removed by filtration. The filter can comprise any suitable filter such that at least a portion of the microbes are thereby retained to produce a retentate comprising one or more microbes and a filtrate comprising at least a portion of the growth medium. In certain embodiments, the filter is configured to retain at least 20, 30, 40, 50, 60, 70, 80, 85, 90, 95, 99, or 100% of the microbes in the growth medium. The filter can comprise a first filter layer. The first filter layer can comprise a pore size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um. In certain embodiments, the first filter layer comprises a pore size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for

example, 0.2-300 um, preferably 120-240 um, more preferably 160-220 um. The filter can further comprise a second filter layer under the first filter layer comprising a pore size smaller than the first filter layer. The second filter layer can comprise a pore size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 20-100 um, more preferably 40-80 um. In certain embodiments, the portion of microbes retained comprises at least 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.5, 99.9, or 100% of the microbes, for example at least 50, preferably at least 70, more preferably at least 90, even more preferably at least 95, yet more preferably at least 98, still more preferably at least 99%. In certain embodiments, after filtering, the microbes are removed from the filter and placed in a collection vessel. Additionally or alternatively, the microbes can be spray dried and/or lyophilized.

[00181] In certain embodiments, after filtration, the microbes retained on the filter are further dried, for example in a laminar flow hood. In certain embodiments, at least 50, 60, 70, 80, 90, 95, 99, or 100% of the excess water is removed from the microbes. In certain embodiments, the dried microbes comprise less than 5, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05, 0.01, 0.005, or 0.001% water by weight, for example less than 1, preferably less than 0.5, more preferably less than 0.1, even more preferably less than 0.01, yet more preferably less than 0.005, still more preferably less than 0.001%.

[00182] In certain embodiments, the dried microbes are then processed into a powder. In certain embodiments, the powder comprises a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um. Any suitable technique can be used to process the dried first population of microbes to the desired median particle size, for example blending.

[00183] Once dried, the dried microbes may be processed into a powder and stored until further use. In certain embodiments, the dried microbes are combined with one or more agriculturally acceptable adjuvants. As shown in Figures 1a and 1d, powdered stocks of microbes (101) may then be combined to form any one of the compositions as disclosed herein (103), and, optionally, mixed with one or more agriculturally acceptable adjuvants (102), as disclosed herein, for example one or more liquid carriers, solid carriers, surfactants, viscosity modifiers, thickeners, rheology additives, structuring agents, preservatives, biocides or biostatic agents, antifreezes, crystallization inhibitors, suspending agents, dyes, anti-oxidants, foaming agents,

light absorbers, light blockers, mixing auxiliaries, antifoams, complexing agents, neutralizing or pH-modifying substances and buffers, corrosion inhibitors, fragrances, wetting agents, take-up enhancers, micronutrients, plasticizers, glidants, lubricants, and dispersants.an emulsifier, a carrier, a stabilizer, or a combination thereof. Any suitable number of stocks can be propagated and then combined, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 stocks.

[00184] In certain embodiments, the dried microbes are then combined with one or more agriculturally acceptable adjuvant. Any suitable agriculturally acceptable adjuvant can be used, such as an emulsifier, *e.g.*, a surfactant, and/or a carrier.

[00185] In certain embodiments, the agriculturally acceptable adjuvant comprises an agent that helps the powder composition dissolve in water, *e.g.*, a wetting agent. In certain embodiments, the emulsifier comprises a surfactant and/or a lipid, for example soy lecithin, yucca powder, Tween 20, and/or Tween 80. In certain embodiments, the emulsifier is at a concentration of at least 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, or 9 wt% and/or no more than 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, 9, or 10 wt%, for example 0.5-10 wt%, preferably 1-3 wt%, more preferably 1.8-2.2 wt%. In certain embodiments, the carrier comprises a saccharide, for example a monosaccharide, di-saccharide, tri-saccharide, and/or a polysaccharide, *e.g.*, glucose, lactose, maltose, and/or galactose. In certain embodiments, the carrier comprises glucose. In certain embodiments, the carrier is at a concentration of at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 wt% and/or no more than 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 wt%, for example 50-100 wt%, preferably 70-100 wt%, more preferably 80-100 wt%, even more preferably 90-100 wt%, still more preferably 95-100 wt%.

[00186] In certain embodiments, the one or more carriers comprise a monosaccharide, a polysaccharide, a lipid, or a combination thereof. In certain embodiments, the one or more carriers comprises a monosaccharide. In certain embodiments, the monosaccharide comprises glucose. In certain embodiments, the concentration of the monosaccharide is at least 20, 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, or 99 wt% and/or not more than 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, 99, 99.5, or 99.9 wt%, for example 20-99 wt%, preferably 70-95 wt%, more preferably 85-95 wt%. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise a polysaccharide. In certain embodiments, the polysaccharide comprises a starch. In certain embodiments, the starch is derived from yucca. In certain embodiments, the starch is derived from oat. In certain embodiments, the concentration of the polysaccharide is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6,

1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%. In certain embodiments, the one or more agriculturally acceptable adjuvants comprises one or more surfactants. In certain embodiments, the surfactant comprises a lipid. In certain embodiments, the lipid comprises a lecithin. In certain embodiments, the lecithin comprises a soy lecithin. In certain embodiments, the concentration of surfactant is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[00187] An exemplary method for propagating and/or processing one or more microbes is shown in Figure 1b. Briefly, a stock of microbes is transferred to solid medium and grown to form colonies. At least a portion of the bacteria within the colonies are transferred to a liquid medium and grown to a desired concentration. Thereafter, the solution of microbes is concentration by removing at least a portion of the liquid medium. The microbes are then dried and, optionally, combined with one or more agriculturally acceptable adjuvants to form a composition comprising dried microbes and one or more agriculturally acceptable adjuvants. Multiple dried stocks of microbes may be combined before or after adding the one or more agriculturally accepted adjuvants.

[00188] An exemplary method for propagating and/or processing one or more microbes is shown in Figure 1c. Specifically, frozen culture of each microbe are separately streaked onto oat agar medium and incubated at 28 °C for 7-10 days until suitable confluency has been achieved. At least a portion, preferably ~50% of the surface area of the plate, are separately harvested and separately inoculated into liquid medium, preferably oat liquid medium and grown at 28 °C for 7-10 days. The microbes are then combined and sieved through a filter. Retained microbes are dried and processed to a powder. The microbe powder is then combined with one or more agriculturally acceptable adjuvants, for example glucose and, optionally, soy lecithin or yucca powder, to produce a composition comprising a plurality of microbes.

[00189] The processed microbes can be stored in any suitable packaging. The packaging may be a sealed bag, that optionally protects the microbes from any environmental stressors, such as UV light.

[00190] In certain embodiments, the microbes comprises a viability of at least 10^6, 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition cfu/g after processing.

[00191] In certain cases, it may be beneficial that the stocks are isolated and/or pure. In other cases, it may be beneficial that the stocks comprise a plurality of different microbes.

[00192] In certain embodiments, the first microbe and the one or more additional microbes are first grown separately, combined, and then grown together. In certain embodiments, growth media (*e.g.*, solid or liquid media) are separately inoculated with a portion of a stock of the respective microbe to be growth in the growth medium, for example in the case of growing two strains a microbes, a first growth medium is inoculated with a portion of a first stock of the first microbe and a second growth medium is separately inoculated with a portion of a second stock of the second microbe. The stock can comprise any suitable stock, such as a cryostock, *e.g.*, a glycerol stock, a solid medium comprising one or more of the microbes, *e.g.*, an agar plate, and/or a liquid medium comprising one or more of the microbes. In certain embodiments, the stock comprises a glycerol stock comprising a glycerol concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50%, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22%. After inoculating the growth medium, the growth medium is incubated at a suitable temperature for a suitable period of time such that the microbes replicate to a suitable level. In certain embodiments, the growth medium is incubated at (*e.g.*, the microbes are grown at) a temperature of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 26, or 38 °C and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 °C, for example 10-40 °C, preferably 20-30 °C, more preferably 26-30 °C. In certain embodiments, the growth medium is incubated for (*e.g.*, the microbes are grown for) at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 days and/or not more than 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days, for example 0.1-15 days, preferably 5-12 days, more preferably 7-10 days. In certain embodiments, for example when the growth medium comprises a solid medium, the suitable level to which the microbe grows comprises a confluency of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95% and/or no more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100%, for example 5-100%, preferably 50-100%, more preferably 70-100%. In certain embodiments, for example when the growth medium comprises a liquid medium, the suitable level to which the first microbe grows comprises a microbe concentration, *e.g.*, turbidity, as measured by optical density, for example at 600 nM (OD_{600}), of at least 0.2, 0.4, 0.6, 0.8, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 20 and/or no more than 0.4, 0.6, 0.8, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, or 50, for example 0.2-50, preferably 0.5-10, more preferably 1-5. Any suitable method can be used to measure the concentration of microbes in the culture, for example

optical density, cell counting, cytometry, dry cell weight, colony forming units, and/or nucleic acid quantification.

[00193] In certain embodiments, provided herein are methods for preparing, *e.g.*, growing, two or more microbes together. In certain embodiments, the method comprises growing a first microbe and one or more additional microbes, such as at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, or 50 additional microbes, for example 1-50 additional microbes, preferably 1-20 additional microbes, more preferably 1-10 additional microbes. Thus, in certain embodiments, the method comprises growing together at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, or 50 microbes, for example 1-50 total microbes, preferably 1-20, more preferably 1-10. In certain embodiments, the first microbe and one or more additional microbes are grown in a first heterologous medium. In certain embodiments, the first microbe and one or more additional microbes are grown from a stock of the first microbe in a first heterologous medium to produce a first population of microbes. At least a portion of the first population of microbes is then transferred to a second heterologous medium and grown to produce a second population of microbes. In certain embodiments, the first population of microbes and/or the second population of microbes are then concentrated, for example at least a portion of the first and/or second heterologous medium are removed thereby concentrating the microbes. In certain embodiments, at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100% of the heterologous medium is removed.

[00194] In certain embodiments, provided herein is a method of growing one or more microbes comprising inoculating a heterologous medium with a first population of microbes, *e.g.*, a stock of microbes comprising any one of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2 , or O-46-O140, and providing suitable conditions for one or more microbes to grow.

[00195] In certain embodiments, the first stock can be, but is not required to be, pure.

[00196] In certain embodiments, the first population comprises Streptomyces designation 1. In certain embodiments, the first population comprises Streptomyces designation 2. In certain embodiments, the first population comprises Streptomyces designation 3. In certain embodiments, the first population comprises Streptomyces designation 4. In certain embodiments, the first population comprises Streptomyces designation 5. In certain embodiments, the first population comprises Streptomyces designation 6. In certain embodiments, the first population comprises Streptomyces designation 7. In certain embodiments, the first population comprises Streptomyces designation 8. In certain embodiments, the first population comprises Streptomyces designation 9. In certain

embodiments, the first population comprises Streptomyces designation 10. In certain embodiments, the first population comprises Streptomyces designation 11. In certain embodiments, the first population comprises Streptomyces designation 12. In certain embodiments, the first population comprises Streptomyces designation 13. In certain embodiments, the first population comprises Streptomyces designation 14. In certain embodiments, the first population comprises Streptomyces designation 15. In certain embodiments, the first population comprises Streptomyces designation 16. In certain embodiments, the first population comprises Streptomyces designation 17. In certain embodiments, the first population comprises Streptomyces designation 18. In certain embodiments, the first population comprises Streptomyces designation 19. In certain embodiments, the first population comprises Streptomyces designation 20. In certain embodiments, the first population comprises Streptomyces designation 21. In certain embodiments, the first population comprises Streptomyces designation 22. In certain embodiments, the first population comprises Streptomyces designation 23. In certain embodiments, the first population comprises Streptomyces designation 24. In certain embodiments, the first population comprises Streptomyces designation 25. In certain embodiments, the first population comprises Streptomyces designation 26. In certain embodiments, the first population comprises Streptomyces designation 27. In certain embodiments, the first population comprises Streptomyces designation 28. In certain embodiments, the first population comprises Streptomyces designation 29. In certain embodiments, the first population comprises Streptomyces designation 30. In certain embodiments, the first population comprises Streptomyces designation 31. In certain embodiments, the first population comprises Streptomyces designation 32. In certain embodiments, the first population comprises Streptomyces designation 33. In certain embodiments, the first population comprises Streptomyces designation 34. In certain embodiments, the first population comprises Streptomyces designation 35. In certain embodiments, the first population comprises Streptomyces designation 36. In certain embodiments, the first population comprises Streptomyces designation 37. In certain embodiments, the first population comprises Streptomyces designation 38. In certain embodiments, the first population comprises Streptomyces designation 39. In certain embodiments, the first population comprises Streptomyces designation 40. In certain embodiments, the first population comprises Streptomyces designation 41. In certain embodiments, the first population comprises Streptomyces designation 42. In certain embodiments, the first population comprises Streptomyces designation 43. In certain embodiments, the first population comprises Streptomyces designation 44. In certain

embodiments, the first population comprises Streptomyces designation 45. In certain embodiments, the first population comprises any one of the microbes in Streptomyces designation 46.

[00197] In certain embodiments, the heterologous medium comprises a solid medium. In certain embodiments, the solid medium comprises agar. In certain embodiments, the concentration of agar is at least 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, or 1.4 and/or no more than 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, or 1.5 g/L, for example 0.3-1.5 g/L, preferably 0.4-1 g/L, more preferably, 0.6-0.8 g/L. In certain embodiments, the heterologous medium comprises a liquid medium. In certain embodiments, the heterologous medium comprises a polysaccharide, a disaccharide, a monosaccharide, a gum, a natural or synthetic derivative thereof. In certain embodiments, the heterologous medium comprises a polysaccharide. In certain embodiments, the polysaccharide comprises a starch. In certain embodiments, the starch is an oat starch. In certain embodiments, the concentration of starch is at least 10, 20, 30, 40, 50, 60, 70, 80, or 90 g/L and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, or 100 g/L, for example 10-100, preferably 20-80, more preferably 30-70. In certain embodiments, the heterologous medium further comprises a vitamin. In certain embodiments, the vitamin comprises Vitamin A, Vitamin C, Vitamin D, Vitamin E, Vitamin B1, Vitamin B2, Niacin, Vitamin B6, Folate, Vitamin B12, Biotin, Pantothenic Acid, Calcium, Iron, Iodine, Magnesium, Zinc, Selenium, Copper, or a combination thereof. In certain embodiments, the vitamin comprises Vitamin A. In certain embodiments, the Vitamin A is present at a concentration of at least 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, or 1400 and/or not more than 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or 1500 ug/L, for example 100-1500, preferably 300-1000, more preferably 500-900, even more preferably 600-800. In certain embodiments, the vitamin comprises Vitamin C. In certain embodiments, the Vitamin C is present at a concentration of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 mg/L, for example 10-50, preferably 50-130, more preferably 70-110, even more preferably 80-100. In certain embodiments, the vitamin comprises Vitamin D. In certain embodiments, the Vitamin D is present at at least 5, 10, 15, 20, 25, 30, 35, 40, or 45 and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, or 50 ug/L, for example 5-50, preferably 10-40, more preferably 15-35, even more preferably 20-30. In certain embodiments, the vitamin comprises Vitamin E. In certain embodiments, the Vitamin E is present at a concentration of at least 5, 7, 9, 11, 13, 15, 17, 19, 21, or 23 and/or not more than 7, 9, 11, 13, 15, 17, 19, 21, 23, or 25 mg/L, for example 5-25, preferably 9-21, more preferably 11-19, even more preferably 13-17. In certain embodiments, the vitamin comprises Vitamin B1. In certain embodiments, the Vitamin B1 is

present at a concentration of at least 1, 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, or 3.8 and/or not more than 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, or 4 mg/L, for example 1-4 mg/L, preferably 1.6-3.2, more preferably 2-2.8, even more preferably 2.2-2.6. In certain embodiments, the vitamin comprises Vitamin B2. In certain embodiments, the Vitamin B2 is present at a concentration of at least 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, or 2.75 and/or not more than 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, 2.75, or 2.85 mg/L, for example 1.25-2.85, preferably 1.55-2.55, more preferably, 1.65-2.45, more preferably 1.85-2.05. In certain embodiments, the vitamin comprises Niacin. In certain embodiments, the Niacin is present at a concentration of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, or 38 and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 mg/L, for example 10-40, preferably 14-36, more preferably 18-32, even more preferably 20-28. In certain embodiments, the vitamin comprises Vitamin B6. In certain embodiments, the Vitamin B6 is present at a concentration of at least 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, or 4.8 and/or not more than 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, 4.8, or 5 mg/L, for example 2-5, preferably 2.6-4.4, more preferably 3-4, even more preferably 3-3.8. In certain embodiments, the vitamin comprises Folic Acid. In certain embodiments, the Folic Acid is present at a concentration of at least 120, 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, or 680 and/or not more than 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, 680, or 720 ug/L, for example 120-720, preferably 240-600, more preferably 320-480, even more preferably 360-440. In certain embodiments, the vitamin comprises Vitamin B12. In certain embodiments, the Vitamin B12 is present at a concentration of at least 5.4, 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, or 13.8 and/or not more than 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, 13.8, or 14.4, for example 5.4-14.4, preferably 7.2-12.6, more preferably 8.4-11.4, even more preferably 9-10.2. In certain embodiments, the vitamin comprises Biotin. In certain embodiments, the Biotin is present at a concentration of at least , 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 and/or not more than 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or 85 ug/L, for example 10-85, preferably 20-75, more preferably 30-65, even more preferably 35-55. In certain embodiments, the vitamin comprises Pantothenic Acid. In certain embodiments, the Pantothenic Acid is present at a concentration of at least 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, or 11 and/or not more than 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, or 11.5 mg/L, for example 4-11.5, preferably 5.5-10, more preferably 6.5-9, even more preferably 7-8. In certain embodiments, the vitamin comprises Calcium. In certain embodiments, the Calcium is present at a concentration of at least 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 and/or not more than 70, 80, 90,

100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 210 mg/L, for example 60-210, preferably 80-190, more preferably 100-170, even more preferably 120-140. In certain embodiments, the vitamin comprises Iron. In certain embodiments, the Iron is present at a concentration of at least 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32 and/or not more than 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 mg/L, for example 6-34, preferably 12-26, more preferably 14-22, even more preferably 16-20. In certain embodiments, the vitamin comprises Iodine. In certain embodiments, the Iodine is present at a concentration of at least 80, 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180, 190, 200, 210, or 220 and/or not more than 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180, 190, 200, 210, 220, or 230 mg/L, for example 80-230, preferably 100-200, more preferably 120-180, even more preferably 140-160. In certain embodiments, the vitamin comprises Magnesium. In certain embodiments, the Magnesium is present at a concentration of at least 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, or 70 and/or not more than 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, 70, or 74 mg/L, for example 18-74, preferably 22-62, more preferably 30-54, even more preferably 38-46. In certain embodiments, the vitamin comprises Zinc. In certain embodiments, the Zinc is present at a concentration of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 mg/L, for example 2-15, preferably 3-13, more preferably 5-11, even more preferably 7-9. In certain embodiments, the vitamin comprises Selenium. In certain embodiments, the Selenium is present at a concentration of at least 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, or 69 and/or not more than 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, or 73 ug/L, for example 13-73, preferably 25-57, more preferably 29-53, even more preferably 37-45. In certain embodiments, the vitamin comprises Copper. In certain embodiments, the Copper is present at a concentration of at least 0.65, 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, or 2.05 and/or not more than 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, or 2.15 mg/L, for example 0.65-2.15, preferably 0.85-1.85, more preferably 1.05-1.65, even more preferably 1.25-1.45.

[00198] In certain embodiments, the first population of microbes is in a stock solution comprising a cryoprotectant prior to inoculating. In certain embodiments, the cryoprotectant comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride, ammonium sulfate, or a combination thereof. In certain embodiments, the cryoprotectant comprises glycerol. In certain embodiments, the glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50% v/v, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22%.

[00199] In certain embodiments, the method further comprises inoculating the heterologous medium with a second population of microbes different from the first. In certain embodiments, the method further comprises inoculating the heterologous medium with a third population of microbes different from the first or the second. In certain embodiments, the method further comprises inoculating the heterologous medium with a fourth population of microbes different from the first, second, or third. In certain embodiments, the method further comprises inoculating the heterologous medium with a fifth population of microbes different from the first, second, third, or fourth.

[00200] In certain embodiments, the method further comprises concentrating the one or more microbes after growing. In certain embodiments, concentrating comprises filtering. In certain embodiments, the filtering is through a filter comprising pores of a size sufficient to retain at least a portion of the microbes. In certain embodiments, the filter comprises a first filter layer comprising pores of a first size and a second filter layer comprising pores of a second size. In certain embodiments, the pores are of a size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um. In certain embodiments, the first size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 120-240 um, more preferably 160-220 um. In certain embodiments, the second size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 20-100 um, more preferably 40-80 um. In certain embodiments, the portion of microbes retained comprises at least 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.5, 99.9, or 100% of the microbes, for example at least 50, preferably at least 70, more preferably at least 90, even more preferably at least 95, yet more preferably at least 98, still more preferably at least 99%. In certain embodiments, concentrating comprises freeze drying. In certain embodiments, concentrating comprises spray drying.

[00201] In certain embodiments, after concentrating, the microbes are transferred to a collection vessel. In certain embodiments, the concentrated microbes comprise less than 5, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05, 0.01, 0.005, or 0.001% water by weight, for example less than 1, preferably less than 0.5, more preferably less than 0.1, even more preferably less than 0.01, yet more preferably less than 0.005, still more preferably less than 0.001%.

[00202] In certain embodiments, the concentrated microbes are combined with one or more agriculturally acceptable adjuvants. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise one or more carriers. In certain embodiments, the one or more

carriers comprise a monosaccharide, a polysaccharide, a lipid, or a combination thereof. In certain embodiments, the one or more carriers comprises a monosaccharide. In certain embodiments, the monosaccharide comprises glucose. In certain embodiments, the concentration of the monosaccharide is at least 20, 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, or 99 wt% and/or not more than 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, 99, 99.5, or 99.9 wt%, for example 20-99 wt%, preferably 70-95 wt%, more preferably 85-95 wt%. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise a polysaccharide. In certain embodiments, the polysaccharide comprises a starch. In certain embodiments, the starch is derived from yucca. In certain embodiments, the concentration of the polysaccharide is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%. In certain embodiments, the starch is derived from an oat. In certain embodiments, the one or more agriculturally acceptable adjuvants comprises one or more surfactants. In certain embodiments, the surfactant comprises a lipid. In certain embodiments, the lipid comprises a lecithin. In certain embodiments, the lecithin comprises a soy lecithin. In certain embodiments, the concentration of surfactant is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[00203] In certain embodiments, the dried microbes are processed to a powder.

[00204] In certain embodiments, the method further comprises placing the microbes in a package. The package may be any suitable package. In certain embodiments the package is opaque and prevents moisture from entering the package, e.g., a vacuum-sealed package under nitrogen. In certain embodiments, provided herein is a package comprising a microbial composition, such as a microbial composition disclosed herein, wherein the package is opaque and prevents moisture from entering, so that over at least 1, 2, 5 days or 1, 2, 5, 10, 20, 30, 40, 50, or 60 weeks the microbial composition retains sufficient viability for its intended purpose. In certain embodiments, provided herein is a method of producing a package comprising a microbial composition, such as a microbial composition disclosed herein, wherein the package is produced by a process comprising vacuum sealing, e.g., vacuume sealing under nitrogen.

[00205] Additionally or alternatively, provided herein is a method comprising combining a first population of microbes comprising microbes of any one of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2 and a second population of microbes, different from the first. The second population of can comprises any one

of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2, different from the first. The first and second populations can be combined with any suitable number of additional microbe populations, such as at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, 30, 32, 35, 37, 40, 42 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, 30, 32, 35, 37, 40, 42, or 43 additional populations of microbes comprising any one of any one of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2, wherein the microbes of each additional population are different from the first and second populations, and the microbes of each additional population are different from each other. At least one of the populations can be a pure population. In certain embodiments, all of the populations are pure populations. In certain embodiments, the populations of microbes are each in a liquid prior to combining. The liquids can then be filtered to remove at least a portion of each liquid and leave a remainder liquid for each, wherein each remainder liquid comprises the microbes or a portion thereof. In certain embodiments, at least a portion of the liquids can be combined before filtering. Additionally or alternatively, the remainder liquids are combined after filtering. Filtering can be performed using any suitable technique, such as through a filter comprising pores of a size sufficient to retain at least a portion of the microbes. The filter can comprise a first filter layer comprising pores of a first size and a second filter layer comprising pores of a second size. Typically, the pores are of a size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um. The pores of the first filter layer can be at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 120-240 um, more preferably 160-220 um. The pores of the second filter layer can be at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 20-100 um, more preferably 40-80 um. In certain embodiments, the portion of microbes retained comprises at least 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.5, 99.9, or 100% of the microbes, for example at least 50, preferably at least 70, more preferably at least 90, even more preferably at least 95, yet more preferably at least 98, still more preferably at least 99%. After filtering, the microbes can be removed from the filter and placed in a collection vessel and/or dried to produce dried microbes. In certain embodiments, the microbes are dried after filtration and combining. In certain embodiments, the microbes are air dried. In certain embodiments, the microbes are lyophilized. In certain embodiments, the dried microbes comprise less than 5, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05, 0.01, 0.005, or 0.001% water by weight, for example

less than 1, preferably less than 0.5, more preferably less than 0.1, even more preferably less than 0.01, yet more preferably less than 0.005, still more preferably less than 0.001%. In certain embodiments, the dried microbes are combined with one or more agriculturally acceptable adjuvants. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise one or more carriers, such as a monosaccharide, a polysaccharide, a lipid, or a combination thereof. In certain embodiments, the one or more carriers comprises a monosaccharide, such as glucose. In certain embodiments, the concentration of the monosaccharide is at least 20, 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, or 99 wt% and/or not more than 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, 99, 99.5, or 99.9 wt%, for example 20-99 wt%, preferably 70-95 wt%, more preferably 85-95 wt%. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise a polysaccharide, such as a starch, for example yucca starch and/or oat starch. In certain embodiments, the concentration of the polysaccharide is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%. In certain embodiments, the one or more agriculturally acceptable adjuvants comprises one or more surfactants, for example a lipid, such as a lecithin, e.g., soy lecithin. In certain embodiments, the concentration of surfactant is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%. In certain embodiments, the dried microbes are processed to a powder. The powder can comprise a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um, and/or a mean particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um. In certain embodiments, the microbes comprises a viability of at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 1011, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of

composition cfu/g after processing. In certain embodiments, the microbes are then placed in a package.

Production compositions

[00206] In certain embodiments, provided herein is a composition comprising an isolated and/or pure of any one of Streptomyces deposited as ATCC Nos. as shown in Table 2 or O-46-O-140 and a heterologous growth medium. In certain embodiments, provided herein is a composition consisting essentially of an isolated and/or pure of any one of Streptomyces deposited as ATCC Nos. 1-45 as shown in Table 2 or O-46-O-140 and a heterologous growth medium.

[00207] In certain embodiments, the composition comprises Streptomyces designation 1. In certain embodiments, the composition comprises Streptomyces designation 2. In certain embodiments, the composition comprises Streptomyces designation 3. In certain embodiments, the composition comprises Streptomyces designation 4. In certain embodiments, the composition comprises Streptomyces designation 5. In certain embodiments, the composition comprises Streptomyces designation 6. In certain embodiments, the composition comprises Streptomyces designation 7. In certain embodiments, the composition comprises Streptomyces designation 8. In certain embodiments, the composition comprises Streptomyces designation 9. In certain embodiments, the composition comprises Streptomyces designation 10. In certain embodiments, the composition comprises Streptomyces designation 11. In certain embodiments, the composition comprises Streptomyces designation 12. In certain embodiments, the composition comprises Streptomyces designation 13. In certain embodiments, the composition comprises Streptomyces designation 14. In certain embodiments, the composition comprises Streptomyces designation 15. In certain embodiments, the composition comprises Streptomyces designation 16. In certain embodiments, the composition comprises Streptomyces designation 17. In certain embodiments, the composition comprises Streptomyces designation 18. In certain embodiments, the composition comprises Streptomyces designation 19. In certain embodiments, the composition comprises Streptomyces designation 20. In certain embodiments, the composition comprises Streptomyces designation 21. In certain embodiments, the composition comprises Streptomyces designation 22. In certain embodiments, the composition comprises Streptomyces designation 23. In certain embodiments, the composition comprises Streptomyces designation 24. In certain embodiments, the composition comprises Streptomyces designation 25. In certain embodiments, the composition comprises Streptomyces designation 26. In certain embodiments, the composition comprises Streptomyces designation 27. In certain embodiments, the composition comprises Streptomyces designation 28. In certain embodiments, the composition

comprises Streptomyces designation 29. In certain embodiments, the composition comprises Streptomyces designation 30. In certain embodiments, the composition comprises Streptomyces designation 31. In certain embodiments, the composition comprises Streptomyces designation 32. In certain embodiments, the composition comprises Streptomyces designation 33. In certain embodiments, the composition comprises Streptomyces designation 34. In certain embodiments, the composition comprises Streptomyces designation 35. In certain embodiments, the composition comprises Streptomyces designation 36. In certain embodiments, the composition comprises Streptomyces designation 37. In certain embodiments, the composition comprises Streptomyces designation 38. In certain embodiments, the composition comprises Streptomyces designation 39. In certain embodiments, the composition comprises Streptomyces designation 40. In certain embodiments, the composition comprises Streptomyces designation 41. In certain embodiments, the composition comprises Streptomyces designation 42. In certain embodiments, the composition comprises Streptomyces designation 43. In certain embodiments, the composition comprises Streptomyces designation 44. In certain embodiments, the composition comprises Streptomyces designation 45. In certain embodiments, the composition comprises any one of Streptomyces designation 46. In certain embodiments, the composition comprises Streptomyces designation O-46. In certain embodiments, the composition comprises Streptomyces designation O-47. In certain embodiments, the composition comprises Streptomyces designation O-48. In certain embodiments, the composition comprises Streptomyces designation O-49. In certain embodiments, the composition comprises Streptomyces designation O-50. In certain embodiments, the composition comprises Streptomyces designation O-51. In certain embodiments, the composition comprises Streptomyces designation O-52. In certain embodiments, the composition comprises Streptomyces designation O-53. In certain embodiments, the composition comprises Streptomyces designation O-54. In certain embodiments, the composition comprises Streptomyces designation O-55. In certain embodiments, the composition comprises Streptomyces designation O-56. In certain embodiments, the composition comprises Streptomyces designation O-57. In certain embodiments, the composition comprises Streptomyces designation O-58. In certain embodiments, the composition comprises Streptomyces designation O-59. In certain embodiments, the composition comprises Streptomyces designation O-60. In certain embodiments, the composition comprises Streptomyces designation O-61. In certain embodiments, the composition comprises Streptomyces designation O-62. In certain embodiments, the composition comprises Streptomyces designation O-63. In certain embodiments, the composition comprises Streptomyces designation O-64. In certain embodiments, the composition comprises

Streptomyces designation O-65. In certain embodiments, the composition comprises Streptomyces designation O-66. In certain embodiments, the composition comprises Streptomyces designation O-67. In certain embodiments, the composition comprises Streptomyces designation O-68. In certain embodiments, the composition comprises Streptomyces designation O-69. In certain embodiments, the composition comprises Streptomyces designation O-70. In certain embodiments, the composition comprises Streptomyces designation O-71. In certain embodiments, the composition comprises Streptomyces designation O-72. In certain embodiments, the composition comprises Streptomyces designation O-73. In certain embodiments, the composition comprises Streptomyces designation O-74. In certain embodiments, the composition comprises Streptomyces designation O-75. In certain embodiments, the composition comprises Streptomyces designation O-76. In certain embodiments, the composition comprises Streptomyces designation O-77. In certain embodiments, the composition comprises Streptomyces designation O-78. In certain embodiments, the composition comprises Streptomyces designation O-79. In certain embodiments, the composition comprises Streptomyces designation O-80. In certain embodiments, the composition comprises Streptomyces designation O-81. In certain embodiments, the composition comprises Streptomyces designation O-82. In certain embodiments, the composition comprises Streptomyces designation O-83. In certain embodiments, the composition comprises Streptomyces designation O-84. In certain embodiments, the composition comprises Streptomyces designation O-85. In certain embodiments, the composition comprises Streptomyces designation O-86. In certain embodiments, the composition comprises Streptomyces designation O-87. In certain embodiments, the composition comprises Streptomyces designation O-88. In certain embodiments, the composition comprises Streptomyces designation O-89. In certain embodiments, the composition comprises Streptomyces designation O-90. In certain embodiments, the composition comprises Streptomyces designation O-91. In certain embodiments, the composition comprises Streptomyces designation O-92. In certain embodiments, the composition comprises Streptomyces designation O-93. In certain embodiments, the composition comprises Streptomyces designation O-94. In certain embodiments, the composition comprises Streptomyces designation O-95. In certain embodiments, the composition comprises Streptomyces designation O-96. In certain embodiments, the composition comprises Streptomyces designation O-97. In certain embodiments, the composition comprises Streptomyces designation O-98. In certain embodiments, the composition comprises Streptomyces designation O-99. In certain embodiments, the composition comprises

Streptomyces designation O-100. In certain embodiments, the composition comprises Streptomyces designation O-101. In certain embodiments, the composition comprises Streptomyces designation O-102. In certain embodiments, the composition comprises Streptomyces designation O-103. In certain embodiments, the composition comprises Streptomyces designation O-104. In certain embodiments, the composition comprises Streptomyces designation O-105. In certain embodiments, the composition comprises Streptomyces designation O-106. In certain embodiments, the composition comprises Streptomyces designation O-107. In certain embodiments, the composition comprises Streptomyces designation O-108. In certain embodiments, the composition comprises Streptomyces designation O-109. In certain embodiments, the composition comprises Streptomyces designation O-110. In certain embodiments, the composition comprises Streptomyces designation O-111. In certain embodiments, the composition comprises Streptomyces designation O-112. In certain embodiments, the composition comprises Streptomyces designation O-113. In certain embodiments, the composition comprises Streptomyces designation O-114. In certain embodiments, the composition comprises Streptomyces designation O-115. In certain embodiments, the composition comprises Streptomyces designation O-116. In certain embodiments, the composition comprises Streptomyces designation O-117. In certain embodiments, the composition comprises Streptomyces designation O-118. In certain embodiments, the composition comprises Streptomyces designation O-119. In certain embodiments, the composition comprises Streptomyces designation O-120. In certain embodiments, the composition comprises Streptomyces designation O-121. In certain embodiments, the composition comprises Streptomyces designation O-122. In certain embodiments, the composition comprises Streptomyces designation O-123. In certain embodiments, the composition comprises Streptomyces designation O-124. In certain embodiments, the composition comprises Streptomyces designation O-125. In certain embodiments, the composition comprises Streptomyces designation O-126. In certain embodiments, the composition comprises Streptomyces designation O-127. In certain embodiments, the composition comprises Streptomyces designation O-128. In certain embodiments, the composition comprises Streptomyces designation O-129. In certain embodiments, the composition comprises Streptomyces designation O-130. In certain embodiments, the composition comprises Streptomyces designation O-131. In certain embodiments, the composition comprises Streptomyces designation O-132. In certain embodiments, the composition comprises Streptomyces designation O-133. In certain embodiments, the composition comprises Streptomyces designation O-134. In certain embodiments, the composition comprises

Streptomyces designation O-135. In certain embodiments, the composition comprises Streptomyces designation O-136. In certain embodiments, the composition comprises Streptomyces designation O-137. In certain embodiments, the composition comprises Streptomyces designation O-138. In certain embodiments, the composition comprises Streptomyces designation O-139. In certain embodiments, the composition comprises Streptomyces designation O-140.

[00208] In certain embodiments, the heterologous medium comprises a solid medium.

[00209] In certain embodiments, the heterologous medium comprises a solid medium. In certain embodiments, the solid medium comprises agar. In certain embodiments, the concentration of agar is at least 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, or 1.4 and/or no more than 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, or 1.5 g/L, for example 0.3-1.5 g/L, preferably 0.4-1 g/L, more preferably, 0.6-0.8 g/L. In certain embodiments, the heterologous medium comprises a liquid medium. In certain embodiments, the heterologous medium comprises a polysaccharide, a disaccharide, a monosaccharide, a gum, a natural or synthetic derivative thereof. In certain embodiments, the heterologous medium comprises a polysaccharide. In certain embodiments, 187. The method of claim 186 wherein the polysaccharide comprises a starch. In certain embodiments, the starch is an oat starch. In certain embodiments, the concentration of starch is at least 10, 20, 30, 40, 50, 60, 70, 80, or 90 g/L and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, or 100 g/L, for example 10-100, preferably 20-80, more preferably 30-70. In certain embodiments, the heterologous medium further comprises a vitamin. In certain embodiments, the vitamin comprises Vitamin A, Vitamin C, Vitamin D, Vitamin E, Vitamin B1, Vitamin B2, Niacin, Vitamin B6, Folate, Vitamin B12, Biotin, Pantothenic Acid, Calcium, Iron, Iodine, Magnesium, Zinc, Selenium, Copper, or a combination thereof. In certain embodiments, the vitamin comprises Vitamin A. In certain embodiments, the Vitamin A is present at a concentration of at least 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, or 1400 and/or not more than 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or 1500 ug/L, for example 100-1500, preferably 300-1000, more preferably 500-900, even more preferably 600-800. In certain embodiments, the vitamin comprises Vitamin C. In certain embodiments, the Vitamin C is present at a concentration of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 mg/L, for example 10-50, preferably 50-130, more preferably 70-110, even more preferably 80-100. In certain embodiments, the vitamin comprises Vitamin D. In certain embodiments, the Vitamin D is present at at least 5, 10, 15, 20, 25, 30, 35, 40, or 45 and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, or 50 ug/L, for example 5-50, preferably 10-40, more preferably 15-35, even more

preferably 20-30. In certain embodiments, the vitamin comprises Vitamin E. In certain embodiments, the Vitamin E is present at a concentration of at least 5, 7, 9, 11, 13, 15, 17, 19, 21, or 23 and/or not more than 7, 9, 11, 13, 15, 17, 19, 21, 23, or 25 mg/L, for example 5-25, preferably 9-21, more preferably 11-19, even more preferably 13-17. In certain embodiments, the vitamin comprises Vitamin B1. In certain embodiments, the Vitamin B1 is present at a concentration of at least 1, 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, or 3.8 and/or not more than 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, or 4 mg/L, for example 1-4 mg/L, preferably 1.6-3.2, more preferably 2-2.8, even more preferably 2.2-2.6. In certain embodiments, the vitamin comprises Vitamin B2. In certain embodiments, the Vitamin B2 is present at a concentration of at least 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, or 2.75 and/or not more than 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, 2.75, or 2.85 mg/L, for example 1.25-2.85, preferably 1.55-2.55, more preferably, 1.65-2.45, more preferably 1.85-2.05. In certain embodiments, the vitamin comprises Niacin. In certain embodiments, the Niacin is present at a concentration of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, or 38 and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 mg/L, for example 10-40, preferably 14-36, more preferably 18-32, even more preferably 20-28. In certain embodiments, the vitamin comprises Vitamin B6. In certain embodiments, the Vitamin B6 is present at a concentration of at least 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, or 4.8 and/or not more than 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, 4.8, or 5 mg/L, for example 2-5, preferably 2.6-4.4, more preferably 3-4, even more preferably 3-3.8. In certain embodiments, the vitamin comprises Folic Acid. In certain embodiments, the Folic Acid is present at a concentration of at least 120, 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, or 680 and/or not more than 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, 680, or 720 ug/L, for example 120-720, preferably 240-600, more preferably 320-480, even more preferably 360-440. In certain embodiments, the vitamin comprises Vitamin B12. In certain embodiments, the Vitamin B12 is present at a concentration of at least 5.4, 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, or 13.8 and/or not more than 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, 13.8, or 14.4, for example 5.4-14.4, preferably 7.2-12.6, more preferably 8.4-11.4, even more preferably 9-10.2. In certain embodiments, the vitamin comprises Biotin. In certain embodiments, the Biotin is present at a concentration of at least , 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 and/or not more than 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or 85 ug/L, for example 10-85, preferably 20-75, more preferably 30-65, even more preferably 35-55. In certain embodiments, the vitamin comprises Pantothenic Acid. In certain embodiments, the Pantothenic Acid is present at a concentration of at least 4, 4.5, 5, 5.5, 6, 6.5,

7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, or 11 and/or not more than 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, or 11.5 mg/L, for example 4-11.5, preferably 5.5-10, more preferably 6.5-9, even more preferably 7-8. In certain embodiments, the vitamin comprises Calcium. In certain embodiments, the Calcium is present at a concentration of at least 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 and/or not more than 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 210 mg/L, for example 60-210, preferably 80-190, more preferably 100-170, even more preferably 120-140. In certain embodiments, the vitamin comprises Iron. In certain embodiments, the Iron is present at a concentration of at least 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32 and/or not more than 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 mg/L, for example 6-34, preferably 12-26, more preferably 14-22, even more preferably 16-20. In certain embodiments, the vitamin comprises Iodine. In certain embodiments, the Iodine is present at a concentration of at least 80, 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180, 190, 200, 210, or 220 and/or not more than 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180, 190, 200, 210, 220, or 230 mg/L, for example 80-230, preferably 100-200, more preferably 120-180, even more preferably 140-160. In certain embodiments, the vitamin comprises Magnesium. In certain embodiments, the Magnesium is present at a concentration of at least 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, or 70 and/or not more than 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, 70, or 74 mg/L, for example 18-74, preferably 22-62, more preferably 30-54, even more preferably 38-46. In certain embodiments, the vitamin comprises Zinc. In certain embodiments, the Zinc is present at a concentration of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 mg/L, for example 2-15, preferably 3-13, more preferably 5-11, even more preferably 7-9. In certain embodiments, the vitamin comprises Selenium. In certain embodiments, the Selenium is present at a concentration of at least 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, or 69 and/or not more than 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, or 73 ug/L, for example 13-73, preferably 25-57, more preferably 29-53, even more preferably 37-45. In certain embodiments, the vitamin comprises Copper. In certain embodiments, the Copper is present at a concentration of at least 0.65, 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, or 2.05 and/or not more than 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, or 2.15 mg/L, for example 0.65-2.15, preferably 0.85-1.85, more preferably 1.05-1.65, even more preferably 1.25-1.45.

[00210] In certain embodiments, the heterologous medium comprises a cryoprotectant. In certain embodiments, the cryoprotectant comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride, ammonium sulfate, or a combination thereof. In certain embodiments, the cryoprotectant comprises glycerol. In certain embodiments,

he glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50% v/v, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22%.

[00211] In certain embodiments, provided herein is a composition comprising one or more of Streptomyces deposited as ATCC Nos. as shown in Table 2 or O-46-O-140. In certain embodiments, the composition comprises Streptomyces designation 1. In certain embodiments, the composition comprises Streptomyces designation 2. In certain embodiments, the composition comprises Streptomyces designation 3. In certain embodiments, the composition comprises Streptomyces designation 4. In certain embodiments, the composition comprises Streptomyces designation 5. In certain embodiments, the composition comprises Streptomyces designation 6. In certain embodiments, the composition comprises Streptomyces designation 7. In certain embodiments, the composition comprises Streptomyces designation 8. In certain embodiments, the composition comprises Streptomyces designation 9. In certain embodiments, the composition comprises Streptomyces designation 10. In certain embodiments, the composition comprises Streptomyces designation 11. In certain embodiments, the composition comprises Streptomyces designation 12. In certain embodiments, the composition comprises Streptomyces designation 13. In certain embodiments, the composition comprises Streptomyces designation 14. In certain embodiments, the composition comprises Streptomyces designation 15. In certain embodiments, the composition comprises Streptomyces designation 16. In certain embodiments, the composition comprises Streptomyces designation 17. In certain embodiments, the composition comprises Streptomyces designation 18. In certain embodiments, the composition comprises Streptomyces designation 19. In certain embodiments, the composition comprises Streptomyces designation 20. In certain embodiments, the composition comprises Streptomyces designation 21. In certain embodiments, the composition comprises Streptomyces designation 22. In certain embodiments, the composition comprises Streptomyces designation 23. In certain embodiments, the composition comprises Streptomyces designation 24. In certain embodiments, the composition comprises Streptomyces designation 25. In certain embodiments, the composition comprises Streptomyces designation 26. In certain embodiments, the composition comprises Streptomyces designation 27. In certain embodiments, the composition comprises Streptomyces designation 28. In certain embodiments, the composition comprises Streptomyces designation 29. In certain embodiments, the composition comprises Streptomyces designation 30. In certain embodiments, the composition comprises Streptomyces designation 31. In certain embodiments, the composition comprises Streptomyces designation 32. In certain embodiments, the composition comprises Streptomyces designation 33. In certain embodiments, the composition

comprises Streptomyces designation 34. In certain embodiments, the composition comprises Streptomyces designation 35. In certain embodiments, the composition comprises Streptomyces designation 36. In certain embodiments, the composition comprises Streptomyces designation 37. In certain embodiments, the composition comprises Streptomyces designation 38. In certain embodiments, the composition comprises Streptomyces designation 39. In certain embodiments, the composition comprises Streptomyces designation 40. In certain embodiments, the composition comprises Streptomyces designation 41. In certain embodiments, the composition comprises Streptomyces designation 42. In certain embodiments, the composition comprises Streptomyces designation 43. In certain embodiments, the composition comprises Streptomyces designation 44. In certain embodiments, the composition comprises Streptomyces designation 45. In certain embodiments, the composition comprises any one of Streptomyces designation 46. In certain embodiments, the composition comprises Streptomyces designation O-46. In certain embodiments, the composition comprises Streptomyces designation O-47. In certain embodiments, the composition comprises Streptomyces designation O-48. In certain embodiments, the composition comprises Streptomyces designation O-49. In certain embodiments, the composition comprises Streptomyces designation O-50. In certain embodiments, the composition comprises Streptomyces designation O-51. In certain embodiments, the composition comprises Streptomyces designation O-52. In certain embodiments, the composition comprises Streptomyces designation O-53. In certain embodiments, the composition comprises Streptomyces designation O-54. In certain embodiments, the composition comprises Streptomyces designation O-55. In certain embodiments, the composition comprises Streptomyces designation O-56. In certain embodiments, the composition comprises Streptomyces designation O-57. In certain embodiments, the composition comprises Streptomyces designation O-58. In certain embodiments, the composition comprises Streptomyces designation O-59. In certain embodiments, the composition comprises Streptomyces designation O-60. In certain embodiments, the composition comprises Streptomyces designation O-61. In certain embodiments, the composition comprises Streptomyces designation O-62. In certain embodiments, the composition comprises Streptomyces designation O-63. In certain embodiments, the composition comprises Streptomyces designation O-64. In certain embodiments, the composition comprises Streptomyces designation O-65. In certain embodiments, the composition comprises Streptomyces designation O-66. In certain embodiments, the composition comprises Streptomyces designation O-67. In certain embodiments, the composition comprises Streptomyces designation O-68. In certain embodiments, the composition comprises Streptomyces designation O-69. In certain

embodiments, the composition comprises Streptomyces designation O-70. In certain embodiments, the composition comprises Streptomyces designation O-71. In certain embodiments, the composition comprises Streptomyces designation O-72. In certain embodiments, the composition comprises Streptomyces designation O-73. In certain embodiments, the composition comprises Streptomyces designation O-74. In certain embodiments, the composition comprises Streptomyces designation O-75. In certain embodiments, the composition comprises Streptomyces designation O-76. In certain embodiments, the composition comprises Streptomyces designation O-77. In certain embodiments, the composition comprises Streptomyces designation O-78. In certain embodiments, the composition comprises Streptomyces designation O-79. In certain embodiments, the composition comprises Streptomyces designation O-80. In certain embodiments, the composition comprises Streptomyces designation O-81. In certain embodiments, the composition comprises Streptomyces designation O-82. In certain embodiments, the composition comprises Streptomyces designation O-83. In certain embodiments, the composition comprises Streptomyces designation O-84. In certain embodiments, the composition comprises Streptomyces designation O-85. In certain embodiments, the composition comprises Streptomyces designation O-86. In certain embodiments, the composition comprises Streptomyces designation O-87. In certain embodiments, the composition comprises Streptomyces designation O-88. In certain embodiments, the composition comprises Streptomyces designation O-89. In certain embodiments, the composition comprises Streptomyces designation O-90. In certain embodiments, the composition comprises Streptomyces designation O-91. In certain embodiments, the composition comprises Streptomyces designation O-92. In certain embodiments, the composition comprises Streptomyces designation O-93. In certain embodiments, the composition comprises Streptomyces designation O-94. In certain embodiments, the composition comprises Streptomyces designation O-95. In certain embodiments, the composition comprises Streptomyces designation O-96. In certain embodiments, the composition comprises Streptomyces designation O-97. In certain embodiments, the composition comprises Streptomyces designation O-98. In certain embodiments, the composition comprises Streptomyces designation O-99. In certain embodiments, the composition comprises Streptomyces designation O-100. In certain embodiments, the composition comprises Streptomyces designation O-101. In certain embodiments, the composition comprises Streptomyces designation O-102. In certain embodiments, the composition comprises Streptomyces designation O-103. In certain embodiments, the composition comprises Streptomyces designation O-104. In certain

embodiments, the composition comprises Streptomyces designation O-105. In certain embodiments, the composition comprises Streptomyces designation O-106. In certain embodiments, the composition comprises Streptomyces designation O-107. In certain embodiments, the composition comprises Streptomyces designation O-108. In certain embodiments, the composition comprises Streptomyces designation O-109. In certain embodiments, the composition comprises Streptomyces designation O-110. In certain embodiments, the composition comprises Streptomyces designation O-111. In certain embodiments, the composition comprises Streptomyces designation O-112. In certain embodiments, the composition comprises Streptomyces designation O-113. In certain embodiments, the composition comprises Streptomyces designation O-114. In certain embodiments, the composition comprises Streptomyces designation O-115. In certain embodiments, the composition comprises Streptomyces designation O-116. In certain embodiments, the composition comprises Streptomyces designation O-117. In certain embodiments, the composition comprises Streptomyces designation O-118. In certain embodiments, the composition comprises Streptomyces designation O-119. In certain embodiments, the composition comprises Streptomyces designation O-120. In certain embodiments, the composition comprises Streptomyces designation O-121. In certain embodiments, the composition comprises Streptomyces designation O-122. In certain embodiments, the composition comprises Streptomyces designation O-123. In certain embodiments, the composition comprises Streptomyces designation O-124. In certain embodiments, the composition comprises Streptomyces designation O-125. In certain embodiments, the composition comprises Streptomyces designation O-126. In certain embodiments, the composition comprises Streptomyces designation O-127. In certain embodiments, the composition comprises Streptomyces designation O-128. In certain embodiments, the composition comprises Streptomyces designation O-129. In certain embodiments, the composition comprises Streptomyces designation O-130. In certain embodiments, the composition comprises Streptomyces designation O-131. In certain embodiments, the composition comprises Streptomyces designation O-132. In certain embodiments, the composition comprises Streptomyces designation O-133. In certain embodiments, the composition comprises Streptomyces designation O-134. In certain embodiments, the composition comprises Streptomyces designation O-135. In certain embodiments, the composition comprises Streptomyces designation O-136. In certain embodiments, the composition comprises Streptomyces designation O-137. In certain embodiments, the composition comprises Streptomyces designation O-138. In certain embodiments, the composition comprises Streptomyces designation O-139. In certain

embodiments, the composition comprises Streptomyces designation O-140. In certain embodiments, the composition comprises at least 5, 10, 15, 20, 25, 30, 35, or 40 of Streptomyces ATCC Deposit Numbers 1-45 and/or O-46 to O-140 and/or not more than 5, 10, 15, 20, 25, 30, 35, or 40 of Streptomyces ATCC Deposit Numbers 1-45 and/or O-46 to O-140, preferably 5-45, more preferably 10-45, even more preferably 20-45, yet more preferably 35-45. In certain embodiments, the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 of Streptomyces ATCC Deposit Numbers 1-45 and/or Streptomyces Designation O-46-O-140, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100. In certain embodiments, the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 of the different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 of the of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) and/or Streptomyces Designation O-46 through O-140, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140, even yet more preferably all of the of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140, are isolated and/or pure.

[00212] In certain embodiments, the composition further comprises a liquid medium in which the one or more microbes are distributed. In certain embodiments, the liquid medium is heterologous to the Streptomyces ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413 or Streptomyces Designation O-46-O-140. In certain embodiments, the liquid medium comprises an aqueous medium. In certain embodiments, the aqueous medium comprises a combination of mediums in which each of the Streptomyces ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413 or Streptomyces Designation O-46- O-140 has been growing.

[00213] In certain embodiments, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 35, 40, 45, or 50 of the different microbes are heterologous to each other, for example at least 2, preferably at least 3, more preferably at least 4, even more preferably at least 5, yet more preferably at least 7, still more preferably at least 10.

[00214] In certain embodiments, total colony forming units (CFUs) per gram of the composition is at least 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16}, preferably 10^9 to 10^{16}, more preferably 10^9 to 10^{14}, even more preferably 10^9 to 10^{13}, yet more preferably 10^9 to 10^{12}. In certain embodiments, each of the different microbes is present at at least 10^6, 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition. In certain embodiments, the different microbes are present in a ratio to each other (CFU to CFU) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25.

[00215] In certain embodiments, less than 0.1%, or less than 0.01%, or less than 0.001% w/w water. In certain embodiments, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 35, 40, 45, or 50 of the microbes are heterologous to each other. In certain embodiments, total colony forming units (CFUs) per gram of the composition is at least 10^8,10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16}, preferably 10^9 to 10^{16}, more preferably 10^9 to 10^{14}, even more preferably 10^9 to 10^{13}, yet more preferably 10^9 to 10^{12}. In certain embodiments, each of the microbes is present at at least 10^6, 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition. In certain embodiments, the microbes are present in a ratio to each other (CFU to CFU) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5. In certain embodiments, the composition consists essentially of, *e.g.*, comprises no adjuvant, the one or more microbes.

[00216] In certain embodiments, the composition comprises a plurality of particles, wherein each particle comprises a composition as disclosed herein. In certain embodiments, the particles have a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um. In certain embodiments, at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, or 99% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, 99, 99.5, or 100%, or 100%, for example 10-100%, preferably 20-100%, more preferably 50-100%, even more preferably 80-100%, still more preferably 90-100% of the

particles have a mean particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[00217] In certain embodiments, the composition comprises a delayed release composition comprising a plurality of particles, each of which comprises a composition as disclosed herein, wherein the composition comprises one or more microbes, and wherein the plurality of particles comprises a first population of particles wherein each particle of the first population comprises one or more first components configured to confine at least a portion of the microbes to the particles, and wherein the one or more first components are such that the one or more first components lose sufficient integrity upon exposure to one or more environmental triggers that at least a portion of the confined microbes are released from the particles. In certain embodiments, the first components are configured to confine at least 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99% of the microbes, for example at least 60%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%. In certain embodiments, the one or more first components form a shell wherein the microbes are confined within, and/or embedded in, and/or associated with a surface of, the shell. In certain embodiments, the one or more first components form a matrix in which the microbes are embedded or otherwise associated. In certain embodiments, the one or more first components form a plurality of lamellae, wherein the particles are confined between, and/or embedded in, and/or associate with a surface of, the lamellae. In certain embodiments, the environmental trigger comprises water, temperature, electromagnetic radiation, or a combination thereof. In certain embodiments, the environmental trigger is water. In certain embodiments, one or more first components and/or structure of the particles are such that exposure to the trigger causes sufficient loss of integrity that at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, or 99% and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, 99, or 100% of the microbes are released. In certain embodiments, 30-100% of the microbes are released. In certain embodiments, 50-100% of the microbes are released. In certain embodiments, 80-100% of the microbes are released. In certain embodiments, 90-100% of the microbes are released. In certain embodiments, 5-80% of the microbes are released. In certain embodiments, 5-60% of the microbes are released. In certain embodiments, 5-40% of the microbes are released. In certain embodiments, 10-40% of the microbes are released. In certain embodiments, 5-30% of the microbes are released. In certain embodiments, 10-30% of the microbes are released. In certain embodiments, 5-25% of the microbes are released. In certain embodiments, 10-25% of the microbes are released. In certain

embodiments, the composition further comprises a second population of particles wherein each particle of the second population comprises one or more second components configured to confine at least a portion of the microbes to the particles, and wherein the one or more second components are such that the one or more second components withstand exposure to the one or more environmental triggers that cause the first components of the first population to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the second population. In certain embodiments, the composition further comprises a third population of particles wherein each particle of the third population comprises one or more third components configured to confine at least a portion of the microbes to the particles, and wherein the one or more third components are such that the one or more third components withstand exposure to the one or more environmental triggers that cause the first and second components of the first population and second populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the third population. In certain embodiments, the composition further comprises a fourth population of particles wherein each particle of the fourth population comprises one or more fourth components configured to confine at least a portion of the microbes to the particles, and wherein the one or more fourth components are such that the one or more fourth components withstand exposure to the one or more environmental triggers that cause the first, second and third components of the first population, second and third populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the fourth population. In certain embodiments, the composition further comprises a fifth population of particles wherein each particle of the fourth population comprises one or more fifth components configured to confine at least a portion of the microbes to the particles, and wherein the one or more fifth components are such that the one or more fifth components withstand exposure to the one or more environmental triggers that cause the first, second, third, and fourth components of the first population, second third, and fourth populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the fifth population.

[00218] In certain embodiments, the composition comprises one or more agriculturally acceptable adjuvants. In certain embodiments, at least one of the agriculturally acceptable adjuvants is heterologous to the one or more microbes of the composition. In certain embodiments, the one or more agriculturally acceptable adjuvants comprise one or more liquid

carriers, solid carriers, surfactants, viscosity modifiers, thickeners, rheology additives, structuring agents, preservatives, biocides or biostatic agents, antifreezes, crystallization inhibitors, suspending agents, dyes, anti-oxidants, foaming agents, light absorbers, light blockers, mixing auxiliaries, antifoams, complexing agents, neutralizing or pH-modifying substances and buffers, corrosion inhibitors, fragrances, wetting agents, take-up enhancers, micronutrients, plasticizers, glidants, lubricants, and dispersants, an emulsifier, a carrier, a stabilizer, or a combination thereof. In certain embodiments, the composition comprises one or more surfactants. In certain embodiments, the one or more surfactants comprise a non-ionic, cationic, or anionic surfactant, or a combination thereof. In certain embodiments, the surfactant comprises Tween 20 or Tween 80. In certain embodiments, the composition comprises soy lecithin or yucca powder or a derivative thereof, or a combination thereof. In certain embodiments, the surfactant is organic. In certain embodiments, the surfactant or surfactants are at a total concentration of at least 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, or 9 wt% and/or no more than 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, 9, or 10 wt%, for example 0.5-10 wt%, preferably 1-3 wt%, more preferably 1.8-2.2 wt%.

[00219] In certain embodiments, the composition is a solid composition.

[00220] In certain embodiments, the composition is a liquid composition.

[00221] In certain embodiments, the composition comprises a carrier. In certain embodiments, the carrier comprises a saccharide, e.g., a monosaccharide, disaccharide, trisaccharide, or polysaccharide. In certain embodiments, the carrier comprises glucose, lactose, maltose, and/or galactose. In certain embodiments, the carrier comprises glucose. In certain embodiments, the carrier is at a concentration in the composition of at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 wt% and/or no more than 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 wt%, for example 50-100 wt%, preferably 70-100 wt%, more preferably 80-100 wt%, even more preferably 90-100 wt%, still more preferably 95-100 wt%.

[00222] In certain embodiments, the composition comprises one or more materials that protect the microbes from one or more aspects of an environment in which the microbes will be stored and/or used. In certain embodiments, the one or more materials comprises a light absorber or light blocker, or a combination thereof. In certain embodiments, the light absorber or light blocker protects the microbes of the composition from ultraviolet (UV) light. In certain embodiments, the microbes are enclosed in the material. In certain embodiments, the material is such that it releases some or all of the microbes upon exposure to one or more environmental triggers. In certain embodiments, the one or more environmental triggers comprises water. In certain embodiments, the composition is stable at temperatures between 4 °C. and 37 °C for at

least 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3 or 4 weeks, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months, or 1, 2, 3, 4, or 5 years, for example, stable at between 4 °C. and 37 °C for at least one week, preferably at least one month, more preferably at least 6 months, even more preferably at least 12 months, yet more preferably at least 2 years.

[00223] In certain embodiments, the composition comprises an antifreeze agent, *e.g.*, a cryoprotectant. In certain embodiments, the composition comprises an antifreeze agent for cold storage at temperature less than -5, -10, -15, -20, -25, -30, -40, -50, -60, -70, -80 °C, for example less than -5, preferably less than -10, more preferably less than -15, even more preferably less than -20 °C. In certain embodiments, the antifreeze agent comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride and ammonium sulfate. In certain embodiments, the antifreeze agent comprises glycerol. In certain embodiments, the glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50%, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22% wt%.

[00224] In certain embodiments, the composition comprises microbes of only one strain. Additionally or alternatively, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10 or more microbial strains.

[00225] In certain embodiments, total colony forming units (CFUs) per gram of the composition is at least 10^8,10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16}, preferably 10^9 to 10^{16}, more preferably 10^9 to 10^{14}, even more preferably 10^9 to 10^{13}, yet more preferably 10^9 to 10^{12}. In certain embodiments, total CFUs per gram of the composition is 10^{10} to 10^{13} per gram. In certain embodiments, total CFUs per gram of the composition is 10^{10} to 10^{12} per gram. In certain embodiments, each of the microbes is present at at least 10^6, 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9,10^{10},10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition.

[00226] In certain embodiments, the composition comprises a plurality of particles, wherein each particle comprises a composition as disclosed herein. In certain embodiments, the particles have a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um. In certain embodiments, at least 10,

20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, or 99% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, 99, 99.5, or 100%, or 100%, for example 10-100%, preferably 20-100%, more preferably 50-100%, even more preferably 80-100%, still more preferably 90-100% of the particles have a mean particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[00227] In certain embodiments, the composition comprises 10-20 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 5-25% of total CFUs. In certain embodiments, the composition comprises 21-30 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 3-10% of total CFUs. In certain embodiments, the composition comprises 31-40 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 2-8% of total CFUs. In certain embodiments, the composition comprises 41-50 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 1-5% of total CFUs. In certain embodiments, the composition comprises 51-60 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.8-4% of total CFUs. In certain embodiments, the composition comprises 61-70 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.6-3.5% of total CFUs. In certain embodiments, the composition comprises 71-80 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.5-3.2% of total CFUs. In certain embodiments, the composition comprises 81-90 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.4-3.0% of total CFUs. In certain embodiments, the composition comprises 91-100 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.4-2.8% of total CFUs. In certain embodiments, the composition comprises 101-110 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.3-2.4%

of total CFUs. In certain embodiments, the composition comprises 111-120 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.2-2% of total CFUs. In certain embodiments, the composition comprises 121-130 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.2-1.5% of total CFUs. In certain embodiments, the composition comprises 131-140 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140 and each is present as 0.1-1.2% of total CFUs.

[00228] In certain embodiments, the composition further comprises cells of one or more additional microbial species or strains different from those of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or Streptomyces Designation O-46 through O-140. In certain embodiments, the additional microbial species comprise fungi, bacteria, or a combination thereof. In certain embodiments, the additional microbial species comprise fungi. In certain embodiments, the fungi comprise mycorrhizal fungi.

[00229]

III. Examples

Example 1: Preparation of microbial composition

[00230] This example demonstrates two different methods of preparation of a composition comprising a plurality of different microbes from 140 different microbe stocks, corresponding to Designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and microbial stocks OATH 46-140. ATCC stock 46 was prepared with microbes from microbial stocks OATH 46-140 and ATCC stock 47 was prepared with microbes from all 140 stocks.

[00231] The compositions were produced using fully aseptic techniques. Microorganisms within each of the 140 different stocks were separately cultured in a laminar airflow cabinet with HEPA filters (0.2 μm). Autoclaves and pressure cookers were used to sterilize the media at 121 °C at 1.5 atmospheric pressure for 30 minutes. After autoclaving, ingredients were stored at room temperature of 20-23 °C until use. The living microbes in the product were stored in the fridge at 4 °C and in liquid glycerol in the freezer at -20 °C. The laboratory, storage area, benches and floors in the laboratory were constantly cleaned and sanitized every day with Lysol, ethyl alcohol and bleach to maintain the highest level of cleanness. During manufacturing all standard methods of sterilization were used including hand washing with medical soap and ethyl alcohol for the technicians. The ingredients (the living microbes and the glucose (dextrose which is the carrier)

were mixed inside laminar airflow cabinet with HEPA filters (0.2 μm) to prevent any possibility of contamination.

[00232] In a first procedure, microbes from each stock were separately grown on oatmeal agar (as below for liquid media, but with the addition of agar). The plates were dried in the laminar airflow hood before using them, to prevent moisture accumulation. The plates were inoculated with the spores from a previous plate and spread with sterilized inoculating loop. Twenty plates were prepared for each of the 140 stocks. The plates were incubated in the incubator for at least 10 days at 28 °C. After 10 days, all the plates (20 plates for each of the 140 stocks) were scraped using scalpel or a strong sharp knife and the cells and spores were combined with 500 g of glucose to make a stock powder. In some cases, a wetting agent such as Yucca powder was also be added to the dry mix as an organic wetting agent. The aliquot was then filled in sterilized and tightly sealed plastic pouches inside laminar airflow cabinet under aseptic techniques. On average, 100 g of stock powder is used to treat 1 acre.

[00233] In a second procedure, the manufacture of the wettable dry products was carried out by growing the microbes in each of the 140 stocks in liquid organic oatmeal broth which contains multivitamins and yeast extract (1gram yeast extract per 1000 mL of water + 0.5 multivitamins per 1000 mL of water). The liquid oatmeal was sterilized in culture bottles at 121 °C for 30 min on three successive days to ensure sterilization. Separately for each stock, liquid oat medium was aseptically inoculated with spore suspensions (5 mL) and incubated with constant shaking at 250 rpm at 28 °C in the dark for 10 days. In some cases, each individual culture was first grown on an agar/oatmeal plate, as above, then scraped or otherwise separated from the agar into the liquid medium. The liquid/microbe mixes were placed on a shaker. After 10 days of incubation on the shaker, the liquid media were generally combined into a single liquid aliquot, and the cells were harvested by normal filtration and centrifugation at 4000 x *g* for 20 min. The harvested spores and cells after centrifugation were completely dried in a laminar airflow cabinet with HEPA filters (0.2 μm) for 2 hours in 500 g of glucose as a stock powder. Organic Yucca powder can also be added to the dry mix as an organic wetting agent. The aliquot was then filled in sterilized and tightly sealed plastic pouches inside laminar airflow cabinet under aseptic techniques. On average, 100 g of stock powder is used to treat 1 acre.

[00234] All pouches were stored up to 20-23 °C in dry conditions. The pouches can stay active for up to 12 months at 20-23 °C in dry conditions.

Example 2: Increase in soil carbon in soil treated with a composition comprising a plurality of different microbes as disclosed herein

[00235] This example demonstrates increased soil organic carbon (SOC) levels and increases in soil microbes after treatment of soil in which turf was grown with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to untreated soil and turf.

[00236] The composition comprising a plurality of different microbes (was applied to low bulk density turf; untreated control with the same soil and plants was also used. At 6 months post-treatment, soil organic carbon levels were measured by loss on ignition for both the treated turf and an untreated control at 6 months post-treatment. Soil organic carbon levels are reported as (weight after heating divided by weight before heating)*100%. Further, abundance of soil microbes was measured for both the treated turf and an untreated control. Briefly, 1 gram of soil was rinsed with water, the water was strained and collected so that the microbe from the soil were present in the strained water, and then cells in a portion of the water were counted under a microscope, and extrapolated to the entire gram of soil. Results are shown in Table 3. The soil organic carbon level 6 months post treatment was 65% higher in treated vs. untreated soil (soil carbon level of 18.70% in treated vs. 11.30% in untreated) The treated turf comprised 4,200,000 microbes per gram of soil as compared to 7,900 microbes per gram of soil in the untreated control, a 531-fold increase in total soil microbes due to treatment of turf with the composition.

Table 3: soil organic carbon level and soil microbe measurements

	Treated	Untreated
Soil organic carbon level [%]	18.70%	11.30%
Microbes per gram soil	4,200,000	7,900

[00237] This example demonstrates surprisingly rapid and large improvement of soil characteristics, including soil organic carbon level (~65% increased SOC) and microbe per gram soil (531-fold increase) in turf treated with the composition comprising a plurality microbes as compared to untreated turf in just six months.

Example 3: Optimized soil bulk density and increased soil moisture content after treatment with a composition comprising a plurality of different microbes as disclosed herein

[00238] This example demonstrates improved soil bulk density (SBD) and increased soil moisture content (SMC) in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to untreated turf soil.

[00239] The composition comprising a plurality different microbes was applied to plots of turf in 3 geographically separate locations. Untreated turf was also used as a control. Treated turf was watered daily for 20 minutes. Untreated turf was watered daily for 40 minutes. After 6 months,

five soil samples were collected at each location from the treated turf and five separate soil samples were collected from untreated control turf. Values for each location were averages of the soil samples for the locations.

[00240] Soil bulk density and soil moisture content were determined for each soil sample as follows.

[00241] SBD was determined by collecting a soil sample by an auger, drying then weighing the sample, and then dividing the weight of the soil sample by its volume. According to USDA soil quality indicators, the ideal soil density for optimum plant growth in Sandy and Silty soils is between 1.40 to 1.60. Soil density which restricts root growth in Sandy and Silty soils is between 1.65 to 1.80. The results of the study are shown in Table 4 and demonstrate an improvement in soil bulk density of turf treated with the composition comprising a plurality of different microbes as compared to an untreated control, with an average change in soil bulk density at the end of six months into the optimum range, compared to untreated, which was above the optimum range.

Table 4: soil bulk density [g cm^{-3}] comparison of treated and untreated soils

	Treated	Untreated
Location 1	1.36	1.62
Location 2	1.78	1.64
Location 3	1.49	1.93
Average	1.54	1.73

[00242] SMC was determined by oven drying the sample at 100 °C for 48 hours, measuring the dried weight of the sample, and the calculating the difference between the fresh soil weight and the dry soil weight. The higher the value of the soil moisture content, the better the soil retains water. The results of the study are shown in Table 5 and demonstrate an improvement in soil moisture content of turf treated with the composition comprising a plurality of different microbes as compared to an untreated control with an average increase in soil moisture content of 107%.

Table 5: soil moisture content [%] comparison of treated and untreated soils

	Treated	Untreated
Location 1	49.67	23.80
Location 2	32.60	14.77
Location 3	47.20	24.00
Average	43.16	20.86

[00243] SMC was further estimated using a neutron probe. Neutron probe readings were taken at each location. The results are shown in Table 6 and correlate with the soil water content as measured above.

Table 6: soil moisture content [%] comparison of treated and untreated soils as estimated by neutron probe measurements

	Treated	Untreated
Location 1	8.00	6.00
Location 2	7.50	6.00
Location 3	7.00	5.00
Average	7.50	5.67

[00244] This example demonstrates surprisingly rapid and large improvement of soil characteristics, including optimized soil bulk density and dramatically increased soil water content (~107% increased SWC) in turf treated with the composition comprising a plurality different microbes as compared to untreated turf, in just six months. On average, treatment of soil with the composition comprising a plurality of different microbes improved soil bulk density to within the USDA's recommended ideal soil density for optimum plant growth.

Example 4: Improvements in soil moisture level and reduced water usage in soil after treatment with a composition comprising a plurality of microbes

[00245] This example demonstrates reduction of the required application of water in minutes of water per day to keep soil moisture percentage levels at a desired set point after treatment with a composition comprising a different microbes (generated as described in Example 1) as compared to an untreated control.

[00246] The following data was compiled over the course of 112 days after treatment of soil in which grass was growing with the composition comprising a plurality of different microbes. Once per week, four soil moisture readings were taken using a water moisture meter from four treated sites and two untreated sites. The four samples included (1) a high moisture area sample, (2) a low moisture area sample, and (3-4) two medium moisture level areas. The average of each site was calculated and documented. Soil moisture content (SMC) was calculated with a digital soil moisture reader for percentages in the top six inches of soil.

[00247] The first 30 days were used as a baseline to identify and sustain SMC levels to the target set point by adjusting the duration of watering. After the first 30 days, the duration of watering was reduced to maintain the desired SMC as the plurality of different microbes amended the soil. The results for the four treated sites and two untreated sites are shown in Table 7 (SMC = soil moisture content [%] and WD = watering duration [min]). Measurements are recorded as % soil water saturation.

Table 7: moisture level and watering duration measurements

	Day 30	Day 60	Day 90	Day 112

	SMC	WD	SMC	WD	SMC	WD	SMC	WD
Treated Location 1	80	40	90	40	90	40	95	20
Treated Location 2	100	40	85	30	75	10	100	10
Treated Location 3	100	40	85	25	60	7	95	15
Treated Location 4	100	40	100	40	100	40	90	25
Untreated Location 5	70	40	50	40	50	40	90	40
Untreated Location 6	100	40	60	40	60	40	80	40

[00248] By day 112, treated location 1 saw a reduction in watering duration from 40 minutes to 20 minutes. The 20 minute watering duration resulted in an average SMC of 95%. By day 112, treated location 2 saw a reduction in watering duration from 40 minutes to 10 minutes. The 10 minute watering duration resulted in an average SMC of 100%. By day 112, treated location 3 saw a reduction in watering duration from 40 minutes to 15 minutes. The 15 minute watering duration resulted in an average SMC of 95%. By day 112, treated location 4 saw a reduction in watering duration from 40 minutes to 25 minutes. The 20 minute watering duration resulted in an average SMC of 90%. The untreated locations required a water duration of 40 minutes to achieve 90% and 80% SMC, respectively. Temperatures at the sites were extremely high, reaching over 100° F. It was the opinion of experts that turf quality was better than control areas in the treated areas, with reduced water usage.

[00249] Further, soil water holding capacity (WHC) of the soil samples were measured. Briefly, two cup cutter cores, one treated and one non-treated, were weighed on an analytical balance, placed into separate tared, plastic buckets, and saturated to run off with tap water twice to make sure that each core retained the maximum amount of water. Fully saturated cores were weighted again and placed on a lab bench at room temperature. The samples were weighed every 24 hours until completely dry. Data is shown in Figure 3. After moisture saturation, treated sample weight increased by 31% while untreated weight increased by 24% moisture, demonstrating a higher initial WHC for treated soil than untreated soil. After 12 days, the untreated sample decreased in weight by 40.69% and was completely dry, while the treated sample decreased in weight by only 17.50% and possessed adequate moisture for plant growth. It was of the opinion of experts that soil texture was noticeably different and more sponge like in treated sample.

[00250] This example demonstrates a substantial increase in WHC and reduction in required watering duration after treatment with a composition comprising a plurality of different microbes as compared to untreated controls. Water requirements were reduced by a minimum of 25% after 30 days and by a minimum of 50% after 90 days, while demonstrated soil water content as good as or better than untreated, after only one application of the soil microbes. Further reductions could likely be achieved in temperatures less extreme than those of this test.

Example 5: Increases in root length and reductions in water usage following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00251] This example demonstrates increased root length and reduced water usage for turf treated with a composition comprising a plurality of different microbes (generated as described in Example 1).

[00252] The soil organic matter of a plot of turf was measured to be 0.2% and the root length was measured to be an average of 1.5". Soil organic matter was measured by loss on ignition as previously described. The composition comprising a plurality of different microbes was then applied to the plot. After 2 months root length was measured. Root length increased from an average of 1.5" to an average of 7" after treatment with the composition comprising a plurality of microbes.

[00253] Further, total water usage was measured monthly and compared to the historical median average for the 4 years prior to treatment. Data is shown in Table 8. For Month 1 following treatment, 8,579,656 gallons of water were used per acre of treated turf as compared to a required 11,518,832 in the years prior to treatment (34.3% reduction in water usage). For Month 2 following treatment, 6,373,645 gallons of water were used per acre of treated turf as compared to a required 13,034,040 in the years prior to treatment (104.5% reduction in water usage). For Month 3 following treatment, 5,089,792 gallons of water were used per acre of treated turf as compared to a required 7,110,068 in the years prior to treatment (39.6% reduction in water usage). For Month 4 following treatment, 4,226,287 gallons of water were used per acre of treated turf as compared to a required 2,701,304 in the years prior to treatment (54.4% increase in water usage). Of note, is that two of the four years, an additional 2 inches of rainfall occurred skewing the median average. For Month 5 following treatment, 2,896,815 gallons of water were used per acre of treated turf as compared to a required 4,425,056 in the years prior to treatment (52.7% reduction in water usage). Four the 5 months tested, an average of 5,433,239 gallons of water were used per acre of treated turf as compared to an average of 7,757,860 gallons of water used per acre of untreated turf, an average reduction of 42.8% water usage.

Table 8: water usage measurements

	Treated [gal/acre]	Prior to treatment [gal/acre]
Month 1	8,579,656	11,518,832
Month 2	6,373,645	13,034,040
Month 3	5,089,792	7,110,068
Month 4 **	4,226,287	2,701,304
Month 5	2,896,815	4,425,056

[00254] This example demonstrates increased root length and significant 42.8% average reduced water usage for turf treated with a composition comprising a plurality of different microbes as compared to the same turf prior to treatment. Further, the increase of root length from an average of 1.5" to an average of 7" after treatment with the plurality of different microbes roughly correlates to root biomass. In the case of root biomass, it is generally thought that increases in root biomass are a major contributor to soil carbon content.

Example 6: Increases in beneficial microbes following treatment with a microbial consortium

[00255] This example demonstrates increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00256] Turf was treated with the composition comprising a plurality of different microbes. Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were 437.5-fold higher in treated soil as compared to untreated soil after 10 days and 7,180-fold higher after 20 days (Table 9).

Table 9: Beneficial microbe measurements per gram of soil

	10 days		20 days	
	Treated	Untreated	Treated	Untreated
Beneficial Fungi & Bacteria	2,100,000	4,800	28,000,000	3,900

[00257] This example demonstrates increases in beneficial microbes in an exceptionally short time after a single treatment with a composition comprising a plurality of different microbes of the type disclosed herein.

Example 7: Increases in beneficial microbe abundance following treatment with a microbial consortium

[00258] This example demonstrates increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00259] Turf was treated with the composition comprising a plurality of different microbes.

Table 10: Beneficial microbe measurements per gram of soil

	Treated	Untreated
Beneficial Fungi & Bacteria	3,500,000	8,800

[00260] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were 397-fold higher in treated soil as compared to untreated soil after 19 days (Table 10).

[00261] These results demonstrate a pioneering example of improvement in soil microbiome after an exceptionally short treatment duration following treatment with a composition comprising a plurality of different microbes of the type as described herein.

Example 8: Increases in beneficial microbe abundance following treatment with a microbial consortium

[00262] This example demonstrates increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00263] Four plots of turf were treated with the composition comprising a plurality of different microbes and two plots of turf were maintained as untreated controls. Beneficial microbes were measured 3 weeks post treatment for the treated group as well as an untreated control (as described above). Data is shown in Table 11.

[00264] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were 2,642-fold higher in treated soil as compared to untreated after 3 weeks.

Table 11: Beneficial microbe measurements per gram of soil

	Untreated #1	Untreated #2	Treated #1	Treated #2	Treated #3	Treated #4
Beneficial Fungi & Bacteria	4,200	6,700	5,600,000	39,000,000	6,200,000	6,800,000

[00265] This Example demonstrates that the microbiome in the treated soil was increased remarkably by the treatment with the composition comprising a plurality of different microbes—over two thousand-fold in beneficial organisms, compared to untreated soil, in just three weeks.

Example 9: Increases in beneficial microbes following treatment with a microbial consortium

[00266] This example demonstrates increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of microbes (generated as described in Example 1) as compared to an untreated control.

[00267] Four plots of turf and shrubs were treated with the composition comprising a plurality different microbes.

Table 12: Beneficial microbe measurements per gram of soil

	Untreated	Treated
Beneficial Fungi & Bacteria	730	4,300,000

[00268] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were 5,890-fold higher in treated soil as compared to untreated soil after 3 months (Table 12).

[00269] This example demonstrates a substantial large and rapid rise in beneficial microbes, as compared to untreated. These results demonstrate a pioneering example of soil amendment and resulting stunning improvement in microbiome after an exceptionally short time after treatment with a composition comprising a plurality of different microbes of the type as disclosed herein.

Example 10: Increases in soil organic carbon levels and increase in beneficial microbe abundance following treatment with a microbial consortium

[00270] This example demonstrates increased soil organic carbon levels and increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00271] Four plots of turf and shrubs were treated with the composition comprising a plurality of different microbes and two plots of turf were maintained as untreated controls. Soil organic carbon levels and beneficial microbes were measured 190 days post treatment for the treated group as well as an untreated control (as described above).

Table 13: Beneficial microbe measurements per gram of soil

	Untreated	Treated
Beneficial Fungi & Bacteria	7,900	4,200,000

[00272] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were 531 -fold higher in treated soil as compared to untreated soil after 3 months (Table 13). Further, soil organic carbon levels were on average 18.7% in treated soil as compared to 11.3% for untreated soil, a 65% increase.

[00273] This example demonstrates an enormous increase in beneficial microbes and a substantial increase in soil carbon after treatment with a composition comprising a plurality of different microbes of the type as disclosed herein. These results demonstrate a pioneering example of soil amendment and resulting astonishing improvement, in both microbiome and carbon content, after an exceptionally time after a single treatment.

Example 11: Increased beneficial microbe abundance following treatment with a microbial consortium

[00274] This example demonstrates increased beneficial microbe abundance in turf soil after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00275] Briefly, plots of turf and shrubs were treated with the composition comprising a plurality of different microbes and plots of turf and shrubs were maintained as untreated controls. Beneficial microbes were measured 190 days post treatment for the treated group as well as an untreated control (as described above). Data is shown in Table 14.

Table 14: Beneficial microbe measurements per gram of soil

	Untreated	Treated
Beneficial Fungi & Bacteria	890	54,000

[00276] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) we're 60.6-fold higher in treated soil as compared to untreated soil after 3 months.

[00277] This example demonstrates a remarkable improvement in soil microbiome after an exceptionally short time after a single treatment with a composition comprising a plurality of different microbes of the type as disclosed herein.

Example 12: Increase in beneficial microbe abundance following treatment of a food crop with a microbial consortium

[00278] This example demonstrates increased beneficial microbe abundance in soil in which blueberries were grown after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) and no improvement, in fact, worsening, in untreated soil over time.

[00279] Soil from 3 locations that was grown with blueberries was treated with the composition comprising a plurality of different microbes. Beneficial microbes were measured at day 0 and the remeasured 17 days post treatment for the treated group as well as an untreated control (as described above).

Table 15: Beneficial microbe measurements as reported treated/untreated*100%

	Location 1		Location 2		Location 3	
	Treated	Untreated	Treated	Untreated	Treated	Untreated
Beneficial	100,000x	0.25x	1500x	0.19x	42,000x	1.58x

[00280] Total counts of beneficial microbes calculated consist of bacteria, fungi and actinomycetes which were determined under a dissecting microscope. Beneficial microbes (fungi and bacteria) were on average 47,833-fold higher than day 0 in treated soil as compared to on average 0.67-fold that of day 0 for untreated soil (Table 15).

[00281] This example demonstrates a substantial large and rapid (only 17 days) increase in beneficial organisms in treated soil, while untreated soil showed a slight increase in one case and significant decrease in two cases. These results demonstrate a pioneering example of soil amendment and enormous increase in beneficial microbes, in soil treated with a composition comprising a plurality of different microbes of the type as disclosed herein over just 17 days, compared to, on average, a decrease in beneficial microbes in untreated soil over 17 days.

Example 13: Increasing growth in existing forests or reforestation with a composition comprising a plurality of different microbes as disclosed herein

[00282] Soils treated with a plurality of different microbes as disclosed herein have been shown to require at least 35% less water than untreated soils, in some cases at least 50% less (see examples above and below). Further soils treated with a plurality of different microbes have been shown to increase tree growth by over at least 50% after 180 days (see examples above and below). Therefore, applying a plurality of different microbes to forested or deforested soils improves tree growth both above- and below-ground, thus sequestering atmospheric carbon, increasing chances of survival and robust growth of seeds or seedlings, and increasing drought tolerance and pest resistance of plants growing in those soils.

[00283] In a first procedure, a composition comprising a plurality of different microbes as disclosed herein is formulated into a plurality of delivery compositions such that they can be delivered aerially to soils to be treated. The aerial delivery device is manned or unmanned, for example a drone. The plurality of delivery compositions is formulated such that they can be loaded onto the aerial delivery device and delivered to the soil. The delivery compositions can be further formulated as a delayed release formulation, such that a percentage of the delivery compositions' contents is released over time rather than immediately upon delivery. The aerial delivery device delivers the compositions to a forested area such that at least a portion of the forested area receives the delivery compositions. After the application, trees grow more robustly, become more drought- and pest-resistant, and sequester significantly more amounts of carbon in

soil compared to before the application. A monetary return may be realized based on the additional carbon sequestered and the price per metric ton of carbon sequestered.

[00284] In a second procedure, a delivery composition is formulated that comprises a plurality of different microbes as disclosed herein and a plurality of seeds or seedlings of forest trees; the delivery composition is formulated as microbes coating the seeds, separate from the seeds, or both. The delivery compositions are loaded onto an aerial delivery device such as a drone and delivered to a forested area with a low or no density of trees, for example an area that recently experienced fire damage or deforestation by other means. The aerial delivery device delivers the delivery compositions such that the delivery compositions preferably enters the ground, where, upon entering the ground, the composition begins to dissolve such that the seed can sprout under appropriate conditions. The aerial delivery device delivers the delivery composition containing a seed or seedling such that the seeds or seedlings will be spaced based on the respective species of tree being planted. Since the plurality of different microbes amends the soil, increasing the rate of seedling growth and reducing the require amounts of water, the seeds and seedlings experience increased survival rate (the amount of viable seedlings per planting) as compared to methods delivering seeds without the plurality of microbes. After the application, the seeds or seedlings grow to mature trees, and sequester significantly more amounts of carbon both in the vegetation of the trees and in soil compared to before the planting and application of microbes. A monetary return may be realized based on the additional carbon sequestered and, e.g., the price per metric ton of carbon sequestered.

Example 14: Increasing carbon sequestration in grasslands following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00285] Soils treated with a plurality of different microbes as disclosed herein have been shown to require approximately 35% less water than untreated soils (see Examples 4 and 9). Further soils treated with a plurality of different microbes have been shown to increase grass growth by over 50% after 180 days (See Examples 5-8) as well as reducing or eliminating pests that can limit grass growth. Therefore, applying a plurality of different microbes to existing grasslands improves plant growth both above- and below-ground, resulting in significant carbon sequestration from the atmosphere.

[00286] In a first procedure, a composition comprising a plurality of different microbes as disclosed herein is formulated into a plurality of delivery compositions such that they can be deployed aerially to soils to be treated. The aerial delivery device is manned or unmanned, for example a drone. The plurality of delivery compositions is formulated such that they can be loaded onto the aerial delivery device and delivered to the soil. The aerial delivery device

delivers the delivery compositions to one or more existing grassland areas comprising, in total, at least 100,000 hectares, for example at least 1,000,000 hectares or at least 100,000,000 hectares, such that the grassland area receives the delivery compositions. After the application, grasses significantly more amounts of carbon in soil compared to before the application, such as at least 2-10 metric tons more per hectare in the first year, with continued carbon sequestration in following years. A monetary return may be realized based on the carbon sequestered and the price per metric ton of carbon sequestered.

[00287] In a second procedure, the delivery compositions are further formulated as a delayed release formulation, such that a percentage of the delivery compositions' contents is released over time rather than immediately upon delivery. The aerial delivery device delivers the delivery compositions to an existing grassland area comprising at least 100,000 hectares, for example at least 1,000,000 hectares such that the grassland area receives the delivery compositions. The delivery compositions release the microbes over time, so that the grasslands have extended application of microbes. After the application, grasses sequester significantly more amounts of carbon in soil compared to before the application, such as at least 2-10 metric tons more per hectare in the first year, with continued carbon sequestration in following years. A monetary return may be realized based on the additional carbon and the price per metric ton of carbon sequestered.

Example 15: increases in shoot biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00288] This example demonstrates increase shoot biomass following treatment of soil with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00289] A 30 square meter plot of turf was treated with the composition comprising a plurality of different microbes. Above ground grass cuttings from the plot were taken on three occasions and weighed for shoot biomass. An equivalent area was sampled from a untreated turf control plot. Application of the composition comprising a plurality of different microbes to the turf showed a 72% increase in shoot biomass by the first cutting, a 68% increase in shoot biomass by the second cutting, and a 135% increase in shoot biomass by the third cutting (Table 16) as compared to the control plot.

Table 16: shoot biomass measurements

	Treated [g]	Untreated [g]
First cutting	898.4	522.1
Second cutting	1211.5	719.8

Third cutting	2763.8	1175.3

[00290] This example demonstrates a substantial increase in shoot biomass after application of a composition comprising a plurality of different microbes as compared to an untreated control.

Example 16: increases in shoot and root biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00291] This example demonstrates increase shoot and root biomass following treatment of soil with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00292] A 30 square meter plot of turf was treated with the composition comprising a plurality of different microbe. Above ground grass cuttings from the plot were taken on three occasions and weighed for shoot biomass and a 1 meter square sample was removed to measure root biomass. Root biomass was measured by thoroughly rinsing the roots to remove any soil, drying, and then weighing. An equivalent area was sample from a untreated turf control plot. Application of the composition comprising a plurality of different microbes to the turf showed a 19% increase in shoot biomass at 21 days, a 36% increase in shoot biomass at 33 days, a 40% increase in shoot biomass at 60 days, and a 20% increase in shoot biomass at 90 days (Table 17) as compared to the control plot. Further, application of the composition comprising a plurality of different microbes to the turf showed a 79% increase in shoot biomass at 21 days, a 60% increase in shoot biomass at 33 days, a 55% increase in shoot biomass at 60 days, and a 56% increase in shoot biomass at 90 days (Table 17) as compared to the control plot.

Table 17: Shoot and root biomass measurements

	Treated		Untreated	
	Shoot biomass [g]	Root biomass [g]	Shoot biomass [g]	Root biomass [g]
21 days	9.3	5.2	7.8	2.9
33 days	14.5	7.7	11.5	4.8
60 days	27.2	15.4	19.4	9.9
90 days	33.8	21.2	28.5	13.6

[00293] This example demonstrates a substantial increase in both shoot and root biomass after application of a composition comprising a plurality of different microbes. In the case of root biomass, it is generally thought that increases in root biomass are a major contributor to soil carbon content, in this case, a remarkable 56% in only 90 days after a single application of the composition comprising a plurality of different microbes.

Example 17: Increases in shoot biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00294] This example demonstrates increase shoot biomass following treatment of soil with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00295] One square meter wooden flats (5" deep) were seeded with Bermuda grass in a greenhouse. Six flats were treated with the composition comprising a plurality of different microbes. Above ground shoot were collected from the six treated flats and six untreated flats, dried at 60 °C, and dried shoot biomass was measured. Data is shown in Table 18. Specifically, dried shoot biomass was increased by 55% at 25 days, 61% at 60 days, and 90% at 90 days as compared to the untreated controls.

Table 18: dried shoot biomass measurements

	Treated [g]	Untreated [g]
25 days	57.92	37.19
60 days	89.43	55.37
90 days	119.44	62.84

[00296] This example demonstrates a substantial increase in shoot biomass after application of a composition comprising a plurality of microbes.

Example 18: increases in shoot biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00297] This example demonstrates increase shoot biomass following treatment of soil with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00298] 15 meter long rows of soil were seeded with tall fescue. The first row was treated with a composition comprising a plurality of different microbes and the second row was untreated. Shoot dry weight was taken three times by mowing a 3 square meter plot, drying at 60 °C, and weighing. Data is shown in Table 19 expressed as dry weight biomass per 1 square meter of turf. Specifically, dry shoot biomass increased by 84% at the first cutting, 109% at the second cutting, and 122% at the third cutting as compared to the untreated control.

Table 19: Dried shoot biomass measurements

	Treated	Untreated
first cutting	17.39	9.42
second cutting	31.22	14.9
third cutting	41.16	18.53

[00299] This example demonstrates a substantial increase in shoot biomass after application of a composition comprising a plurality of microbes.

Example 19: Increases in root weight, shoot weight, shoot height, and percent mycorrhization following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00300] This example demonstrates increased root weight, shoot height, shoot weight, and percent mycorrhization for tree seedlings after treatment with the composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00301] Long leaf pine, bald cypress, and eastern white pine seeds were separately planted in soil in containers 17 inches long by 1.7 inches wide. After planting, the composition comprising a plurality of different microbes was applied to the soil. All seedlings were irrigated with one inch water per week in addition to natural rainfall and once every two weeks were overhead chemigated with a dilute Miracle Grow fertilizer solution. 10 seedlings were harvested at 30, 60, 90, 120, and 180 days. Root weight, shoot height, and shoot weight were measured. Root weight was measured by collecting the roots of the plant, thoroughly rinsing away soil, drying, and then weighing. Shoot weight was measured by cutting the shoot of the plant, drying, and then weighing. Percent mycorrhization of the root system was determined under a dissecting microscope for each seedling.

[00302] Data is shown for bald cypress trees in Table 20. Average root weight was 12%, 5%, 15%, 53%, and 55% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot height was 7%, 1.5%, 10%, 46%, and 38% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot weight was 5%, 4%, 74%, 65%, and 58% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples.

Table 20: Bald cypress measurements

	Treated			Untreated		
	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]
30 days	1.8	3.2	2.1	1.6	3.0	2.0
60 days	4.0	7.1	4.7	3.8	7.0	4.5

90 days	11.3	13.7	19.4	9.8	12.4	11.1
120 Days	18.2	23.7	23.9	11.9	16.2	14.5
180 Days	22.2	27.1	27.5	14.3	19.9	17.3

[00303] Percent mycorrhization was 0, 10, 25, 45, and 75% for days 30, 60, 90, 120, and 180 respectively as compared to 0, 0, 0, 10, and 20% for days 30, 60, 90, 120, and 180 for untreated samples. Mycorrhization was detected by day 30 in the treated samples as compared day 120 for the untreated samples. Further, the relative percent of mycorrhization was 4.5-fold and 3.75-fold higher in the treated samples as compared to the untreated samples for days 120 and 180 respectively.

[00304] Data is shown for long leaf pine trees in Table 21. Average root weight was 18%, 31%, 30%, 49%, and 64% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot height was 16%, 36%, 49%, 65%, and 83% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot weight was 14%, 36%, 109%, 72%, and 117% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples.

Table 21: Long leaf pine measurements

	Treated			Untreated		
	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]
30 days	2.6	4.2	3.1	2.2	3.6	2.7
60 days	5.5	8.3	4.9	4.2	6.1	3.6
90 days	8.2	12.7	9.2	6.3	8.5	4.4
120 Days	12.5	19.4	13.6	8.4	11.7	7.9
180 Days	15.1	22.2	17.4	9.2	12.1	8.0

[00305] Percent mycorrhization was 0, 35, 85, 100, and 100% for days 30, 60, 90, 120, and 180 respectively as compared to 0, 0, 10, 15, and 20% for days 30, 60, 90, 120, and 180 for untreated samples. Mycorrhization was detected by day 30 in the treated samples as compared day 90 for the untreated samples. Treated samples achieve complete mycorrhization after 120 days, where the untreated samples reached a maximum of 20% mycorrhization by 180 days.

Further, the relative percent of mycorrhization was 3.5-fold, 5.6-fold and 5-fold higher in the treated samples as compared to the untreated samples for days 90, 120, and 180 respectively.

[00306] Data is shown for eastern white pine trees in Table 22. Average root weight was 12%, 5%, 23%, 2%, and 42% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot height was 15%, 7%, 22%, 22%, and 37% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples. Average shoot weight was 10%, 12%, 15%, 12%, and 19% increased at 30, 60, 90, 120, and 180 days, respectively, in the treated samples as compared to the untreated samples.

Table 22: Eastern white pine measurements

	Treated			Untreated		
	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]	Root Weight [g]	Shoot Height [cm]	Shoot Weight [g]
30 days	2.7	3.7	3.1	2.4	3.2	2.8
60 days	4.2	5.6	4.4	4.0	5.2	3.9
90 days	8.9	11.6	7.7	7.2	9.5	6.7
120 Days	11.1	17.3	9.3	9.9	14.1	8.3
180 Days	17.4	23.9	13.2	12.2	17.4	11.1

[00307] Percent mycorrhization was 0, 25, 55, 90, and 100% for days 30, 60, 90, 120, and 180 respectively as compared to 0, 10, 15, 35, and 50% for days 30, 60, 90, 120, and 180 for untreated samples. Mycorrhization was detected by day 30 in both the treated samples and untreated samples. Treated samples achieve complete mycorrhization after 180 days, where the untreated samples reached a maximum of 50% mycorrhization by 180 days. Further, the relative percent of mycorrhization was 2.5-fold, 3.6-fold, 2.5-fold and 2-fold higher in the treated samples as compared to the untreated samples for days 60, 90, 120, and 180 respectively.

[00308] This example demonstrates a substantial increase in root biomass for seedlings treated with a composition comprising a plurality of different microbes after only 180 days, with an average of 54% increase in root weight, 52% increase in shoot height, and 65% in shoot weight. Further this example demonstrates an improvement in root mycorrhization for treated samples as compared to untreated samples without supplementation of any mycorrhizal microbes, suggesting that the composition comprising a plurality of different microbes of the type as disclosed herein stimulate mycorrhizal microbes growth and root colonization.

Example 20: Increases in root biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00309] This example demonstrates increased root biomass for turf after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00310] Turf was treated with the composition comprising a plurality of different microbes. Dry root biomass per 40 cubic centimeters of turf core was measured 10 days and 20 days post treatment along with an untreated control by harvesting 40 cubic cm of turf core, thoroughly rinsing the soil from the roots, drying, and then weighing. At 10 days post treatment, dry root biomass for the treated turf was 6.59 g as compared to 4.28 g for the untreated control, a 65% increase. At 20 days post treatment, dry root biomass for the treat turf was 198.6 g as compared to 79.5 g for the untreated control, a 149% increase.

[00311] This example demonstrates a substantial, 65% increase after only 10 days and a 149% increase after only 20 days in root biomass for seedlings treated with a single application of a composition comprising a plurality of different microbes of the type as disclosed herein compared to untreated.

Example 21: Increases in grape quality following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00312] This example demonstrates increases in crop quality following treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control crop.

[00313] Soil containing grape plants were treated with 100 g/acre of the composition comprising a plurality of different microbes. 4 rows of grape plants were treated and four rows of grape plants were maintained as an untreated control. Total above ground plant wet biomass at harvest was collected and the anthocyanin concentrations in the fruit were measured. Average anthocyanin concentration in grapes from plants grown in the treated soil was 232 mg/L as compared to 112 mg/L for grapes from plants grown in the untreated soil, an increase in anthocyanin concentration of 107%.

[00314] This example demonstrates increases in grape anthocyanin concentration by more than 2-fold following only a single treatment with a composition comprising a plurality of different microbes of the type as disclosed herein as compared to an untreated control crop. It is generally thought that anthocyanin concentration is an indicator of grape quality, thus, the single treatment with a microbial consortium of the type disclosed herein yielded a crop of grapes with higher quality than the untreated control.

Example 22: Increases in agricultural yield following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00315] This example demonstrates increases in crop yield following treatment with the composition comprising a plurality of different microbes as compared to an untreated control crop.

[00316] Three rows of soil planted with tomato seeds was treated with a composition comprising a plurality of different microbes (Example 1), and three rows of soil planted with tomato seeds was maintained as an untreated control. Total above ground fruit production was measured at harvest for both the treated and untreated groups. Tomato plant biomass for the 3 rows was 49.6 kg as compared to 27.8 kg for the untreated control, a 68.67% increase.

[00317] This example demonstrates a substantial increase in crop yield after only a single treatment with the composition comprising a plurality of microbes.

Example 23: 16S rRNA sequencing

[00318] This example demonstrates the ribotype diversity present in the 140 different microbe stocks (see Example 1), available for preparation of a composition comprising a plurality of different microbes.

[00319] Briefly, DNA extraction and 16S gene sequencing was carried out at the Arizona Genomics Institute, University of Arizona. DNA was extracted using ZymoBIOMIC DNA Kit (Zymo Research Inc.) All PCR reactions were performed using the NEB Q5 high-fidelity polymerase kit (New England BioLabs Inc.). Each PCR was done in triplicate with 20 cycles. The bacterial full-length 16S rRNA PCR primers included designated PacBio barcodes. PCR products were purified with AMPure XP beads (BeckmanCoulter Inc.). The amplified DNA was sequenced using the PacBio SMRT sequencing technology according to the standard manufacturers' conditions. DNA concentration was determined by Qubit quantification using Qubit 2.0 fluorometer and the high sensitivity DNA reagents (Invitrogen). Samples were pooled in equimolar concentration and gel purified using The Wizard® SV Gel and PCR Clean-Up System (Promega). The library size was confirmed on a Tape station (Agilent Technologies) before sequencing. 16S gene data was quality checked and filtered and bacterial identities were determined using the BARRNAP tool (https://github.com/tseemann/barrnap). Phylogenetic topography of the 16S sequences was determined using the PhyML Maximum-Likelihood approach (https://ngphylogeny.fr/). The resulting Newick tree was imported into iTOL for visualization and labelling of branches and leaves.

[00320] Figure 2 shows the topography of a Maximum-Likelihood phylogentic tree displaying 195 ribotype gene signatures representing the OSL probiotic culture collection. Ten genera are

presented with *Steptomyces* bacteria comprising the most diverse genus. In the central portion of the radial tree, the most distant and common ancestor of all species is observed, and it bears a close relation to *Streptomyces*. This genus evolved approximately 450 million years ago, taking the form of branched filamentous organisms adapted for the utilization of plant remains. The outermost leaf tips of the tree represent the 195 potential ribotypes available for generating a composition comprising a plurality of different microbes. Starting from *Lysinibacillus* and moving counterclockwise, the genera are (1) *Lysinibacillus*, (2) *Paenibacillus*, (3) *Aureimonas*, (4) *Bradyrhizobium*, (5) *Microvirga*, (6) *Pseudomonas*, (7) *Streptomyces*, (8) *Amycolatopsis*, (9) *Rhodococcus*, (10) *Micrococcus*, and (11) *Strepomyces*. The species for each left are, starting from Lysinibacillus and moving counterclockwise: 162 *Lysinibacillus capsici* (SEQ ID NO: 1), 161 *Lysinibacillus capsici* (SEQ ID NO: 2), 159 *Lysinibacillus capsici* (SEQ ID NO: 3), 150 *Lysinibacillus capsici* (SEQ ID NO: 4), 155 *Lysinibacillus capsici* (SEQ ID NO: 5), 174 *Lysinibacillus capsici* (SEQ ID NO: 6), 166 *Lysinibacillus capsici* (SEQ ID NO: 7), 160 *Lysinibacillus capsici* (SEQ ID NO: 8), 163 *Lysinibacillus capsici* (SEQ ID NO: 9), 56 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 10), 59 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 11), 62 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 12), 41 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 13), 67 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 14), 49 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 15), 65 *Paenibacillus cellulositrophicus* A (SEQ ID NO: 16), 206 *Paenibacillus illinoisensis* (SEQ ID NO: 17), 199 *Aureimonas* A sp001425485 (SEQ ID NO: 18), 112 *Aureimonas* A sp001425485 (SEQ ID NO: 19), 86 *Aureimonas* A sp001425485 (SEQ ID NO: 20), 87 *Aureimonas* A sp001425485 (SEQ ID NO: 21), 209 *Bradyrhizobium elkanii* (SEQ ID NO: 22), 191 *Bradyrhizobium elkanii* (SEQ ID NO: 23), 136 *Bradyrhizobium elkanii* (SEQ ID NO: 24), 182 *Bradyrhizobium elkanii* (SEQ ID NO: 25), 188 *Bradyrhizobium elkanii* (SEQ ID NO: 26), 145 *Bradyrhizobium elkanii* (SEQ ID NO: 27), 121 *Bradyrhizobium elkanii* (SEQ ID NO: 28), 144 *Bradyrhizobium elkanii* (SEQ ID NO: 29), 115 *Bradyrhizobium elkanii* (SEQ ID NO: 30), 133 *Bradyrhizobium denitrificans* (SEQ ID NO: 31), 122 *Bradyrhizobium denitrificans* (SEQ ID NO: 32), 130 *Bradyrhizobium denitrificans* (SEQ ID NO: 33), 193 *Bradyrhizobium denitrificans* (SEQ ID NO: 34), 97 *Bradyrhizobium denitrificans* (SEQ ID NO: 35), 181 *Bradyrhizobium denitrificans* (SEQ ID NO: 36), 186 *Bradyrhizobium denitrificans* (SEQ ID NO: 37), 21 *Microvirga* sp OATH 1 (SEQ ID NO: 38), 14 *Pseudomonas poae* (SEQ ID NO: 39), 30 *Pseudomonas* sp OATH 2 (SEQ ID NO: 40), 33 *Pseudomonas* sp OATH 3 (SEQ ID NO: 41), 44 *Pseudomonas* sp OATH6 (SEQ ID NO: 42), 76 *Pseudomonas poae* (SEQ ID NO: 43), 77 *Pseudomonas* sp OATH 16 (SEQ ID NO: 44), 69 *Pseudomonas* sp OATH 14 (SEQ ID NO: 45), 158 *Pseudomonas azotoformans* (SEQ ID NO: 46), 180 *Pseudomonas azotoformans* (SEQ ID NO: 47), 167 *Pseudomonas azotoformans* (SEQ

ID NO: 48), 156 *Pseudomonas azotoformans* (SEQ ID NO: 49), 24 *Pseudomonas azotoformans* (SEQ ID NO: 50), 82 *Pseudomonas fluorescens* (SEQ ID NO: 51), 80 *Pseudomonas fluorescens* (SEQ ID NO: 52), 42 *Pseudomonas* E sp002836515 (SEQ ID NO: 53), 147 *Pseudomonas* sp OATH 53 (SEQ ID NO: 54), 165 *Pseudomonas* sp OATH 56 (SEQ ID NO: 55), 200 *Pseudomonas* E sp003253735 (SEQ ID NO: 56), 207 *Pseudomonas* E sp003253735 (SEQ ID NO: 57), 152 *Pseudomonas straminea* (SEQ ID NO: 58), 164 *Pseudomonas* sp OATH 55 (SEQ ID NO: 59), 52 *Pseudomonas koreensis* (SEQ ID NO: 60), 70 *Pseudomonas koreensis* (SEQ ID NO: 61), 134 *Pseudomonas* sp OATH 45 (SEQ ID NO: 62), 142 *Pseudomonas* sp OATH 51 (SEQ ID NO: 63), 28 *Pseudomonas koreensis* (SEQ ID NO: 64), 61 *Pseudomonas koreensis* (SEQ ID NO: 65), 71 *Pseudomonas* sp OATH 15 (SEQ ID NO: 66), 39 *Pseudomonas* sp OATH 4 (SEQ ID NO: 67), 114 *Streptomyces violaceorectus* (SEQ ID NO: 68), 110 *Streptomyces* sp OATH 38 (SEQ ID NO: 69), 116 *Streptomyces* sp OATH 40 (SEQ ID NO: 70), 123 *Streptomyces rochei* (SEQ ID NO: 71), 113 *Streptomyces labedae* (SEQ ID NO: 72), 189 *Streptomyces rochei* (SEQ ID NO: 73), 102 *Streptomyces griseoincarnatus* (SEQ ID NO: 74), 23 *Streptomyces griseoincarnatus* (SEQ ID NO: 75), 202 *Streptomyces griseoincarnatus* (SEQ ID NO: 76), 75 *Streptomyces griseoincarnatus* (SEQ ID NO: 77), 74 *Streptomyces griseoincarnatus* (SEQ ID NO: 78), 73 *Streptomyces nigra* (SEQ ID NO: 79), 48 *Streptomyces* sp OATH 8 (SEQ ID NO: 80), 60 *Streptomyces* sp OATH 12 (SEQ ID NO: 81), 90 *Streptomyces* sp OATH 22 (SEQ ID NO: 82), 95 *Streptomyces viridochromogenes* (SEQ ID NO: 83), 72 *Streptomyces* sp001509795 (SEQ ID NO: 84), 81 *Streptomyces flavoviridis* (SEQ ID NO: 85), 117 *Streptomyces* sp OATH 41 (SEQ ID NO: 86), 27 *Streptomyces flavoviridis* (SEQ ID NO: 87), 11 *Streptomyces fimbriatus* (SEQ ID NO: 88), 16 *Streptomyces rochei* (SEQ ID NO: 89), 19 *Streptomyces rochei* (SEQ ID NO: 90), 125 *Streptomyces rochei* (SEQ ID NO: 91), 127 *Streptomyces misionensis* (SEQ ID NO: 92), 129 *Streptomyces misionensis* (SEQ ID NO: 93), 128 *Streptomyces misionensis* (SEQ ID NO: 94), 55 *Streptomyces misionensis* (SEQ ID NO: 95), 37 *Streptomyces misionensis* (SEQ ID NO: 96), 35 *Streptomyces misionensis* (SEQ ID NO: 97), 131 *Streptomyces misionensis* (SEQ ID NO: 98), 3 *Streptomyces misionensis* (SEQ ID NO: 99), 36 *Streptomyces misionensis* (SEQ ID NO: 100), 47 *Streptomyces misionensis* (SEQ ID NO: 101), 184 *Streptomyces griseoviridis* A (SEQ ID NO: 102), 50 *Streptomyces griseoviridis* A (SEQ ID NO: 103), 66 *Streptomyces griseoviridis* A (SEQ ID NO: 104), 2 *Streptomyces griseofuscus* (SEQ ID NO: 105), 54 *Streptomyces* sp OATH 10 (SEQ ID NO: 106), 135 *Streptomyces griseofuscus* (SEQ ID NO: 107), 17 *Streptomyces misionensis* (SEQ ID NO: 108), 53 *Streptomyces misionensis* (SEQ ID NO: 109), 149 *Amycolatopsis lurida* (SEQ ID NO: 110), 153 *Amycolatopsis* OATH 54 (SEQ ID NO: 111), 194 *Amycolatopsis lurida* (SEQ ID NO: 112), 151 *Amycolatopsis lurida* (SEQ ID NO: 113), 168 *Amycolatopsis lurida* (SEQ ID NO: 114), 154

Amycolatopsis lurida (SEQ ID NO: 115), 187 *Rhodococcus qingshengii* (SEQ ID NO: 116), 146 *Rhodococcus erythropolis* (SEQ ID NO: 117), 32 *Micrococcus luteus* (SEQ ID NO: 118), 43 *Micrococcus luteus* (SEQ ID NO: 119), 126 *Streptomyces* sp OATH 44 (SEQ ID NO: 120), 210 *Streptomyces* sp OATh 66 (SEQ ID NO: 121), 204 *Streptomyces* sp OATH 63 (SEQ ID NO: 122), 143 *Streptomyces* sp OATH 52 (SEQ ID NO: 123), 5 *Streptomyces* sp OATH B (SEQ ID NO: 124), 170 *Streptomyces* sp OATH 57 (SEQ ID NO: 125), 140 *Streptomyces* sp OATH 49 (SEQ ID NO: 126), 34 *Streptomyces* sp OATH G (SEQ ID NO: 127), 46 *Streptomyces* sp OATH 7 (SEQ ID NO: 128), 40 *Streptomyces* sp OATH 5 (SEQ ID NO: 129), 51 *Streptomyces* sp OATH 9 (SEQ ID NO: 130), 68 *Streptomyces* sp OATH 13 (SEQ ID NO: 131), 137 *Streptomyces* sp OATH 46 (SEQ ID NO: 132), 63 *Streptomyces* sp OATH 12 (SEQ ID NO: 133), 45 *Streptomyces lydicus* (SEQ ID NO: 134), 203 *Streptomyces lydicus* (SEQ ID NO: 135), 78 *Streptomyces lydicus* (SEQ ID NO: 136), 79 *Streptomyces* sp OATH 17 (SEQ ID NO: 137), 7 *Streptomyces* sp OATH D (SEQ ID NO: 138), 141 *Streptomyces* sp OATH 50 (SEQ ID NO: 139), 94 *Streptomyces* sp OATH 26 (SEQ ID NO: 140), 26 *Streptomyces griseoaurantiacus* (SEQ ID NO: 141), 18 *Streptomyces griseoaurantiacus* (SEQ ID NO: 142), 208 *Streptomyces* sp OATH 65 (SEQ ID NO: 143), 57 *Streptomyces* sp OATH 27 (SEQ ID NO: 144), 197 *Streptomyces* sp OATH 61 (SEQ ID NO: 145), 173 *Streptomyces* sp AOTH 58 (SEQ ID NO: 146), 4 *Streptomyces* sp OATH A (SEQ ID NO: 147), 10 *Streptomyces* sp OATH E (SEQ ID NO: 148), 201 *Streptomyces* sp OATH 62 (SEQ ID NO: 149), 85 *Streptomyces* sp OATH 20 (SEQ ID NO: 150), 99 *Streptomyces* sp OATH 30 (SEQ ID NO: 151), 96 *Streptomyces* OATH 28 (SEQ ID NO: 152), 205 *Streptomyces* sp OATH 64 (SEQ ID NO: 153), 13 *Streptomyces* sp OATH F (SEQ ID NO: 154), 89 *Streptomyces* sp OATH 22 (SEQ ID NO: 155), 132 *Streptomyces* sp OATH 44 (SEQ ID NO: 156), 124 *Streptomyces* sp OATH 43 (SEQ ID NO: 157), 179 *Streptomyces* sp OATH 59 (SEQ ID NO: 158), 25 *Streptomyces* sp900105755 (SEQ ID NO: 159), 20 *Streptomyces* sp900105755 (SEQ ID NO: 160), 196 *Streptomyces* sp900105755 (SEQ ID NO: 161), 58 *Streptomyces* sp OATH 11 (SEQ ID NO: 162), 84 *Streptomyces* sp OATH 19 (SEQ ID NO: 163), 108 *Streptomyces* sp OATH 36 (SEQ ID NO: 164), 138 *Streptomyces* sp OATH 47 (SEQ ID NO: 165), 139 *Streptomyces* sp OATH 48 (SEQ ID NO: 166), 6 *Streptomyces* sp OATH C (SEQ ID NO: 167), 22 *Streptomyces antibioticus* B (SEQ ID NO: 168), 185 *Streptomyces antibioticus* B (SEQ ID NO: 169), 120 *Streptomyces globosus* (SEQ ID NO: 170), 198 *Streptomyces globosus* (SEQ ID NO: 171), 119 *Streptomyces globosus* (SEQ ID NO: 172), 31 *Streptomyces globosus* (SEQ ID NO: 173), 1 *Streptomyces globosus* (SEQ ID NO: 174), 183 *Streptomyces globosus* (SEQ ID NO: 175), 157 *Streptomyces globosus* (SEQ ID NO: 176), 176 *Streptomyces globosus* (SEQ ID NO: 177), 178 *Streptomyces globosus* (SEQ ID NO: 178), 175 *Streptomyces globosus* (SEQ ID NO: 179), 177 *Streptomyces globosus* (SEQ ID

NO: 180), 172 *Streptomyces globosus* (SEQ ID NO: 181), 171 *Streptomyces globosus* (SEQ ID NO: 182), 169 *Streptomyces globosus* (SEQ ID NO: 183), 12 *Streptomyces bikiniensis* (SEQ ID NO: 184), 101 *Streptomyces* sp OATH 32 (SEQ ID NO: 185), 111 *Streptomyces* sp OATH 39 (SEQ ID NO: 186), 109 *Streptomyces* sp OAT 37 (SEQ ID NO: 187), 100 *Streptomyces* sp OATH 31 (SEQ ID NO: 188), 190 *Streptomyces* sp OATH 60 (SEQ ID NO: 189), 118 *Streptomyces* sp OATH 42 (SEQ ID NO: 190), 64 *Streptomyces cavourensis* (SEQ ID NO: 191), 15 *Streptomyces bacillaris* (SEQ ID NO: 192), 91 *Streptomyces* sp OATH 23 (SEQ ID NO: 193), 29 *Streptomyces bacillaris* (SEQ ID NO: 194), 38 *Streptomyces cavourensis* (SEQ ID NO: 195), 211 *Streptomyces bacillaris* (SEQ ID NO: 196).

[00321] *Streptomyces* bacteria constitute the most abundant and potentially significant group of soil *Actinobacteria*, comprising 10% to 70% of the total bacterial populations in global soils. They are widely recognized as ideal soil probiotics due to their positive impact on nutrient availability in soil ecosystems and plant health. Their lifestyle is diverse, encompassing both freeliving and saprophytic capabilities, as well as the ability to colonize plants. *Streptomyces* are renowned for their exceptional genetic capacity to produce unique enzymes that catalyze the biosynthesis of antimicrobial compounds, effectively preventing pathogen invasion in soil. Additionally, they excel in the transformation of complex plant polymers such as cellulose, lignin, chitin, and xylan, making them the primary agents responsible for recycling macro and micronutrients. The byproducts generated during primary decomposition serve as substrates for the growth and energy production of other microbes, including fungi and bacteria, as well as plants that would otherwise struggle to access essential building blocks for growth. Furthermore, the majority of *Streptomyces* species are non-pathogenic, ensuring their compatibility with sustainable agricultural practices and their ability to make positive contributions to soil and plant dynamics. No pathogenic species are included in the consortia as disclosed herein.

[00322] Consortia signatures of carbon sequestration: CO_2 sequestration and fixation by microbes is widespread in bacterial domains, including *Aquificae, Actinobacteria, Chlorobi, Chloroflexi, Firmicutes, Proteobacteria,* and *Thermodesulfobacteria* phyla. Enzymes such as ribulose 1,5-bisphosphate carboxylase/oxygenase (RuBisCO) and carbonic anhydrase (CA) are extensively studied in these domains. Consortia as disclosed herein harbor bacteria from three of these phyla, namely Actinobacteria, Firmicutes, and Proteobacteria, which utilize the non-photosynthetic pathways. These pathways involve the CA enzyme that plays a key role in hydrating CO_2 to bicarbonate. Critical to this process is also the release of the urease enzyme, which catalyzes the formation of urea, maintaining the alkaline pH that promotes the calcification process (the formation of stable calcium carbonate). Of the currently ten identified genera all, except *Paenibacillus* and *Micrococcus* harbor genes encoding CA enzymes and are

therefore also highly likely involved in CO_2 sequestration and a long-term solution of storing carbon in soil.

[00323] Consortia signatures of plant health promoting factors: Several species of nitrogen fixing bacteria are represented in the consortia as disclosed herein and belong to the *Paenibacillus, Bradyrhizobium, Lysinibacillus, Auerimonas, Micrococcus* and *Microvirga* genera. These bacteria offer several additional beneficial functions to the plant host. *Paenibacillus, Pseudomonas,* and *Lysinibacillus* bacteria have demonstrated their capacity to directly enhance crop health by facilitating phosphate solubilization and releasing siderophores that assist plants in acquiring essential metals like iron, magnesium, and manganese. Similar enzymatic capacities exist for the hydrolysis of immobile potassium. Taken together, these abilities to dissolve otherwise inert phosphorus and potassium soil complexes, chelate critical elements from soil, as well as fix nitrogen from the atmosphere, play an important role in promoting plant health, root growth, and can reduce the need for additional N-P-K fertilizers.

[00324] Soil structure and water conservation: *Streptomyces* bacteria (such as those within consortia as disclosed herein) are renowned for their ability to produce filamentous hyphae, a feature that significantly contributes to the formation of mycelial networks within the soil. These hyphae intricately intertwine with other soil particles, fungal hyphae, and plant roots, establishing a complex and interconnected network that plays a crucial role in stabilizing soil structure, effectively preventing erosion, and bolstering overall soil stability. The networks also offer other benefits such as enhancing soil porosity, which, in turn, facilitates improved water infiltration and air exchange—factors critical for healthy root growth and nutrient availability. Furthermore, the presence of *Streptomyces* hyphae (such as *Streptomyces* within consortia as disclosed herein) creates microhabitats within the soil, providing refuge for various other microbes, thereby promoting biodiversity and facilitating interactions among different soil organisms.

[00325] Soil bacteria such as *Streptomyces* (such as those within consortia as disclosed herein) significantly contribute to water conservation by promoting the formation of soil aggregates through the secretion of gel-like substances like Extracellular Polymeric Substances (EPS). EPS helps stabilize soil structure, preventing water loss through evaporation or flooding. In addition to EPS role in soil structure, they directly shield plant roots from desiccation, further emphasizing their importance in preserving soil moisture. The gel-like EPS matrix not only enhances plant root growth but also improves water infiltration, ultimately assisting in maintaining a balanced water table at a shallower depth.

[00326] In conclusion, these findings underscore the substantial contributions of the beneficial soil microbiome and highlights the beneficial function that can be provided by consortia as

disclosed herein. The application of consortia as disclosed herein presents groundbreaking opportunities to advance soil carbon sequestration, boost crop production, enhance nutrient content in crops, promote water conservation through improved soil structure, reduce reliance on chemical fertilizers, and ensure the long-term fertility and resilience of soils.

Example 24: Improved germination rates, root biomass, and shoot biomass from grass seed coated with a composition comprising a plurality of different microbes as disclosed herein

[00327] This example demonstrates improved germination rates, increased root biomass, and increased shoot biomass for seeds coated with a composition comprising a plurality of different microbes (generated as described in Example 1) compared to untreated seeds.

[00328] Briefly, Fescue grass seeds were either coated with the composition comprising a plurality of different microorganisms or untreated and placed onto steam/heat sterilized turf field soil in flats, 6 flats per treatment group. The flats were 30 inches by 22 inches by 4.5 inches. The seeds were grown under standard greenhouse conditions at 24 °C and were watered three times per week for 21 days. Germination rate and time was documented. Germination rate was determined as the number of germinated seeds per planted seed 10 days post seeding. Seedlings were the destructively harvested and evaluated for root and shoot biomass.

[00329] Data is shown in Table 23 and Figure 4 shows a comparison of turf resulting from treated (right) and untreated (left) seeds. The treated seeds shown higher germination rates, and increased root and shoot biomass. Specifically, average fresh root biomass for seeds treated with the composition comprising a plurality of different microbes was 11.96 g as compared to 5.23 g for untreated seeds, a 2.28-fold increase. Average fresh shoot biomass for seeds treated with the composition comprising a plurality of different microbes was 16.32 g as compared to 7.27 g for untreated seeds, a 2.24-fold increase. Further, germination rate was increased by 9% in for treated seeds.

Table 23: Measurements

Treatment	Average fresh root biomass (g)	Average fresh shoot biomass (g)	Percent germination
Untreated seeds	5.23	7.27	89%
Treated seeds	11.96	16.32	98%

[00330] This example demonstrates a substantial increase in both root biomass and shoot biomass for seeds treated with a composition comprising a plurality of different microbes as disclosed herein compared to untreated seeds, > ~2-fold increase. Further, coating seeds with a composition comprising a plurality of different microbes as disclosed herein improved seed germination rates.

Example 25: Increased root weight, shoot weight, and fruit weight following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00331] This example demonstrates increased root weight, shoot weight, and fruit weight (*i.e.*, yield) after treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to an untreated control.

[00332] Tomatoes were grown under constant recycled hydroponic greenhouse conditions. 50 trellis trained Burpee Bigboy tomato plants grown under standard conditions were compared to 50 trellis trained Burpee Bigboy tomato plants treated with a single treatment of 1 tablespoon per 5 gallons root irrigation of the composition comprising a plurality of different microbes. At the end of the growing cycle all of the plants were destructively tested for the total root weight, total shoot weight (not including fruit), and the total fruit weight of the free tissue tomatoes. Results are provided as an average per 50 plants.

Table 24: Measurements

Treatment	Average total root weight (g)	Average total shoot weight (g)	Average total fruit weight (g)
Untreated	721.4	802.2	2764.9
Treated	1169.8	1268.3	3904.7

[00333] Data is shown in Table 24. Plants treated with the composition comprising a plurality of different microbes shown increased total root weight, increased total shoot weight, and increased total fruit weight as compared to the untreated plants. Specifically, average total root weight increased by 1.62-fold, average total shoot weight increased by 1.58-fold, and average total fruit weight increased by 1.41-fold for treated plants as compared to untreated plants.

[00334] This example demonstrates a substantial increase in total root weight, total shoot weight, and total fruit weight following just a single treatment with a composition comprising a plurality of different microbes as disclosed herein. This represents a surprising and unexpected increase in yield by 41% with only a single treatment of the composition.

Example 26: Improved yield and fruit quality of pineapple plants treated with a composition comprising a plurality of different microbes as disclosed herein

[00335] This example demonstrates increased pineapple yield and fruit quality for plants following treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to untreated plants.

[00336] Briefly, pineapple plants were treated with 369 g/ha/application of the composition comprising a plurality of different microbes at days 14 and 29. Brix, acid %, pH, Vitamin C, carotene, shell firmness, porosity, translucency, blemish, and yield were measured.

[00337] Treatment with the composition comprising a plurality of different microbes increased Brix to 16.64 as compared to 15.90 for untreated plants (p-value = 0.001). Likewise, Vitamin C increased to 106.2 mg/6 fluid ounce as compared to 93 mg/6 fluid ounce for untreated plants (p-value < 0.001). Acid % (treated: 0.53, untreated 0.53, p-value = 0.81), pH (treated: 3.73, untreated 3.75, p-value = 0.48), and carotene (treated: 5.7, untreated 5.9, p-value = 0.42) were similar between the two treatment groups. Shell firmness (treated: 8.12, untreated 8.20, p-value = 0.61), porosity (treated: 1.85, untreated 1.63, p-value = 0.045), and translucency (treated: 2.38, untreated 2.20, p-value = 0.06) were also similar between the two treatment groups. While porosity was significantly higher for fruit harvested from treated plants as compared to untreated plants, the average rating was lower than 2, which implies acceptable trace to moderate porosity for both treatments.

[00338] Plants treated with the composition comprising a plurality of different microbes produced 747 more boxes of marketable idea 6-8 sizes of pineapples (6,303 total boxes as compared to 5,556 total boxes) and 325 fewer non-marketable boxes (undersized fruits, 880 as compared to 1,205 boxes). Further, plants treated with the composition comprising a plurality of different microbes had 456 more fresh fruit boxes (10,751 as compared to 10,295). Plants treated with the composition comprising a plurality of different microbes resulted in 6.3 ton/ha more idea cannery sizes and 5.7 ton/ha more total tonnage than untreated plants. The average fruit weight was similar between the two treatment groups.

[00339] This example demonstrates increased pineapple yield and fruit quality for plants following treatment with a composition comprising a plurality of different microbes as compared to untreated plants.

Example 27: Improved soybean yield from plants treated with a composition comprising a plurality of different microbes as disclosed herein

[00340] This example demonstrates improved soybean yield from plants treated with a composition comprising a plurality of different microbes (generated as described in Example 1) compared to untreated plants.

[00341] Briefly 30 square meter plots of soybeans (Glycine Max) were planted with soybean seeds, a first having been treated with the composition comprising a plurality of different microbes at 16 oz/acre and the second untreated. Standard fertilization, pesticides, and irrigation protocols were used on both plots. Soybean pods were harvested when foliage had turned brown and bean pods were ripe and dry. Weight of soybeans (*i.e.*, yield) was measured in the first year and in the second year. In the first year, treated plants produced 17.7 kg of soybeans as compared

to 9.9 kg for the untreated plants, a 1.8-fold increase. In the second year, treated plants produced 21.9 kg of soybeans as compared to 13.7 kg for the untreated plants, a 1.6-fold increase.

[00342] This example demonstrates a substantial increase in soybean yield in the first and second years for plants treated with a composition comprising a plurality of different microbes as disclosed herein as compared to untreated plants.

Example 28: Improved bell pepper yield from plants treated with a composition comprising a plurality of different microbes as disclosed herein

[00343] This example demonstrates improved bell pepper yield from plants treated with a composition comprising a plurality of different microbes (generated as described in Example 1) compared to untreated plants.

[00344] Briefly 200 6" pots containing steam sterilized field soil were planted with a single bell pepper seed. Half of the pots were treated with 16 oz/acre of the composition comprising a plurality of different microbes while the other half were untreated. Plants were grown under controlled greenhouse conditions subject to routine irrigation, fertilization, and pesticide application. Total fresh weight of fruit was measured for the 100 treated and untreated pots at day 55, day 80, and day 110. At day 55, treated plants produced 22.6 kg of bell peppers as compared to 17.3 kg for the untreated plants, a 1.3-fold increase. At day 80, treated plants produced 26.1 kg of bell peppers as compared to 16.9 kg for the untreated plants, a 1.5-fold increase. At day 110, treated plants produced 25.0 kg of bell peppers as compared to 17.2 kg for the untreated plants, a 1.5-fold increase. In total, over the 110 days, treated plants produced 73.7 kg of bell peppers while untreated plants produced 51.4 kg of bell peppers, equating to ~44% more fruit by weight.

[00345] This example demonstrates a substantial increase in bell pepper yield in the first and second years for plants treated with a composition comprising a plurality of different microbes as disclosed herein as compared to untreated plants.

Example 29: Increased growth of trees treated with a composition comprising a plurality of different microbes as disclosed herein

[00346] This example demonstrates increased tree growth, for example tree ring growth and diameter at breast height (dbh), in trees following treatment with a composition comprising a plurality of different microbes (generated as described in Example 1) compared to untreated trees.

[00347] Briefly, Aleppo pine (*Pinus halepensis*) trees were treated with the composition comprising a plurality of different microbes ~3 times per year, with each subsequent treatment applied approximately every 30 days. ~0.5 g of the composition comprising a plurality of

different microbes was mixed into 1 gallon of water and poured evenly around the base of the tree. Treated trees were treated in 2022.

[00348] Tree ring growth was determined as follows. Core samples were taken using a coring tool. One core per treated tree and two cores from a single untreated tree were collected. Cores were approximately 12-16 inches in length. The core samples were glued to wooden mounts with the cross-sectional surface facing upwards. Samples were polished to better view the earlywood and latewood ring boundaries using a random orbital sander with progressively finer sandpaper (400, 600, 800, and 1200 grit). An air compressor equipped with a high-pressure nozzle was then used to remove remnant dust particles. The samples were then hand buffer and any remaining dust and debris was removed with the air compressor. The samples were imaged under the microscope and sequential calendar years were assigned to the rings of each sample, starting with the outermost complete ring and moving inward to Ca. 5 years (Stokes and Smiley, 1996). All samples were then scanned individually into the computer at 2400 dpi using an Epson V600 scanner and the scanning program SilverFast 9. Using the dendrochronology software CooRecorder 9.6 (Maxwell and Larsson, 2021), the ring-width for each sample was measured to the nears 0.001 mm starting with the known outermost year. Samples were assigned annual dates based on careful attention to tracheid anatomical detail. Special care was taken to account for all possible rings that could be misinterpreted, and these were recorded in detail.

[00349] All treated trees experienced growth following treatment with the composition comprising a plurality of different microbes (Table 25). There were variations in the amount of growth between trees, but all treated trees showed substantial increases in secondary growth (radial growth) in 2023 than in 2022 (2023 mean growth: 1.644 mm, 2022 mean growth: 0.381 mm, one tail P-value using a Two-sample t-Test assuming unequal variances: 0.007). Treated trees on average showed a 4.3-fold increase in mean growth from 2023 to 2022. The untreated tree did not show an increase in growth rate in the same time period. The mean growth in 2023 was less than in 2022 (2023 mean growth: 0.828 mm, 2022 mean growth: 1.088 mm). These results demonstrate a substantial difference in ring mean growth between treated and untreated trees.

Table 25: Tree-ring measurements

	Annual tree-ring measurements [mm]			
	2020	2021	2022	2023
Treated #1	0.545	1.034	0.278	2.090
Treated #2	0.341	0.403	0.117	0.826
Treated #3	0.665	1.461	0.594	2.987
Treated #4	0.277	0.497	0.470	1.224
Treated #5	-	-	0.446	2.817

Treated #6	0.234	0.670	0.657	1.266
Treated #7	0.130	0.128	0.106	0.297
Untreated #1a	0.171	1.698	1.493	1.103
Untreated #1b	0.114	0.880	0.683	0.552

- Data not available.

[00350] Tree dbh was calculated by measuring the width of a tree at a height of approximately 4 feet. Average dbh for trees treated with the composition comprising a plurality of different microbes was ~71 cm as compared to 43.5 cm for the untreated tree (Table 26). These results show a substantial 1.62-fold increase in average tree diameter for treated trees as compared to untreated trees.

Table 26: Tree diameter measurements

	Diameter at breast height (dbh) [cm]
Treated #1	80
Treated #2	90
Treated #3	65
Treated #4	53
Treated #5	74
Treated #6	72
Treated #7	62
Untreated #1	43.5

[00351] This example demonstrates that trees treated with a composition comprising a plurality of different microbes as disclosed herein demonstrate substantial increases in annual tree growth (~4.3-fold) and diameter at breast height (~1.62-fold). This is a pioneering example of soil amendment that improves annual tree growth. Thus, the compositions comprising a plurality of different microbes as disclosed herein show utility in a number of applications, for example those of reforestation where increased annual growth rates would greatly aid in reforestation efforts.

Example 30: Improved oil content, soil beneficial microbes, and plant biomass hemp treated with a composition comprising a plurality of different microbes as disclosed herein

[00352] This example demonstrates improved growth and plant properties of hemp treated with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to untreated plants. Specifically, this example demonstrates reduction of THC content due to cultivar genetic expression enhancement and increased in CBD oil content in treated plants as compared to untreated plants.

[00353] Briefly, 1,000 2-month old potted CHERRY CROSS clones (bred for low THC and high CBD) were planted on a 10 acre tract of sandy loam soil. All plants were drip irrigated and

treated with standard fertilization with 140 lbs/acre Nitrogen, 70 lbs/acre Potassium, and 45 lbs/acre Phosphorous. Fertilizer determinations were made via NCDA soil analysis. Half of the plants (500) were treated with the composition comprising a plurality of different microbes. The season was very challenging regarding insects (aphids and spider mites), which were treated with pyrethrin, neem oil, and chromobacterium sprays on a regular basis. After 3 months, the plants were harvested, flowering heads stripped, and dried at ambient temperature with vigorous air flow. Samples of these plants were sent to Botanacor Services for oil extraction, which is Certified by the State of Colorado for official Cannabis analysis. Leaf nutrient content analysis, plant biomass, and total oil production was analyzed.

[00354] Total cannabinoid content in treated plants substantially higher than in untreated plants, 15.1% as compared to 8.8% respectively, a 1.71-fold increase. Oil content analysis is shown in Table 27. Specifically, THC was undetectable in treated plants as compared to untreated plants. CBDa and CBD increased by 1.82-fold and 1.46-fold respectively for treated plants as compared to untreated plants. Interestingly, more than 50% of the untreated plants tested above legal limits for THC, classifying them as marijuana, while less than 4% of the treated plants had a total THC content over 0.03% with the remaining 96% of treated plants below the legal limits.

Table 27: Oil content analysis

	Mean average [mg/g]					
	THCa	THC	CBDa	CBD	CBN	CBG
Treated	0.313	0	13.093	1.676	0	0
Untreated	0.397	0.075	7.181	1.146	0	0

[00355] Seven days post-treatment, beneficial microbes were quantified as described above. Beneficial microbes were present at an average of 33,100 beneficial microbes per gram of untreated soil as compared to an average of 52,500,000,000 beneficial microbes per gram of treated soil.

[00356] After drying, plant biomass was recorded for 100 treated and 100 untreated plants. There was a substantial 1.47-fold increase in plant biomass for treated plants as compared to untreated plants (mean treated: 2851 g, mean untreated: 1934 g, one tail P-value using a Two-sample t-Test assuming unequal variances: 5E-51). The data is also visually represented as a box and whiskers chart in Figure 5.

[00357] Petiole samples were taken from hemp plants and processed by the North Carolina Department of Agriculture. The results are shown in Table 28. There was a 1.38-fold, 1.58-fold, 1.64-fold, 2.1-fold, 2.3-fold, and 1.7-fold increase in total leaf Nitrogen, Potassium, Phosphorus, Magnesium, Calcium, and Sulfur for treated plants compared to untreated plants respectively.

Table 28: Nutrient analysis

	Total Leaf Nutrients [%]					
	Nitrogen	Potassium	Phosphorus	Magnesium	Calcium	Sulfur
Treated	2.45	1.77	0.46	0.59	0.98	0.53
Untreated	1.77	1.12	0.28	0.28	0.42	0.31

[00358] This example demonstrates a dramatic improvement in oil content, soil beneficial microbes, and plant biomass following treatment with a composition comprising a plurality of different microbes as disclosed herein. In general flowing heads (containing oil bearing trichomes) were larger and more robust, the oil content per gram of flower was consistently higher in treated plants, and CDB yield is double that of non-treated cannabis plants.

Example 31: Increased hemp plant properties following treatment with a composition comprising a plurality of different microbes as disclosed herein

[00359] This example demonstrates increase overall health and vitality of plants root, shoot, and flower tissues, increased number of leaf bearing trichomes, increased number and weight of flower tissues, and double-triple CDB, CDB-A, CBG, and CBG-A cannabinoid and aromatic terpene content in hemp plants treated with a composition comprising a plurality of different microbes (generated as described in Example 1) as compared to untreated plants.

[00360] Briefly, hemp cultivar T1 was grown with or without treatment with the composition comprising a plurality of different microbes. Plants were harvested and analyzed following, 1, 2, and 3 treatments and compared to untreated plants. The plants were grown using standard agronomic practices in a challenging environment with temperatures exceeding 40 °C with periods of both drought and high rainfall in addition to high insect and pathogen populations.

[00361] Plant height for untreated plants averaged 34.3 cm, for 1x treated plants averaged 71.4 cm, for 2x treated plants averaged 99.8 cm, and for 3x treated plant averaged 137.7 cm. 1x treated plants were 108% taller on average, 2x treated plants were 191% taller on average, and 3x treated plants on average were 301% taller than the untreated plants.

[00362] Stem diameter at the root collar for untreated plants averaged 7.1 mm, for 1x treated plants averaged 13.6 mm, for 2x treated plants averaged 14.2 mm, and for 3x treated plants averaged 17.3 mm. 1x treated plants had a 91% wider root collar diameter on average, 2x treated plants had a 100% wider root collar diameter on average, and 3x treated plants had a 144% wider root collar diameter on average than the untreated plants.

[00363] Root weight for untreated plants averaged 492 g, for 1x treated plants averaged 689 g, for 2x treated plants averaged 1001 g, and for 3x treated plants averaged 1097 g. 1x treated plants had 40% higher root weight on average, 2x treated plants had 103% higher root weight on average, and 3x treated plants had 123% higher root weight on average than untreated plants.

[00364] Fine root weight for untreated plants averaged 188 g, for 1x treated plants averaged 301 g, for 2x treated plants averaged 529 g, and for 3x treated plants averaged 718 g. 1x treated plants had 60% higher fine root weight on average, 2x treated plants had181% higher fine root weight on average, and 3x treated plants had 282% higher fine root weight than untreated plants.

[00365] It will be appreciated that fine root weight is an indication of available surface area for production of one or more substances (e.g., root exudates) that hold carbon or are precursors to such substances. Thus, the surprisingly large increase in fine root weight indicates a greatly increased carbon deposition in and around the plants.

[00366] Fresh shoot weight for untreated plants averaged 793 g, for 1x treated plants averaged 1201 g, for 2x treated plants averaged 1442 g, and for 3x treated plants averaged 1893 g. 1x treated plants had 51% higher fresh shoot weight on average, 2x treated plants had 82% higher fresh shoot weight on average, and 3x treated plants had 139% higher fresh shoot weight on average than untreated plants.

[00367] Average total fresh flower weight for untreated plants averaged 362 g, for 1x treated plants averaged 697 g, for 2x treated plants averaged 864 g, and for 3x treated plants averaged 930 g. 1x treated plants had 92% higher fresh flower weight on average, 2x treated plants had 139% higher fresh flower weight on average, and 3x treated plants had 157% higher fresh flower weight on average than untreated plants.

[00368] The average number of flowering heads per plant for untreated plants averaged 4.6 g, for 1x treated plants averaged 13.9 g, for 2x treated plants averaged 15.2 g, and for 3x treated plants averaged 17.4 g. 1x treated plants had 202% more flowering heads, 2x treated plants had 230% more flowering heads, and 3x treated plants had 278% more flowering heads than untreated plants.

[00369] Flowering head weight per plant for untreated plants averaged 13.4 g, for 1x treated plants averaged 48.6 g, for 2x treated plants averaged 67.4 g, for 3x treated plants averaged 91.7 g. 1x treated plants had 263% higher flowering head weight, 2x treated plants had 403% higher flowering head weight, and 3x treated plants had 584% higher flowering head weight than untreated plants.

[00370] Terminal leaf trichomes per square centimeter (cm) on the leaf surface for untreated plants averaged 13.2 per square cm, for 1x treated plants averaged 37.7 per square cm, for 2x treated plants averaged 59.0 per square cm, and for 3x treated plants averaged 71.0 per square cm. 1x treated plants had 185.6% more trichomes per square cm, 2x treated plants had 347% more trichomes per square cm, and 3x treated plant had 438% more trichomes per square cm than untreated plants.

[00371] Average shoot growth at 30, 60 and 90 days post-treatment for untreated plants averaged 31.2, 57.3, and 99.3 cm respectively. For 1x treated plants, average shoot growth at 30, 60, and 90 days post-treatment averaged 58.7, 77.9, and 132.7 cm respectively. For 2x treated plants, average shoot growth at 60 and 90 days post-treatment averaged 84.2 and 132.7 cm respectively. For 3x treated plants, average shoot growth at 90 days post-treatment averaged 161.0 cm. At harvest, average shoot growth for untreated plants averaged 103.9 cm, for 1x treated plants averaged 159.7 cm, for 2x treated plants averaged 181.9 cm, and for 3x treated plants averaged 198.2 cm. Percentage increases compared to untreated are shown in Table 29.

Table 29: % increase in ave. shoot growth of treated plants compared to untreated plants

	Increase compared to untreated [%]		
	1x treated	2x treated	3x treated
30 days	88.14		
60 days	35.95	46.94	
90 days	131.58	131.58	
Harvest	53.70	75.07	90.76

[00372] Terpene analysis was conducted by Avazyme for untreated plants and harvested 3x treated plants. The data is shown in Table 30. Total terpenes increased by 2-fold in 3x treated plants as compared to 1x treated plants. Alpha pinene levels were 85% higher on average, Mycene levels were 204% higher on average, Limonene levels were 18% higher on average, Beta caryphylene levels were 102% higher on average, and Alpha humulene levels were 228% higher on average for the 3x treated plants than the untreated plants.

Table 30: Terpene analysis

	Untreated	3x treated
Alpha pinene	0.4	0.737
Myrcene	1.585	3.821
Limonene	1.53	1.814
Beta caryphylene	4.967	10.052
Alpha humulene	0.545	1.789
Total Terpenes	9.027	18.213

[00373] Cannabinoid analysis was simultaneously conducted by Avazyme for untreated plants and for 3x treated plants. The data is shown in Table 31. Total CBD increased by 94% and total CBG increased by 196% for 3x treated plants as compared to untreated plants. CBD levels increased 193% on average, CBD-A levels increased 78% on average, and CDG-A levels increased 119% on average for 3x treated plants as compared to control plants.

Table 31: Cannabinoid analysis

	Untreated	Treated
CBD	4.76	13.95
CBG	0.00	1.78
CBD-A	41.79	74.38
CBG-A	2.61	5.71
Total CBD (CBD+CBD-A*0.877)	41.41	79.18
Total CBG (CBG+CBG-A*0.877)	2.29	6.79

[00374] Treatments with the composition comprising a plurality of different microbes as disclosed herein doubled the terpene content, tripled total CBD concentration, and significantly enhanced the growth, development, and final yield/oil concentrations. Treated plants demonstrated highly statistically significant differences in all categories of collected data and illustrated that soil additives such as those disclosed herein substantially impact the phenology, growth, yield, and quality of industrial hemp grown for cannabinoid and terpene extraction

IV. Embodiments

[00375] In embodiment 1 provided herein is a composition comprising one or more *Streptomyces* microbes, wherein the one or more *Streptomyces* microbes comprise a 16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5 identical, or 100% identical, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to a nucleic acid sequence to one or more of SEQ ID NOs: 68-109 and 120-196.

[00376] In embodiment 2 provided herein is the composition of embodiment 1 comprising microbes of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, yet even more preferably 10-30 different *Streptomyces* strains.

[00377] In embodiment 3 provided herein is the composition of embodiment 1 or embodiment 2 further comprising one or more non-*Streptomyces* microbes.

[00378] In embodiment 4 provided herein is the composition of any one of the previous embodiments comprising one or more *Pseudomonas* microbes.

[00379] In embodiment 5 provided herein is the composition of any one of the previous embodiments comprising one or more *Microvirga* microbes.

[00380] In embodiment 6 provided herein is the composition of any one of the previous embodiments comprising one or more *Micrococcus* microbes.

[00381] In embodiment 7 provided herein is the composition of any one of the previous embodiments comprising one or more *Paenibacillus* microbes.

[00382] In embodiment 8 provided herein is the composition of any one of the previous embodiments comprising one or more *Aureimonas* microbes.

[00383] In embodiment 9 provided herein is the composition of any one of the previous embodiments comprising one or more *Bradyrhizobium* microbes.

[00384] In embodiment 10 provided herein is the composition of any one of the previous embodiments comprising one or more *Rhodococcus* microbes.

[00385] In embodiment 11 provided herein is the composition of any one of the previous embodiments comprising one or more *Amycolatopsis* microbes.

[00386] In embodiment 12 provided herein is the composition of any one of the previous embodiments comprising one or more *Lysinibacillus* microbes.

[00387] In embodiment 13 provided herein is the composition of any one of the previous embodiments wherein two or more of the microbes are heterologous to each other.

[00388] In embodiment 14 provided herein is a composition comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, further preferably 10-30, different *Streptomyces* microbes.

[00389] In embodiment 15 provided herein is the composition of embodiment 14 further comprising one or more non-*Streptomyces* microbes.

[00390] In embodiment 16 provided herein is the composition of embodiment 14 or embodiment 15 wherein two or more of the microbes are heterologous to each other.

[00391] In embodiment 17 provided herein is the composition of embodiment 15 or embodiment 16 wherein the one or more non-*Streptomyces* microbes comprise a *Pseudomonas*, *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

[00392] In embodiment 18 provided herein is the composition of embodiment 15 or embodiment 16 wherein the one or more non-*Streptomyces* microbes comprise a *Pseudomonas*, *Microvirga*, *Micrococcus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

[00393] In embodiment 19 provided herein is the composition of embodiment 15 or embodiment 16 wherein the one or more non-*Streptomyces* microbes comprise a *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

[00394] In embodiment 20 provided herein is the composition of embodiment 17 or embodiment 18 wherein the one or more non-*Streptomyces* microbes comprise one or more *Pseudomonas* microbes.

[00395] In embodiment 21 provided herein is the composition of any one of embodiments 17 through 20 comprising a *Microvirga* microbe.

[00396] In embodiment 22 provided herein is the composition of any one of embodiments 17 through 21 wherein the one or more non-*Streptomyces* microbes comprise one or more *Micrococcus* microbes.

[00397] In embodiment 23 provided herein is the composition of any one of embodiments 17 through 22 wherein the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes.

[00398] In embodiment 24 provided herein is the composition of any one of embodiments 17 through 23 wherein the one or more non-*Streptomyces* microbes comprise one or more *Aureimonas* microbes.

[00399] In embodiment 25 provided herein is the composition of any one of embodiments 17 through 24 wherein the one or more non-*Streptomyces* microbes comprise one or more *Bradyrhizobium* microbes.

[00400] In embodiment 26 provided herein is the composition of any one of embodiments 17 through 25 wherein the one or more non-*Streptomyces* microbes comprise one or more *Rhodococcus* microbes.

[00401] In embodiment 27 provided herein is the composition of any one of embodiments 17 through 26 wherein the one or more non-*Streptomyces* microbes comprise one or more *Amycolatopsis* microbes.

[00402] In embodiment 28 provided herein is the composition of any one of embodiments 17 through 27 wherein the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes.

[00403] In embodiment 29 provided herein is a composition comprising *Streptomyces* spp. microbes and at least one, two, three, four, five, 6, or 7 and/or not more than one, two, three, four, five, 6, 7, or 8, preferably 2-8, more preferably 2-6, yet more preferably 3-8, such as 2, 3, 4, 5, 6, 7, 8, or 8 additional microbes selected from the group consisting of *Pseudomonas* spp.,

Microvirga spp., *Paenibacillus* spp., *Aureimonas* spp., *Bradyrhizobium* spp., *Rhodococcus* spp., *Amycolatopsis* spp., and *Lysinibacillis* spp.

[00404] In embodiment 30 provided herein is the composition of embodiment 29 comprising at least 2, 3, 5, 7, 10, 12, 15, 20, 30, 40, or 50 and/or not more than 3, 5, 7, 10, 12, 15, 20, 30, 40, 50, 60, 80, or 100 different *Streptomyces* microbes, for example 2-100 different *Streptomyces* microbes.

[00405] In embodiment 31 provided herein is the composition of embodiment 29 or embodiment 30 comprising *Pseudomonas* spp. microbes.

[00406] In embodiment 32 provided herein is the composition of embodiment 31 comprising at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 different *Pseudomonas* microbes, for example 2-24 different *Pseudomonas* microbes.

[00407] In embodiment 33 provided herein is the composition any one of embodiments 29 through 32 comprising *Microvirga* spp. microbes.

[00408] In embodiment 34 provided herein is the composition any one of embodiments 29 through 33 comprising *Micrococcus* spp. microbes.

[00409] In embodiment 35 provided herein is the composition of embodiment 34 comprising at least 2, 3, 4, 5 and/or not more than 3, 4, 5, or 6 different *Micrococcus* microbes, for example 2-6 different *Micrococcus* microbes.

[00410] In embodiment 36 provided herein is the composition of any one of embodiments 29 through 35 comprising *Paenibacillus* spp. microbes.

[00411] In embodiment 37 provided herein is the composition of embodiment 36 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Paenibacillus* microbes, for example 2-10 different *Paenibacillus* microbes.

[00412] In embodiment 38 provided herein is the composition of any one of embodiments 29 through 37 comprising *Aureimonas* spp. microbes.

[00413] In embodiment 39 provided herein is the composition of embodiment 38 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Aureimonas* microbes, for example 2-10 different *Aureimonas* microbes.

[00414] In embodiment 40 provided herein is the composition of any one of embodiments 29 through 39 comprising *Bradyrhizobium* spp. microbes.

[00415] In embodiment 41 provided herein is the composition of embodiment 40 comprising at least 2, 3, 4, 5, 6, 7, 8, 10, 12, or 14 and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, or 16 different *Bradyrhizobium* microbes, for example 2-16 different *Bradyrhizobium* microbes.

[00416] In embodiment 42 provided herein is the composition of any one of embodiments 29 through 41 comprising *Rhodococcus* spp. microbes.

[00417] In embodiment 43 provided herein is the composition of embodiment 42 comprising at least 2 different *Rhodococcus* microbes.

[00418] In embodiment 44 provided herein is the composition of any one of embodiments 29 through 43 comprising *Amycolatopsis* spp. microbes.

[00419] In embodiment 45 provided herein is the composition of embodiment 44 comprising at least 2, 3, 4, or 5 and/or not more than 3, 4, 5, or 6 different *Amycolatopsis* microbes, for example 2-6 different *Amycolatopsis* microbes.

[00420] In embodiment 46 provided herein is the composition of any one of embodiments 29 through 45 comprising *Lysinibacillis* spp. microbes.

[00421] In embodiment 47 provided herein is the composition of embodiment 47 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Lysinibacillus* microbes, for example 2-10 different *Lysinibacillus* microbes.

[00422] In embodiment 48 provided herein is a composition comprising one or more *Streptomyces* microbes and at least one non-*Streptomyces* microbe, wherein the non-*Streptomyces* microbe is a nitrogen-fixing microbe.

[00423] In embodiment 49 provided herein is the composition of embodiment 48 comprising at least 2, 3, 5, 7, 10, 12, 15, 20, 30, 40, or 50 and/or not more than 3, 5, 7, 10, 12, 15, 20, 30, 40, 50, 60, 80, or 100 different *Streptomyces* strains, for example 2-100 different *Streptomyces* microbes.

[00424] In embodiment 50 provided herein is the composition of embodiment 48 or embodiment 49 wherein the nitrogen-fixing, non-*Streptomyces* microbe comprises a *Pseudomonas* spp., *Microvirga* spp., *Bradyrhizobium* spp., *Aureimonas* spp., *Paenibacillus* spp., and/or *Lysinibacillus* spp. microbe.

[00425] In embodiment 51 provided herein is the composition of embodiment 50 comprising one or more *Pseudomonas* spp. microbe.

[00426] In embodiment 52 provided herein is the composition of embodiment 48 or 49 wherein the nitrogen-fixing, non-*Streptomyces* microbe comprises a *Microvirga* spp., *Bradyrhizobium* spp., *Aureimonas* spp., *Paenibacillus* spp., and/or *Lysinibacillus* spp. microbe.

[00427] In embodiment 53 provided herein is the composition of any one of embodiments 48 through 52 comprising one or more *Microvirga* spp. microbe.

[00428] In embodiment 54 provided herein is the composition of any one of embodiments 48 through 53 comprising one or more *Micrococcus* spp. microbe.

[00429] In embodiment 55 provided herein is the composition of any one of embodiments 48 through 54 comprising one or more *Paenibacillus* spp. microbe.

[00430] In embodiment 56 provided herein is the composition of any one of embodiments 48 through 55 comprising one or more *Aureimonas* spp. microbe.

[00431] In embodiment 57 provided herein is the composition of any one of embodiments 48 through 56 comprising one or more *Bradyrhizobium* spp. microbe.

[00432] In embodiment 58 provided herein is the composition of any one of embodiments 48 through 57 comprising one or more *Lysinibacillus* spp. microbe.

[00433] In embodiment 59 provided herein is the composition of any one of the previous embodiments wherein the one or more *Streptomyces* microbes comprise one or more of *Streptomyces antibioticus* B, *Streptomyces bacillaris*, *Streptomyces bikiniensis*, *Streptomyces cavourensis*, *Streptomyces fimbriatus*, *Streptomyces flavoviridis*, *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces griseofuscus*, *Streptomyces griseoincarnatus*, *Streptomyces griseoviridis* A, *Streptomyces labedae*, *Streptomyces lydicus*, *Streptomyces misionensis*, *Streptomyces nigra*, *Streptomyces rochei*, *Streptomyces* sp. OATH_5, *Streptomyces* sp. OATH_7, *Streptomyces* sp. OATH_8, *Streptomyces* sp. OATH_9, *Streptomyces* sp. OATH_10, *Streptomyces* sp. OATH_11, *Streptomyces* sp. OATH_12, *Streptomyces* sp. OATH_13, *Streptomyces* sp. OATH_17, *Streptomyces* sp. OATH_19, *Streptomyces* sp. OATH_20, *Streptomyces* sp. OATH_22A, *Streptomyces* sp. OATH_22B, *Streptomyces* sp. OATH_23, *Streptomyces* sp. OATH_26, *Streptomyces* sp. OATH_27, *Streptomyces* sp. OATH_28, *Streptomyces* sp. OATH_30, *Streptomyces* sp. OATH_31, *Streptomyces* sp. OATH_34, *Streptomyces* sp. OATH_36, *Streptomyces* sp. OATH_37, *Streptomyces* sp. OATH_38, *Streptomyces* sp. OATH_39, *Streptomyces* sp. OATH_40, *Streptomyces* sp. OATH_41, *Streptomyces* sp. OATH_42, *Streptomyces* sp. OATH_43, *Streptomyces* sp. OATH_44, *Streptomyces* sp. OATH_46, *Streptomyces* sp. OATH_47, *Streptomyces* sp. OATH_48, *Streptomyces* sp. OATH_49, *Streptomyces* sp. OATH_50, *Streptomyces* sp. OATH_52, *Streptomyces* sp. OATH_57, *Streptomyces* sp. OATH_58, *Streptomyces* sp. OATH_59, *Streptomyces* sp. OATH_60, *Streptomyces* sp. OATH_61, *Streptomyces* sp. OATH_62, *Streptomyces* sp. OATH_63, *Streptomyces* sp. OATH_64, *Streptomyces* sp. OATH_65, *Streptomyces* sp. OATH_66, *Streptomyces* sp. OATH_A, *Streptomyces* sp. OATH_B, *Streptomyces* sp. OATH_C, *Streptomyces* sp. OATH_D, *Streptomyces* sp. OATH_E, *Streptomyces* sp. OATH_F, *Streptomyces* sp. OATH_G, *Streptomyces* sp001509795, *Streptomyces* sp900105755, and/or *Streptomyces violaceorectus*.

[00434] In embodiment 60 provided herein is the composition of any one of the previous embodiments comprising the one or more *Streptomyces* microbes comprise one or more of

Streptomyces sp. OATH_5, *Streptomyces* sp. OATH_7, *Streptomyces* sp. OATH_8, *Streptomyces* sp. OATH_9, *Streptomyces* sp. OATH_10, *Streptomyces* sp. OATH_11, *Streptomyces* sp. OATH_12, *Streptomyces* sp. OATH_13, *Streptomyces* sp. OATH_17, *Streptomyces* sp. OATH_19, *Streptomyces* sp. OATH_20, *Streptomyces* sp. OATH_22A, *Streptomyces* sp. OATH_22B, *Streptomyces* sp. OATH_23, *Streptomyces* sp. OATH_26, *Streptomyces* sp. OATH_27, *Streptomyces* sp. OATH_28, *Streptomyces* sp. OATH_30, *Streptomyces* sp. OATH_31, *Streptomyces* sp. OATH_34, *Streptomyces* sp. OATH_36, *Streptomyces* sp. OATH_37, *Streptomyces* sp. OATH_38, *Streptomyces* sp. OATH_39, *Streptomyces* sp. OATH_40, *Streptomyces* sp. OATH_41, *Streptomyces* sp. OATH_42, *Streptomyces* sp. OATH_43, *Streptomyces* sp. OATH_44, *Streptomyces* sp. OATH_46, *Streptomyces* sp. OATH_47, *Streptomyces* sp. OATH_48, *Streptomyces* sp. OATH_49, *Streptomyces* sp. OATH_50, *Streptomyces* sp. OATH_52, *Streptomyces* sp. OATH_57, *Streptomyces* sp. OATH_58, *Streptomyces* sp. OATH_59, *Streptomyces* sp. OATH_60, *Streptomyces* sp. OATH_61, *Streptomyces* sp. OATH_62, *Streptomyces* sp. OATH_63, *Streptomyces* sp. OATH_64, *Streptomyces* sp. OATH_65, *Streptomyces* sp. OATH_66, *Streptomyces* sp. OATH_A, *Streptomyces* sp. OATH_B, *Streptomyces* sp. OATH_C, *Streptomyces* sp. OATH_D, *Streptomyces* sp. OATH_E, *Streptomyces* sp. OATH_F, *Streptomyces* sp. OATH_G.

[00435] In embodiment 61 provided herein is the composition of any one of the previous embodiments wherein the one or more *Streptomyces* microbes have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 68-109 and 120-196.

[00436] In embodiment 62 provided herein is the composition of any one of embodiments 4-13, 17-47, or 50-61 wherein the one or more *Pseudomonas* microbes comprise a first *Pseudomonas* strain.

[00437] In embodiment 63 provided herein is the composition of embodiment 62 wherein the one or more *Pseudomonas* microbes comprise a second *Pseudomonas* strain, wherein the second *Pseudomonas* strain is different from the first *Pseudomonas* strain.

[00438] In embodiment 64 provided herein is the composition of embodiment 63 wherein the one or more *Pseudomonas* microbes comprise a third *Pseudomonas* strain, wherein the third *Pseudomonas* strain is different from the first and second *Pseudomonas* strains.

[00439] In embodiment 65 provided herein is the composition of embodiment 64 wherein the one or more *Pseudomonas* microbes comprise a fourth *Pseudomonas* strain, wherein the fourth *Pseudomonas* strain is different from the first, second, and third *Pseudomonas* strains.

[00440] In embodiment 66 provided herein is the composition of embodiment 65 wherein the one or more *Pseudomonas* microbes comprise a fifth *Pseudomonas* strain, wherein the fifth *Pseudomonas* strain is different from the first, second, third, and fourth *Pseudomonas* strains.

[00441] In embodiment 67 provided herein is the composition of any one of embodiments 62 through 66 wherein the first, second, third, fourth, and/or fifth *Pseudomonas* strains comprise one or more of *Pseudomonas* E sp003253735, *Pseudomonas fluorescens*, *Pseudomonas koreensis*, *Pseudomonas poae*, *Pseudomonas* sp. OATH_2, *Pseudomonas* sp. OATH_3, *Pseudomonas* sp. OATH_4, *Pseudomonas* sp. OATH_6, *Pseudomonas* sp. OATH_14, *Pseudomonas* sp. OATH_15, *Pseudomonas* sp. OATH_16, *Pseudomonas* sp. OATH_45 *Pseudomonas* sp. OATH_51 *Pseudomonas* sp. OATH_53, *Pseudomonas* sp. OATH_55, *Pseudomonas* sp. OATH_56, *Pseudomonas* sp.002836515, and/or *Pseudomonas straminea.*

[00442] In embodiment 68 provided herein is the composition of any one of embodiments 62 through 67 wherein the first, second, third, fourth, and/or fifth *Pseudomonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 39-67.

[00443] In embodiment 69 provided herein is the composition of any one of embodiments 5-13, 21-28, 33-47 or 53-61 wherein the *Microvirga* microbe comprises a first *Microvirga* strain comprising *Microvirga* sp. OATH1.

[00444] In embodiment 70 provided herein is the composition of embodiment 69 wherein the first *Microvirga* strain has a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NO: 38.

[00445] In embodiment 71 provided herein is the composition of any one of embodiments 6-13, 22-28, 34-47 or 54-61 wherein the one or more *Micrococcus* microbes comprise a first *Micrococcus* strain.

[00446] In embodiment 72 provided herein is the composition of embodiment 71 wherein the one or more *Micrococcus* microbes comprise a second *Micrococcus* strain, wherein the second *Micrococcus* strain is different from the first strain.

[00447] In embodiment 73 provided herein is the composition of embodiment 71 or embodiment 72 wherein the first or second *Micrococcus* strains comprise *Micrococcus luteus*.

[00448] In embodiment 74 provided herein is the composition of any one of embodiments 71 through 73 wherein the first and/or second *Micrococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 118-119.

[00449] In embodiment 75 provided herein is the composition of any one of embodiments 7-13, 17, 19-28, 36-47, or 55-61 wherein the one or more *Paenibacillus* microbes comprise a first *Paenibacillus* strain.

[00450] In embodiment 76 provided herein is the composition of embodiment 75 wherein the one or more *Paenibacillus* microbes comprise second *Paenibacillus* strain, wherein the second *Paenibacillus* strain is different from the first *Paenibacillus* strain.

[00451] In embodiment 77 provided herein is the composition of embodiment 76 wherein the one or more *Paenibacillus* microbes comprise a third *Paenibacillus* strain, wherein the third *Paenibacillus* strain is different from the first and second *Paenibacillus* strains.

[00452] In embodiment 78 provided herein is the composition of embodiment 77 wherein the one or more *Paenibacillus* microbes comprise a fourth *Paenibacillus* strain, wherein the fourth *Paenibacillus* strain is different from the first, second, and third *Paenibacillus* strains.

[00453] In embodiment 79 provided herein is the composition of embodiment 78 wherein the one or more *Paenibacillus* microbes comprise a fifth *Paenibacillus* strain, wherein the fifth *Paenibacillus* strain is different from the first, second, third, and fourth *Paenibacillus* strains.

[00454] In embodiment 80 provided herein is the composition of any one of embodiments 75 through 79 wherein the first, second, third, fourth, and/or fifth *Paenibacillus* strains comprise *Paenibacillus cellulositrophicus* A and/or *Paenibacillus illinoisensis*.

[00455] In embodiment 81 provided herein is the composition of any one of embodiments 75 through 80 wherein the first, second, third, fourth, and/or fifth *Paenibacillus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 10-17.

[00456] In embodiment 82 provided herein is the composition of any one of embodiments 8-13, 24-28, 38-47 or 56-61 wherein the one or more *Aureimonas* microbes comprise a first *Aureimonas* strain.

[00457] In embodiment 83 provided herein is the composition of embodiment 82 wherein the one or more *Aureimonas* microbes comprise a second *Aureimonas* strain, wherein the second *Aureimonas* strain is different from the first *Aureimonas* strain.

[00458] In embodiment 84 provided herein is the composition of embodiment 83 wherein the one or more *Aureimonas* microbes comprise a third *Aureimonas* strain, wherein the third *Aureimonas* strain is different from the first and second *Aureimonas* strains.

[00459] In embodiment 85 provided herein is the composition of embodiment 84 wherein the one or more *Aureimonas* microbes comprise a fourth *Aureimonas* strain, wherein the fourth *Aureimonas* strain is different from the first, second, and third *Aureimonas* strains.

[00460] In embodiment 86 provided herein is the composition of any one of embodiments 82 through 85 wherein the first, second, third, and/or fourth *Aureimonas* strains comprise *Aureimonas* A sp001425485.

[00461] In embodiment 87 provided herein is the composition of any one of embodiments 82 through 86 wherein the first, second, third, and/or fourth *Aureimonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 18-21.

[00462] In embodiment 88 provided herein is the composition of any one of embodiments 9-13, 25-28, 40-47 or 57-61 wherein the one or more *Bradyrhizobium* microbes comprise a first *Bradyrhizobium* strain.

[00463] In embodiment 89 provided herein is the composition of embodiment 88 wherein the one or more *Bradyrhizobium* microbes a second *Bradyrhizobium* strain, wherein the second *Bradyrhizobium* strain is different from the first *Bradyrhizobium* strain.

[00464] In embodiment 90 provided herein is the composition of embodiment 89 wherein the one or more *Bradyrhizobium* microbes comprise third *Bradyrhizobium* strain, wherein the third *Bradyrhizobium* strain is different from the first and second *Bradyrhizobium* strains.

[00465] In embodiment 91 provided herein is the composition of embodiment 90 wherein the one or more *Bradyrhizobium* microbes comprise a fourth *Bradyrhizobium* strain, wherein the fourth *Bradyrhizobium* strain is different from the first, second, and third *Bradyrhizobium* strains.

[00466] In embodiment 92 provided herein is the composition of embodiment 91 wherein the one or more *Bradyrhizobium* microbes comprise a fifth *Bradyrhizobium* strain, wherein the fifth *Bradyrhizobium* strain is different from the first, second, third, and fourth *Bradyrhizobium* strains.

[00467] In embodiment 93 provided herein is the composition of any one of embodiments 88 through 92 wherein first, second, third, fourth, and/or fifth *Bradyrhizobium* stains comprise *Bradyrhizobium denitrificans* and/or *Bradyrhizobium elkanii*.

[00468] In embodiment 94 provided herein is the composition of any one of embodiments 88 through 93 wherein the first, second, third, fourth, and/or fifth *Bradyrhizobium* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 22-37.

[00469] In embodiment 95 provided herein is the composition of any one of embodiments 10-13, 26-28, 42-47 or 59-61 wherein the one or more *Rhodococcus* microbes comprise a first *Rhodococcus* strain.

[00470] In embodiment 96 provided herein is the composition of embodiment 95 wherein the one or more *Rhodococcus* microbes comprise a second *Rhodococcus* strain, wherein the second *Rhodococcus* strain is different from the first *Rhodococcus* strain.

[00471] In embodiment 97 provided herein is the composition of embodiment 95 or 96 wherein the first and/or second *Rhodococcus* strains comprise *Rhodococcus erythropolis* and/or *Rhodococcus qingshengii*.

[00472] In embodiment 98 provided herein is the composition of any one of embodiments 95 through 97 wherein first and/or second *Rhodococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 116-117.

[00473] In embodiment 99 provided herein is the composition of any one of embodiments 11-13, 27-28, 44-47 or 59-61 wherein the one or more *Amycolatopsis* microbes comprise a first *Amycolatopsis* strain.

[00474] In embodiment 100 provided herein is the composition of embodiment 99 wherein the one or more *Amycolatopsis* microbes comprise a second *Amycolatopsis* strain, wherein the second *Amycolatopsis* strains is different from the first *Amycolatopsis* strain.

[00475] In embodiment 101 provided herein is the composition of embodiment 100 wherein the one or more *Amycolatopsis* microbes comprise a third *Amycolatopsis* strain, wherein the third *Amycolatopsis* strains is different from the first and second *Amycolatopsis* strains.

[00476] In embodiment 102 provided herein is the composition of embodiment 101 wherein the one or more *Amycolatopsis* microbes comprise a fourth *Amycolatopsis* strain, wherein the fourth *Amycolatopsis* strains is different from the first, second, and third *Amycolatopsis* strains.

[00477] In embodiment 103 provided herein is the composition of embodiment 102 wherein the one or more *Amycolatopsis* microbes comprise a fifth *Amycolatopsis* strain, wherein the fifth *Amycolatopsis* strains is different from the first, second, third, and fourth *Amycolatopsis* strains.

[00478] In embodiment 104 provided herein is the composition of any one of embodiments 99-103 wherein the first, second, third, fourth, and/or fifth *Amycolatopsis* strains comprise *Amycolatopsis lurida* and/or *Amycolatopsis*_OATH_54.

[00479] In embodiment 105 provided herein is the composition of any one of embodiments 99-104 wherein the first, second, third, fourth, and/or fifth *Amycolatopsis* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 110-115.

[00480] In embodiment 106 provided herein is the composition of any one of embodiments 12-13, 28, 46-47 or 58-61 wherein the one or more *Lysinibacillus* microbes comprise a first *Lysinibacillus* strain.

[00481] In embodiment 107 provided herein is the composition of embodiment 106 wherein the one or more *Lysinibacillus* microbes comprise a second *Lysinibacillus* strain, wherein the second *Lysinibacillus* strain is different from the first *Lysinibacillus* strain.

[00482] In embodiment 108 provided herein is the composition of embodiment 107 wherein the one or more *Lysinibacillus* microbes comprise a third *Lysinibacillus* strain, wherein the third *Lysinibacillus* strain is different from the first and second *Lysinibacillus* strains.

[00483] In embodiment 109 provided herein is the composition of embodiment 108 wherein the one or more *Lysinibacillus* microbes comprise a fourth *Lysinibacillus* strain, wherein the fourth *Lysinibacillus* strain is different from the first, second, and third *Lysinibacillus* strains.

[00484] In embodiment 110 provided herein is the composition of embodiment 109 wherein the one or more *Lysinibacillus* microbes comprise a fifth *Lysinibacillus* strain, wherein the fifth *Lysinibacillus* strain is different from the first, second, third, and fourth *Lysinibacillus* strains.

[00485] In embodiment 111 provided herein is the composition of any one of embodiments 106 through 110 wherein the first, second, third, fourth, and/or fifth *Lysinibacillus* strains comprise *Lysinibacillus capsici*.

[00486] In embodiment 112 provided herein is the composition of any one of embodiments 106 through 111 wherein the first, second, third, fourth, and/or fifth *Lysinibacillus* strains have a

16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 1-9.

[00487] In embodiment 113 provided herein is a composition comprising one or more microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2.

[00488] In embodiment 114 provided herein is the composition of any one of the previous embodiments comprising one or more microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2.

[00489] In embodiment 115 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 1.

[00490] In embodiment 116 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 2.

[00491] In embodiment 117 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 3.

[00492] In embodiment 118 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 4.

[00493] In embodiment 119 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 5.

[00494] In embodiment 120 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 6.

[00495] In embodiment 121 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 7.

[00496] In embodiment 122 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 8.

[00497] In embodiment 123 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 9.

[00498] In embodiment 124 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 10.

[00499] In embodiment 125 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 11.

[00500] In embodiment 126 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 12.

[00501] In embodiment 127 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 13.

[00502] In embodiment 128 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 14.

[00503] In embodiment 129 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 15.

[00504] In embodiment 130 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 16.

[00505] In embodiment 131 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 17.

[00506] In embodiment 132 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 18.

[00507] In embodiment 133 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 19.

[00508] In embodiment 134 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 20.

[00509] In embodiment 135 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 21.

[00510] In embodiment 136 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 22.

[00511] In embodiment 137 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 23.

[00512] In embodiment 138 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 24.

[00513] In embodiment 139 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 25.

[00514] In embodiment 140 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 26.

[00515] In embodiment 141 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 27.

[00516] In embodiment 142 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 28.

[00517] In embodiment 143 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 29.

[00518] In embodiment 144 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 30.

[00519] In embodiment 145 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 31.

[00520] In embodiment 146 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 32.

[00521] In embodiment 147 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 33.

[00522] In embodiment 148 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 34.

[00523] In embodiment 149 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 35.

[00524] In embodiment 150 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 36.

[00525] In embodiment 151 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 37.

[00526] In embodiment 152 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 38.

[00527] In embodiment 153 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 39.

[00528] In embodiment 154 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 40.

[00529] In embodiment 155 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 41.

[00530] In embodiment 156 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 42.

[00531] In embodiment 157 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 43.

[00532] In embodiment 158 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 44.

[00533] In embodiment 159 provided herein is the composition of any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit of Table 2, designation 45.

[00534] In embodiment 160 provided herein is the composition of any preceding any one of the previous embodiments wherein the composition comprises one or more microbes of ATCC deposit designation 46.

[00535] In embodiment 161 provided herein is the composition of any one of the previous embodiments comprising one or more microbes of one or more of *Streptomyces* designation O-46 through O-140.

[00536] In embodiment 162 provided herein is the composition of embodiment 161 which comprises one or more microbes of *Streptomyces* designation O-46.

[00537] In embodiment 163 provided herein is the composition of embodiment 161 or embodiment 162 which comprises one or more microbes of *Streptomyces* designation O-47.

[00538] In embodiment 164 provided herein is the composition of any one of embodiments 161 through 163 which comprises one or more microbes of *Streptomyces* designation O-48.

[00539] In embodiment 165 provided herein is the composition of any one of embodiments 161 through 164 which comprises one or more microbes of *Streptomyces* designation O-49.

[00540] In embodiment 166 provided herein is the composition of any one of embodiments 161 through 165 which comprises one or more microbes of *Streptomyces* designation O-50.

[00541] In embodiment 167 provided herein is the composition of any one of embodiments 161 through 166 which comprises one or more microbes of *Streptomyces* designation O-51.

[00542] In embodiment 168 provided herein is the composition of any one of embodiments 161 through 167 which comprises one or more microbes of *Streptomyces* designation O-52.

[00543] In embodiment 169 provided herein is the composition of any one of embodiments 161 through 168 which comprises one or more microbes of *Streptomyces* designation O-53.

[00544] In embodiment 170 provided herein is the composition of any one of embodiments 161 through 169 which comprises one or more microbes of *Streptomyces* designation O-54.

[00545] In embodiment 171 provided herein is the composition of any one of embodiments 161 through 170 which comprises one or more microbes of *Streptomyces* designation O-55.

[00546] In embodiment 172 provided herein is the composition of any one of embodiments 161 through 171 which comprises one or more microbes of *Streptomyces* designation O-56.

[00547] In embodiment 173 provided herein is the composition of any one of embodiments 161 through 172 which comprises one or more microbes of *Streptomyces* designation O-57.

[00548] In embodiment 174 provided herein is the composition of any one of embodiments 161 through 173 which comprises one or more microbes of *Streptomyces* designation O-58.

[00549] In embodiment 175 provided herein is the composition of any one of embodiments 161 through 174 which comprises one or more microbes of *Streptomyces* designation O-59.

[00550] In embodiment 176 provided herein is the composition of any one of embodiments 161 through 175 which comprises one or more microbes of *Streptomyces* designation O-60.

[00551] In embodiment 177 provided herein is the composition of any one of embodiments 161 through 176 which comprises one or more microbes of *Streptomyces* designation O-61.

[00552] In embodiment 178 provided herein is the composition of any one of embodiments 161 through 177 which comprises one or more microbes of *Streptomyces* designation O-62.

[00553] In embodiment 179 provided herein is the composition of any one of embodiments 161 through 178 which comprises one or more microbes of *Streptomyces* designation O-63.

[00554] In embodiment 180 provided herein is the composition of any one of embodiments 161 through 179 which comprises one or more microbes of *Streptomyces* designation O-64.

[00555] In embodiment 181 provided herein is the composition of any one of embodiments 161 through 180 which comprises one or more microbes of *Streptomyces* designation O-65.

[00556] In embodiment 182 provided herein is the composition of any one of embodiments 161 through 181 which comprises one or more microbes of *Streptomyces* designation O-66.

[00557] In embodiment 183 provided herein is the composition of any one of embodiments 161 through 182 which comprises one or more microbes of *Streptomyces* designation O-67.

[00558] In embodiment 184 provided herein is the composition of any one of embodiments 161 through 183 which comprises one or more microbes of *Streptomyces* designation O-68.

[00559] In embodiment 185 provided herein is the composition of any one of embodiments 161 through 184 which comprises one or more microbes of *Streptomyces* designation O-69.

[00560] In embodiment 186 provided herein is the composition of any one of embodiments 161 through 185 which comprises one or more microbes of *Streptomyces* designation O-70.

[00561] In embodiment 187 provided herein is the composition of any one of embodiments 161 through 186 which comprises one or more microbes of *Streptomyces* designation O-71.

[00562] In embodiment 188 provided herein is the composition of any one of embodiments 161 through 187 which comprises one or more microbes of *Streptomyces* designation O-72.

[00563] In embodiment 189 provided herein is the composition of any one of embodiments 161 through 188 which comprises one or more microbes of *Streptomyces* designation O-73.

[00564] In embodiment 190 provided herein is the composition of any one of embodiments 161 through 189 which comprises one or more microbes of *Streptomyces* designation O-74.

[00565] In embodiment 191 provided herein is the composition of any one of embodiments 161 through 190 which comprises one or more microbes of *Streptomyces* designation O-75.

[00566] In embodiment 192 provided herein is the composition of any one of embodiments 161 through 191 which comprises one or more microbes of *Streptomyces* designation O-76.

[00567] In embodiment 193 provided herein is the composition of any one of embodiments 161 through 192 which comprises one or more microbes of *Streptomyces* designation O-77.

[00568] In embodiment 194 provided herein is the composition of any one of embodiments 161 through 193 which comprises one or more microbes of *Streptomyces* designation O-78.

[00569] In embodiment 195 provided herein is the composition of any one of embodiments 161 through 194 which comprises one or more microbes of *Streptomyces* designation O-79.

[00570] In embodiment 196 provided herein is the composition of any one of embodiments 161 through 195 which comprises one or more microbes of *Streptomyces* designation O-80.

[00571] In embodiment 197 provided herein is the composition of any one of embodiments 161 through 196 which comprises one or more microbes of *Streptomyces* designation O-81.

[00572] In embodiment 198 provided herein is the composition of any one of embodiments 161 through 197 which comprises one or more microbes of *Streptomyces* designation O-82.

[00573] In embodiment 199 provided herein is the composition of any one of embodiments 161 through 198 which comprises one or more microbes of *Streptomyces* designation O-83.

[00574] In embodiment 200 provided herein is the composition of any one of embodiments 161 through 199 which comprises one or more microbes of *Streptomyces* designation O-84.

[00575] In embodiment 201 provided herein is the composition of any one of embodiments 161 through 200 which comprises one or more microbes of *Streptomyces* designation O-85.

[00576] In embodiment 202 provided herein is the composition of any one of embodiments 161 through 201 which comprises one or more microbes of *Streptomyces* designation O-86.

[00577] In embodiment 203 provided herein is the composition of any one of embodiments 161 through 202 which comprises one or more microbes of *Streptomyces* designation O-87.

[00578] In embodiment 204 provided herein is the composition of any one of embodiments 161 through 203 which comprises one or more microbes of *Streptomyces* designation O-88.

[00579] In embodiment 205 provided herein is the composition of any one of embodiments 161 through 204 which comprises one or more microbes of *Streptomyces* designation O-89.

[00580] In embodiment 206 provided herein is the composition of any one of embodiments 161 through 205 which comprises one or more microbes of *Streptomyces* designation O-90.

[00581] In embodiment 207 provided herein is the composition of any one of embodiments 161 through 206 which comprises one or more microbes of *Streptomyces* designation O-91.

[00582] In embodiment 208 provided herein is the composition of any one of embodiments 161 through 207 which comprises one or more microbes of *Streptomyces* designation O-92.

[00583] In embodiment 209 provided herein is the composition of any one of embodiments 161 through 208 which comprises one or more microbes of *Streptomyces* designation O-93.

[00584] In embodiment 210 provided herein is the composition of any one of embodiments 161 through 209 which comprises one or more microbes of *Streptomyces* designation O-94.

[00585] In embodiment 211 provided herein is the composition of any one of embodiments 161 through 210 which comprises one or more microbes of *Streptomyces* designation O-95.

[00586] In embodiment 212 provided herein is the composition of any one of embodiments 161 through 211 which comprises one or more microbes of *Streptomyces* designation O-96.

[00587] In embodiment 213 provided herein is the composition of any one of embodiments 161 through 212 which comprises one or more microbes of *Streptomyces* designation O-97.

[00588] In embodiment 214 provided herein is the composition of any one of embodiments 161 through 213 which comprises one or more microbes of *Streptomyces* designation O-98.

[00589] In embodiment 215 provided herein is the composition of any one of embodiments 161 through 214 which comprises one or more microbes of *Streptomyces* designation O-99.

[00590] In embodiment 216 provided herein is the composition of any one of embodiments 161 through 215 which comprises one or more microbes of *Streptomyces* designation O-100.

[00591] In embodiment 217 provided herein is the composition of any one of embodiments 161 through 216 which comprises one or more microbes of *Streptomyces* designation O-101.

[00592] In embodiment 218 provided herein is the composition of any one of embodiments 161 through 217 which comprises one or more microbes of *Streptomyces* designation O-102.

[00593] In embodiment 219 provided herein is the composition of any one of embodiments 161 through 218 which comprises one or more microbes of *Streptomyces* designation O-103.

[00594] In embodiment 220 provided herein is the composition of any one of embodiments 161 through 219 which comprises one or more microbes of *Streptomyces* designation O-104.

[00595] In embodiment 221 provided herein is the composition of any one of embodiments 161 through 220 which comprises one or more microbes of *Streptomyces* designation O-105.

[00596] In embodiment 222 provided herein is the composition of any one of embodiments 161 through 221 which comprises one or more microbes of *Streptomyces* designation O-106.

[00597] In embodiment 223 provided herein is the composition of any one of embodiments 161 through 222 which comprises one or more microbes of *Streptomyces* designation O-107.

[00598] In embodiment 224 provided herein is the composition of any one of embodiments 161 through 223 which comprises one or more microbes of *Streptomyces* designation O-108.

[00599] In embodiment 225 provided herein is the composition of any one of embodiments 161 through 224 which comprises one or more microbes of *Streptomyces* designation O-109.

[00600] In embodiment 226 provided herein is the composition of any one of embodiments 161 through 225 which comprises one or more microbes of *Streptomyces* designation O-110.

[00601] In embodiment 227 provided herein is the composition of any one of embodiments 161 through 226 which comprises one or more microbes of *Streptomyces* designation O-111.

[00602] In embodiment 228 provided herein is the composition of any one of embodiments 161 through 227 which comprises one or more microbes of *Streptomyces* designation O-112.

[00603] In embodiment 229 provided herein is the composition of any one of embodiments 161 through 228 which comprises one or more microbes of *Streptomyces* designation O-113.

[00604] In embodiment 230 provided herein is the composition of any one of embodiments 161 through 229 which comprises one or more microbes of *Streptomyces* designation O-114.

[00605] In embodiment 231 provided herein is the composition of any one of embodiments 161 through 230 which comprises one or more microbes of *Streptomyces* designation O-115.

[00606] In embodiment 232 provided herein is the composition of any one of embodiments 161 through 231 which comprises one or more microbes of *Streptomyces* designation O-116.

[00607] In embodiment 233 provided herein is the composition of any one of embodiments 161 through 232 which comprises one or more microbes of *Streptomyces* designation O-117.

[00608] In embodiment 234 provided herein is the composition of any one of embodiments 161 through 233 which comprises one or more microbes of *Streptomyces* designation O-118.

[00609] In embodiment 235 provided herein is the composition of any one of embodiments 161 through 234 which comprises one or more microbes of *Streptomyces* designation O-119.

[00610] In embodiment 236 provided herein is the composition of any one of embodiments 161 through 235 which comprises one or more microbes of *Streptomyces* designation O-120.

[00611] In embodiment 237 provided herein is the composition of any one of embodiments 161 through 236 which comprises one or more microbes of *Streptomyces* designation O-121.

[00612] In embodiment 238 provided herein is the composition of any one of embodiments 161 through 237 which comprises one or more microbes of *Streptomyces* designation O-122.

[00613] In embodiment 239 provided herein is the composition of any one of embodiments 161 through 238 which comprises one or more microbes of *Streptomyces* designation O-123.

[00614] In embodiment 240 provided herein is the composition of any one of embodiments 161 through 239 which comprises one or more microbes of *Streptomyces* designation O-124.

[00615] In embodiment 241 provided herein is the composition of any one of embodiments 161 through 240 which comprises one or more microbes of *Streptomyces* designation O-125.

[00616] In embodiment 242 provided herein is the composition of any one of embodiments 161 through 241 which comprises one or more microbes of *Streptomyces* designation O-126.

[00617] In embodiment 243 provided herein is the composition of any one of embodiments 161 through 242 which comprises one or more microbes of *Streptomyces* designation O-127.

[00618] In embodiment 244 provided herein is the composition of any one of embodiments 161 through 243 which comprises one or more microbes of *Streptomyces* designation O-128.

[00619] In embodiment 245 provided herein is the composition of any one of embodiments 161 through 244 which comprises one or more microbes of *Streptomyces* designation O-129.

[00620] In embodiment 246 provided herein is the composition of any one of embodiments 161 through 245 which comprises one or more microbes of *Streptomyces* designation O-130.

[00621] In embodiment 247 provided herein is the composition of any one of embodiments 161 through 246 which comprises one or more microbes of *Streptomyces* designation O-131.

[00622] In embodiment 248 provided herein is the composition of any one of embodiments 161 through 247 which comprises one or more microbes of *Streptomyces* designation O-132.

[00623] In embodiment 249 provided herein is the composition of any one of embodiments 161 through 248 which comprises one or more microbes of *Streptomyces* designation O-133.

[00624] In embodiment 250 provided herein is the composition of any one of embodiments 161 through 249 which comprises one or more microbes of *Streptomyces* designation O-134.

[00625] In embodiment 251 provided herein is the composition of any one of embodiments 161 through 250 which comprises one or more microbes of *Streptomyces* designation O-135.

[00626] In embodiment 252 provided herein is the composition of any one of embodiments 161 through 251 which comprises one or more microbes of *Streptomyces* designation O-136.

[00627] In embodiment 253 provided herein is the composition of any one of embodiments 161 through 252 which comprises one or more microbes of *Streptomyces* designation O-137.

[00628] In embodiment 254 provided herein is the composition of any one of embodiments 161 through 253 which comprises one or more microbes of *Streptomyces* designation O-138.

[00629] In embodiment 255 provided herein is the composition of any one of embodiments 161 through 254 which comprises one or more microbes of *Streptomyces* designation O-139.

[00630] In embodiment 256 provided herein is the composition of any one of embodiments 161 through 255 which comprises one or more microbes of *Streptomyces* designation O-140.

[00631] In embodiment 257 provided herein is the composition of any one of the previous embodiments comprising at least 5, 10, 15, 20, 25, 30, 35, or 40 and/or not more than 5, 10, 15, 20, 25, 30, 35, or 45 microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2, preferably 5-45, more preferably 10-45, even more preferably 20-45, yet more preferably 35-45.

[00632] In embodiment 258 provided herein is the composition of any one of the previous embodiments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 of *Streptomyces* Designation O-46 through O-140, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[00633] In embodiment 259 provided herein is the composition of any previous embodiment wherein the composition comprises one or more microbes of ATCC deposit designation 47.

[00634] In embodiment 260 provided herein is the composition of any one of the previous embodiments further comprising a liquid medium in which the one or more microbes are distributed.

[00635] In embodiment 261 provided herein is the composition of embodiment 260 wherein the liquid medium is heterologous to one or more of the microbes.

[00636] In embodiment 262 provided herein is the composition of embodiment 260 or embodiment 261 wherein the liquid medium comprises an aqueous medium.

[00637] In embodiment 263 provided herein is the composition of embodiment 262 wherein the aqueous medium comprises a combination of mediums in which microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2 or *Streptomyces* Designation O-46 through O-140, or combinations thereof, has been growing.

[00638] In embodiment 264 provided herein is the composition of any one of the previous embodiments wherein at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 35, 40, 45, or 50 of the different microbes are heterologous to each other, for example at least 2, preferably at least 3, more preferably at least 4, even more preferably at least 5, yet more preferably at least 7, still more preferably at least 10.

[00639] In embodiment 265 provided herein is the composition of any one of the previous embodiments wherein the different microbes are present in a ratio to each other (CFU to CFU) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25.

[00640] In embodiment 266 provided herein is the composition of any one of the previous embodiments wherein the different microbes are present in a ratio to each other (wt:wt) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25.

[00641] In embodiment 267 provided herein is a composition comprising a plurality of particles, wherein each particle comprises a composition of any one of embodiments 1 through 259.

[00642] In embodiment 268 provided herein is the composition of any one of embodiments 1 through 259 or embodiment 267 comprising less than 5, 4, 3, 2, 1, 0.5, 0.1%, or less than 0.01%, or less than 0.001% w/w water.

[00643] In embodiment 269 provided herein is the composition of any one of the previous embodiments wherein total colony forming units (CFUs) per gram of the composition is at least 10^5,10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^7 to 10^{11}, still more preferably 10^8 to 10^{11}CFU/gm.

[00644] In embodiment 270 provided herein is the composition of any one of the previous embodiments wherein each of the microbes is present at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition.

[00645] In embodiment 271 provided herein is the composition of any one of the previous embodiments wherein the different microbes are present in a ratio to each other (CFU to CFU) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25.

[00646] In embodiment 272 provided herein is the composition of any one of the previous embodiments wherein the different microbes are present in a ratio to each other (wt:wt) of 20:1 to 1:20, preferably 10:1 to 1:10, more preferably 5:1 to 1:5, even more preferably 2:1 to 1:2, yet more preferably 1.5:1 to 1:1.5, even more preferably 1.25:1 to 1:1.25.

[00647] In embodiment 273 provided herein is the composition of any one of embodiments 267 through 270 wherein the particles have a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[00648] In embodiment 274 provided herein is the composition of any one of embodiments 267 through 271 wherein at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, or 99% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 95, 97, 98, 99, 99.5, or 100%, or 100%, for example 10-100%, preferably 20-100%, more preferably 50-100%, even more preferably 80-100%, still more preferably 90-100% of the particles have a mean particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[00649] In embodiment 275 provided herein is the composition of any one of the previous embodiments wherein the composition comprises 10-20 different strains of microbes, and each strain is present as 5-25% of total CFUs.

[00650] In embodiment 276 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 21-30 different strains of microbes, and each strain is present as 3-10% of total CFUs.

[00651] In embodiment 277 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 31-40 different strains of microbes, and each strain is present as 2-8% of total CFUs.

[00652] In embodiment 278 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 41-50 different strains of microbes, and each strain is present as 1-5% of total CFUs.

[00653] In embodiment 279 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 51-60 different strains of microbes, and each strain is present as 0.8-4% of total CFUs.

[00654] In embodiment 280 provided herein is the composition any one of embodiments 1 through 274 wherein the composition comprises 61-70 different strains of microbes, and each strain is present as 0.6-3.5% of total CFUs.

[00655] In embodiment 281 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 71-80 different strains of microbes, and each strain is present as 0.5-3.2% of total CFUs.

[00656] In embodiment 282 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 81-90 different strains of microbes, and each strain is present as 0.4-3.0% of total CFUs.

[00657] In embodiment 283 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 91-100 different strains of microbes, and each strain is present as 0.4-2.8% of total CFUs.

[00658] In embodiment 284 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 101-110 different strains of microbes, and each strain is present as 0.3-2.4% of total CFUs.

[00659] In embodiment 285 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 111-120 different strains of microbes, and each strain is present as 0.2-2% of total CFUs.

[00660] In embodiment 286 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 121-130 different strains of microbes, and each strain is present as 0.2-1.5% of total CFUs.

[00661] In embodiment 287 provided herein is the composition of any one of embodiments 1 through 274 wherein the composition comprises 131-140 different strains of microbes, and each strain is present as 0.1-1.2% of total CFUs.

[00662] In embodiment 288 provided herein is a delayed release composition comprising a plurality of particles, wherein the particles comprises one or more microbes, and wherein the plurality of particles comprises a first population of particles wherein each particle of the first population comprises one or more first components configured to confine at least a portion of the microbes to the particles, and wherein the one or more first components are such that the one or more first components lose sufficient integrity upon exposure to one or more environmental triggers that at least a portion of the confined microbes are released from the particles.

[00663] In embodiment 289 provided herein is the composition of embodiment 288 comprising the composition of any one of embodiments 1 through 259.

[00664] In embodiment 290 provided herein is the composition of embodiment 288 or embodiment 289 wherein the first components are configured to confine at least 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99% of the microbes, for example at least 60%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%.

[00665] In embodiment 291 provided herein is the composition of any one of embodiments 288 through 290 wherein the one or more first components form a shell wherein the microbes are confined within, and/or embedded in, and/or associated with a surface of, the shell.

[00666] In embodiment 292 provided herein is the composition of any one of embodiments 288 through 291 wherein the one or more first components form a matrix in which the microbes are embedded or otherwise associated.

[00667] In embodiment 293 provided herein is the composition of any one of embodiments 288 through 292 wherein the one or more first components form a plurality of lamellae, wherein the particles are confined between, and/or embedded in, and/or associate with a surface of, the lamellae.

[00668] In embodiment 294 provided herein is the composition of any one of embodiments 288 through 293 wherein the environmental trigger comprises water, temperature, electromagnetic radiation, or a combination thereof.

[00669] In embodiment 295 provided herein is the composition of any one of embodiments 288 through 294 wherein the environmental trigger is water.

[00670] In embodiment 296 provided herein is the composition of any one of embodiments 288 through 295 wherein one or more first components and/or structure of the particles are such that exposure to the trigger causes sufficient loss of integrity that at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, or 99% and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, 99, or 100% of the microbes are released. and for a suitable duration.

[00671] In embodiment 297 provided herein is the composition of embodiment 296 wherein 30-100% of the microbes are released.

[00672] In embodiment 298 provided herein is the composition of embodiment 296 wherein 50-100% of the microbes are released.

[00673] In embodiment 299 provided herein is the composition of embodiment 296 wherein 80-100% of the microbes are released.

[00674] In embodiment 300 provided herein is the composition of embodiment 296 wherein 90-100% of the microbes are released.

[00675] In embodiment 301 provided herein is the composition of embodiment 296 wherein 5-80% of the microbes are released.

[00676] In embodiment 302 provided herein is the composition of embodiment 296 wherein 5-60% of the microbes are released.

[00677] In embodiment 303 provided herein is the composition of embodiment 296 wherein 5-40% of the microbes are released.

[00678] In embodiment 304 provided herein is the composition of embodiment 296 wherein 10-40% of the microbes are released.

[00679] In embodiment 305 provided herein is the composition of embodiment 296 wherein 5-30% of the microbes are released.

[00680] In embodiment 306 provided herein is the composition of embodiment 296 wherein 10-30% of the microbes are released.

[00681] In embodiment 307 provided herein is the composition of embodiment 296 wherein 5-25% of the microbes are released.

[00682] In embodiment 308 provided herein is the composition of embodiment 296 wherein 10-25% of the microbes are released.

[00683] In embodiment 309 provided herein is the composition of any one of embodiments 288 through 308 further comprising a second population of particles wherein each particle of the second population comprises one or more second components configured to confine at least a portion of the microbes to the particles, and wherein the one or more second components are such that the one or more second components withstand exposure to the one or more environmental triggers that cause the first components of the first population to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the second population.

[00684] In embodiment 310 provided herein is the composition of embodiment 309 further comprising a third population of particles wherein each particle of the third population comprises one or more third components configured to confine at least a portion of the microbes to the particles, and wherein the one or more third components are such that the one or more third components withstand exposure to the one or more environmental triggers that cause the first and second components of the first population and second populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the third population.

[00685] In embodiment 311 provided herein is the composition of embodiment 310 further comprising a fourth population of particles wherein each particle of the fourth population comprises one or more fourth components configured to confine at least a portion of the microbes to the particles, and wherein the one or more fourth components are such that the one or more fourth components withstand exposure to the one or more environmental triggers that cause the first, second and third components of the first population, second and third populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more

environmental triggers that at least a portion of the confined microbes are released from the particles of the fourth population.

[00686] In embodiment 312 provided herein is the composition of any one of the previous embodiments further comprising one or more agriculturally acceptable adjuvants.

[00687] In embodiment 313 provided herein is the composition of embodiment 312 wherein at least one of the agriculturally acceptable adjuvants is heterologous to the one or more microbes of the composition.

[00688] In embodiment 314 provided herein is the composition of embodiment 312 or embodiment 313 wherein the one or more agriculturally acceptable adjuvants comprise one or more liquid carriers, solid carriers, surfactants, viscosity modifiers, thickeners, rheology additives, structuring agents, preservatives, biocides or biostatic agents, antifreezes, crystallization inhibitors, suspending agents, dyes, anti-oxidants, foaming agents, light absorbers, light blockers, mixing auxiliaries, antifoams, complexing agents, neutralizing or pH-modifying substances and buffers, corrosion inhibitors, fragrances, wetting agents, take-up enhancers, micronutrients, plasticizers, glidants, lubricants, and dispersants.an emulsifier, a carrier, a stabilizer, or a combination thereof.

[00689] In embodiment 315 provided herein is the composition of embodiment 314 comprising one or more surfactants.

[00690] In embodiment 316 provided herein is the composition of embodiment 315 wherein the one or more surfactants comprise a non-ionic, cationic, or anionic surfactant, or a combination thereof.

[00691] In embodiment 317 provided herein is the composition of embodiment 316 comprising Tween 20 or Tween 80.

[00692] In embodiment 318 provided herein is the composition of embodiment 315 comprising soy lecithin or yucca powder or a derivative thereof, or a combination thereof, preferably soy lecithin.

[00693] In embodiment 319 provided herein is the composition of any one of embodiment 315 through 318 wherein the surfactant is organic.

[00694] In embodiment 320 provided herein is the composition of any one of embodiment 315 through 319 wherein the surfactant or surfactants are at a total concentration of at least 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, or 9 wt% and/or no more than 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 3, 4, 5, 6, 7, 8, 9, or 10 wt%, for example 0.5-10 wt%, preferably 1-3 wt%, more preferably 1.8-2.2 wt%.

[00695] In embodiment 321 provided herein is the composition of any one of embodiments 1 through 259 that is a solid composition.

[00696] In embodiment 322 provided herein is the composition of any one of embodiments 1 through 259 that is a liquid composition.

[00697] In embodiment 323 provided herein is the composition of any one of embodiments 314 through 322 comprising a carrier.

[00698] In embodiment 324 provided herein is the composition of embodiment 323 wherein the carrier comprises an alcohol and/or a saccharide, and/or saccharide, *e.g.*, a monosaccharide, disaccharide, trisaccharide, or polysaccharide.

[00699] In embodiment 325 provided herein is the composition of embodiment 323 wherein the carrier comprises inulin, glycerol glucose, lactose, maltose, and/or galactose.

[00700] In embodiment 326 provided herein is the composition of embodiment 323 wherein the carrier comprises glucose.

[00701] In embodiment 327 provided herein is the composition of any one of embodiments 323 through 326 wherein the carrier is at a concentration in the composition of at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 wt% and/or no more than 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 wt%, for example 50-100 wt%, preferably 70-100 wt%, more preferably 80-100 wt%, even more preferably 90-100 wt%, still more preferably 95-100 wt%.

[00702] In embodiment 328 provided herein is the composition of any one of embodiments 314 through 327 comprising one or more materials that protect the microbes from one or more aspects of an environment in which the microbes will be stored and/or used.

[00703] In embodiment 329 provided herein is the composition of embodiment 328 wherein the one or more materials comprises a light absorber or light blocker, or a combination thereof.

[00704] In embodiment 330 provided herein is the composition of embodiment 329 wherein the light absorber or light blocker protects the microbes of the composition from ultraviolet (UV) light.

[00705] In embodiment 331 provided herein is the composition of embodiment 329 or embodiment 330 wherein the microbes are enclosed in the material.

[00706] In embodiment 332 provided herein is the composition of any one of embodiments 331 wherein the material is such that it releases some or all of the microbes upon exposure to one or more environmental triggers.

[00707] In embodiment 333 provided herein is the composition of embodiment 332 wherein the one or more environmental triggers comprises water.

[00708] In embodiment 334 provided herein is the composition of embodiment 332 or embodiment 333 wherein the material comprises a water soluble material.

[00709] In embodiment 335 provided herein is the composition of any one of the previous embodiments wherein the composition is stable at temperatures between 4 °C. and 37 °C for at least 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3 or 4 weeks, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months, or 1, 2, 3, 4, or 5 years, for example, stable at between 4 °C. and 37 °C for at least one week, preferably at least one month, more preferably at least 6 months, even more preferably at least 12 months, yet more preferably at least 2 years.

[00710] In embodiment 336 provided herein is the composition of any one of embodiments 260 through 263 or embodiment 322 comprising an antifreeze agent for cold storage at temperature less than -5, -10, -15, -20, -25, -30, -40, -50, -60, -70, -80 °C, for example less than -5, preferably less than -10, more preferably less than -15, even more preferably less than -20 °C.

[00711] In embodiment 337 provided herein is the composition of embodiment 336 wherein the antifreeze agent comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride and ammonium sulfate.

[00712] In embodiment 338 provided herein is the composition of embodiment 337 wherein the antifreeze agent comprises glycerol.

[00713] In embodiment 339 provided herein is the composition of embodiment 338 wherein the glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50%, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22% wt%.

[00714] In embodiment 340 provided herein is the composition of any one of embodiments 336 through 339 wherein the composition comprises microbes of only one strain.

[00715] In embodiment 341 provided herein is the composition of any one of the previous embodiments wherein total colony forming units (CFUs) per gram of the composition is at least 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14} and/or not more than 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16}, preferably 10^9 to 10^{16}, more preferably 10^9 to 10^{14}, even more preferably 10^9 to 10^{13}, yet more preferably 10^9 to 10^{12}.

[00716] In embodiment 342 provided herein is the composition of embodiment 341 wherein total CFUs per gram of the composition is 10^{10} to 10^{13} per gram.

[00717] In embodiment 343 provided herein is the composition of embodiment 342 wherein total CFUs per gram of the composition is 10^{10} to 10^{12} per gram.

[00718] In embodiment 344 provided herein is a population of seeds, seedlings, or other plant propagules comprising at least 10, 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, or and/or

not more than 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, or 120 different microbes, wherein at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, of the microbes are heterologous to the seeds, seedlings, or other plant propagules, wherein at least a portion of the microbes of the composition are associated with the seeds, seedlings, or other plant propagules.

[00719] In embodiment 345 provided herein is the population of embodiment 344 comprising a composition of any one of embodiments 1 through 259 wherein at least a portion of the microbes of the composition are associated with the seeds, seedlings, or other plant propagules.

[00720] In embodiment 346 provided herein is the population of embodiment 344 or embodiment 345 wherein at least 50, 60, 70, 80, 85, 90, 95, 97, or 99% of the seeds, seedlings, or other plant propagules of the population, for example at least 50%, preferably at least 60%, more preferably at least 80%, yet more preferably at least 85%, and even yet more preferably at least 90%, each has at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of *Streptomyces* designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or *Streptomyces* designations O-46 to O-140 associated with it, for example at least 10, preferably at least 20, more preferably at least 30, even more preferably at least 40, yet more preferably at least 50.

[00721] In embodiment 347 provided herein is the population of any one of embodiments 344 through 346 wherein the microbes are present on each seed, seedling, or other plant propagule in an average total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, or 50,000 and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, or 1M CFU per seed, seedling, or other plant propagule, for example, 10-1M, preferably 100-500,000, more preferably 500-500,000, even more preferably 1000-500,000, yet more preferably 5000-500,000, yet more preferably 5000-1M.

[00722] In embodiment 348 provided herein is the population of any one of embodiments 344 through 347 wherein the population of seeds, seedlings, or other plant propagules comprises all of *Streptomyces* designations 1-45 (ATCC Nos. PTA-127367 to PTA-127411) and/or *Streptomyces* designations O-46 to O-140.

[00723] In embodiment 349 provided herein is the population of any one of embodiments 344 through 348 wherein the microbes of the composition are disposed on surfaces, in pores, or a combination thereof, of the seeds, seedlings, or other plant propagules.

[00724] In embodiment 350 provided herein is the population of any one of embodiments 344 through 349 comprising at least 100, 500, 1000, 5000, 10,000, 50,000, 100,000, or 1M seeds, seedlings, other plant propagules, for example at least 1000, preferably at least 10,000, more preferably at least 100,000.

[00725] In embodiment 351 provided herein is the population of any one of embodiments 344 through 350 that is configured to be suitable for aerial deposition.

[00726] In embodiment 352 provided herein is the population of any one of embodiments 344 through 351 comprising seeds, wherein the seeds are contained in a bag or container suitable for commercial sale.

[00727] In embodiment 353 provided herein is the population of any one of embodiments 344 through 352 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the seed, seedling, or other plant propagule.

[00728] In embodiment 354 provided herein is a composition comprising soil in which plants are growing or have grown wherein the soil comprises at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, or 100 and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40, or 1-150, preferably 1-100, more preferably 2-80, even more preferably 2.

[00729] In embodiment 355 provided herein is the composition of embodiment 354 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[00730] In embodiment 356 provided herein is the composition of embodiment 354 or embodiment 355 wherein the soil has a water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[00731] In embodiment 357 provided herein is the composition of any one of embodiments 354 through 356 wherein the soil has a concentration of beneficial microbes of at least 1M, 2M,

5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[00732] In embodiment 358 provided herein is the composition of any one of embodiments 354 through 357 wherein the soil has a soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[00733] In embodiment 359 provided herein is the composition of any one of embodiments 354 through 358 wherein the soil does not comprise a significant amount or concentration of synthetic fertilizer.

[00734] In embodiment 360 provided herein is the composition of any one of embodiments 354 through 359 wherein the soil does not comprise a detectable amount or concentration of synthetic fertilizer.

[00735] In embodiment 361 provided herein is the composition of any one of embodiments 354 through 360 wherein the soil does not comprise a significant amount or concentration of synthetic herbicide.

[00736] In embodiment 362 provided herein is the composition of any one of embodiments 354 through 361 wherein the soil does not comprise a detectable amount or concentration of synthetic herbicide.

[00737] In embodiment 363 provided herein is the composition of any one of embodiments 354 through 362 comprising a composition of any one of embodiments 1 through 259.

[00738] In embodiment 364 provided herein is a composition comprising soil in which plants are growing or have grown wherein the soil comprises at least 1, 2, 5, 10, 15, 20, 30, 35, 40, or 45 different microbes comprising composition of any one of embodiments 1 through 259.

[00739] In embodiment 365 provided herein is the composition of embodiment 364 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[00740] In embodiment 366 provided herein is the composition of embodiment 364 or embodiment 365 wherein the soil has a water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[00741] In embodiment 367 provided herein is the composition of any one of embodiments 364 through 366 wherein the soil has a concentration of beneficial microbes of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[00742] In embodiment 368 provided herein is the composition of any one of embodiments 364 through 367 wherein the soil has a soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[00743] In embodiment 369 provided herein is the composition of any one of embodiments 364 through 368 wherein the soil does not comprise a significant amount or concentration of synthetic fertilizer.

[00744] In embodiment 370 provided herein is the composition of any one of embodiments 364 through 369 wherein the soil does not comprise a detectable amount or concentration of synthetic fertilizer.

[00745] In embodiment 371 provided herein is the composition of any one of embodiments 364 through 370 wherein the soil does not comprise a significant amount or concentration of synthetic herbicide.

[00746] In embodiment 372 provided herein is the composition of any one of embodiments 364 through 371 wherein the soil does not comprise a detectable amount or concentration of synthetic herbicide.

[00747] In embodiment 373 provided herein is the composition of any one of embodiments 364 through 372 further comprising the plants or part of the plants.

[00748] In embodiment 374 provided herein is the composition of embodiment 373 wherein the part of the plants comprises roots of the plants.

[00749] In embodiment 375 provided herein is the composition of embodiment 374 wherein the microbes are disposed on or in the roots.

[00750] In embodiment 376 provided herein is the composition of embodiment 373 or embodiment 374 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, *e.g.*, 10-10^{16}, preferably 100-10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[00751] In embodiment 377 provided herein is the composition of any one of embodiments 364 through 376 further comprising mycorrhizal fungi.

[00752] In embodiment 378 provided herein is a plant or plant part comprising one or more microbes of the composition of any one of embodiments 1 through 259 disposed on or in the plant or plant part.

[00753] In embodiment 379 provided herein is the plant or plant part of embodiment 378 wherein the one or more microbes are disposed on or in a plant part comprising a root of the plant.

[00754] In embodiment 380 provided herein is the plant or plant part of embodiment 378 or embodiment 379 wherein at least 1, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the plant or plant part.

[00755] In embodiment 381 provided herein is the plant or plant part of embodiment 379 or embodiment 380 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, *e.g.*, 10-10^{16}, preferably 100-10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[00756] In embodiment 382 provided herein is the plant or plant part of any one of embodiments 378 through 381 further comprising mycorrhizal fungi.

[00757] In embodiment 383 provided herein is a composition comprising a population of plants wherein the plants or part of the plants comprises the microbe or microbes of the composition of any one of embodiments 1 through 259 disposed on or in the plant or plant part.

[00758] In embodiment 384 provided herein is the composition of embodiment 383 comprising at least 100, 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 3M, 5M, 10M, 50M, 100M, 500M, 1B, 2B, 5B, 10B, 50B, 100B, 1T, 10T, 100T plants and/or not more than 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 3M, 5M, 10M, 50M, 100M, 500M, 1B, 2B, 5B, 10B, 50B, 100B, 1T, 10T, 100T, or 500T plants.

[00759] In embodiment 385 provided herein is the composition of embodiment 383 or embodiment 384 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition are heterologous to the plant or plant part.

[00760] In embodiment 386 provided herein is the composition of any one of embodiments 383 through 385 wherein the one or more microbes are disposed on or in a plant part comprising a root of the plant.

[00761] In embodiment 387 provided herein is the composition of embodiment 386 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the root, *e.g.*, 10-10^{16}, preferably 100- 10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[00762] In embodiment 388 provided herein is the composition of embodiment 386 or embodiment 387 further comprising mycorrhizal fungi.

[00763] In embodiment 389 provided herein is the composition of any one of embodiments 383 through 388 wherein the population of plants is distributed over an area of at least 0.1, 0.5, 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, or 100,000 square miles and/or not more than 0.5, 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000 50,000, 100,000, 500,000, 1M, 2M, 10M, or 50M square miles, for example, 0.1 to 50M square miles, preferably 0.1 to 10M square miles, more preferably 1 to 10M square miles, yet more preferably 10 to 10M square miles, still more preferably 100 to 10M square miles, yet still more preferably 1000 to 1M square miles.

[00764] In embodiment 390 provided herein is the composition of any one of embodiments 383 though 389 comprising roots of the plant and further comprising soil in which the plant is growing or have grown.

[00765] In embodiment 391 provided herein is the composition of embodiment 390 wherein the soil is within 1 cm of roots of the plant.

[00766] In embodiment 392 provided herein is the composition of embodiment 390 wherein the soil is within 2 cm of roots of the plant.

[00767] In embodiment 393 provided herein is the composition of embodiment 390 wherein the soil is within 3 cm of roots of the plant.

[00768] In embodiment 394 provided herein is the composition of embodiment 390 wherein the soil is within 5 cm of roots of the plant.

[00769] In embodiment 395 provided herein is the composition of embodiment 390 wherein the soil is within 7 cm of roots of the plant.

[00770] In embodiment 396 provided herein is the composition of embodiment 390 wherein the soil is within 10 cm of roots of the plant.

[00771] In embodiment 397 provided herein is the composition of embodiment 390 wherein the soil is within 15 cm of roots of the plant.

[00772] In embodiment 398 provided herein is the composition of embodiment 390 wherein the soil is within 20 cm of roots of the plant.

[00773] In embodiment 399 provided herein is the composition of embodiment 390 wherein the soil is within 50 cm of roots of the plant.

[00774] In embodiment 400 provided herein is the composition of embodiment 390 wherein the soil is within 100 cm of roots of the plant.

[00775] In embodiment 401 provided herein is the composition of embodiment 390 wherein the soil is within 100 cm of roots of the plant.

[00776] In embodiment 402 provided herein is the composition of any one of embodiment 390 through 401 wherein the microbes of the composition comprise at least 0.01, 0.05, 0.1, 0.5, 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least at least 0.01%, or at least 0.1%, or 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[00777] In embodiment 403 provided herein is the composition of any one of embodiment 390 through 402 further comprising mycorrhizal fungi.

[00778] In embodiment 404 provided herein is the composition of embodiment 403 wherein the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[00779] In embodiment 405 provided herein is the composition of any one of embodiment 390 through 404 wherein beneficial microbes other than the microbes of the composition comprising

microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[00780] In embodiment 406 provided herein is the composition of any one of embodiment 390 through 405 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[00781] In embodiment 407 provided herein is the composition of any one of embodiment 390 through 406 wherein the soil has an average water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[00782] In embodiment 408 provided herein is the composition of any one of embodiment 390 through 407 wherein the soil has an average carbon content of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20% and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, or 40% (w/w), for example, 5-30%, preferably 7-30%, more preferably 10-30%, yet more preferably 10-25%.

[00783] In embodiment 409 provided herein is the composition of any one of embodiments 390 through 408 wherein the soil does not comprise a significant amount or concentration of synthetic fertilizer.

[00784] In embodiment 410 provided herein is the composition of any one of embodiments 390 through 408 wherein the soil does not comprise a detectable amount or concentration of synthetic fertilizer.

[00785] In embodiment 411 provided herein is the composition of any one of embodiments 390 through 410 wherein the soil does not comprise a significant amount or concentration of synthetic herbicide.

[00786] In embodiment 412 provided herein is the composition of any one of embodiments 390 through 410 wherein the soil does not comprise a detectable amount or concentration of synthetic herbicide.

[00787] In embodiment 413 provided herein is the composition of any one of embodiments 390 through 412 wherein the soil does not comprise a significant amount or concentration of synthetic pesticide.

[00788] In embodiment 414 provided herein is the composition of any one of embodiments 390 through 412 wherein the soil does not comprise a detectable amount or concentration of synthetic pesticide.

[00789] In embodiment 415 provided herein is the composition of embodiment 414 wherein the soil does not comprise a significant amount or concentration of synthetic insecticide.

[00790] In embodiment 416 provided herein is the composition of embodiment 414 wherein the soil does not comprise a detectable amount or concentration of synthetic insecticide.

[00791] In embodiment 417 provided herein is the composition of embodiment 414 wherein the soil does not comprise a significant amount or concentration of synthetic fungicide.

[00792] In embodiment 418 provided herein is the composition of embodiment 414 wherein the soil does not comprise a detectable amount or concentration of synthetic fungicide.

[00793] In embodiment 419 provided herein is the composition of embodiment 414 wherein the soil does not comprise a significant amount or concentration of synthetic bactericide.

[00794] In embodiment 420 provided herein is the composition of embodiment 414 wherein the soil does not comprise a detectable amount or concentration of synthetic bactericide.

[00795] In embodiment 421 provided herein is the composition of embodiment 414 wherein the soil does not comprise a significant amount or concentration of synthetic nematicide.

[00796] In embodiment 422 provided herein is the composition of embodiment 414 wherein the soil does not comprise a detectable amount or concentration of synthetic nematicide.

[00797] In embodiment 423 provided herein is the composition of any one of embodiments 383 through 422 further comprising soil in which the plants grow.

[00798] In embodiment 424 provided herein is the composition of embodiment 423 wherein the microbes comprise at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[00799] In embodiment 425 provided herein is the composition of embodiment 423 or embodiment 424 further comprising mycorrhizal fungi.

[00800] In embodiment 426 provided herein is the composition of embodiment 425 wherein the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at

least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[00801] In embodiment 427 provided herein is the composition of any one of embodiments 423 through 426 wherein beneficial microbes other than the microbes of the composition comprising microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[00802] In embodiment 428 provided herein is the composition of any one of embodiments 423 through 427 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[00803] In embodiment 429 provided herein is the composition of any one of embodiments 423 through 428 wherein the soil has an average water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[00804] In embodiment 430 provided herein is the composition of any one of embodiments 423 through 429 wherein the soil and plant parts in the soil have an average carbon content of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20% and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, or 40% (w/w), for example, 5-30%, preferably 7-30%, more preferably 10-30%, yet more preferably 10-25.

[00805] In embodiment 431 provided herein is the composition of any one of embodiments 423 through 430 wherein the soil and plant parts in the soil have an average carbon content of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 35, 37, 40, 42, 45, 50, 55, or 60 and/or not more than 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 35, 37, 40, 42, 45, 50, 55, 60, or 70 metric ton per hectare for example 10-70, preferably 10-60, more preferably 15-60, yet more preferably 15-50, still more preferably 18-60, even still more preferably 18-55 metric ton per hectare.

[00806] In embodiment 432 provided herein is the composition of any one of embodiments 423 through 431 wherein the soil is to a depth of at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90,

100, or 150 cm and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, or 200 cm, for example not more than 100 cm, preferably not more than 80 cm, more preferably not more than 60 cm, even more preferably not more than 40 cm, yet more preferably not more than 30 cm, still more preferably not more than 20 cm, or to the depth of roots of the plants.

[00807] In embodiment 433 provided herein is a method comprising applying the composition of any one of embodiments 1 through 259, or a derivative thereof, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a first application.

[00808] In embodiment 434 provided herein is the method of embodiment 433 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes in the composition are at a concentration that is at least 2, 5, 10, 50, 100, 500, or 1000x the concentration of the same microbe found or detected in an untreated control plant, or a part thereof, and/or soil or other growth medium in which the plant grows or will grow, preferably at 2x, more preferably at least 5x, even more preferably at least 10x, yet more preferably at least 50x, still more preferably at least 500x.

[00809] In embodiment 435 provided herein is the method of embodiment 433 or embodiment 434 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes in the composition are undetectable in an untreated control plant, or a part thereof, and/or to soil in which the plant grows or will grow.

[00810] In embodiment 436 provided herein is the method of any one of embodiments 433 through 435 wherein the derivative composition is an aqueous composition.

[00811] In embodiment 437 provided herein is the method of any one of embodiments 433 through 436 further comprising applying the composition of any one of embodiments 1 through 259, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a second application.

[00812] In embodiment 438 provided herein is the method of any one of embodiments 433 through 436 further comprising applying the composition of any one of embodiments 1 through 259, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a third application.

[00813] In embodiment 439 provided herein is the method of any one of embodiments 433 through 436 further comprising applying the composition of any one of embodiments 1 through

259, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a fourth application.

[00814] In embodiment 440 provided herein is the method of any one of embodiments 433 through 436 further comprising applying the composition of any one of embodiments 1 through 259, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a fifth application.

[00815] In embodiment 441 provided herein is the method of any one of embodiments 433 through 436 further comprising applying the composition of any one of embodiments 1 through 259, or a derivative produced from the composition, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a sixth application.

[00816] In embodiment 442 provided herein is the method of any one of embodiments 437 through 441 wherein the applications are separated by at least 1, 2, 3, 4, 5, or 6 days, or 1, 2, 3, or 4 weeks, or 1, 2, 3, 4, 5, 6, 8, or 10 months, or 1, 2, 3, 4, or 5 years and/or not more than 2, 3, 4, 5, or 6 days, or 1, 2, 3, or 4 weeks, or 1, 2, 3, 4, 5, 6, 8, or 10 months, or 1, 2, 3, 4, 5 or 10 years.

[00817] In embodiment 443 provided herein is the method of any one of embodiments 433 through 442 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[00818] In embodiment 444 provided herein is the method of any one of embodiments 433 through 443 wherein the application of the composition leads to a concentration of at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the microbes that is at least 2, 5, 10, 50, 100, 500, 1000, 10,000, 50,000, or 100,000x higher than the concentration of the same microbe found or detected in an untreated control plant or soil or other growth medium in which the plant grows or will grow, for example at least 100x, preferably at least 500x, more preferably at least 1000x, yet more preferably at least 5000, still more preferably at least 50,000x.

[00819] In embodiment 445 provided herein is the method of any one of embodiments 433 through 444 further comprising applying one or more soil amendments to the soil.

[00820] In embodiment 446 provided herein is the method of embodiment 445 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[00821] In embodiment 447 provided herein is the method of embodiment 445 or embodiment 446 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[00822] In embodiment 448 provided herein is the method of any one of embodiments 433 through 447 further comprising growing the plant in the soil.

[00823] In embodiment 449 provided herein is the method of any one of embodiments 433 through 448 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition colonize roots of the plants, for example at least 10, preferably at least 20, more preferably at least 40, yet more preferably at least 60, still more preferably at least 80%.

[00824] In embodiment 450 provided herein is the method of any one of embodiments 433 through 449 wherein the composition or derivative is applied to a plurality of plants, or a parts thereof, and/or to soil or other growth medium in which the plurality of plants grow or will grow.

[00825] In embodiment 451 provided herein is the method of embodiment 450 wherein the plurality comprises at least 10, 20, 50, 100, 500, 1000, 5000, 10,000, 100,000, 500,000, 1M, 2M, 5M, 10M, 50M, 100M, 500M, 1B, 5B, 10B, 50B, or 100B of the plants, for example at least 100, preferably at least 1000, more preferably at least 100,000, even more preferably at least 10M, yet more preferably at least 100M, still more preferably at least 1B.

[00826] In embodiment 452 provided herein is a method comprising applying a composition comprising a plurality of microbes to an area comprising soil by aerial application.

[00827] In embodiment 453 provided herein is the method of embodiment 452 wherein the area further comprises plants growing in the soil.

[00828] In embodiment 454 provided herein is the method of embodiment 453 wherein the plants comprise grasses or trees.

[00829] In embodiment 455 provided herein is the method of embodiment 454 wherein the plants comprise grasses.

[00830] In embodiment 456 provided herein is the method of embodiment 454 wherein the plants comprise trees.

[00831] In embodiment 457 provided herein is the method of embodiment 453 wherein the area is a grassland.

[00832] In embodiment 458 provided herein is the method of embodiment 453 wherein the area is a forest.

[00833] In embodiment 459 provided herein is the method of embodiment 452 or embodiment 453 wherein the area comprising soil is a degraded soil ecosystem.

[00834] In embodiment 460 provided herein is the method of embodiment 459 wherein the area comprising soil is a deforested area.

[00835] In embodiment 461 provided herein is the method of embodiment 459 wherein the area comprising soil is a forested area.

[00836] In embodiment 462 provided herein is the method of embodiment 453 wherein the area comprising soil is a rangeland for livestock grazing.

[00837] In embodiment 463 provided herein is the method of embodiment 453 wherein the area comprising soil is an agricultural land.

[00838] In embodiment 464 provided herein is the method of any one of embodiments 453 through 463 wherein the aerial application is by unmanned aerial delivery vehicle.

[00839] In embodiment 465 provided herein is the method of embodiment 464 wherein the aerial application comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 separate applications by the unmanned aerial delivery vehicle, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[00840] In embodiment 466 provided herein is the method of embodiment 465 wherein each of the separate applications is to a part of the area at least a portion of which is different from a part of the area of the other applications.

[00841] In embodiment 467 provided herein is the method of any one of embodiments 453 through 463 wherein the application is by a plurality of unmanned aerial delivery devices.

[00842] In embodiment 468 provided herein is the method of embodiment 467 wherein the plurality comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 unmanned aerial delivery vehicles, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[00843] In embodiment 469 provided herein is the method of any one of embodiments 453 through 468 wherein the composition or derivative produced from the composition is applied over an area of at least 10, 100, 1000, 10,000, 100,000, 1M, 10M, 100M, or 1B hectares, for example at least 10, preferably at least 100, more preferably at least 10,000, even more preferably at least 1M, yet more preferably at least 10M, still more preferably at least 100M.

[00844] In embodiment 470 provided herein is the method of any one of embodiments 453 through 469 further comprising applying one or more soil amendments to the soil.

[00845] In embodiment 471 provided herein is the method of embodiment 470 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[00846] In embodiment 472 provided herein is the method of any one of embodiments 453 through 471 further comprising determining a carbon content of soil of the area before the application or applications.

[00847] In embodiment 473 provided herein is the method of any one of embodiments 453 through 472 further comprising determining a carbon content of soil of the area after the application or applications.

[00848] In embodiment 474 provided herein is the method of any one of embodiments 452 through 473 wherein the composition comprising a plurality of microbes comprises the composition of any one of embodiments 1 through 259, or a derivative thereof.

[00849] In embodiment 475 provided herein is a method comprising applying to a plant growth medium (a) a plurality of microbes, and (b) one or more macronutrients, (c) one or more micronutrients, and/or (d) one or more carbon sources, wherein a composition and/or effective amount of (a), (b), (c) and/or (d) is determined at least in part by one or more results of a first test on one or more samples comprising growth medium to which the plurality of microbes is to be applied or has been applied and/or a component of a plant or plants growing in the growth medium.

[00850] In embodiment 476 provided herein is the method of embodiment 475 wherein the plants are not cannabis.

[00851] In embodiment 477 provided herein is the method of embodiment 475 or embodiment 476 wherein the growth medium comprises soil.

[00852] In embodiment 478 provided herein is the method of any one of embodiments 475 through 477 wherein the composition and/or effective amount of (a), (b), and/or (c) is further determined, at least in part, by a type of plant or plants in the growth medium.

[00853] In embodiment 479 provided herein is the method of any one of embodiments 475 through 478 wherein the plurality of microbes is applied to the plant growth medium at an amount of at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, or 400 and/or not more than 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400, or 500 g microbes/acre, for example 5-5-500 or 5-200 or 5-100 or 5-50 g/acre, preferably 50-200 g microbes/acre, more preferably 75-125 g/acre, even more preferably 100 g/acre.

[00854] In embodiment 480 provided herein is the method of embodiment 479 wherein the plurality of microbes is present at a concentration of at least 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, or

10^{12} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, or 10^{13} cfu/g, for example 10^5-10^{13} cfu/g, preferably 10^7-10^{11} cfu/g, more preferably 10^8-10^{10} cfu/g.

[00855] In embodiment 481 provided herein is the method of any one of embodiments 475 through 480 wherein the plurality of microbes applied to the plant growth medium at an amount of at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} and/or not more than 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} cfu/acre, for example 10^6-10^{16} cfu/acre, preferably 10^8-10^{14} cfu/acre, more preferably 10^9-10^{13} cfu/acre, even more preferably 10^{10}-10^{12} cfu/acre.

[00856] In embodiment 482 provided herein is the method of any one of embodiments 475 through 481 wherein the plurality of microbes is applied 2, 3, 4, 5, 6, 7, 8, 9, or 10 times during a growing season, for example 1-10 times, preferably 3-8 times.

[00857] In embodiment 483 provided herein is the method of embodiment 482 wherein the time between applications is 1 week to 1 year.

[00858] In embodiment 484 provided herein is the method of any one of embodiments 475 through 483 wherein the plurality of microbes is applied via irrigation and/or aerial delivery vehicle.

[00859] In embodiment 485 provided herein is the method of embodiment 484 wherein the plurality of microbe is applied via irrigation.

[00860] In embodiment 486 provided herein is the method of embodiment 484 wherein the plurality of microbe is applied via aerial delivery vehicle.

[00861] In embodiment 487 provided herein is the method of any one of embodiments 475 through 486 wherein the first test comprises testing for organic materials, pH, macronutrients, micronutrients, or a combination thereof.

[00862] In embodiment 488 provided herein is the method of embodiment 487 wherein macronutrients comprise ammonium, nitrate, phosphate, potassium, sodium, calcium, magnesium, or a combination thereof.

[00863] In embodiment 489 provided herein is the method of embodiment 488 wherein the amount of nitrate in the growth medium is determined and compared to a preferred range of nitrate in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of nitrate within the preferred range after treatment.

[00864] In embodiment 490 provided herein is the method of embodiment 489 wherein the preferred range of nitrate comprises at least 10, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, or 140 and/or not more than 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 35-90 lbs/acre.

[00865] In embodiment 491 provided herein is the method of any one of embodiments 488 through 490 wherein the amount of phosphate in the growth medium is determined and

compared to a preferred range of phosphate in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of phosphate within the preferred range after treatment.

[00866] In embodiment 492 provided herein is the method of embodiment 491 wherein the preferred range of phosphate comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 50-100 lbs/acre.

[00867] In embodiment 493 provided herein is the method of any one of embodiments 488 through 492 wherein the amount of potassium in the growth medium is determined and compared to a preferred range of potassium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of potassium within the preferred range after treatment.

[00868] In embodiment 494 provided herein is the method of embodiment 493 wherein the preferred range of potassium comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 75-100 lbs/acre.

[00869] In embodiment 495 provided herein is the method of any one of embodiments 488 through 494 wherein the amount of calcium in the growth medium is determined and compared to a preferred range of calcium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of calcium within the preferred range after treatment.

[00870] In embodiment 496 provided herein is the method of embodiment 495 wherein the preferred range of calcium comprises at least 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, or 150 lbs/acre, preferably 60-120 lbs/acre.

[00871] In embodiment 497 provided herein is the method of any one of embodiments 488 through 496 wherein the amount of magnesium in the growth medium is determined and compared to a preferred range of magnesium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of magnesium within the preferred range after treatment.

[00872] In embodiment 498 provided herein is the method of embodiment 497 wherein the preferred range of magnesium comprises at least 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, or 40 and/or not more than 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50 lbs/acre, preferably 13-20 lbs/acre.

[00873] In embodiment 499 provided herein is the method of any one of embodiments 488 through 498 wherein the amount of sodium in the growth medium is determined and compared to a preferred range of sodium in the plant growth medium and the plant growth medium is treated such that the plant growth medium comprises an amount of sodium within the preferred range after treatment.

[00874] In embodiment 500 provided herein is the method of embodiment 499 wherein the preferred range of sodium comprises no more than 500, 400, 300, 200, 150, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 lbs/acre, preferably no more than 100 lbs/acre.

[00875] In embodiment 501 provided herein is the method of any one of embodiments 487 through 500 wherein micronutrients comprise zinc, iron, manganese, copper, cobalt, molybdenum, selenium, nickel, boron, silicon, aluminum, chloride, or a combination thereof.

[00876] In embodiment 502 provided herein is the method of any one of embodiments 475 through 501 wherein the one or more minerals comprises sea minerals.

[00877] In embodiment 503 provided herein is the method of any one of embodiments 475 through 502 wherein the carbon source comprises humates or humic acid.

[00878] In embodiment 504 provided herein is the method of embodiment 503 wherein the carbon source further comprises fulvic acid.

[00879] In embodiment 505 provided herein is the method of any one of embodiments 475 through 504 further comprising applying fertilizer, compost, or the like to the plant growth medium.

[00880] In embodiment 506 provided herein is the method of any one of embodiments 475 through 505 further comprising performing a second test on the plant growth medium to provide a second result comprising an amount of one or more microbes in the plurality of microbe after application to the plant growth medium.

[00881] In embodiment 507 provided herein is the method of embodiment 506 wherein the test comprises determining whether or not, or to what extent, the microbes have grown in the soil and/or on the plants.

[00882] In embodiment 508 provided herein is the method of any one of embodiments 475 through 507 comprising performing a third test on a sample comprising a plant component to provide a third result.

[00883] In embodiment 509 provided herein is the method of embodiment 508 wherein the plant component comprises sap, a leaf, a petiole, a root, a flower, or a fruit.

[00884] In embodiment 510 provided herein is the method of embodiment 509 wherein the plant component comprises a petiole.

[00885] In embodiment 511 provided herein is the method of any one of embodiments 508 through 510 further comprising applying an effective composition and/or amount of one or more amendments to the plant growth medium and/or plant, wherein the effective composition and/or amount of one or more amendments is determined at least in part by the third result.

[00886] In embodiment 512 provided herein is the method of embodiment 511 wherein the effective composition and/or amount of one or more amendments is applied to the plant growth medium and/or plant via a foliar spray or irrigation.

[00887] In embodiment 513 provided herein is the method of any one of embodiments 475 through 512 comprising performing a fourth test for carbon content of soil to provide a fourth result.

[00888] In embodiment 514 provided herein is the method of any one of embodiments 475 through 513 comprising performing a fifth test on the plant growth medium to provide a fifth result.

[00889] In embodiment 515 provided herein is the method of embodiment 514 wherein the fifth test is performed at the end of the growing season.

[00890] In embodiment 516 provided herein is the method of embodiment 515 wherein the fifth test comprises a carbon content test.

[00891] In embodiment 517 provided herein is the method of any one of embodiments 475 through 516 further comprising performing a pathogen analysis, a toxin analysis, a water analysis, a soil bulk density test, a soil water content test, or a combination thereof.

[00892] In embodiment 518 provided herein is the method of any one of embodiments 475 through 517 wherein a plant in the plant growth medium and/or the growth medium, *e.g.*, soil, exhibits one or more improved properties as compared to reference plant and/or growth medium, *e.g.*, soil, wherein the improved properties comprise: (i) reduced water consumption; (ii) increased soil water holding capacity; (iii) improved soil density; (iv) increased soil carbon content; (v) increased rate of soil carbon content increase; (vi) increased density of beneficial microbes in soil; (vii) increased yield; or (viii) increased nutrient density.

[00893] In embodiment 519 provided herein is the method of any one of embodiments 475 through 518 wherein the composition and/or effective amount is further determined at least in part by one or more desired results, a duration for to achieve the desired results, and/or a type of cultivation practice to be used to cultivate one or more plant in the plant growth medium.

[00894] In embodiment 520 provided herein is the method of any one of embodiments 475 through 519 wherein at least 20, 40, 50, 60, 70, 80, 90, 95, 97 98, 99 or 100% of the microbes in the plurality of microbes are *Streptomyces*.

[00895] In embodiment 521 provided herein is the method of any one of embodiments 475 through 520 wherein the plurality of microbes comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 of *Streptomyces janthinus*, *Streptomyces cinerochromogenes*, *Streptomyces chromofuscus*, *Streptomyces atratus*, *Streptomyces aurantiogriseus*, *Streptomyces rimosus*, *Streptomyces venezuelae*, *Streptomyces violaceus*, *Streptomyces violascens*, *Streptomyces viridodiasticus*, *Streptomyces griseus*, *Streptoverticillium rectiverticillatum*, or *Bacillus subtilis*.

[00896] In embodiment 522 provided herein is the method of any one of embodiments 475 through 521 wherein the plurality of microbes comprises one or more strains of mycorrhizae.

[00897] In embodiment 523 provided herein is the method of any one of embodiments 475 through 522 wherein the plurality of microbes comprises a composition of any one of embodiments 1 through 259.

[00898] In embodiment 524 provided herein is a method comprising contacting a surface of a seed, seedling, or other plant propagule with a composition of any one of embodiments 1 through 259, or a derivative produced from the composition.

[00899] In embodiment 525 provided herein is the method of embodiment 524 wherein the seed, seedling, or other plant propagule is coated with and/or comprises within pores of the seed, seedling, or other plant propagule at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition.

[00900] In embodiment 526 provided herein is the method of embodiment 524 or embodiment 525 comprising contacting the surface of a seed with the composition.

[00901] In embodiment 527 provided herein is the method of any one of embodiments 524 through 526 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the microbes are heterologous to the seed, seedling, or other plant propagule.

[00902] In embodiment 528 provided herein is the method of any one of embodiments 524 through 527 comprising contacting the surface of the seed, seedling, or other plant propagule with at least 10, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 2000, 5000, 10,000, 50,000, or 100,000 CFUS of the microbes of the composition or derivative, for example at least 10, preferably at least 50, more preferably at least 100, even more preferably at least 200, yet more preferably at least 500, still more preferably at least 1000.

[00903] In embodiment 529 provided herein is the method of any one of embodiments 524 through 528 further comprising placing the seeds, seedlings, or other plant propagules in soil and exposing it to suitable conditions for growth.

[00904] In embodiment 530 provided herein is the method of embodiment 529 further comprising applying one or more soil amendments to the soil.

[00905] In embodiment 531 provided herein is the method of embodiment 530 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[00906] In embodiment 532 provided herein is the method of embodiment 530 or embodiment 531 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plant grows or will grow.

[00907] In embodiment 533 provided herein is the method of any one of embodiments 529 through 532 further comprising growing the plant in the soil.

[00908] In embodiment 534 provided herein is the method of any one of embodiments 524 through 533 wherein the seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of grass or trees.

[00909] In embodiment 535 provided herein is a method comprising contacting surfaces of a populations of seeds, seedlings, or other plant propagules with a composition of any one of embodiments 1 through 259, or a derivative produced from the composition.

[00910] In embodiment 536 provided herein is the method of embodiment 535 wherein individual seeds, seedlings, or other plant propagules of the population are coated with and/or comprise within pores of the seeds, seedlings, or other plant propagules at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes of the composition.

[00911] In embodiment 537 provided herein is the method of embodiment 535 or embodiment 536 wherein at least 50, 60, 70, 80, 90, 95, or 99%, or 100%, of the different microbes in the composition are present in the population of seeds, seedlings, or other plant propagules of the population, for example at least 50, preferably at least 60, more preferably at least 80, even more preferably at least 90, yet more preferably at least 95, still more preferably at least 99, and even still more preferably 100%.

[00912] In embodiment 538 provided herein is the method of any one of embodiments 535 through 537 wherein at least at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%

of the different microbes of the composition is heterologous to the seeds, seedlings, or other plant propagule preferably at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 40.

[00913] In embodiment 539 provided herein is the method of any one of embodiments 535 through 538 wherein the population comprises at least 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 200,000, 500,000, or 1M seeds, seedlings, or other plant propagules.

[00914] In embodiment 540 provided herein is the method of any one of embodiments 535 through 539 comprising contacting the population of seeds, seedlings, or other plant propagules with a sufficient quantity of the composition or derivative so that each seed, seedling, or other plant propagule is contacted with at least 10, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 2000, 5000, 10,000, 50,000, or 100,000 CFUS of the microbes of the composition or derivative, for example at least 10, preferably at least 50, more preferably at least 100, even more preferably at least 200, yet more preferably at least 500, still more preferably at least 1000.

[00915] In embodiment 541 provided herein is the method of any one of embodiments 535 through 540 further comprising placing the seeds, seedlings, or other plant propagules in soil and exposing them to suitable conditions for growth.

[00916] In embodiment 542 provided herein is the method of any one of embodiments 535 through 541 further comprising applying one or more soil amendments to the soil.

[00917] In embodiment 543 provided herein is the method of embodiment 542 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[00918] In embodiment 544 provided herein is the method of embodiment 542 or embodiment 543 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[00919] In embodiment 545 provided herein is the method of any one of embodiments 541 through 544 further comprising growing the plant in the soil.

[00920] In embodiment 546 provided herein is the method of embodiment 545 wherein at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, or 99%, or 100%, of the microbes of the composition colonize roots of the plants, for example at least 10, preferably at least 20, more preferably at least 40, yet more preferably at least 60, still more preferably at least 80%.

[00921] In embodiment 547 provided herein is the method of any one of embodiments 535 through 546 wherein the seeds, seedling, or other plant propagules comprise seeds, seedlings, or other plant propagules of grass or trees.

[00922] In embodiment 548 provided herein is use of the composition of any one of embodiments 1 through 259 in reducing methane production in soil in which plants grow compared to before use of the composition.

[00923] In embodiment 549 provided herein is use of the composition of any one of embodiments 1 through 259 in coating a surface of seeds, seedlings, or other plant propagules with one or more microbes of the composition.

[00924] In embodiment 550 provided herein is use of the composition of any one of embodiments 1 through 259 in in increasing beneficial organisms in soil in which plants grow and to which composition applied, compared to without.

[00925] In embodiment 551 provided herein is use of the composition of any one of embodiments 1 through 259 in transitioning to organic farming in 3 years or less, or 2 years or less, or 1.5 years or less.

[00926] In embodiment 552 provided herein is use of the composition of any one of embodiments 1 through 259 in improving soil density, soil water holding capacity, soil water retention capacity, in soil in which plants grow, compared to without.

[00927] In embodiment 553 provided herein is use of the composition of any one of embodiments 1 through 259 in increasing mycorrhizal fungi on or in roots of plant, compared to a reference plant.

[00928] In embodiment 554 provided herein is use of the composition of any one of embodiments 1 through 259 in preventing or reducing flooding.

[00929] In embodiment 555 provided herein is use of the composition of any one of embodiments 1 through 259 in decreasing use of synthetic fertilizer, herbicide, and/or pesticide on plants or soil in which plants grow, compared to without.

[00930] In embodiment 556 provided herein is use of the composition of any one of embodiments 1 through 259 in increasing nutrient uptake by a plant grown in soil to which composition applied compared to without.

[00931] In embodiment 557 provided herein is use of the composition of any one of embodiments 1 through 259 in decreasing uptake of one or more toxins, e.g., heavy metals, by plants grown in soil comprising composition.

[00932] In embodiment 558 provided herein is use of the composition of any one of embodiments 1 through 259 in increasing plant nutrient density of a plant grown in soil to which composition applied compared to without.

[00933] In embodiment 559 provided herein is use of the composition of any one of embodiments 1 through 259 in reducing carbon footprint for raising livestock.

[00934] In embodiment 560 provided herein is use of the composition of any one of embodiments 1 through 259 in increasing oil production of a plant not cannabis.

[00935] In embodiment 561 provided herein is use of the composition of any one of embodiments 1 through 259 in regenerating degraded soil.

[00936] In embodiment 562 provided herein is a method comprising combining a first population of microbes comprising microbes of any one of *Streptomyces* designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2 and a second population of microbes, different from the first.

[00937] In embodiment 563 provided herein is the method of embodiment 562 wherein the first population of microbes comprises microbes of a composition of any one of embodiments 1 through 259.

[00938] In embodiment 564 provided herein is the method of embodiment 562 or embodiment 563 wherein the second population of microbes comprises any one of *Streptomyces* designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2, different from the first.

[00939] In embodiment 565 provided herein is the composition of embodiment 564 wherein the second population of microbes comprises microbes of a composition of any one of embodiments 1 through 259.

[00940] In embodiment 566 provided herein is the method of any one of embodiments 562 through 564 further comprising combining the first and second populations with at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, 30, 32, 35, 37, 40, 42 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, 30, 32, 35, 37, 40, 42, or 43 additional populations of microbes comprising any one of any one of *Streptomyces* designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2, wherein the microbes of each additional population are different from the first and second populations, and the microbes of each additional population are different from each other.

[00941] In embodiment 567 provided herein is the method of any one of embodiments 562 through 566 wherein at least one of the populations is pure population.

[00942] In embodiment 568 provided herein is the method of embodiment 567 wherein all of the populations are pure populations.

[00943] In embodiment 569 provided herein is the method of any one of embodiments 562 through 568 wherein the populations of microbes are each in a liquid prior to combining.

[00944] In embodiment 570 provided herein is the method of embodiment 569 comprising filtering each of the liquids to remove at least a portion of each liquid and leave a remainder liquid for each, wherein each remainder liquid comprises the microbes or a portion thereof.

[00945] In embodiment 571 provided herein is the method of embodiment 570 comprising combining the liquids before filtering.

[00946] In embodiment 572 provided herein is the method of embodiment 570 comprising combining the remainder liquids after filtering.

[00947] In embodiment 573 provided herein is the method of any one of embodiments 570 through 572 wherein the filtering is through a filter comprising pores of a size sufficient to retain at least a portion of the microbes.

[00948] In embodiment 574 provided herein is the method of embodiment any one of embodiments 570 through 573 wherein the filter comprises a first filter layer comprising pores of a first size and a second filter layer comprising pores of a second size.

[00949] In embodiment 575 provided herein is the method of any one of embodiments 570 through 574 wherein the pores are of a size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um.

[00950] In embodiment 576 provided herein is the method of embodiment 574 wherein the first size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 120-240 um, more preferably 160-220 um.

[00951] In embodiment 577 provided herein is the method of embodiment 574 wherein the second size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 20-100 um, more preferably 40-80 um.

[00952] In embodiment 578 provided herein is the method of embodiment 573 wherein the portion of microbes retained comprises at least 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.5, 99.9, or 100% of the microbes, for example at least 50, preferably at least 70, more preferably at least 90, even more preferably at least 95, yet more preferably at least 98, still more preferably at least 99%.

[00953] In embodiment 579 provided herein is the method of embodiment 570 through 578 wherein the microbes are removed from the filter and placed in a collection vessel.

[00954] In embodiment 580 provided herein is the method of any one of embodiments 562 through 579 wherein the microbes are dried to produce dried microbes.

[00955] In embodiment 581 provided herein is the method of embodiment 580 wherein the microbes are dried after filtration and combining.

[00956] In embodiment 582 provided herein is the method of embodiment 580 wherein the microbes are air dried.

[00957] In embodiment 583 provided herein is the method of embodiment 580 wherein the microbes are spray dried.

[00958] In embodiment 584 provided herein is the method of embodiment 580 wherein the microbes are lyophilized.

[00959] In embodiment 585 provided herein is the method of any one of embodiments 580 through 584 wherein the dried microbes comprise less than 5, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05, 0.01, 0.005, or 0.001% water by weight, for example less than 1, preferably less than 0.5, more preferably less than 0.1, even more preferably less than 0.01, yet more preferably less than 0.005, still more preferably less than 0.001%.

[00960] In embodiment 586 provided herein is the method of any one of embodiments 580 through 585 wherein the dried microbes are combined with one or more agriculturally acceptable adjuvants.

[00961] In embodiment 587 provided herein is the method of any one of embodiments 580 through 586 wherein the one or more agriculturally acceptable adjuvants comprise one or more carriers.

[00962] In embodiment 588 provided herein is the method of embodiment 587 wherein the one or more carriers comprise a monosaccharide, a polysaccharide, a lipid, or a combination thereof.

[00963] In embodiment 589 provided herein is the method of embodiment 588 wherein the one or more carriers comprises a monosaccharide.

[00964] In embodiment 590 provided herein is the method of embodiment 589 wherein the monosaccharide comprises glucose.

[00965] In embodiment 591 provided herein is the method embodiment 589 or embodiment 590 wherein the concentration of the monosaccharide is at least 20, 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, or 99 wt% and/or not more than 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, 99, 99.5, or 99.9 wt%, for example 20-99 wt%, preferably 70-95 wt%, more preferably 85-95 wt%.

[00966] In embodiment 592 provided herein is the method of any one of embodiments 586 through 591 wherein the one or more agriculturally acceptable adjuvants comprise a polysaccharide.

[00967] In embodiment 593 provided herein is the method of embodiment 592 wherein the polysaccharide comprises a starch.

[00968] In embodiment 594 provided herein is the method of embodiment 593 wherein the starch is derived from yucca.

[00969] In embodiment 595 provided herein is the method of any one of embodiments 592 through 594 wherein the concentration of the polysaccharide is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[00970] In embodiment 596 provided herein is the method any one of embodiments 592 through 595 wherein the starch is derived from an oat.

[00971] In embodiment 597 provided herein is the method of any one of embodiments 586 through 596 wherein the one or more agriculturally acceptable adjuvants comprises one or more surfactants.

[00972] In embodiment 598 provided herein is the method of embodiment 597 wherein the surfactant comprises a lipid.

[00973] In embodiment 599 provided herein is the method of embodiment 598 wherein the lipid comprises a lecithin.

[00974] In embodiment 600 provided herein is the method of embodiment 599 wherein the lecithin comprises a soy lecithin.

[00975] In embodiment 601 provided herein is the method of any one of embodiments 597 through 600 wherein the concentration of surfactant is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[00976] In embodiment 602 provided herein is the method of any one of embodiments 580 through 601 wherein the dried microbes are processed to a powder.

[00977] In embodiment 603 provided herein is the method of embodiment 602 wherein the powder comprises a median particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um, and/or a mean particle size of at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 um and/or no more than 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 270, 300, 400, or 500 um, for example 20-500 um, preferably 90-270 um, more preferably 140-220 um, even more preferably 160-200 um, still more preferably 170-190 um.

[00978] In embodiment 604 provided herein is the method of any one of embodiments 562 through 603 wherein the microbes comprises a viability of at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or 10^{14}, and/or not more than 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or 10^{15} CFU/gm of composition, preferably 10^6 to 10^{15}, more preferably 10^7 to 10^{14}, even more preferably 10^7 to 10^{13}, yet more preferably 10^7 to 10^{11}, even yet more preferably 10^8 to 10^{11} CFU/gm of composition cfu/g after processing.

[00979] In embodiment 605 provided herein is the method of any one of embodiments 562 through 604 further comprising placing the microbes in a package.

[00980] In embodiment 606 provided herein is a method of growing one or more microbes comprising inoculating a heterologous medium with a first population of microbes comprising microbes of the composition of any one of embodiments of embodiments 1 through 259 and providing suitable conditions for one or more microbes to grow.

[00981] In embodiment 607 provided herein is the method of embodiment 606 wherein the first population is a pure population.

[00982] In embodiment 608 provided herein is the method of embodiment 606 or embodiment 607 wherein the heterologous medium comprises a solid medium.

[00983] In embodiment 609 provided herein is the method of embodiment 608 wherein the solid medium comprises agar.

[00984] In embodiment 610 provided herein is the method of embodiment 609 wherein the concentration of agar is at least 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, or 1.4 and/or no more than 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, or 1.5 g/L, for example 0.3-1.5 g/L, preferably 0.4-1 g/L, more preferably, 0.6-0.8 g/L.

[00985] In embodiment 611 provided herein is the method of any one of embodiments 606 through 610 wherein the heterologous medium comprises a liquid medium.

[00986] In embodiment 612 provided herein is the method of any one of embodiments 608 through 611 wherein the heterologous medium comprises a polysaccharide, a disaccharide, a monosaccharide, a gum, a natural or synthetic derivative thereof.

[00987] In embodiment 613 provided herein is the method of embodiment 612 wherein the heterologous medium comprises a polysaccharide.

[00988] In embodiment 614 provided herein is the method of embodiment 613 wherein the polysaccharide comprises a starch.

[00989] In embodiment 615 provided herein is the method of embodiment 614 wherein the starch is an oat starch.

[00990] In embodiment 616 provided herein is the method of embodiment 614 or embodiment 615 wherein the concentration of starch is at least 10, 20, 30, 40, 50, 60, 70, 80, or 90 g/L and/or

not more than 20, 30, 40, 50, 60, 70, 80, 90, or 100 g/L, for example 10-100, preferably 20-80, more preferably 30-70.

[00991] In embodiment 617 provided herein is the method of any one of embodiments 608 through 616 wherein the heterologous medium further comprises a vitamin.

[00992] In embodiment 618 provided herein is the method of embodiment 617 wherein the vitamin comprises Vitamin A, Vitamin C, Vitamin D, Vitamin E, Vitamin B1, Vitamin B2, Niacin, Vitamin B6, Folate, Vitamin B12, Biotin, Pantothenic Acid, Calcium, Iron, Iodine, Magnesium, Zinc, Selenium, Copper, or a combination thereof.

[00993] In embodiment 619 provided herein is the method of embodiment 618 wherein the vitamin comprises Vitamin A.

[00994] In embodiment 620 provided herein is the method of embodiment 619 wherein the Vitamin A is present at a concentration of at least 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, or 1400 and/or not more than 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or 1500 ug/L, for example 100-1500, preferably 300-1000, more preferably 500-900, even more preferably 600-800.

[00995] In embodiment 621 provided herein is the method of any one of embodiments 618 through 620 wherein the vitamin comprises Vitamin C.

[00996] In embodiment 622 provided herein is the method of embodiment 621 wherein the Vitamin C is present at a concentration of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, or 140 and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 mg/L, for example 10-50, preferably 50-130, more preferably 70-110, even more preferably 80-100.

[00997] In embodiment 623 provided herein is the method of any one of embodiments 618 through 622 wherein the vitamin comprises Vitamin D.

[00998] In embodiment 624 provided herein is the method of embodiment 623 wherein the Vitamin D is present at least 5, 10, 15, 20, 25, 30, 35, 40, or 45 and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, or 50 ug/L, for example 5-50, preferably 10-40, more preferably 15-35, even more preferably 20-30.

[00999] In embodiment 625 provided herein is the method of any one of embodiments 618 through 624 wherein the vitamin comprises Vitamin E.

[001000] In embodiment 626 provided herein is the method of embodiment 625 wherein the Vitamin E is present at a concentration of at least 5, 7, 9, 11, 13, 15, 17, 19, 21, or 23 and/or not more than 7, 9, 11, 13, 15, 17, 19, 21, 23, or 25 mg/L, for example 5-25, preferably 9-21, more preferably 11-19, even more preferably 13-17.

[001001] In embodiment 627 provided herein is the method of any one of embodiments 618 through 626 wherein the vitamin comprises Vitamin B1.

[001002] In embodiment 628 provided herein is the method of embodiment 627 wherein the Vitamin B1 is present at a concentration of at least 1, 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, or 3.8 and/or not more than 1.2, 1.4, 1.6, 1.8, 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, or 4 mg/L, for example 1-4 mg/L, preferably 1.6-3.2, more preferably 2-2.8, even more preferably 2.2-2.6.

[001003] In embodiment 629 provided herein is the method of any one of embodiments 618 through 628 wherein the vitamin comprises Vitamin B2.

[001004] In embodiment 630 provided herein is the method of embodiment 629 wherein the Vitamin B2 is present at a concentration of at least 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, or 2.75 and/or not more than 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, 2.15, 2.25, 2.35, 2.45, 2.55, 2.65, 2.75, or 2.85 mg/L, for example 1.25-2.85, preferably 1.55-2.55, more preferably, 1.65-2.45, more preferably 1.85-2.05.

[001005] In embodiment 631 provided herein is the method of any one of embodiments 618 through 630 wherein the vitamin comprises Niacin.

[001006] In embodiment 632 provided herein is the method of embodiment 631 wherein the Niacin is present at a concentration of at least 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, or 38 and/or not more than 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, or 40 mg/L, for example 10-40, preferably 14-36, more preferably 18-32, even more preferably 20-28.

[001007] In embodiment 633 provided herein is the method of any one of embodiments 618 through 632 wherein the vitamin comprises Vitamin B6.

[001008] In embodiment 634 provided herein is the method of embodiment 633 wherein the Vitamin B6 is present at a concentration of at least 2, 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, or 4.8 and/or not more than 2.2, 2.4, 2.6, 2.8, 3, 3.2, 3.4, 3.6, 3.8, 4, 4.2, 4.4, 4.6, 4.8, or 5 mg/L, for example 2-5, preferably 2.6-4.4, more preferably 3-4, even more preferably 3-3.8.

[001009] In embodiment 635 provided herein is the method of any one of embodiments 618 through 634 wherein the vitamin comprises Folic Acid.

[001010] In embodiment 636 provided herein is the method of embodiment 635 wherein the Folic Acid is present at a concentration of at least 120, 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, or 680 and/or not more than 160, 200, 240, 280, 320, 360, 400, 440, 480, 520, 560, 600, 640, 680, or 720 ug/L, for example 120-720, preferably 240-600, more preferably 320-480, even more preferably 360-440.

[001011] In embodiment 637 provided herein is the method of any one of embodiments 618 through 636 wherein the vitamin comprises Vitamin B12.

[001012] In embodiment 638 provided herein is the method of embodiment 637 wherein the Vitamin B12 is present at a concentration of at least 5.4, 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, or 13.8 and/or not more than 6, 6.6, 7.2, 7.8, 8.4, 9.0, 9.6, 10.2, 10.8, 11.4, 12, 12.6, 13.2, 13.8, or 14.4, for example 5.4-14.4, preferably 7.2-12.6, more preferably 8.4-11.4, even more preferably 9-10.2.

[001013] In embodiment 639 provided herein is the method of any one of embodiments 618 through 638 wherein the vitamin comprises Biotin.

[001014] In embodiment 640 provided herein is the method of embodiment 639 wherein the Biotin is present at a concentration of at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 and/or not more than 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or 85 ug/L, for example 10-85, preferably 20-75, more preferably 30-65, even more preferably 35-55.

[001015] In embodiment 641 provided herein is the method of any one of embodiments 618 through 640 wherein the vitamin comprises Pantothenic Acid.

[001016] In embodiment 642 provided herein is the method of embodiment 641 wherein the Pantothenic Acid is present at a concentration of at least 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, or 11 and/or not more than 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, or 11.5 mg/L, for example 4-11.5, preferably 5.5-10, more preferably 6.5-9, even more preferably 7-8.

[001017] In embodiment 643 provided herein is the method of any one of embodiments 618 through 642 wherein the vitamin comprises Calcium.

[001018] In embodiment 644 provided herein is the method of embodiment 643 wherein the Calcium is present at a concentration of at least 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 and/or not more than 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 210 mg/L, for example 60-210, preferably 80-190, more preferably 100-170, even more preferably 120-140.

[001019] In embodiment 645 provided herein is the method of any one of embodiments 618 through 644 wherein the vitamin comprises Iron.

[001020] In embodiment 646 provided herein is the method of embodiment 645 wherein the Iron is present at a concentration of at least 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32 and/or not more than 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 mg/L, for example 6-34, preferably 12-26, more preferably 14-22, even more preferably 16-20.

[001021] In embodiment 647 provided herein is the method of any one of embodiments 618 through 646 wherein the vitamin comprises Iodine.

[001022] In embodiment 648 provided herein is the method of embodiment 647 wherein the Iodine is present at a concentration of at least 80, 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180, 190, 200, 210, or 220 and/or not more than 90, 100, 110, 120, 130, 140, 150, 160 ,170, 180,

190, 200, 210, 220, or 230 mg/L, for example 80-230, preferably 100-200, more preferably 120-180, even more preferably 140-160.

[001023] In embodiment 649 provided herein is the method of any one of embodiments 618 through 648 wherein the vitamin comprises Magnesium.

[001024] In embodiment 650 provided herein is the method of embodiment 649 wherein the Magnesium is present at a concentration of at least 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, or 70 and/or not more than 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, 70, or 74 mg/L, for example 18-74, preferably 22-62, more preferably 30-54, even more preferably 38-46.

[001025] In embodiment 651 provided herein is the method of any one of embodiments 618 through 650 wherein the vitamin comprises Zinc.

[001026] In embodiment 652 provided herein is the method of embodiment 651 wherein the Zinc is present at a concentration of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 mg/L, for example 2-15, preferably 3-13, more preferably 5-11, even more preferably 7-9.

[001027] In embodiment 653 provided herein is the method of any one of embodiments 618 through 652 wherein the vitamin comprises Selenium.

[001028] In embodiment 654 provided herein is the method of embodiment 653 wherein the Selenium is present at a concentration of at least 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, or 69 and/or not more than 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, or 73 ug/L, for example 13-73, preferably 25-57, more preferably 29-53, even more preferably 37-45.

[001029] In embodiment 655 provided herein is the method of any one of embodiments 618 through 654 wherein the vitamin comprises Copper.

[001030] In embodiment 656 provided herein is the method of embodiment 655 wherein the Copper is present at a concentration of at least 0.65, 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, or 2.05 and/or not more than 0.75, 0.85, 0.95, 1.05, 1.15, 1.25, 1.35, 1.45, 1.55, 1.65, 1.75, 1.85, 1.95, 2.05, or 2.15 mg/L, for example 0.65-2.15, preferably 0.85-1.85, more preferably 1.05-1.65, even more preferably 1.25-1.45.

[001031] In embodiment 657 provided herein is the method of any one of embodiments 606 through 656 wherein the first population of microbes is in a stock solution comprising a cryoprotectant prior to inoculating.

[001032] In embodiment 658 provided herein is the method of embodiment 657 wherein the cryoprotectant comprises glycerol, ethylene glycol, propylene glycol, urea, calcium chloride, sodium nitrate, magnesium chloride, ammonium sulfate, or a combination thereof.

[001033] In embodiment 659 provided herein is the method of embodiment 658 wherein the cryoprotectant comprises glycerol.

[001034] In embodiment 660 provided herein is the method of embodiment 659 wherein the glycerol is present at a concentration of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, or 45% and/or no more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 35, 40, 45, or 50% v/v, for example 1-50%, preferably 10-30%, more preferably 15-25%, even more preferably 18-22%.

[001035] In embodiment 661 provided herein is the method of any one of embodiments 606 through 660 further comprising inoculating the heterologous medium with a second population of microbes different from the first.

[001036] In embodiment 662 provided herein is the method of embodiment 661 further comprising inoculating the heterologous medium with a third population of microbes different from the first or the second.

[001037] In embodiment 663 provided herein is the method of embodiment 662 further comprising inoculating the heterologous medium with a fourth population of microbes different from the first, second, or third.

[001038] In embodiment 664 provided herein is the method of embodiment 663 further comprising inoculating the heterologous medium with a fifth population of microbes different from the first, second, third, or fourth.

[001039] In embodiment 665 provided herein is the method of any one of embodiments 606 through 664 further comprising concentrating the one or more microbes after growing.

[001040] In embodiment 666 provided herein is the method of embodiment 665 wherein concentrating comprises filtering.

[001041] In embodiment 667 provided herein is the method of embodiment 666 wherein the filtering is through a filter comprising pores of a size sufficient to retain at least a portion of the microbes.

[001042] In embodiment 668 provided herein is the method of embodiment 667 wherein the filter comprises a first filter layer comprising pores of a first size and a second filter layer comprising pores of a second size.

[001043] In embodiment 669 provided herein is the method of embodiment 668 wherein the pores are of a size of at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um.

[001044] In embodiment 670 provided herein is the method of embodiment 668 wherein the first size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 120-240 um, more preferably 160-220 um.

[001045] In embodiment 671 provided herein is the method of embodiment 668 or embodiment 670 wherein the second size is at least 0.2, 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, or 280 and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 um, for example, 0.2-300 um, preferably 20-100 um, more preferably 40-80 um.

[001046] In embodiment 672 provided herein is the method of any one of embodiments 667 through 671 wherein the portion of microbes retained comprises at least 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.5, 99.9, or 100% of the microbes, for example at least 50, preferably at least 70, more preferably at least 90, even more preferably at least 95, yet more preferably at least 98, still more preferably at least 99%.

[001047] In embodiment 673 provided herein is the method of embodiment 665 wherein concentrating comprises freeze drying.

[001048] In embodiment 674 provided herein is the method of embodiment 665 wherein concentrating comprises spray drying.

[001049] In embodiment 675 provided herein is the method of any one of embodiments 665 through 674 wherein, after concentrating, the microbes are transferred to a collection vessel.

[001050] In embodiment 676 provided herein is the method of any one of embodiments 665 through 675 wherein the concentrated microbes comprise less than 5, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1, 0.05, 0.01, 0.005, or 0.001% water by weight, for example less than 1, preferably less than 0.5, more preferably less than 0.1, even more preferably less than 0.01, yet more preferably less than 0.005, still more preferably less than 0.001%.

[001051] In embodiment 677 provided herein is the method of any one of embodiments 665 through 676 wherein the concentrated microbes are combined with one or more agriculturally acceptable adjuvants.

[001052] In embodiment 678 provided herein is the method of embodiment 677 wherein the one or more agriculturally acceptable adjuvants comprise one or more carriers.

[001053] In embodiment 679 provided herein is the method of embodiment 678 wherein the one or more carriers comprise a monosaccharide, a polysaccharide, a lipid, or a combination thereof.

[001054] In embodiment 680 provided herein is the method of embodiment 679 wherein the one or more carriers comprises a monosaccharide.

[001055] In embodiment 681 provided herein is the method of embodiment 680 wherein the monosaccharide comprises glucose.

[001056] In embodiment 682 provided herein is the method embodiment 679 or embodiment 680 wherein the concentration of the monosaccharide is at least 20, 30, 40, 50, 60, 70, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, or 99 wt% and/or not more than 30, 40, 50, 60, 70, 80,

85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 98, 99, 99.5, or 99.9 wt%, for example 20-99 wt%, preferably 70-95 wt%, more preferably 85-95 wt%.

[001057] In embodiment 683 provided herein is the method of any one of embodiments 677 through 682 wherein the one or more agriculturally acceptable adjuvants comprise a polysaccharide.

[001058] In embodiment 684 provided herein is the method of embodiment 683 wherein the polysaccharide comprises a starch.

[001059] In embodiment 685 provided herein is the method of embodiment 684 wherein the starch is derived from yucca.

[001060] In embodiment 686 provided herein is the method of any one of embodiments 677 through 685 wherein the concentration of the polysaccharide is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[001061] In embodiment 687 provided herein is the method any one of embodiments 683 through 686 wherein the starch is derived from an oat.

[001062] In embodiment 688 provided herein is the method of any one of embodiments 677 through 687 wherein the one or more agriculturally acceptable adjuvants comprises one or more surfactants.

[001063] In embodiment 689 provided herein is the method of embodiment 688 wherein the surfactant comprises a lipid.

[001064] In embodiment 690 provided herein is the method of embodiment 689 wherein the lipid comprises a lecithin.

[001065] In embodiment 691 provided herein is the method of embodiment 690 wherein the lecithin comprises a soy lecithin.

[001066] In embodiment 692 provided herein is the method of any one of embodiments 688 through 691 wherein the concentration of surfactant is at least 0.2, 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, or 4 and/or not more than 0.4, 0.6, 0.8, 1, 1.2, 1.4, 1.6, 1.8. 2, 2.2, 2.4, 2.6, 2.8, 3, 4, or 5 wt%, for example, 0.2-5 wt%, preferably 1-3 wt%, more preferably 1.4-2.6 wt%, even more preferably 1.8-2.2 wt%.

[001067] In embodiment 693 provided herein is the method of any one of embodiments 665 through 692 wherein the dried microbes are processed to a powder.

[001068] In embodiment 694 provided herein is the method of any one of embodiments 665 through 693 further comprising placing the microbes in a package.

[001069] In embodiment 695 provided herein is a composition comprising a pure population of microbes of the composition of any one of embodiments of embodiments 1 through 259 and a heterologous growth medium.

[001070] In embodiment 696 provided herein is a composition consisting essentially of a pure population of microbes of the composition of any one of embodiments of embodiments 1 through 259 and a heterologous growth medium.

[001071] In embodiment 697 provided herein is a kit comprising an apparatus for obtaining a soil sample or a plant or plant part sample and packaging to contain the apparatus.

[001072] In embodiment 698 provided herein is a method comprising collecting a soil sample or a plant sample, wherein the sample is collected with a kit of any embodiment 697.

[001073] In embodiment 699 provided herein is a method for enhancing a rate at which atmospheric carbon is converted to carbon products in soil in which plants are grown and/or in the plants comprising applying a composition comprising one or more microbes to the plants and/or soil, in a first application, wherein the rate is greater than that for reference soil and/or plants in which the plants are grown without the composition.

[001074] In embodiment 700 provided herein is the method of embodiment 699 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001075] In embodiment 701 provided herein is the method of embodiment 699 or embodiment 700 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001076] In embodiment 702 provided herein is the method of any one of embodiments 699 through 701 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001077] In embodiment 703 provided herein is the method of any one of embodiments 699 through 702 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or

100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001078] In embodiment 704 provided herein is the method of any one of embodiments 699 through 703 wherein the different microbes are *Streptomyces*.

[001079] In embodiment 705 provided herein is the method of any one of embodiments 699 through 704 wherein the composition comprising microbes comprises the composition of any one of embodiments of embodiments 1 through 259 or progeny and/or mutants thereof.

[001080] In embodiment 706 provided herein is the method of embodiment 705 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001081] In embodiment 707 provided herein is the method of any one of embodiments 699 through 706 wherein the rate of conversion of atmospheric carbon to carbon products in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300%.

[001082] In embodiment 708 provided herein is the method of any one of embodiments 699 through 707 wherein the enhancement of rate of conversion results in an increase in soil carbon content of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare/year and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare/year, wherein the soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare/year, compared to reference soil.

[001083] In embodiment 709 provided herein is the method of any one of embodiments 699 through 708 wherein the enhancement of rate of conversion results in an increase in soil carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3/year, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3/year, wherein carbon content is measured to a depth of 20 cm, compared to reference soil.

[001084] In embodiment 710 provided herein is the method of any one of embodiments 699 through 709 further comprising applying one or more soil amendments to the soil.

[001085] In embodiment 711 provided herein is the method of embodiment 445 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001086] In embodiment 712 provided herein is the method of embodiment 445 or embodiment 446 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001087] In embodiment 713 provided herein is the method of any one of embodiments 699 through 447 wherein the plants are not cannabis plants.

[001088] In embodiment 714 provided herein is the method of any one of embodiments 699 through 713 further comprising applying the composition in a second application.

[001089] In embodiment 715 provided herein is the method of embodiment 714 further comprising applying the composition in a third application.

[001090] In embodiment 716 provided herein is the method of any one of embodiments 699 through 715 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001091] In embodiment 717 provided herein is the method of any one of embodiments 699 through 716 wherein carbon content of the soil is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 400, or 500%, for example at least 20, preferably at least 40, more preferably at least 60, even more preferably at least 70, yet more preferably at least 80, still more preferably at least 90% in a period of time after the first application.

[001092] In embodiment 718 provided herein is the method of embodiment 718 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4

weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[001093] In embodiment 719 provided herein is the method of embodiment 717 or embodiment 718 wherein carbon content is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 400, or 500%, for example at least 20, preferably at least 40, more preferably at least 60, even more preferably at least 70, yet more preferably at least 80, still more preferably at least 90%.

[001094] In embodiment 720 provided herein is the method of any one of embodiments 717 through 719 wherein the soil carbon content is increased by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton/hectare, wherein the soil carbon content is measured to a depth of 20 cm soil.

[001095] In embodiment 721 provided herein is the method of any one of embodiments 699 through 720 wherein the increased soil carbon content comprises an increase in at least one of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001096] In embodiment 722 provided herein is the method of any one of embodiments 699 through 720 wherein the increased soil carbon content comprises an increase in at least two of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001097] In embodiment 723 provided herein is the method of any one of embodiments 699 through 720 wherein the increased soil carbon content comprises an increase in at least three of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001098] In embodiment 724 provided herein is the method of any one of embodiments 699 through 720 wherein the increased soil carbon content comprises an increase in at least four of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001099] In embodiment 725 provided herein is the method of any one of embodiments 699 through 720 wherein the increased soil carbon content comprises an increase in all of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001100] In embodiment 726 provided herein is the method of any one of embodiments 699 through 725 wherein the soil is in an area of at least 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 500,000, 1M, 5M, 10M, 50M, 100M, or 500M hectares and or not more than 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 500,000, 1M, 5M, 10M, 50M, 100M, 500M or 1B hectares, for example, at least 10 hectare, preferably at least 100 hectare, more preferably at least 1000, even more preferably at least 100,000 hectare, yet more preferably at least 1M hectare, still more preferably at least 10M hectare, or for example 10 to 1B, preferably 100 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B, yet more preferably 10M to 1B, still more preferably 100M to 1B hectare.

[001101] In embodiment 727 provided herein is the method of any one of embodiments 699 through 726 wherein the application is aerial application.

[001102] In embodiment 728 provided herein is the method of embodiment 727 wherein the aerial application is by unmanned aerial application device.

[001103] In embodiment 729 provided herein is the method of embodiment 727 or embodiment 728 wherein the aerial application comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 separate applications by the unmanned aerial application device, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001104] In embodiment 730 provided herein is the method of embodiment 729 wherein each of the separate applications is to a part of the area at least a portion of which is different from a part of the area of the other applications.

[001105] In embodiment 731 provided herein is the method of embodiment 729 or embodiment 730 wherein the application is by a plurality of unmanned aerial delivery devices.

[001106] In embodiment 732 provided herein is the method of embodiment 731 wherein the plurality comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 unmanned aerial delivery devices, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001107] In embodiment 733 provided herein is the method of any one of embodiments 708 through 732 wherein the carbon content of the soil comprises soil organic carbon (SOC).

[001108] In embodiment 734 provided herein is the method of anyone of embodiments 699 through 733 comprising reducing soil methane production.

[001109] In embodiment 735 provided herein is the method of any one of embodiments 699 through 734 further obtaining a carbon credit based at least in part on the increased soil carbon content.

[001110] In embodiment 736 provided herein is the method of embodiment 735 further comprising obtaining financial benefit from the plants.

[001111] In embodiment 737 provided herein is the method of embodiment 736 wherein the financial benefit comprises payment for the plants or parts of the plants.

[001112] In embodiment 738 provided herein is the method of embodiment 736 wherein the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants.

[001113] In embodiment 739 provided herein is the method of embodiment 738 wherein the plants are trees.

[001114] In embodiment 740 provided herein is the method of any one of embodiments 736 through 739 further comprising realizing a financial benefit from animals that eat the plants.

[001115] In embodiment 741 provided herein is the method of any one of embodiments 699 through 740 further comprising, as compared to without application of the composition, at least one of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001116] In embodiment 742 provided herein is the method of embodiment 741 wherein the method comprises decreasing water use to grow plants.

[001117] In embodiment 743 provided herein is the method of embodiment 741 or embodiment 742 wherein the method comprises decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers, to grow the plants.

[001118] In embodiment 744 provided herein is the method of any one of embodiments 741 through 743 wherein the method comprises increasing nutrient density of the plants.

[001119] In embodiment 745 provided herein is the method of any one of embodiments 741 through 744 further comprising realizing a financial benefit from decreased water use; decreased herbicide, pesticide, and/or fertilizer use; and/or increased nutrient density of the plants.

[001120] In embodiment 746 provided herein is the method of any one of embodiments 735 through 745 wherein the composition comprising microbes is supplied by a first entity and the

plants and soil are controlled by a second entity, different from the first, wherein the first and second entities share in one or more of (i) carbon credit; (ii) a financial benefit from the plants; (iii) a financial benefit from one or more animals that eat the plants; or (iii) a financial benefit from decreased water use; decreased herbicide, pesticide, and/or fertilizer use; and/or increased nutrient density of the plants.

[001121] In embodiment 747 provided herein is a method of increasing soil carbon content comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, and/or the plants, a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby increasing soil carbon content.

[001122] In embodiment 748 provided herein is the method of embodiment 747 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[001123] In embodiment 749 provided herein is the method of embodiment 747 or embodiment 748 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001124] In embodiment 750 provided herein is the method of embodiment 749 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001125] In embodiment 751 provided herein is the method of any embodiment 749 or embodiment 750 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least

80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001126] In embodiment 752 provided herein is the method of any one of embodiments 749 through 751 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001127] In embodiment 753 provided herein is the method of any one of embodiments 749 through 752 wherein the different microbes are *Streptomyces*.

[001128] In embodiment 754 provided herein is the method of any one of embodiments 747 through 753 wherein the composition comprising microbes comprises one or more composition of any one of embodiments 1 through 259.

[001129] In embodiment 755 provided herein is the method of embodiment 754 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 of different microbes of the composition of any one of embodiments 1 through 259, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001130] In embodiment 756 provided herein is the method of any one of embodiments 747 through 755 wherein a rate of increase in soil carbon content in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300% in the period of time.

[001131] In embodiment 757 provided herein is the method of any one of embodiments 747 through 756 wherein the increase in soil carbon content is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare/year and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare/year, wherein the soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least

15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare/year, compared to reference soil.

[001132] In embodiment 758 provided herein is the method of any one of embodiments 747 through 757 further comprising applying one or more soil amendments to the soil.

[001133] In embodiment 759 provided herein is the method of embodiment 758 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001134] In embodiment 760 provided herein is the method of embodiment 758 or embodiment 759 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001135] In embodiment 761 provided herein is the method of any one of embodiments 758 through 760 further comprising applying the composition in a second application.

[001136] In embodiment 762 provided herein is the method of embodiment 761 further comprising applying the composition in a third application.

[001137] In embodiment 763 provided herein is the method of embodiment 762 further comprising applying the composition in a fourth application.

[001138] In embodiment 764 provided herein is the method of any one of embodiments 747 through 763 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001139] In embodiment 765 provided herein is the method of any one of embodiments 747 through 764 wherein the increased soil carbon content comprises an increase in at least one of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001140] In embodiment 766 provided herein is the method of any one of embodiments 747 through 764 wherein the increased soil carbon content comprises an increase in at least two of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001141] In embodiment 767 provided herein is the method of any one of embodiments 747 through 764 wherein the increased soil carbon content comprises an increase in at least three of

(i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001142] In embodiment 768 provided herein is the method of any one of embodiments 747 through 764 wherein the increased soil carbon content comprises an increase in at least four of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001143] In embodiment 769 provided herein is the method of any one of embodiments 747 through 764 wherein the increased soil carbon content comprises an increase in all of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001144] In embodiment 770 provided herein is the method of any one of embodiments 747 through 769 wherein a protocol is established for treatment of the soil during and/or after the time period.

[001145] In embodiment 771 provided herein is the method of embodiment 770 wherein the protocol comprises reduced or eliminated tillage.

[001146] In embodiment 772 provided herein is the method of any one of embodiments 747 through 771 further comprising obtaining a carbon credit based on a net amount of carbon increase in the soil, or a value derived from the net amount of carbon increase.

[001147] In embodiment 773 provided herein is the method of embodiment 772 wherein the carbon credit is further based on a time period for carbon permanence.

[001148] In embodiment 774 provided herein is the method of embodiment 773 wherein the time period is less than 100 years.

[001149] In embodiment 775 provided herein is the method of any one of embodiments 747 through 774 wherein the soil carbon content is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 400, or 500%, for example at least 20, preferably at least 40, more preferably at least 60, even more preferably at least 70, yet more preferably at least 80, still more preferably at least 90%.

[001150] In embodiment 776 provided herein is the method of any one of embodiments 747 through 775 wherein the soil carbon content is increased by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare, wherein the soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3,

more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare.

[001151] In embodiment 777 provided herein is the method of any one of embodiments 747 through 776 wherein the soil is in an area of at least 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 500,000, 1M, 5M, 10M, 50M, 100M, or 500M hectares and or not more than 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, 100,000, 500,000, 1M, 5M, 10M, 50M, 100M, 500M or 1B hectares, for example, at least 10 hectare, preferably at least 100 hectare, more preferably at least 1000, even more preferably at least 100,000 hectare, yet more preferably at least 1M hectare, still more preferably at least 10M hectare, or for example 10 to 1B, preferably 100 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B, yet more preferably 10M to 1B, still more preferably 100M to 1B hectare.

[001152] In embodiment 778 provided herein is the method of any one of embodiments 747 through 777 wherein the application is aerial application.

[001153] In embodiment 779 provided herein is the method of embodiment 778 wherein the aerial application is by unmanned aerial application device.

[001154] In embodiment 780 provided herein is the method of embodiment 778 or embodiment 779 wherein the aerial application comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 separate applications by the unmanned aerial 467 delivery vehicle, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001155] In embodiment 781 provided herein is the method of embodiment 780 wherein each of the separate applications is to a part of the area at least a portion of which is different from a part of the area of the other applications.

[001156] In embodiment 782 provided herein is the method of any one of embodiments 778 through 781 wherein the application is by a plurality of unmanned aerial delivery devices.

[001157] In embodiment 783 provided herein is the method of embodiment 782 wherein the plurality comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 unmanned aerial delivery vehicles, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001158] In embodiment 784 provided herein is the method of any one of embodiments 747 through 783 wherein the carbon content of the soil comprises soil organic carbon (SOC).

[001159] In embodiment 785 provided herein is the method of any one of embodiments 747 through 784 further comprising reducing soil methane production.

[001160] In embodiment 786 provided herein is the method of any one of embodiments 747 through 785 further obtaining a carbon credit based at least in part on the increased soil carbon content.

[001161] In embodiment 787 provided herein is the method of embodiment 786 further comprising obtaining financial benefit from the plants.

[001162] In embodiment 788 provided herein is the method of embodiment 787 wherein the financial benefit comprises payment for the plants or parts of the plants.

[001163] In embodiment 789 provided herein is the method of embodiment 787 wherein the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants.

[001164] In embodiment 790 provided herein is the method of embodiment 789 wherein the plants are trees.

[001165] In embodiment 791 provided herein is the method of any one of embodiments 786 through 790 further comprising realizing a financial benefit from animals that eat the plants.

[001166] In embodiment 792 provided herein is the method of any one of embodiments 747 through 791 further comprising, as compared to before application of the composition, at least one of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001167] In embodiment 793 provided herein is the method of embodiment 792 wherein the method comprises decreasing water use to grow plants.

[001168] In embodiment 794 provided herein is the method of embodiment 792 or embodiment 793 wherein the method comprises decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers, to grow the plants.

[001169] In embodiment 795 provided herein is the method of any one of embodiments 792 through 794 wherein the method comprises increasing nutrient density of the plants.

[001170] In embodiment 796 provided herein is the method of any one of embodiments 792 through 795 further comprising realizing a financial benefit from decreased water use; decreased herbicide, pesticide, and/or fertilizer use; and/or increased nutrient density of the plants.

[001171] In embodiment 797 provided herein is the method of any one of embodiments 792 through 796 wherein the composition comprising microbes is supplied by a first entity and the

plants and soil are controlled by a second entity, different from the first, wherein the first and second entities share in one or more of (i) carbon credit; (ii) a financial benefit from the plants; (iii) a financial benefit from one or more animals that eat the plants; (iii) a financial benefit from decreased water use; decreased herbicide, pesticide, and/or fertilizer use; and/or increased nutrient density of the plants.

[001172] In embodiment 798 provided herein is the method of any one of embodiments 747 through 797 wherein the plants comprise grasses, trees, or commercial crops.

[001173] In embodiment 799 provided herein is the method of any one of embodiments 747 through 798 further comprising applying one or more minerals and/or one or more carbon sources to the soil.

[001174] In embodiment 800 provided herein is the method of embodiment 799 wherein the type and/or amount of the one or more minerals and/or one or more carbon sources is determined at least in part by one or more results of a first test on one or more samples comprising the growth medium and/or a component of a plant growing in the growth medium.

[001175] In embodiment 801 provided herein is the method of any one of embodiments 747 through 800 wherein the plants are not cannabis plants.

[001176] In embodiment 802 provided herein is the method of any one of embodiments 747 through 801 wherein the carbon content is organic carbon content.

[001177] In embodiment 803 provided herein is the method of any one of embodiments 747 through 802 wherein soil carbon content is increased to at least 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 12, or 15 ton/acre and/or not more than 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 12, 15, or 20 ton/acre, wherein carbon content is measured to a depth of 20 cm soil.

[001178] In embodiment 804 provided herein is a composition comprising soil and plants growing in the soil, wherein the plants comprise parts in the soil, *e.g.*, roots, and wherein the soil and plant parts comprise (i) a carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil; and (ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, or microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40.

[001179] In embodiment 805 provided herein is the composition of embodiment 804 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%,

yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001180] In embodiment 806 provided herein is the composition of embodiment 804 or embodiment 805 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001181] In embodiment 807 provided herein is the composition of any one of embodiments 804 through 806 wherein the different microbes are *Streptomyces*.

[001182] In embodiment 808 provided herein is the composition of any one of embodiments 804 through 807 wherein the composition comprises one or more of microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001183] In embodiment 809 provided herein is the composition of embodiment 808 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbe of microbes of the composition of any one of embodiments 1 through 259, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001184] In embodiment 810 provided herein is the composition of any one of embodiments 804 through 809 wherein the microbes of the composition comprise at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001185] In embodiment 811 provided herein is the composition of any one of embodiments 804 through 810 wherein the one or more microbes are disposed on or in a plant part comprising a root of the plant.

[001186] In embodiment 812 provided herein is the composition of embodiment 811 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or

10^{16} CFU per gram dry weight of the roots, *e.g.*, 10-10^{16}, preferably 100- 10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[001187] In embodiment 813 provided herein is the composition of any one of embodiments 804 through 812 further comprising mycorrhizal fungi.

[001188] In embodiment 814 provided herein is the composition of embodiment 813 wherein the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001189] In embodiment 815 provided herein is the composition of any one of embodiments 804 through 814 wherein beneficial microbes, other than the microbes of the composition comprising microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[001190] In embodiment 816 provided herein is the composition of any one of embodiments 804 through 815 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm^3 dry weight of soil.

[001191] In embodiment 817 provided herein is the composition of any one of embodiments 804 through 816 wherein the soil has an average water holding capacity (WHC) of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%.

[001192] In embodiment 818 provided herein is the composition of any one of embodiments 804 through 816 wherein the soil does not comprise a significant amount or concentration of synthetic herbicide, pesticide and/or fertilizer.

[001193] In embodiment 819 provided herein is the composition of any one of embodiments 804 through 818 wherein the soil comprises an area of at least 0.1, 0.5, 1, 5, 10, 50, 100, 500, 1000, 5000, 10,000, 50,000, or 100,000 square miles and/or not more than 0.5, 1, 5, 10, 50, 100,

500, 1000, 5000, 10,000 50,000, 100,000, 500,000, 1M, 2M, 10M, or 50M square miles, for example, 0.1 to 50M square miles, preferably 0.1 to 10M square miles, more preferably 1 to 10M square miles, yet more preferably 10 to 10M square miles, still more preferably 100 to 10M square miles, yet still more preferably 1000 to 1M square miles.

[001194] In embodiment 820 provided herein is a method of obtaining a carbon credit comprising allowing plants to grow in an area of soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing conditions for the plants to grow in the soil; (iii) determining the increase in soil carbon content over the period of time in the area of soil; and (iv) based at least in part on (iii), obtaining a carbon credit.

[001195] In embodiment 821 provided herein is the method of embodiment 820 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001196] In embodiment 822 provided herein is the method of embodiment 820 or embodiment 821 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001197] In embodiment 823 provided herein is the method of any one of embodiments 820 through 822 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001198] In embodiment 824 provided herein is the method of any one of embodiments 820 through 823 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001199] In embodiment 825 provided herein is the method of any one of embodiments 820 through 824 wherein the different microbes are *Streptomyces*.

[001200] In embodiment 826 provided herein is the method of any one of embodiments 820 through 825 wherein the composition comprises one or more of microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001201] In embodiment 827 provided herein is the method of embodiment 826 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001202] In embodiment 828 provided herein is a method of reducing soil methane production comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing conditions for the plants to grow in the soil; thereby increasing decreasing soil methane production.

[001203] In embodiment 829 provided herein is a method of transferring atmospheric carbon to soil in which plants grow comprising (i) applying a composition comprising a plurality of different microbes to the soil, plants, plant parts, and/or seed of the plants, wherein the composition is applied over an area of at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares; and (ii) providing conditions suitable for growth of the plants for a period of time, thereby transferring atmospheric carbon to the soil to increase carbon content of the soil.

[001204] In embodiment 830 provided herein is a method of reducing an overall carbon footprint for raising domesticated animals comprising feeding the animals, and/or allowing the animals to feed on, plants or parts of plants, wherein the plants have been or are growing in soil to which has been applied a composition comprising a plurality of different microbes, wherein the composition (i) increases carbon dioxide transfer from atmosphere to soil thus increasing carbon content of the soil, compared to without the composition; (ii) increases biomass of the

plants in a given area, compared to without the composition, so that carbon produced per unit biomass of plants is decreased; and (iii) increases nutrient density of the plants, compared to without the composition, so that less biomass of plants is used to produce a given amount of increase in economically valuable attribute of the domesticated animals or a combination thereof, thus decreasing overall carbon footprint for raising the domesticated animals.

[001205] In embodiment 831 provided herein is the method of embodiment 830 wherein the economically valuable attribute comprises weight of the animal.

[001206] In embodiment 832 provided herein is the method of embodiment 830 wherein the economically valuable attribute comprises nutritional value of a material supplied by the animal.

[001207] In embodiment 833 provided herein is the method of embodiment 830 wherein the economically valuable attribute comprises an amount of a product produced by the animal.

[001208] In embodiment 834 provided herein is the method of embodiment 830 wherein the economically valuable attribute comprises increased nutrient density of a material or material from the animal that is consumed by humans.

[001209] In embodiment 835 provided herein is the method of embodiment 834 wherein the material comprises meat, organs, milk, or eggs.

[001210] In embodiment 836 provided herein is the method of embodiment 834 or embodiment 835 wherein the increased nutrient density comprises increased protein content, increased mineral content, increased vitamin content, or a combination thereof.

[001211] In embodiment 837 provided herein is the method of any one of embodiments 834 through 836 wherein the increased nutrient density comprises increased mineral content, wherein mineral content comprises calcium, magnesium, iron, or a combination thereof.

[001212] In embodiment 838 provided herein is the method of any one of embodiments 830 through 837 wherein the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses.

[001213] In embodiment 839 provided herein is the method of any one of embodiments 830 through 837 wherein the animals are cattle.

[001214] In embodiment 840 provided herein is the method of any one of embodiments 830 through 839 wherein the plants or parts of plants that the cattle are feed or feed on, for at least part of their growth, comprise grasses.

[001215] In embodiment 841 provided herein is the method of embodiment 840 wherein the grasses comprise pasture or range grasses.

[001216] In embodiment 842 provided herein is the method of any one of embodiments 830 through 839 wherein the plants or parts of plants that the cattle are feed or feed on, for at least part of their growth comprise grain.

[001217] In embodiment 843 provided herein is the method of any one of embodiments 830 through 842 wherein at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99%, or 100%, of the plants or plant parts which the animals are fed and/or allowed to feed on are plants or plant parts from plants have been or are growing in soil to which has been applied the composition comprising a plurality of microbes.

[001218] In embodiment 844 provided herein is the method of any one of embodiments 830 through 843 wherein methane production from the soil in which the plants have been grown or are growing is reduced.

[001219] In embodiment 845 provided herein is the method of any one of embodiments 830 through 844 wherein the carbon footprint is reduced at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, for example, at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 50%, yet more preferably at least 80%, still more preferably at least 90%.

[001220] In embodiment 846 provided herein is the method of any one of embodiments 830 through 845 wherein the raising of the domesticated animals is overall carbon negative.

[001221] In embodiment 847 provided herein is the method of any one of embodiments 830 through 846 further comprising realizing an additional economic benefit compared to without use of the composition.

[001222] In embodiment 848 provided herein is the method of embodiment 847 wherein the economic benefit results from one or more of increasing carbon content of soil, decreasing carbon produced per unit biomass of plants, decreasing biomass consumed per unit economically valuable attribute of the animals, or a combination thereof.

[001223] In embodiment 849 provided herein is the method of embodiment 847 or embodiment 848 wherein the economic benefit comprises a carbon credit based on carbon avoided, carbon sequestered, or a combination thereof.

[001224] In embodiment 850 provided herein is the method of embodiment 847 wherein the economic benefit comprises greater price per animal.

[001225] In embodiment 851 provided herein is the method of any one of embodiments 830 through 850 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001226] In embodiment 852 provided herein is the method of any one of embodiments 830 through 851 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001227] In embodiment 853 provided herein is the method of any one of embodiments 830 through 852 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001228] In embodiment 854 provided herein is the method of any one of embodiments 830 through 853 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001229] In embodiment 855 provided herein is the method of any one of embodiments 830 through 854 wherein the different microbes are *Streptomyces*.

[001230] In embodiment 856 provided herein is the method of any one of embodiments 830 through 855 wherein the composition comprises one or more of microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001231] In embodiment 857 provided herein is the method of embodiment 856 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001232] In embodiment 858 provided herein is a method of obtaining carbon credit or other economic benefit comprising (i) determining an increase in carbon content of soil in which plants grow after (a) applying a composition comprising a plurality of different microbes to the soil, plants, plant parts, and/or seed of the plants, wherein the composition is applied over an area of at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more

than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares, and (b) providing conditions suitable for growth of the plants for a period of time, thereby transferring atmospheric carbon to the soil to increase carbon content of the soil; and (ii) obtaining the carbon credit and/or other economic benefit based, at least in part, on the increase in carbon content determined in (i).

[001233] In embodiment 859 provided herein is the method of embodiment 858 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1.5 year.

[001234] In embodiment 860 provided herein is the method of embodiment 858 or embodiment 859 wherein the period of time is 1 year.

[001235] In embodiment 861 provided herein is the method of any one of embodiments 858 through 860 wherein the composition is applied to soil.

[001236] In embodiment 862 provided herein is the method of any one of embodiments 858 through 861 wherein soil carbon content is increased at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare/year and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare/year, wherein the soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare/year.

[001237] In embodiment 863 provided herein is the method of any one of embodiments 858 through 862 wherein soil carbon content is determined at the end of the period of time and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, or 50 additional times after the period of time.

[001238] In embodiment 864 provided herein is the method of embodiment 863 wherein the period of time is 4 months to 1.5 year, for example, 1 year, and the additional times start one year after the period of time and continue yearly thereafter.

[001239] In embodiment 865 provided herein is the method of embodiment 864 wherein the increase in soil carbon content after the period of time is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001240] In embodiment 866 provided herein is the method of embodiment 865 wherein the increase in soil carbon content after the additional times is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001241] In embodiment 867 provided herein is the method of any one of embodiments 858 through 866 wherein soil carbon content is measured to a depth of at least 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, or 90 cm and/or not more than 15, 20, 25, 30, 40, 50, 60, 70, 80, 90 or 100 cm, for example, 10-100 cm, preferably 10-80 cm, more preferably 15-75 cm, even more preferably 15-60 cm, yet more preferably 15-50 cm, still more preferably 15-30 cm; in some cases 20 cm.

[001242] In embodiment 868 provided herein is the method of any one of embodiments 858 through 867 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001243] In embodiment 869 provided herein is the method of any one of embodiments 858 through 868 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001244] In embodiment 870 provided herein is the method of any one of embodiments 858 through 869 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001245] In embodiment 871 provided herein is the method of any one of embodiments 858 through 870 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or

100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001246] In embodiment 872 provided herein is the method of any one of embodiments 858 through 871 wherein the different microbes are *Streptomyces*.

[001247] In embodiment 873 provided herein is the method of any one of embodiments 858 through 872 wherein the composition comprises one or more of microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001248] In embodiment 874 provided herein is the method of embodiment 873 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 of different microbes of the composition of any one of embodiments 1 through 259, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001249] In embodiment 875 provided herein is the method of any one of embodiments 858 through 874 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001250] In embodiment 876 provided herein is the method of any one of embodiments 858 through 875 wherein the increased soil carbon content comprises an increase in at least one of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001251] In embodiment 877 provided herein is the method of any one of embodiments 858 through 875 wherein the increased soil carbon content comprises an increase in at least two of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001252] In embodiment 878 provided herein is the method of any one of embodiments 858 through 875 wherein the increased soil carbon content comprises an increase in at least three of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-

associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001253] In embodiment 879 provided herein is the method of any one of embodiments 858 through 875 wherein the increased soil carbon content comprises an increase in at least four of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001254] In embodiment 880 provided herein is the method of any one of embodiments 858 through 875 wherein the increased soil carbon content comprises an increase in at least five of (i) total soil carbon, (ii) total soil organic carbon, (iii) total soil inorganic carbon, (iv) mineral-associated organic matter (MAOM), (v) particulate organic matter (POM), (vi) microbial necromass, (vii) soil aggregates, and/or (viii) root biomass, or a component of root biomass.

[001255] In embodiment 881 provided herein is the method of any one of embodiments 858 through 880 wherein the composition is a delayed release composition comprising a plurality of particles, wherein the composition comprises one or more microbes, and wherein the plurality of particles comprises a first population of particles wherein each particle of the first population comprises one or more first components configured to confine at least a portion of the microbes to the particles, and wherein the one or more first components are such that the one or more first components lose sufficient integrity upon exposure to one or more environmental triggers that at least a portion of the confined microbes are released from the particles.

[001256] In embodiment 882 provided herein is the method of embodiment 881 wherein the first components are configured to confine at least 50, 60, 70, 80, 90, 95, 96, 97, 98, or 99% of the microbes, for example at least 60%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%.

[001257] In embodiment 883 provided herein is the method of embodiment 881 or embodiment 882 wherein the one or more first components form a shell wherein the microbes are confined within, and/or embedded in, and/or associated with a surface of, the shell.

[001258] In embodiment 884 provided herein is the method of any one of embodiments 881 through 883 wherein the one or more first components form a matrix in which the microbes are embedded or otherwise associated.

[001259] In embodiment 885 provided herein is the method of any one of embodiments 881 through 884 wherein the one or more first components form a plurality of lamellae, wherein the particles are confined between, and/or embedded in, and/or associate with a surface of, the lamellae.

[001260] In embodiment 886 provided herein is the method of any one of embodiments 881 through 885 wherein the environmental trigger comprises water, temperature, electromagnetic radiation, or a combination thereof.

[001261] In embodiment 887 provided herein is the method of any one of embodiments 881 through 886 wherein the environmental trigger is water.

[001262] In embodiment 888 provided herein is the method of any one of embodiments 881 through 887 wherein one or more first components and/or structure of the particles are such that exposure to the trigger causes sufficient loss of integrity that at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, or 99% and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 98, 99, or 100% of the microbes are released. and for a suitable duration.

[001263] In embodiment 889 provided herein is the method of embodiment 888 wherein 30-100% of the microbes are released.

[001264] In embodiment 890 provided herein is the method of embodiment 888 wherein 50-100% of the microbes are released.

[001265] In embodiment 891 provided herein is the method of embodiment 888 wherein 80-100% of the microbes are released.

[001266] In embodiment 892 provided herein is the method of embodiment 888 wherein 90-100% of the microbes are released.

[001267] In embodiment 893 provided herein is the method of embodiment 888 wherein 5-80% of the microbes are released.

[001268] In embodiment 894 provided herein is the method of embodiment 888 wherein 5-60% of the microbes are released.

[001269] In embodiment 895 provided herein is the method of embodiment 888 wherein 5-40% of the microbes are released.

[001270] In embodiment 896 provided herein is the method of embodiment 888 wherein 10-40% of the microbes are released.

[001271] In embodiment 897 provided herein is the method of embodiment 888 wherein 5-30% of the microbes are released.

[001272] In embodiment 898 provided herein is the method of embodiment 888 wherein 10-30% of the microbes are released.

[001273] In embodiment 899 provided herein is the method of embodiment 888 wherein 5-25% of the microbes are released.

[001274] In embodiment 900 provided herein is the method of embodiment 888 wherein 10-25% of the microbes are released.

[001275] In embodiment 901 provided herein is the method of any one of embodiments 881 through 900 further comprising a second population of particles wherein each particle of the second population comprises one or more second components configured to confine at least a portion of the microbes to the particles, and wherein the one or more second components are such that the one or more second components withstand exposure to the one or more environmental triggers that cause the first components of the first population to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the second population.

[001276] In embodiment 902 provided herein is the method of embodiment 901 further comprising a third population of particles wherein each particle of the third population comprises one or more third components configured to confine at least a portion of the microbes to the particles, and wherein the one or more third components are such that the one or more third components withstand exposure to the one or more environmental triggers that cause the first and second components of the first population and second populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the second population.

[001277] In embodiment 903 provided herein is the method of embodiment 902 further comprising a fourth population of particles wherein each particle of the fourth population comprises one or more fourth components configured to confine at least a portion of the microbes to the particles, and wherein the one or more fourth components are such that the one or more fourth components withstand exposure to the one or more environmental triggers that cause the first, second and third components of the first population, second and third populations to lose integrity, but that lose sufficient integrity upon further exposure to the one or more environmental triggers that at least a portion of the confined microbes are released from the particles of the third population.

[001278] In embodiment 904 provided herein is the method of any one of embodiments 858 through 903 wherein the application comprises aerial application.

[001279] In embodiment 905 provided herein is the method of embodiment 904 wherein the aerial application is by unmanned aerial application device.

[001280] In embodiment 906 provided herein is the method of embodiment 904 or embodiment 905 wherein the aerial application comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 separate applications by the unmanned aerial delivery vehicle, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001281] In embodiment 907 provided herein is the method of embodiment 906 wherein each of the separate applications is to a part of the area at least a portion of which is different from a part of the area of the other applications.

[001282] In embodiment 908 provided herein is the method of any one of embodiments 904 through 907 wherein the application is by a plurality of unmanned aerial delivery devices.

[001283] In embodiment 909 provided herein is the method of embodiment 908 wherein the plurality comprises at least 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, 70, 100, 200, 500, or 1000 unmanned aerial delivery vehicles, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 50, yet more preferably at least 100, still more preferably at least 500.

[001284] In embodiment 910 provided herein is the method of any one of embodiments 858 through 909 wherein the carbon content of the soil comprises soil organic carbon (SOC).

[001285] In embodiment 911 provided herein is the method of any one of embodiments 858 through 910 further comprising reducing soil methane production.

[001286] In embodiment 912 provided herein is the method of any one of embodiments 858 through 911 further comprising obtaining financial benefit from the plants.

[001287] In embodiment 913 provided herein is the method of embodiment 912 wherein the financial benefit comprises payment for the plants or parts of the plants.

[001288] In embodiment 914 provided herein is the method of embodiment 912 wherein the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants.

[001289] In embodiment 915 provided herein is the method of embodiment 914 wherein the plants are trees.

[001290] In embodiment 916 provided herein is the method of any one of embodiments 858 through 915 further comprising realizing a financial benefit from animals that eat the plants.

[001291] In embodiment 917 provided herein is the method of any one of embodiments 858 through 916 further comprising at least one of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001292] In embodiment 918 provided herein is the method of any one of embodiments 858 through 916 further comprising at least two of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding

capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001293] In embodiment 919 provided herein is the method of any one of embodiments 858 through 916 further comprising at least three of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001294] In embodiment 920 provided herein is the method of any one of embodiments 858 through 916 further comprising at least four of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001295] In embodiment 921 provided herein is the method of any one of embodiments 858 through 916 further comprising at least five of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001296] In embodiment 922 provided herein is the method of any one of embodiments 858 through 916 further comprising at least six of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides,

pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001297] In embodiment 923 provided herein is the method of any one of embodiments 858 through 916 further comprising all of (i) moving density of soil toward optimum for growing the plants; (ii) decreasing water use to grow plants; (iii) increasing water holding capacity of the soil; (iv) increasing nutrient uptake of the plants from the soil; (v) increasing nutrient content of the plants; (vi) increasing concentration of beneficial microbes in the soil and/or on the plants or plant parts; or (vii) decreasing use of one or more of herbicides, pesticides, or fertilizers, for example, synthetic herbicides, pesticides, or fertilizers to grow the plants.

[001298] In embodiment 924 provided herein is a system comprising (i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more second entities; (ii) the second entity, or a plurality of second entities, that (a) owns, controls, or otherwise has rights to land in an area of land on which plants grow and (b) uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities, wherein the area of land at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares; (iii) an agreement between the first and second entities or between the first entity and each of the plurality of second entities that delineates an apportionment of the economic benefits between the first and second entities or between the first entity and each of the plurality of second entities; and (iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines an apportionment between the first and second entities or between the first entity and each of the plurality of second entities and communicates information comprising the apportionment to the first and/or second entities.

[001299] In embodiment 925 provided herein is the system of embodiment 924 wherein the second entity comprises a governmental entity.

[001300] In embodiment 926 provided herein is the system of embodiment 924 wherein the second entity comprises a private entity.

[001301] In embodiment 927 provided herein is the system of any one of embodiments 924 through 926 comprising a plurality of second entities wherein the plurality of second entities

comprises at least 5, 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, or 50,000 entities and/or not more than 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, 50,000, or 100,000 entities.

[001302] In embodiment 928 provided herein is the system of embodiment 927 wherein at least 10, 20, 30, 50, 70, 80, 90, 95, or 99% of the second entities are private farming entities.

[001303] In embodiment 929 provided herein is the system of any one of embodiments 924 through 928 wherein the economic benefit comprises a carbon credit based, at least in part, on an increase of carbon in the soil.

[001304] In embodiment 930 provided herein is the system of any one of embodiments 924 through 928 wherein the economic benefit comprises a financial benefit attributable to the plants.

[001305] In embodiment 931 provided herein is the system of embodiment 930 wherein the financial benefit comprises payment for the plants or parts of the plants.

[001306] In embodiment 932 provided herein is the system of embodiment 931 wherein the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants.

[001307] In embodiment 933 provided herein is the system of any one of embodiments 924 through 932 wherein the plants are trees.

[001308] In embodiment 934 provided herein is the system of embodiment 933 wherein the financial benefit comprises a financial benefit realized from animals that eat the plants.

[001309] In embodiment 935 provided herein is the system of any one of embodiments 924 through 934 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001310] In embodiment 936 provided herein is the system of any one of embodiments 924 through 935 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001311] In embodiment 937 provided herein is the method of any one of embodiments 924 through 936 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least

80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001312] In embodiment 938 provided herein is the system of any one of embodiments 924 through 937 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001313] In embodiment 939 provided herein is the system of any one of embodiments 924 through 938 wherein the different microbes are *Streptomyces*.

[001314] In embodiment 940 provided herein is the system of any one of embodiments 924 through 939 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001315] In embodiment 941 provided herein is the system of embodiment 940 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001316] In embodiment 942 provided herein is a method of obtaining an economic benefit from land on which plants are grown, wherein the land comprises at least 10, 100, 1000, 10,000, 100,000, 1M, or 10M, hectacres, comprising (i) obtaining and using one or more compositions comprising a microbial consortium, wherein (a) the one or more compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity, or plurality of second entities that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity; (b) the second entity or plurality of second entities uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities; (ii) determining a quantity of the one or more economic benefits; and (iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities.

[001317] In embodiment 943 provided herein is the method of embodiment 942 wherein the apportioning is done according to an agreement or agreements between the first and second entities or between the first entity and each of the plurality of second entities.

[001318] In embodiment 944 provided herein is the method of embodiment 943 wherein the apportioning is done by a processor that receives information regarding the one or more economic benefits and the agreement, processes the information to determine a quantitative value or values for economic benefits for apportionment between the first and second entities, or between the first entity and each of the plurality of second entities, and communicates the quantitative value or values to the first and/or second entities.

[001319] In embodiment 945 provided herein is the method of any one of embodiments 942 through 944 wherein the second entity comprises a governmental entity.

[001320] In embodiment 946 provided herein is the method of any one of embodiments 942 through 944 wherein the second entity comprises a private entity.

[001321] In embodiment 947 provided herein is the method of any one of embodiments 942 through 946 comprising a plurality of second entities wherein the plurality of second entities comprises at least 5, 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, or 50,000 entities and/or not more than 10, 20, 50, 70, 100, 150, 200, 250, 500, 1000, 5000, 10,000, 50,000, or 100,000 entities.

[001322] In embodiment 948 provided herein is the method of embodiment 947 wherein at least 10, 20, 30, 50, 70, 80, 90, 95, or 99% of the second entities are private farming entities.

[001323] In embodiment 949 provided herein is the method of any one of embodiments 942 through 948 wherein the economic benefit comprises a carbon credit based, at least in part, on an increase of carbon in the soil.

[001324] In embodiment 950 provided herein is the method of any one of embodiments 942 through 948 wherein the economic benefit comprises a financial benefit attributable to the plants.

[001325] In embodiment 951 provided herein is the method of embodiment 950 wherein the financial benefit comprises payment for the plants or parts of the plants.

[001326] In embodiment 952 provided herein is the method of embodiment 951 wherein the financial benefit comprises obtaining a further carbon credit for carbon stored in the plants.

[001327] In embodiment 953 provided herein is the method of any one of embodiments 942 through 952 wherein the plants are trees.

[001328] In embodiment 954 provided herein is the method of any one of embodiments 942 through 952 wherein the financial benefit comprises a financial benefit realized from animals that eat the plants.

[001329] In embodiment 955 provided herein is the method of any one of embodiments 942 through 954 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001330] In embodiment 956 provided herein is the method of any one of embodiments 942 through 955 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001331] In embodiment 957 provided herein is the method of any one of embodiments 942 through 956 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001332] In embodiment 958 provided herein is the method of any one of embodiments 942 through 957 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001333] In embodiment 959 provided herein is the method of any one of embodiments 942 through 958 wherein the different microbes are *Streptomyces*.

[001334] In embodiment 960 provided herein is the method of any one of embodiments 942 through 959 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001335] In embodiment 961 provided herein is the method of embodiment 960 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95,

preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001336] In embodiment 962 provided herein is a method of reducing water use for growth and/or maintenance of plants in soil comprising allowing the plants to grow and/or be maintained in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil, the plants, a first application of a composition comprising a plurality of different microbes or a derivative thereof; and (ii) providing suitable conditions for the plants to grow and/or be maintained in the soil for a period of time; thereby decreasing the amount of water necessary to produce a given amount of biomass from the plants and/or to maintain the plants in a desired state, compared to the amount of water necessary to produce the biomass and/or maintain the plants in a desired state for reference soil and plants, for the period of time.

[001337] In embodiment 963 provided herein is the method of embodiment 962 wherein the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 5-22, yet more preferably 6-20, still more preferably 6-18 months.

[001338] In embodiment 964 provided herein is the method of embodiment 963 wherein the period of time is 6-18 months.

[001339] In embodiment 965 provided herein is the method of any one of embodiments 962 through 964 wherein water use is decreased by at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90%, for example at least 10, preferably at least 15, more preferably at least 20, even more preferably at least 30, yet more preferably at least 35, still more preferably at least 40%.

[001340] In embodiment 966 provided herein is the method of any one of embodiments 962 through 965 comprising increasing water holding capacity (WHC) of the soil compared to reference in the period of time.

[001341] In embodiment 967 provided herein is the method of embodiment 966 wherein WHC is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001342] In embodiment 968 provided herein is the method of embodiment 966 or embodiment 967 wherein WHC is increased to at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%,

preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55% in the period of time.

[001343] In embodiment 969 provided herein is the method of any one of embodiments 962 through 968 comprising increasing water retention of the soil compared to reference in the period of time.

[001344] In embodiment 970 provided herein is the method of embodiment 969 wherein water retention is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001345] In embodiment 971 provided herein is the method of any one of embodiments 962 through 970 comprising modulating a density of the soil, so that the density moves from outside an optimal range for growth and/or maintenance of the plants to within an optimal range for growth and/or maintenance of the plants, in the period of time.

[001346] In embodiment 972 provided herein is the method of embodiment 971 wherein the density is modulated to at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm^3 dry weight of soil.

[001347] In embodiment 973 provided herein is the method of any one of embodiments 962 through 972 comprising increasing carbon content of the soil compared to reference in the period of time.

[001348] In embodiment 974 provided herein is the method of embodiment 973 wherein carbon content in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300% in the period of time compared to reference.

[001349] In embodiment 975 provided herein is the method of embodiment 973 or embodiment 974 wherein the increase in soil carbon content is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare, wherein the soil carbon

content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare, compared to reference.

[001350] In embodiment 976 provided herein is the method of any one of embodiments 973 through 975 wherein the increase in soil carbon content after the period of time is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001351] In embodiment 977 provided herein is the method of embodiment 975 or embodiment 976 wherein soil carbon content is measured to a depth of at least 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, or 90 cm and/or not more than 15, 20, 25, 30, 40, 50, 60, 70, 80, 90 or 100 cm, for example, 10-100 cm, preferably 10-80 cm, more preferably 15-75 cm, even more preferably 15-60 cm, yet more preferably 15-50 cm, still more preferably 15-30 cm; in some cases 20 cm.

[001352] In embodiment 978 provided herein is the method of any one of embodiments 962 through 977 further comprising increasing a density of beneficial microbes in the soil in the period of time.

[001353] In embodiment 979 provided herein is the method of embodiment 978 wherein the density of beneficial microbes is increased at least 20, 50, 100, 200, 500, 1,000, or 10,000% and/or not more than 50, 100, 200, 500, 1,000, 10,000, or 100,000%, for example, at least 100%, preferably at least 500%, more preferably at least 1000%.

[001354] In embodiment 980 provided herein is the method of any one of embodiments 962 through 979 comprising increasing a nutrient density of the plants compared to reference.

[001355] In embodiment 981 provided herein is the method of any one of embodiments 962 through 980 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001356] In embodiment 982 provided herein is the method of any one of embodiments 962 through 981 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even

more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001357] In embodiment 983 provided herein is the method of any one of embodiments 962 through 982 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001358] In embodiment 984 provided herein is the method of any one of embodiments 962 through 983 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001359] In embodiment 985 provided herein is the method of any one of embodiments 962 through 984 wherein the different microbes are *Streptomyces*.

[001360] In embodiment 986 provided herein is the method of any one of embodiments 962 through 985 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001361] In embodiment 987 provided herein is the method of embodiment 986 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbe of the composition of any one of embodiments 1 through 259, or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001362] In embodiment 988 provided herein is the method of any one of embodiments 962 through 987 further comprising applying one or more soil amendments to the soil.

[001363] In embodiment 989 provided herein is the method of embodiment 988 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001364] In embodiment 990 provided herein is the method of embodiment 988 or embodiment 989 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001365] In embodiment 991 provided herein is the method of any one of embodiments 962 through 990 further comprising applying the composition in a second application.

[001366] In embodiment 992 provided herein is the method of embodiment 991 further comprising applying the composition in a third application.

[001367] In embodiment 993 provided herein is the method of embodiment 992 further comprising applying the composition in a fourth application.

[001368] In embodiment 994 provided herein is the method of any one of embodiments 962 through 993 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001369] In embodiment 995 provided herein is a method of increasing water holding capacity of soil in which plants are grown comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes or a derivative thereof; and (ii) providing suitable conditions for the plants to grow in the soil for a period of time; thereby increasing the water holding capacity of the soil, compared to reference soil and plants.

[001370] In embodiment 996 provided herein is the method of embodiment 995 wherein the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 5-22, yet more preferably 6-20, still more preferably 6-18 months.

[001371] In embodiment 997 provided herein is the method of embodiment 996 wherein the period of time is 6-18 months.

[001372] In embodiment 998 provided herein is the method of any one of embodiments 995 through 997 wherein WHC is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001373] In embodiment 999 provided herein is the method of any one of embodiments 995 through 998 wherein WHC is increased to at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-

70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55% in the period of time.

[001374] In embodiment 1000 provided herein is the method of any one of embodiments 995 through 999 comprising increasing water retention of the soil compared to reference in the period of time.

[001375] In embodiment 1001 provided herein is the method of embodiment 1000 wherein water retention is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001376] In embodiment 1002 provided herein is the method of any one of embodiments 995 through 1001 comprising modulating a density of the soil, so that the density moves from outside an optimal range for growth and/or maintenance of the plants to within an optimal range for growth and/or maintenance of the plants, in the period of time.

[001377] In embodiment 1003 provided herein is the method of embodiment 1002 wherein the density is modulated to at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[001378] In embodiment 1004 provided herein is the method of any one of embodiments 995 through 1003 comprising increasing carbon content of the soil compared to reference in the period of time.

[001379] In embodiment 1005 provided herein is the method of embodiment 1004 wherein carbon content in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300% in the period of time compared to reference.

[001380] In embodiment 1006 provided herein is the method of embodiment 1004 or embodiment 1005 wherein the increase in soil carbon content is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare, wherein the

soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare, compared to reference.

[001381] In embodiment 1007 provided herein is the method of any one of embodiments 1004 through 1006 wherein the increase in soil carbon content after the period of time is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001382] In embodiment 1008 provided herein is the method of embodiment 1006 or embodiment 1007 wherein soil carbon content is measured to a depth of at least 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, or 90 cm and/or not more than 15, 20, 25, 30, 40, 50, 60, 70, 80, 90 or 100 cm, for example, 10-100 cm, preferably 10-80 cm, more preferably 15-75 cm, even more preferably 15-60 cm, yet more preferably 15-50 cm, still more preferably 15-30 cm; in some cases 20 cm.

[001383] In embodiment 1009 provided herein is the method of any one of embodiments 995 through 1008 further comprising increasing a density of beneficial microbes in the soil in the period of time.

[001384] In embodiment 1010 provided herein is the method of embodiment 1009 wherein the density of beneficial microbes is increased at least 20, 50, 100, 200, 500, 1,000, or 10,000% and/or not more than 50, 100, 200, 500, 1,000, 10,000, or 100,000%, for example, at least 100%, preferably at least 500%, more preferably at least 1000%.

[001385] In embodiment 1011 provided herein is the method of any one of embodiments 995 through 1010 comprising increasing a nutrient density of the plants compared to reference.

[001386] In embodiment 1012 provided herein is the method of any one of embodiments 995 through 1011 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001387] In embodiment 1013 provided herein is the method of any one of embodiments 995 through 1012 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even

more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001388] In embodiment 1014 provided herein is the method of any one of embodiments 995 through 1013 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001389] In embodiment 1015 provided herein is the method of any one of embodiments 995 through 1014 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001390] In embodiment 1016 provided herein is the method of any one of embodiments 995 through 1015 wherein the different microbes are *Streptomyces*.

[001391] In embodiment 1017 provided herein is the method of any one of embodiments 995 through 1016 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001392] In embodiment 1018 provided herein is the method of embodiment 1017 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001393] In embodiment 1019 provided herein is the method of any one of embodiments 995 through 1018 further comprising applying one or more soil amendments to the soil.

[001394] In embodiment 1020 provided herein is the method of embodiment 1019 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001395] In embodiment 1021 provided herein is the method of embodiment 1019 or embodiment 1019 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001396] In embodiment 1022 provided herein is the method of any one of embodiments 995 through 1021 further comprising applying the composition in a second application.

[001397] In embodiment 1023 provided herein is the method of embodiment 1022 further comprising applying the composition in a third application.

[001398] In embodiment 1024 provided herein is the method of embodiment 1023 further comprising applying the composition in a fourth application.

[001399] In embodiment 1025 provided herein is the method of any one of embodiments 995 through 1024 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001400] In embodiment 1026 provided herein is a composition comprising soil in which plants are growing or have grown wherein the soil comprises (i) a water holding capacity of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%; and (ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, or 100, and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40, or preferably 1-150, more preferably 1-100, even more preferably 1-70, yet more preferably 1-50.

[001401] In embodiment 1027 provided herein is the composition of embodiment 1026 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001402] In embodiment 1028 provided herein is the composition of embodiment 1026 or embodiment 1027 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001403] In embodiment 1029 provided herein is the composition of any one of embodiments 1026 through 1028 wherein the different microbes are *Streptomyces*.

[001404] In embodiment 1030 provided herein is the composition of any one of embodiments 1026 through 1029 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001405] In embodiment 1031 provided herein is the composition of embodiment 1030 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001406] In embodiment 1032 provided herein is the composition of any one of embodiments 1026 through 1031 wherein the microbes of the composition comprise at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001407] In embodiment 1033 provided herein is the composition of any one of embodiments 1026 through 1032 wherein the one or more microbes are disposed on or in a plant part comprising a root of the plant.

[001408] In embodiment 1034 provided herein is the composition of any one of embodiments 1026 through 1033 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the roots, *e.g.*, 10-10^{16}, preferably 100- 10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[001409] In embodiment 1035 provided herein is the composition of any one of embodiments 1026 through 1034 further comprising mycorrhizal fungi.

[001410] In embodiment 1036 provided herein is the composition of embodiment 1035 wherein the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at

least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001411] In embodiment 1037 provided herein is the composition of any one of embodiments 1026 through 1036 wherein beneficial microbes other than the microbes of the composition comprising microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[001412] In embodiment 1038 provided herein is the composition of any one of embodiments 1026 through 1037 wherein the soil has an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil.

[001413] In embodiment 1039 provided herein is the composition of any one of embodiments 1026 through 1038 wherein the soil has a carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001414] In embodiment 1040 provided herein is a composition comprising soil in which plants are growing or have grown wherein the soil comprises (i) an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil; and (ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, or 100, and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40 or preferably 1-150, more preferably 1-100, even more preferably 1-70, yet more preferably 1-50.

[001415] In embodiment 1041 provided herein is the composition of embodiment 1040 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at

least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001416] In embodiment 1042 provided herein is the composition of embodiment 1040 or embodiment 1041 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001417] In embodiment 1043 provided herein is the composition of any one of embodiments 1040 through 1042 wherein the different microbes are *Streptomyces*.

[001418] In embodiment 1044 provided herein is the composition of any one of embodiments 1040 through 1043 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001419] In embodiment 1045 provided herein is the composition of embodiment 1044 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001420] In embodiment 1046 provided herein is the composition of any one of embodiments 1040 through 1045 wherein the microbes of the composition comprise at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil, for example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001421] In embodiment 1047 provided herein is the composition of any one of embodiments 1040 through 1046 wherein the one or more microbes are disposed on or in a plant part comprising a root of the plant.

[001422] In embodiment 1048 provided herein is the composition of any one of embodiments 1040 through 1047 wherein the one or more microbes are present in a total amount of at least 10, 100, 200, 500, 700, 1000, 1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} and/or not more than 100, 200, 500, 700, 1000,

1500, 2000, 3000, 5000, 7000, 10,000, 20,000, 50,000, 100,000, 500,000, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU per gram dry weight of the roots, *e.g.*, 10-10^{16}, preferably 100- 10^{16}, more preferably 100 to 10^{16}, even more preferably 100,000 to 10^{16}, yet more preferably 10^6 to 10^{16}, yet still more preferably 10^7 to 10^{16}, and even yet more preferably 10^{12} to 10^{16}.

[001423] In embodiment 1049 provided herein is the composition of any one of embodiments 1040 through 1048 further comprising mycorrhizal fungi.

[001424] In embodiment 1050 provided herein is the composition of embodiment 1049 wherein the mycorrhizal fungi make up at least 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of a total number of microbes in the composition comprising soil or example, at least 1%, preferably at least 2%, even more preferably at least 5%, yet more preferably at least 10%, still more preferably at least 20%, even still more preferably at least 40%.

[001425] In embodiment 1051 provided herein is the composition of any one of embodiments 1040 through 1050 wherein beneficial microbes other than the microbes of the composition comprising microbes, are present at a concentration of at least 1M, 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, or 100M and/or not more than 2M, 5M, 10M, 15M, 20M, 25M, 30M, 35M, 40M, 50M, 70M, 80M, 100M, or 1B per gram soil dry weight, for example 1M to 1B, preferably 10M to 1B, more preferably 20M to 1B, even more preferably 20M to 100M, yet more preferably 20M to 80M, still more preferably 30M to 80M per gram soil dry weight.

[001426] In embodiment 1052 provided herein is the composition of any one of embodiments 1040 through 1051 wherein the soil has a carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001427] In embodiment 1053 provided herein is a method of modulating, *e.g.*, improving, one or more characteristics of soil in which plants grow and/or are maintained, comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by (i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby modulating, *e.g.*, improving the one or more characteristics compared to reference soil and plants.

[001428] In embodiment 1054 provided herein is the method of embodiment 1053 wherein the one or more characteristics comprises density of the soil, wherein density of the soil is improved.

[001429] In embodiment 1055 provided herein is the method of embodiment 1054 wherein soil density before the first application is outside of an optimal range.

[001430] In embodiment 1056 provided herein is the method of embodiment 1053 or embodiment 1054 wherein soil density after the period of time is within an optimal range.

[001431] In embodiment 1057 provided herein is the method of any one of embodiments 1053 through 1056 wherein the density is modulated to at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm^3 dry weight of soil.

[001432] In embodiment 1058 provided herein is the method of any one of embodiments 1053 through 1057 wherein the one or more characteristics comprises water holding capacity (WHC) of the soil, wherein WHC of the soil is increased.

[001433] In embodiment 1059 provided herein is the method of embodiment 1058 wherein WHC is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001434] In embodiment 1060 provided herein is the method of embodiment 1058 or embodiment 1059 wherein WHC is increased to at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55% in the period of time.

[001435] In embodiment 1061 provided herein is the method of any one of embodiments 1053 through 1060 wherein the one or more characteristics comprises water retention of the soil, wherein the water retention of the soil is increased.

[001436] In embodiment 1062 provided herein is the method of embodiment 1061 wherein water retention is increased at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 400, 500% compared to reference, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, yet more preferably at least 25, still more preferably at least 30% in the period of time.

[001437] In embodiment 1063 provided herein is the method of any one of embodiments 1053 through 1062 wherein the one or more characteristics comprise a density of beneficial microbes in the soil, wherein the density is increased.

[001438] In embodiment 1064 provided herein is the method of embodiment 1063 wherein the density of beneficial microbes is increased at least 20, 50, 100, 200, 500, 1,000, or 10,000%

and/or not more than 50, 100, 200, 500, 1,000, 10,000, or 100,000%, for example, at least 100%, preferably at least 500%, more preferably at least 1000%.

[001439] In embodiment 1065 provided herein is the method of any one of embodiments 1053 through 1064 wherein the one or more characteristics comprises bioavailability of one or more plant nutrients in the soil, wherein bioavailability of the one or more nutrients is increased.

[001440] In embodiment 1066 provided herein is the method of any one of embodiments 1053 through 1065 wherein the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months.

[001441] In embodiment 1067 provided herein is the method of any one of embodiments 1053 through 963 further comprising increasing carbon content of the soil compared to reference in the period of time.

[001442] In embodiment 1068 provided herein is the method of embodiment 1067 wherein carbon content in soil in which the plants are grown is increased at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, or 400% and/or not more than 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 250, 300, 350, 400 or 500% for example at least 20%, preferably at least 40%, more preferably at least 60%, even more preferably at least 80%, still more preferably at least 100%, or, for example 10-500%, preferably 20-500%, more preferably 40-400%, even more preferably 40-350%, yet more preferably 50-300%, still more preferably 60-300% in the period of time compared to reference.

[001443] In embodiment 1069 provided herein is the method of embodiment 1067 or embodiment 1068 wherein the increase in soil carbon content is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, or 30 metric ton carbon/hectare and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 23, 25, 27, 30, 35, 40, 45, or 50 metric ton carbon/hectare, wherein the soil carbon content is measured to a depth of 20 cm soil, for example, at least 1, preferably at least 3, more preferably at least 5, even more preferably at least 10, yet more preferably at least 15, still more preferably at least 20, or for example 1-50, preferably 3-40, more preferably 5-40, even more preferably 10-40, yet more preferably 10-35, still more preferably 10-30 metric ton carbon/hectare, compared to reference.

[001444] In embodiment 1070 provided herein is the method of any one of embodiments 1067 through 1069 wherein the increase in soil carbon content after the period of time is at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil.

[001445] In embodiment 1071 provided herein is the method of any one of embodiments 1067 through 1070 wherein soil carbon content is measured to a depth of at least 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, or 90 cm and/or not more than 15, 20, 25, 30, 40, 50, 60, 70, 80, 90 or 100 cm, for example, 10-100 cm, preferably 10-80 cm, more preferably 15-75 cm, even more preferably 15-60 cm, yet more preferably 15-50 cm, still more preferably 15-30 cm; in some cases 20 cm.

[001446] In embodiment 1072 provided herein is the method of any one of embodiments 1053 through 1071 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001447] In embodiment 1073 provided herein is the method of any one of embodiments 1053 through 1072 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001448] In embodiment 1074 provided herein is the method of any one of embodiments 1053 through 1073 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001449] In embodiment 1075 provided herein is the method of any one of embodiments 1053 through 1074 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001450] In embodiment 1076 provided herein is the method of any one of embodiments 1053 through 1075 wherein the different microbes are *Streptomyces*.

[001451] In embodiment 1077 provided herein is the method of embodiment 1076 wherein the composition comprises one or more one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001452] In embodiment 1078 provided herein is the method of embodiment 1077 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001453] In embodiment 1079 provided herein is the method of any one of embodiments 1053 through 1078 further comprising applying the composition in a second application.

[001454] In embodiment 1080 provided herein is the method of embodiment 1079 further comprising applying the composition in a third application.

[001455] In embodiment 1081 provided herein is the method of embodiment 1080 further comprising applying the composition in a fourth application.

[001456] In embodiment 1082 provided herein is the method of any one of embodiments 1053 through 1081 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001457] In embodiment 1083 provided herein is a method of regenerating vegetation in a soil that has been partially or completely depleted of one or more types of vegetation and/or has reduced capacity to grow and/or maintain new vegetation, comprising (i) applying to the soil, plants growing or to be grown in the soil, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for a period of time.

[001458] In embodiment 1084 provided herein is the method of embodiment 1083 further comprising placing seeds, seedlings, or other plant propagules of the plants on or in the soil.

[001459] In embodiment 1085 provided herein is the method of embodiment 1083 or embodiment 1084 wherein the vegetation comprises one or more grasses and has been partially or completely depleted by overgrazing.

[001460] In embodiment 1086 provided herein is the method of embodiment 1083 or embodiment 1084 wherein the vegetation comprises one or more trees and has been partially or completely depleted by tree clearing.

[001461] In embodiment 1087 provided herein is the method of embodiment 1083 or embodiment 1084 wherein the vegetation comprises one or more commercial crops and has been partially or completely depleted by poor management practice.

[001462] In embodiment 1088 provided herein is the method of any one of embodiments 1083 through 1087 wherein vegetation is regenerated in and on at least 10, 1000, 10,000, 100,000, or 1M acres.

[001463] In embodiment 1089 provided herein is the method of any one of embodiments 1083 through 1088 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001464] In embodiment 1090 provided herein is the method of any one of embodiments 1083 through 1089 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001465] In embodiment 1091 provided herein is the method of any one of embodiments 1083 through 1090 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001466] In embodiment 1092 provided herein is the method of any one of embodiments 1083 through 1091 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001467] In embodiment 1093 provided herein is the method of any one of embodiments 1083 through 1092 wherein the different microbes are *Streptomyces*.

[001468] In embodiment 1094 provided herein is the method of embodiment 1093 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001469] In embodiment 1095 provided herein is the method of embodiment 1094 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001470] In embodiment 1096 provided herein is the method of any one of embodiments 1083 through 1095 further comprising applying the composition in a second application.

[001471] In embodiment 1097 provided herein is the method of embodiment 1096 further comprising applying the composition in a third application.

[001472] In embodiment 1098 provided herein is the method of embodiment 1097 further comprising applying the composition in a fourth application.

[001473] In embodiment 1099 provided herein is the method of any one of embodiments 1094 through 1098 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001474] In embodiment 1100 provided herein is a method of repairing damaged or degraded soil comprising (i) applying to the soil a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for plants to grow in the soil for the period of time.

[001475] In embodiment 1101 provided herein is the method of embodiment 1100 further comprising placing seeds, seedlings, or other plant propagules of the plants on or in the soil.

[001476] In embodiment 1102 provided herein is the method of embodiment 1100 or embodiment 1101 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001477] In embodiment 1103 provided herein is the method of any one of embodiments 1100 through 1102 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or

100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001478] In embodiment 1104 provided herein is the method of any one of embodiments 1100 through 1103 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001479] In embodiment 1105 provided herein is the method of any one of embodiments 1100 through 1104 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001480] In embodiment 1106 provided herein is the method of any one of embodiments 1100 through 1105 wherein the different microbes are *Streptomyces*.

[001481] In embodiment 1107 provided herein is the method of embodiment 1106 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001482] In embodiment 1108 provided herein is the method of embodiment 1107 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001483] In embodiment 1109 provided herein is the method of any one of embodiments 1100 through 1108 further comprising applying the composition in a second application.

[001484] In embodiment 1110 provided herein is the method of embodiment 1109 further comprising applying the composition in a third application.

[001485] In embodiment 1111 provided herein is the method of embodiment 1110 further comprising applying the composition in a fourth application.

[001486] In embodiment 1112 provided herein is the method of any one of embodiments 1100 through 1111 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001487] In embodiment 1113 provided herein is a method for decreasing or eliminating flooding on land that has experienced or is likely to experience flooding, wherein soil of the land has grown, is growing, or will grow plants, comprising (i) applying to the soil, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and (ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby decreasing or eliminating flooding on the land.

[001488] In embodiment 1114 provided herein is the method of embodiment 1113 wherein the period of time is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, or 24 months and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 30, or 36 months, for example 1-36, preferably 2-30, more preferably 4-24, even more preferably 4-12, yet more preferably 6-20, still more preferably 6-18 months.

[001489] In embodiment 1115 provided herein is the method of embodiment 1113 or embodiment 1114 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001490] In embodiment 1116 provided herein is the method of any one of embodiments 1113 through 1115 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001491] In embodiment 1117 provided herein is the method of any one of embodiments 1113 through 1116 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001492] In embodiment 1118 provided herein is the method of any one of embodiments 1113 through 1117 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001493] In embodiment 1119 provided herein is the method of any one of embodiments 1113 through 1118 wherein the different microbes are *Streptomyces*.

[001494] In embodiment 1120 provided herein is the method of embodiment 1119 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001495] In embodiment 1121 provided herein is the method of embodiment 1120 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001496] In embodiment 1122 provided herein is the method of any one of embodiments 1113 through 1121 further comprising applying the composition in a second application.

[001497] In embodiment 1123 provided herein is the method of embodiment 1122 further comprising applying the composition in a third application.

[001498] In embodiment 1124 provided herein is the method of embodiment 1123 further comprising applying the composition in a fourth application.

[001499] In embodiment 1125 provided herein is the method of any one of embodiments 1113 through 1124 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001500] In embodiment 1126 provided herein is a method for increasing density of one or more nutrients in plants or plant parts, e.g., plants or plant parts to be consumed by animals, comprising (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/or the plants; and (ii) providing conditions

suitable for growth of the plants for a period of time, e.g., a period of time sufficient for the plants or plant parts to be suitable for consumption by the animals; thereby increasing density of the one or nutrients in the plants or plant parts compared to reference plants or plant parts.

[001501] In embodiment 1127 provided herein is the method of embodiment 1126 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[001502] In embodiment 1128 provided herein is the method of embodiment 1126 or embodiment 1127 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001503] In embodiment 1129 provided herein is the method of any one of embodiments 1126 through 1128 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001504] In embodiment 1130 provided herein is the method of any one of embodiments 1126 through 1129 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001505] In embodiment 1131 provided herein is the method of any one of embodiments 1126 through 1130 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001506] In embodiment 1132 provided herein is the method of any one of embodiments 1126 through 1131 wherein the different microbes are *Streptomyces*.

[001507] In embodiment 1133 provided herein is the method of any one of embodiments 1126 through 1132 wherein the composition comprising a plurality of microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001508] In embodiment 1134 provided herein is the method of embodiment 1133 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001509] In embodiment 1135 provided herein is the method of any one of embodiments 1126 through 1134 further comprising applying one or more soil amendments to the soil.

[001510] In embodiment 1136 provided herein is the method of embodiment 1135 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001511] In embodiment 1137 provided herein is the method of embodiment 1135 or embodiment 1136 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001512] In embodiment 1138 provided herein is the method of any one of embodiments 1135 through 1137 further comprising applying the composition in a second application.

[001513] In embodiment 1139 provided herein is the method of embodiment 1138 further comprising applying the composition in a third application.

[001514] In embodiment 1140 provided herein is the method of embodiment 1139 further comprising applying the composition in a fourth application.

[001515] In embodiment 1141 provided herein is the method of any one of embodiments 1126 through 1140 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001516] In embodiment 1142 provided herein is the method of any one of embodiments 1126 through 1141 wherein the one or more nutrients is increased in density by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[001517] In embodiment 1143 provided herein is the method of any one of embodiments 1126 through 1142 wherein the animals comprise humans or domesticated animals.

[001518] In embodiment 1144 provided herein is the method of embodiment 1143 wherein the animals comprise humans.

[001519] In embodiment 1145 provided herein is the method of embodiment 1143 wherein the animals comprise domesticated animals.

[001520] In embodiment 1146 provided herein is the method of embodiment 1145 wherein the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses.

[001521] In embodiment 1147 provided herein is the method of embodiment 1145 wherein the animals are cattle.

[001522] In embodiment 1148 provided herein is the method of any one of embodiments 1126 through 1147 wherein the increased nutrient density comprises increased protein density, increased mineral density, increased vitamin density, or a combination thereof.

[001523] In embodiment 1149 provided herein is the method of embodiment 1148 wherein the increased nutrient density comprises increased protein density.

[001524] In embodiment 1150 provided herein is the method of embodiment 1148 wherein the increased nutrient density comprises increased vitamin density.

[001525] In embodiment 1151 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin A density.

[001526] In embodiment 1152 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_1 (thiamine) density.

[001527] In embodiment 1153 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_2 (riboflavin) density.

[001528] In embodiment 1154 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_3 (niacin, nicotinic acid) density.

[001529] In embodiment 1155 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_5 (pantothenic acid) density.

[001530] In embodiment 1156 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_6 (pyridoxal, pyridoxine, or pyridoxamine) density.

[001531] In embodiment 1157 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_7 (biotin) density.

[001532] In embodiment 1158 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_9 (folic acid) density.

[001533] In embodiment 1159 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin B_{12} density.

[001534] In embodiment 1160 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin C density.

[001535] In embodiment 1161 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased choline density.

[001536] In embodiment 1162 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin D density.

[001537] In embodiment 1163 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin E density.

[001538] In embodiment 1164 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin K1 density.

[001539] In embodiment 1165 provided herein is the method of embodiment 1150 wherein the increased vitamin density comprises increased vitamin K2 density.

[001540] In embodiment 1166 provided herein is the method of embodiment 1148 wherein the increased nutrient density comprises increased mineral density.

[001541] In embodiment 1167 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased calcium density.

[001542] In embodiment 1168 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased magnesium density.

[001543] In embodiment 1169 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased sodium density.

[001544] In embodiment 1170 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased potassium density.

[001545] In embodiment 1171 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased iron density.

[001546] In embodiment 1172 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased copper density.

[001547] In embodiment 1173 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased manganese density.

[001548] In embodiment 1174 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased zinc density.

[001549] In embodiment 1175 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased iodine density.

[001550] In embodiment 1176 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased chromium density.

[001551] In embodiment 1177 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased molybdenum density.

[001552] In embodiment 1178 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased phosphorus density.

[001553] In embodiment 1179 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased molybdenum density.

[001554] In embodiment 1180 provided herein is the method of embodiment 1166 wherein the increased mineral density comprises increased selenium density.

[001555] In embodiment 1181 provided herein is the method of any one of embodiments 1126 through 1180 further comprising increasing biomass of the plants or plant parts.

[001556] In embodiment 1182 provided herein is a method for increasing uptake of one or more plant nutrients by plants grown in soil comprising (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/or the plants; and (ii) providing conditions suitable for growth of the plants and proliferation and/or other actions of the microbes for a suitable duration for plant nutrient uptake to increase; whereby plant nutrient uptake by the plants is increased.

[001557] In embodiment 1183 provided herein is the method of embodiment 1182 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[001558] In embodiment 1184 provided herein is the method of embodiment 1182 or embodiment 1183 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45,

50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001559] In embodiment 1185 provided herein is the method of any one of embodiments 1182 through 1184 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001560] In embodiment 1186 provided herein is the method of any one of embodiments 1182 through 1185 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001561] In embodiment 1187 provided herein is the method of any one of embodiments 1182 through 1186 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001562] In embodiment 1188 provided herein is the method of any one of embodiments 1182 through 1187 wherein the different microbes are *Streptomyces*.

[001563] In embodiment 1189 provided herein is the method of any one of embodiments 1182 through 1188 wherein the composition comprising microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001564] In embodiment 1190 provided herein is the method of embodiment 1189 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95,

preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001565] In embodiment 1191 provided herein is the method of any one of embodiments 1182 through 1190 further comprising applying one or more soil amendments to the soil.

[001566] In embodiment 1192 provided herein is the method of embodiment 1191 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001567] In embodiment 1193 provided herein is the method of embodiment 1191 or embodiment 1192 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001568] In embodiment 1194 provided herein is the method of any one of embodiments 1191 through 1193 further comprising applying the composition in a second application.

[001569] In embodiment 1195 provided herein is the method of embodiment 1194 further comprising applying the composition in a third application.

[001570] In embodiment 1196 provided herein is the method of embodiment 1195 further comprising applying the composition in a fourth application.

[001571] In embodiment 1197 provided herein is the method of any one of embodiments 1182 through 1196 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001572] In embodiment 1198 provided herein is the method of any one of embodiments 1182 through 1197 wherein uptake of the one or more plant nutrients by the plants is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[001573] In embodiment 1199 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is nitrogen, phosphorus, potassium, or a combination thereof.

[001574] In embodiment 1200 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is nitrogen.

[001575] In embodiment 1201 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is phosphorus.

[001576] In embodiment 1202 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is potassium.

[001577] In embodiment 1203 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is calcium (Ca), magnesium (Mg), sulfur (S), sodium (Na), iron (Fe), manganese (Mn), zinc (Zn), copper (Cu), nickel (Ni), boron (B), molybdenum (Mo), silicon (Si), cobalt (Co), selenium (Se), or chloride (Cl), or a combination thereof.

[001578] In embodiment 1204 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is calcium (Ca).

[001579] In embodiment 1205 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is magnesium (Mg).

[001580] In embodiment 1206 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is sulfur (S).

[001581] In embodiment 1207 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is sodium (Na).

[001582] In embodiment 1208 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is iron (Fe).

[001583] In embodiment 1209 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is manganese (Mn).

[001584] In embodiment 1210 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is zinc (Zn).

[001585] In embodiment 1211 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is copper (Cu).

[001586] In embodiment 1212 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is nickel (Ni).

[001587] In embodiment 1213 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is boron (B).

[001588] In embodiment 1214 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is molybdenum (Mo).

[001589] In embodiment 1215 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is silicon (Si).

[001590] In embodiment 1216 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is cobalt (Co).

[001591] In embodiment 1217 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is selenium (Se).

[001592] In embodiment 1218 provided herein is the method of any one of embodiments 1182 through 1198 wherein the nutrient is chloride (Cl).

[001593] In embodiment 1219 provided herein is the method of any one of embodiments 1182 through 1218 further comprising reducing or eliminating toxin uptake by the plants.

[001594] In embodiment 1220 provided herein is the method of any one of embodiments 1182 through 1219 further comprising reducing water use by the plants.

[001595] In embodiment 1221 provided herein is the method of any one of embodiments 1182 through 1220 further comprising increasing water holding capacity of the soil.

[001596] In embodiment 1222 provided herein is the method of any one of embodiments 1182 through 1221 further comprising increasing uptake of atmospheric carbon by the plants and conversion of atmospheric carbon to soil carbon.

[001597] In embodiment 1223 provided herein is a method for converting one or more plant nutrients in soil in which plants are grown from non-bioavailable to bioavailable form (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/or the plants; and (ii) providing conditions suitable for growth of the plants and proliferation and/or other actions of the microbes for a duration sufficient for the one or more plant nutrients in the soil to convert from non-bioavailable to bioavailable form; whereby the one or more plant nutrients are converted from non-bioavailable to bioavailable form.

[001598] In embodiment 1224 provided herein is the method of embodiment 1223 wherein the period of time is at least 1, 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 years and or not more than 2, 3, or 4 weeks or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 years, for example 1 month to 20 years, preferably 1 month to 10 years, more preferably 3 months to 5 years, even more preferably 3 months to 2 years, yet more preferably 3 months to one year, still more preferably 4 months to 1 year.

[001599] In embodiment 1225 provided herein is the method of embodiment 1223 or embodiment 1224 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001600] In embodiment 1226 provided herein is the method of any one of embodiments 1223 through 1225 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001601] In embodiment 1227 provided herein is the method of any one of embodiments 1223 through 1226 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001602] In embodiment 1228 provided herein is the method of any one of embodiments 1223 through 1227 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001603] In embodiment 1229 provided herein is the method of any one of embodiments 1223 through 1228 wherein the different microbes are *Streptomyces*.

[001604] In embodiment 1230 provided herein is the method of any one of embodiments 1223 through 1229 wherein the composition comprising microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001605] In embodiment 1231 provided herein is the method of embodiment 1230 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 microbe different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001606] In embodiment 1232 provided herein is the method of any one of embodiments 1223 through 1231 further comprising applying one or more soil amendments.

[001607] In embodiment 1233 provided herein is the method of embodiment 1232 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001608] In embodiment 1234 provided herein is the method of embodiment 1232 or embodiment 1233 wherein a content of the soil amendments is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001609] In embodiment 1235 provided herein is the method of any one of embodiments 1232 through 1234 further comprising second amendment.

[001610] In embodiment 1236 provided herein is the method of embodiment 1235 further comprising a third amendment.

[001611] In embodiment 1237 provided herein is the method of embodiment 1236 further comprising a fourth amendment.

[001612] In embodiment 1238 provided herein is the method of any one of embodiments 1223 through 1237 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001613] In embodiment 1239 provided herein is the method of any one of embodiments 1223 through 1238 wherein bioavailable form of the plant nutrient is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[001614] In embodiment 1240 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is nitrogen, phosphorus, potassium, or a combination thereof.

[001615] In embodiment 1241 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is nitrogen.

[001616] In embodiment 1242 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is phosphorus.

[001617] In embodiment 1243 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is potassium.

[001618] In embodiment 1244 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is calcium (Ca), magnesium (Mg), sulfur (S), sodium (Na), iron (Fe), manganese (Mn), zinc (Zn), copper (Cu), nickel (Ni), boron (B), molybdenum (Mo), silicon (Si), cobalt (Co), selenium (Se), or chloride (Cl), or a combination thereof.

[001619] In embodiment 1245 provided herein is the method of any one of embodiments 1223 through 1239 wherein the plant nutrient is calcium (Ca).

[001620] In embodiment 1246 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is magnesium (Mg).

[001621] In embodiment 1247 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is sulfur (S).

[001622] In embodiment 1248 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is sodium (Na).

[001623] In embodiment 1249 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is iron (Fe).

[001624] In embodiment 1250 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is manganese (Mn).

[001625] In embodiment 1251 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is zinc (Zn).

[001626] In embodiment 1252 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is copper (Cu).

[001627] In embodiment 1253 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is nickel (Ni).

[001628] In embodiment 1254 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is boron (B).

[001629] In embodiment 1255 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is molybdenum (Mo).

[001630] In embodiment 1256 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is silicon (Si).

[001631] In embodiment 1257 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is cobalt (Co).

[001632] In embodiment 1258 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is selenium (Se).

[001633] In embodiment 1259 provided herein is the method of any one of embodiments 1223 through 1239 wherein the nutrient is chloride (Cl).

[001634] In embodiment 1260 provided herein is the method of any one of embodiments 1223 through 1259 further comprising reducing or eliminating toxin uptake by the plants.

[001635] In embodiment 1261 provided herein is the method of any one of embodiments 1223 through 1260 further comprising reducing water use by the plants.

[001636] In embodiment 1262 provided herein is the method of any one of embodiments 1223 through 1261 further comprising increasing water holding capacity of the soil.

[001637] In embodiment 1263 provided herein is the method of any one of embodiments 1223 through 1262 further comprising increasing uptake of atmospheric carbon by the plants and conversion of atmospheric carbon to soil carbon.

[001638] In embodiment 1264 provided herein is a composition comprising a plant comprising (i) an above-ground portion; and (ii) a below-ground portion, wherein the below-ground portion comprises roots of the plant and soil associated with the roots, wherein the below-ground portion comprises (a) one or more microbes heterologous to the soil and/or plant; and (b) a concentration of bio-available nutrient that is greater than reference plant and soil.

[001639] In embodiment 1265 provided herein is the composition of embodiment 1264 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100, that are heterologous to the plant.

[001640] In embodiment 1266 provided herein is the composition of embodiment 1264 or embodiment 1265 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001641] In embodiment 1267 provided herein is the composition of any one of embodiments 1264 through 1266 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001642] In embodiment 1268 provided herein is the composition of any one of embodiments 1264 through 1267 wherein the different microbes are *Streptomyces*.

[001643] In embodiment 1269 provided herein is the composition of any one of embodiments 1264 through 1268 comprising one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001644] In embodiment 1270 provided herein is the composition of embodiment 1269 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001645] In embodiment 1271 provided herein is the composition of any one of embodiments 1264 through 1270 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001646] In embodiment 1272 provided herein is a composition comprising a plant, *e.g.*, wherein the plant or part of the plant is for animal consumption, and soil in which the plant is growing, wherein (i) the soil and/or roots of the plant in the soil comprise one or more microbes heterologous to the soil and/or plant; and (ii) the plant or plant part comprises a density of one or more nutrients, e.g., one or more nutrients for the animal, that is greater than reference plant or plant part.

[001647] In embodiment 1273 provided herein is the composition of embodiment 1272 comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100 that are heterologous to the plant and/or soil.

[001648] In embodiment 1274 provided herein is the composition of embodiment 1272 or embodiment 1273 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least

80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001649] In embodiment 1275 provided herein is the composition of any one of embodiments 1272 through 1274 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001650] In embodiment 1276 provided herein is the composition of any one of embodiments 1272 through 1275 wherein the different microbes are *Streptomyces*.

[001651] In embodiment 1277 provided herein is the composition of any one of embodiments 1272 through 1276 wherein the composition comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001652] In embodiment 1278 provided herein is the composition of embodiment 1277 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001653] In embodiment 1279 provided herein is the composition of any one of embodiments 1272 through 1278 wherein nutrient density of the one or more animal nutrients is increased by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least 50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[001654] In embodiment 1280 provided herein is the composition of any one of embodiments 1272 through 1279 wherein the one or more nutrients is increased in density by at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, or 400% and/or not more than 0, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, 300, 350, 400, 500, 700, or 1000%, for example, at least 5, preferably at least 10, more preferably at least 15, even more preferably at least 20, still more preferably at least 30, yet more preferably at least

50%, or for example at least 5-1000, preferably 5-700, more preferably 10-1000, even more preferably 10-700, still more preferably 10-500, yet more preferably 20-500%.

[001655] In embodiment 1281 provided herein is the composition of any one of embodiments 1272 through 1280 through wherein the animals comprise humans or domesticated animals.

[001656] In embodiment 1282 provided herein is the composition of embodiment 1281 wherein the animals comprise humans.

[001657] In embodiment 1283 provided herein is the composition of embodiment 1281 wherein the animals comprise domesticated animals.

[001658] In embodiment 1284 provided herein is the composition of embodiment 1283 wherein the animals comprise cattle, bison, goats, sheep, dairy cows, fowl (such as chickens, geese, and ducks), pigs, or horses.

[001659] In embodiment 1285 provided herein is the composition of embodiment 1283 wherein the animals are cattle.

[001660] In embodiment 1286 provided herein is the composition of any one of embodiments 1272 through 1285 wherein the increased nutrient density comprises increased protein density, increased mineral density, increased vitamin density, or a combination thereof.

[001661] In embodiment 1287 provided herein is the composition of embodiment 1286 wherein the increased nutrient density comprises increased protein density.

[001662] In embodiment 1288 provided herein is the composition of embodiment 1286 wherein the increased nutrient density comprises increased vitamin density.

[001663] In embodiment 1289 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin A density.

[001664] In embodiment 1290 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_1 (thiamine) density.

[001665] In embodiment 1291 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_2 (riboflavin) density.

[001666] In embodiment 1292 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_3 (niacin, nicotinic acid) density.

[001667] In embodiment 1293 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_5 (pantothenic acid) density.

[001668] In embodiment 1294 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_6 (pyridoxal, pyridoxine, or pyridoxamine) density.

[001669] In embodiment 1295 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_7 (biotin) density.

[001670] In embodiment 1296 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_9 (folic acid) density.

[001671] In embodiment 1297 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin B_{12} density.

[001672] In embodiment 1298 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin C density.

[001673] In embodiment 1299 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased choline density.

[001674] In embodiment 1300 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin D density.

[001675] In embodiment 1301 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin E density.

[001676] In embodiment 1302 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin K1 density.

[001677] In embodiment 1303 provided herein is the composition of embodiment 1288 wherein the increased vitamin density comprises increased vitamin K2 density.

[001678] In embodiment 1304 provided herein is the composition of embodiment 1286 wherein the increased nutrient density comprises increased mineral density.

[001679] In embodiment 1305 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased calcium density.

[001680] In embodiment 1306 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased magnesium density.

[001681] In embodiment 1307 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased sodium density.

[001682] In embodiment 1308 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased potassium density.

[001683] In embodiment 1309 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased iron density.

[001684] In embodiment 1310 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased copper density.

[001685] In embodiment 1311 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased manganese density.

[001686] In embodiment 1312 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased zinc density.

[001687] In embodiment 1313 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased iodine density.

[001688] In embodiment 1314 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased chromium density.

[001689] In embodiment 1315 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased molybdenum density.

[001690] In embodiment 1316 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased phosphorus density.

[001691] In embodiment 1317 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased molybdenum density.

[001692] In embodiment 1318 provided herein is the composition of embodiment 1304 wherein the increased mineral density comprises increased selenium density.

[001693] In embodiment 1319 provided herein is a method to convert non-organic agricultural practice to organic agricultural practice comprising (i) applying a composition comprising a plurality of microbes to plants, and/or to soil in which the plants grow or will grow, in a first application at a first time, wherein up to the first time the plants and soil were subject to non-organic farming practice; (ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time, wherein after the period of time the non-organic agricultural practice has been converted to an organic agricultural practice.

[001694] In embodiment 1320 provided herein is the method of embodiment 1319 wherein the period of time is not more than 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, or 5 years, for example not more than 5, preferably not more than 4, more preferably not more than 3.5, even more preferably not more than 3, yet more preferably not more than 2.5, still more preferably not more than 2, yet still more preferably not more than 1.5 years.

[001695] In embodiment 1321 provided herein is the method of embodiment 1319 or embodiment 1320 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001696] In embodiment 1322 provided herein is the method of any one of embodiments 1319 through 1321 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even

more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001697] In embodiment 1323 provided herein is the method of any one of embodiments 1318 through 1322 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001698] In embodiment 1324 provided herein is the method of any one of embodiments 1318 through 1323 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001699] In embodiment 1325 provided herein is the method of any one of embodiments 1318 through 1324 wherein the different microbes are *Streptomyces*.

[001700] In embodiment 1326 provided herein is the method of any one of embodiments 1318 through 1325 wherein the composition comprising a plurality of microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001701] In embodiment 1327 provided herein is the method of embodiment 1326 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001702] In embodiment 1328 provided herein is the method of any one of embodiments 1318 through 1327 further comprising applying one or more soil amendments to the soil.

[001703] In embodiment 1329 provided herein is the method of embodiment 1328 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001704] In embodiment 1330 provided herein is the method of embodiment 1328 or embodiment 1329 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001705] In embodiment 1331 provided herein is the method of any one of embodiments 1318 through 1330 wherein the plants are not cannabis plants.

[001706] In embodiment 1332 provided herein is the method of any one of embodiments 1318 through 1331 further comprising applying the composition in a second application.

[001707] In embodiment 1333 provided herein is the method of embodiment 1332 further comprising applying the composition in a third application.

[001708] In embodiment 1334 provided herein is the method of any one of embodiments 1318 through 1333 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001709] In embodiment 1335 provided herein is the method of any one of embodiments 1318 through 1334 further comprising reducing water use to grow the plants after the period of time.

[001710] In embodiment 1336 provided herein is the method of any one of embodiments 1318 through 1335 further comprising increasing nutrient density of the plants or plant parts after the period of time.

[001711] In embodiment 1337 provided herein is a method for reducing concentration of a toxin in a soil, reducing uptake of the toxin by plants growing in the soil, and/or reducing a concentration of the toxin in the plants or plant parts, comprising (i) applying a composition comprising a plurality of microbes to the plants, or parts thereof, and/or to the soil, in a first application; (ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time, wherein after the period of time concentration of the toxin in the soil, uptake of the toxin by plants growing in the soil, and/or concentration of the toxin in the plants or plant parts is reduced compared to before the first application.

[001712] In embodiment 1338 provided herein is the method of embodiment 1337 wherein the period of time is at least 1, 2, 5, 7, 10, 12, 18, or 24 months and/or 2, 5, 7, 10, 12, 18, 24, or 36 months for example 1-36 months, preferably 2-25 months, more preferably 5-18 months.

[001713] In embodiment 1339 provided herein is the method of embodiment 1337 or embodiment 1338 wherein the reduction is at least 5, 10, 20, 30, 40, 50, 60, 70, 80, 85, 90, 92, 95, 96, 97, 98, or 99%, or 100%.

[001714] In embodiment 1340 provided herein is the method of any one of embodiments 1337 through 1339 wherein the toxin comprises a synthetic pesticide, such as a synthetic pesticide, or impurity thereof, or an herbicide, such as a synthetic herbicide, or impurity thereof.

[001715] In embodiment 1341 provided herein is the method of any one of embodiments 1337 through 1339 wherein the toxin comprises a hydrocarbon.

[001716] In embodiment 1342 provided herein is the method of embodiment 1341 wherein the hydrocarbon comprises a petroleum hydrocarbon.

[001717] In embodiment 1343 provided herein is the method of embodiment 1341 wherein the hydrocarbon comprises a polynuclear aromatic hydrocarbon.

[001718] In embodiment 1344 provided herein is the method of any one of embodiments 1337 through 1339 wherein the toxin comprises a heavy metal.

[001719] In embodiment 1345 provided herein is the method of embodiment 1344 wherein the heavy metal comprises lead, arsenic, cadmium, chromium, or mercury.

[001720] In embodiment 1346 provided herein is the method of any one of embodiments 1337 through 1345 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001721] In embodiment 1347 provided herein is the method of embodiment any one of embodiments 1337 through 1346 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001722] In embodiment 1348 provided herein is the method of any one of embodiments 1337 through 1347 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001723] In embodiment 1349 provided herein is the method of any one of embodiments 1337 through 1348 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least

80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001724] In embodiment 1350 provided herein is the method of any one of embodiments 1337 through 1349 wherein the different microbes are *Streptomyces*.

[001725] In embodiment 1351 provided herein is the method of any one of embodiments 1337 through 1350 wherein the composition comprising a plurality of microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001726] In embodiment 1352 provided herein is the method of embodiment 1351 wherein the composition comprises at least 2, 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 and/or not more than 5, 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90 or 95 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 2, preferably at least 5, more preferably at least 10, even more preferably at least 20, yet more preferably at least 30, still more preferably at least 50, or for example 2-95, preferably 10-95, more preferably 20-95, even more preferably 30-95, yet more preferably 40-95, still more preferably 50-95.

[001727] In embodiment 1353 provided herein is the method of any one of embodiments 1337 through 1352 further comprising applying one or more soil amendments to the soil.

[001728] In embodiment 1354 provided herein is the method of embodiment 1353 wherein the soil amendments comprise one or more minerals and/or one or more carbon sources for the microbes.

[001729] In embodiment 1355 provided herein is the method of embodiment 1354 or embodiment 1355 wherein a content of the soil amendment is determined at least in part by one or more results of one or more analyses of the soil in which the plants grow or will grow.

[001730] In embodiment 1356 provided herein is the method of any one of embodiments 1337 through 1355 wherein the plants are not cannabis plants.

[001731] In embodiment 1357 provided herein is the method of any one of embodiments 1337 through 1356 further comprising applying the composition in a second application.

[001732] In embodiment 1358 provided herein is the method of embodiment 1357 further comprising applying the composition in a third application.

[001733] In embodiment 1359 provided herein is the method of any one of embodiments 1337-1358 wherein each application comprises at least 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} and/or not more than 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, or 10^{16} CFU of microbes of the composition per acre, for example, 10^6 to 10^{16}, preferably 10^7 to 10^{15}, more

preferably 10^8 to 10^{14}, even more preferably 10^9 to 10^{14}, yet more preferably 10^{10} to 10^{13}, still more preferably 10^{10} to 10^{12} CFU of microbes of the composition per acre.

[001734] In embodiment 1360 provided herein is a system comprising (i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more other entities; (ii) a second entity, or a third entity controlled directly or indirectly, at least in part, by the second entity, that obtains, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, are achieved for the second entity; (iii) an agreement between the first and second entities that delineates an apportionment of the economic benefits between the first and second entities; and (iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines the apportionment between the first and second entities, and communicates information comprising the apportionment to the first and/or second entities.

[001735] In embodiment 1361 provided herein is the system of embodiment 1360 wherein the second entity is (i) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts; (ii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold; (iii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration; or (iv) an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions.

[001736] In embodiment 1362 provided herein is the system of embodiment 1361 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts.

[001737] In embodiment 1363 provided herein is the system of embodiment 1361 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold.

[001738] In embodiment 1364 provided herein is the system of embodiment 1363 wherein the land comprises pastureland.

[001739] In embodiment 1365 provided herein is the system of embodiment 1363 wherein the land comprises rangeland.

[001740] In embodiment 1366 provided herein is the system of embodiment 1363 wherein the land comprises land on which grass is grown for feed for the animals.

[001741] In embodiment 1367 provided herein is the system of embodiment 1363 wherein the land comprises land on which grain is grown for feed for the animals.

[001742] In embodiment 1368 provided herein is the system of embodiment 1361 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration.

[001743] In embodiment 1369 provided herein is the system of embodiment 1368 wherein the use of the land comprises a sport, game, or other recreation or entertainment.

[001744] In embodiment 1370 provided herein is the system of embodiment 1361 wherein the second entity is an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions.

[001745] In embodiment 1371 provided herein is the system of embodiment 1370 wherein the land is grassland, forest, or rangeland.

[001746] In embodiment 1372 provided herein is the system of any one of embodiments 1360 through 1371 wherein the second entity is a governmental entity.

[001747] In embodiment 1373 provided herein is the system of any one of embodiments 1360 through 1372 wherein the second entity is a private entity.

[001748] In embodiment 1374 provided herein is the system of any one of embodiments 1360 through 1373 wherein the one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, comprises (i) reduced costs due to decreased water use for the plants; (ii) reduced costs due to decreased use of fertilizer for the plants; (iii) reduced costs due to decreased use of herbicides for the plants; (iv) reduced costs due to decreased use of pesticides for the plants; (v) increased biomass of the plants; (vi) increased price per plant or plant product or unit thereof; (vii) ability to use a greater area of land to grow or maintain the plants; (viii) ability to grow plants in a wider range of environmental conditions; (ix) a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants; (x) a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; (xi) a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants;(xii) a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants; or a combination thereof.

[001749] In embodiment 1375 provided herein is the system of embodiment 1374 wherein the one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, comprises a carbon credit or other economic benefit due, in whole or in part, to

increased soil carbon; a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants, or a combination thereof.

[001750] In embodiment 1376 provided herein is the system of embodiment 1374 or embodiment 1375 wherein the one or more economic benefits comprise reduced costs due to decreased water use for the plants.

[001751] In embodiment 1377 provided herein is the system of embodiment 1374 or embodiment 1375 wherein the one or more economic benefits comprise increased price per plant or plant product or unit thereof.

[001752] In embodiment 1378 provided herein is the system of embodiment 1374 or embodiment 1375 wherein the one or more economic benefits comprise a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants.

[001753] In embodiment 1379 provided herein is the system of embodiment 1378 wherein the animals are cattle.

[001754] In embodiment 1380 provided herein is the system of embodiment 1378 wherein the animals are dairy animals, *e.g.*, cows, goats, or sheep.

[001755] In embodiment 1381 provided herein is the system of embodiment 1378 wherein the animals are poultry.

[001756] In embodiment 1382 provided herein is the system of embodiment 1381 wherein the poultry are raised for slaughter.

[001757] In embodiment 1383 provided herein is the system of embodiment 1381 wherein the poultry are egg layers.

[001758] In embodiment 1384 provided herein is the system of any one of embodiments 1360 through 1383 comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 500, or 1000 other entities, different from the first entity, that obtain, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for each of the entities; agreements between the first entity and each other entity that delineates an apportionment of the economic benefits between the first entity and each of the other entities; and one or more processors that receives information regarding each of the agreements and information regarding the one or more economic benefits for each of the other entities,

determines the apportionment between the first entity and each of the other entities, and communicates information comprising the apportionment to the first entity and/or each of the other entities.

[001759] In embodiment 1385 provided herein is the system of any one of embodiments 1360 through 1384 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001760] In embodiment 1386 provided herein is the system of any one of embodiments 1360 through 1385 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001761] In embodiment 1387 provided herein is the system of any one of embodiments 1360 through 1386 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001762] In embodiment 1388 provided herein is the system of any one of embodiments 1360 through 1387 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001763] In embodiment 1389 provided herein is the system of any one of embodiments 1360 through 1388 wherein the different microbes are *Streptomyces*.

[001764] In embodiment 1390 provided herein is the system of any one of embodiments 1360 through 1389 wherein the composition comprising a plurality of microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001765] In embodiment 1391 provided herein is the system of embodiment 1390 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, or 40 and/or not more than 5, 10, 15, 20,

25, 30, 35, or 40 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001766] In embodiment 1392 provided herein is the system of embodiment 1390 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001767] In embodiment 1393 provided herein is the system of embodiment 1392 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 of the different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100 are biologically pure.

[001768] In embodiment 1394 provided herein is a method of obtaining an economic benefit from land on which plants are grown comprising (i) obtaining and using one or more compositions comprising a plurality of different microbes, wherein (a) the one or more compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity, and (b) the second entity uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity; (ii) determining a quantity of the one or more economic benefits; and (iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities.

[001769] In embodiment 1395 provided herein is the method of embodiment 1394 wherein the apportioning is done according to an agreement or agreements between the first and second entities.

[001770] In embodiment 1396 provided herein is the method of embodiment 1395 wherein the apportioning is done by a processor that receives information regarding the one or more economic benefits and the agreement, processes the information to determine a quantitative value or values for economic benefits for apportionment between the first and second entities, and communicates the quantitative value or values to the first and/or second entities.

[001771] In embodiment 1397 provided herein is the method of any one of embodiments 1394 through 1396 wherein the second entity is (i) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts; (ii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold; (iii) an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration; or (iv) an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions.

[001772] In embodiment 1398 provided herein is the method of embodiment 1397 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for sale of the plants or plant parts.

[001773] In embodiment 1399 provided herein is the method of embodiment 1397 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown primarily for feeding animals that are sold.

[001774] In embodiment 1400 provided herein is the method of embodiment 1399 wherein the land comprises pastureland.

[001775] In embodiment 1401 provided herein is the method of embodiment 1399 wherein the land comprises rangeland.

[001776] In embodiment 1402 provided herein is the method of embodiment 1399 wherein the land comprises land on which grass is grown for feed for the animals.

[001777] In embodiment 1403 provided herein is the method of embodiment 1399 wherein the land comprises land on which grain is grown for feed for the animals.

[001778] In embodiment 1404 provided herein is the method of embodiment 1397 wherein the second entity is an entity that owns, controls, manages, or otherwise has rights to land in which plants are grown, for use of the land in which plants are grown for which the entity receives consideration.

[001779] In embodiment 1405 provided herein is the method of embodiment 1404 wherein the use of the land comprises a sport, game, or other recreation or entertainment.

[001780] In embodiment 1406 provided herein is the method of embodiment 1397 wherein the second entity is (iv) an entity that owns, controls, manages or otherwise has rights to land in which plants are grown with no or minimal alteration to plant or soil conditions.

[001781] In embodiment 1407 provided herein is the method of embodiment 1406 wherein the land is grassland, forest, or rangeland.

[001782] In embodiment 1408 provided herein is the method of any one of embodiments 1394 through 1407 wherein the second entity is a governmental entity.

[001783] In embodiment 1409 provided herein is the method of any one of embodiments 1394 through 1408 wherein the second entity is a private entity.

[001784] In embodiment 1410 provided herein is the method of any one of embodiments 1394 through 1409 wherein the one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, comprises (i) reduced costs due to decreased water use for the plants; (ii) reduced costs due to decreased use of fertilizer for the plants; (iii) reduced costs due to decreased use of herbicides for the plants; (iv) reduced costs due to decreased use of pesticides for the plants; (v) increased biomass of the plants; (vi) increased price per plant or plant product or unit thereof; (vii) ability to use a greater area of land to grow or maintain the plants; (viii) ability to grow plants in a wider range of environmental conditions; (ix) a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants; (x) a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; (xi) a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; (xii) a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants; or a combination thereof.

[001785] In embodiment 1411 provided herein is the method of embodiment 1410 wherein the one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, comprises a carbon credit or other economic benefit due, in whole or in part, to increased soil carbon; a carbon credit or other economic benefit due, in whole or in part, to increased carbon in the plants; a carbon credit or other economic benefit due, in whole or in part, to carbon avoided in raising the plants, or a combination thereof.

[001786] In embodiment 1412 provided herein is the method of embodiment 1411 or embodiment 1412 wherein the one or more economic benefits comprise reduced costs due to decreased water use for the plants.

[001787] In embodiment 1413 provided herein is the method of embodiment 1411 or embodiment 1412 wherein the one or more economic benefits comprise increased price per plant or plant product or unit thereof.

[001788] In embodiment 1414 provided herein is the method of embodiment 1411 or embodiment 1412 wherein the one or more economic benefits comprise a financial benefit realized from reduced costs to raise and/or maintain animals that eat the plants and/or increased price for animals that eat the plants.

[001789] In embodiment 1415 provided herein is the method of embodiment 1414 wherein the animals are cattle.

[001790] In embodiment 1416 provided herein is the method of embodiment 1414 wherein the animals are dairy animals, *e.g.*, cows, goats, or sheep.

[001791] In embodiment 1417 provided herein is the method of embodiment 1414 wherein the animals are poultry.

[001792] In embodiment 1418 provided herein is the method of embodiment 1417 wherein the poultry are raised for slaughter.

[001793] In embodiment 1419 provided herein is the method of embodiment 1417 wherein the poultry are egg layers.

[001794] In embodiment 1420 provided herein is the method of any one of embodiments 1394 through 1419 wherein the one or more compositions are supplied by the first entity that produces, distributes, or otherwise supplies the one or more compositions to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 300, 500, or 1000 other entities, different from the first entity, that obtain, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for each of the entities; wherein the apportioning is done according to an agreement or agreements between the first entity and each other entity that delineates an apportionment of the economic benefits between the first entity and each of the other entities; and wherein the apportioning is done by one or more processors that receives information regarding each of the agreements and information regarding the one or more economic benefits for each of the other entities, determines the apportionment between the first entity and each of the other entities, and communicates information comprising the apportionment to the first entity and/or each of the other entities.

[001795] In embodiment 1421 provided herein is the method of any one of embodiments 1394 through 1420 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 different microbes and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110,

115, 120, 125, 130, 135 or 140 different microbes, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001796] In embodiment 1422 provided herein is the method of any one of embodiments 1394 through 1421 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80% of the different microbes are heterologous to the soil and/or plants.

[001797] In embodiment 1423 provided herein is the method of any one of embodiments 1394 through 1422 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are rhizobacteria.

[001798] In embodiment 1424 provided herein is the method of any one of embodiments 1394 through 1423 wherein at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, or 99%, or 100%, for example at least 10%, preferably at least 20%, more preferably at least 30%, even more preferably at least 40%, yet more preferably at least 60%, still more preferably at least 80%, yet more preferably at least 95%, yet still more preferably 100% of the different microbes are saprophytic.

[001799] In embodiment 1425 provided herein is the method of any one of embodiments 1394 through 1424 wherein the different microbes are *Streptomyces*.

[001800] In embodiment 1426 provided herein is the method of any one of embodiments 1394 through 1425 wherein the composition comprising a plurality of microbes comprises one or more different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof.

[001801] In embodiment 1427 provided herein is the method of embodiment 1426 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, or 40 and/or not more than 5, 10, 15, 20, 25, 30, 35, or 40 different microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, preferably 5-45, more preferably 10-45, even more preferably 20-45, yet more preferably 35-45.

[001802] In embodiment 1428 provided herein is the method of embodiment 1426 wherein the composition comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, or 135 and/or not more than 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135 or 140 different

microbes of the composition of any one of embodiments 1 through 259 or progeny and/or mutants thereof, for example at least 20, in certain cases at least 50, in yet other cases at least 70, or preferably 10-140, more preferably 20-120, even more preferably 40-100, yet more preferably 50-100.

[001803] In embodiment 1429 provided herein is a method of improving one or more characteristics of a tree rooted in soil comprising (i) providing one or more nutrients to the soil in which the tree is rooted; and (ii) providing a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil and/or the tree in a first application.

[001804] In embodiment 1430 provided herein is a method of revitalizing a dormant tree comprising applying to the soil in which the tree is rooted and/or the tree a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil in wherein the microbial composition the tree is rooted in a first application and allowing the tree to grow for a duration of time.

[001805] In embodiment 1431 provided herein is a kit comprising (i) a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes in a first package; and (ii) a composition comprising at least 1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, or 200 and/or not more than 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, 200 or 500 nutrients in a second package, different from the first.

[001806] In embodiment 1432 provided herein is the composition or method of any one of embodiments 344 through 1428 wherein the plants are not cannabis.

[001807] In embodiment 1433 provided herein is the composition or method of any one of embodiments 344 through 1428 wherein the plants comprise grasses, trees, commercial crops, and/or ornamental plants.

[001808] In embodiment 1434 provided herein is the method of embodiment 1432 or embodiment 1433 wherein the plants are grasses.

[001809] In embodiment 1435 provided herein is the method of embodiment 1434 wherein the grasses are turf grasses.

[001810] In embodiment 1436 provided herein is the method of embodiment 1434 wherein the plants are grassland grasses.

[001811] In embodiment 1437 provided herein is the method of embodiment 1432 or embodiment 1433 wherein the plants are trees.

[001812] In embodiment 1438 provided herein is the method of embodiment 1437 wherein the trees are deciduous trees.

[001813] In embodiment 1439 provided herein is the method of embodiment 1437 wherein the trees are evergreen trees.

[001814] In embodiment 1440 provided herein is the method of embodiment 1437 wherein the trees are forest trees.

[001815] In embodiment 1441 provided herein is the method of embodiment 1432 or embodiment 1433 wherein the plant is a commercial crop.

[001816] In embodiment 1442 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a cereal crop.

[001817] In embodiment 1443 provided herein is the method of embodiment 1442 wherein the cereal crop comprises corn, sweet corn, popcorn, seed corn, silage corn, field corn, rice, wheat, barley, or sorghum.

[001818] In embodiment 1444 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a berry.

[001819] In embodiment 1445 provided herein is the method of embodiment 1444 wherein the berry comprises blueberry, blackberry, raspberry, loganberry, huckleberry, cranberry, gooseberry, elderberry, currant, caneberry, or bushberry.

[001820] In embodiment 1446 provided herein is the method of embodiment 1441 wherein the commercial crop comprises an oilseed plant.

[001821] In embodiment 1447 provided herein is the method of embodiment 1446 wherein the oilseed plant canola, castor, coconut, cotton, flax, oil palm, olive, peanut, rapeseed, safflower, sesame, sunflower, or soybean.

[001822] In embodiment 1448 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a tree nut.

[001823] In embodiment 1449 provided herein is the method of embodiment 1448 wherein the tree nut comprises almond, pistachio, pecan, walnut, filberts, chestnut, cashew, beechnut, butternut, or macadamia.

[001824] In embodiment 1450 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a brassica vegetable.

[001825] In embodiment 1451 provided herein is the method of embodiment 1450 wherein the brassica vegetable comprises broccoli, cabbage, cauliflower, brussels sprouts, collards, kale, mustard greens, or kohlrabi.

[001826] In embodiment 1452 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a cucurbit vegetable.

[001827] In embodiment 1453 provided herein is the method of embodiment 1452 wherein the cucurbit vegetable comprises cucumber, cantaloupe, melon, muskmelon, squash, watermelon, pumpkin, or eggplant.

[001828] In embodiment 1454 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a bulb vegetable.

[001829] In embodiment 1455 provided herein is the method of embodiment 1454 wherein the bulb vegetable comprises onion, garlic, or shallots.

[001830] In embodiment 1456 provided herein is the method of embodiment 1441 wherein the commercial crop comprises citrus.

[001831] In embodiment 1457 provided herein is the method of embodiment 1456 wherein the citrus comprises orange, grapefruit, lemon, tangerine, tangelo, or pummelo.

[001832] In embodiment 1458 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a fruiting vegetable.

[001833] In embodiment 1459 provided herein is the method of embodiment 1458 wherein the fruiting vegetable comprises pepper, tomato, ground cherry, tomatillo, okra, or grape.

[001834] In embodiment 1460 provided herein is the method of embodiment 1441 wherein the commercial crop comprises legume or vegetable such as beans.

[001835] In embodiment 1461 provided herein is the method of embodiment 1460 wherein the legume or vegetable such as beans comprise green beans, snap beans, shell beans, soybeans, dry beans, garbanzo beans, lima beans, peas, chickpeas, split peas, lentils, or peanuts.

[001836] In embodiment 1462 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a pome fruit.

[001837] In embodiment 1463 provided herein is the method of embodiment 1462 wherein the pome fruit comprises apple, crabapple, pear, quince, or mayhaw.

[001838] In embodiment 1464 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a root, tuber, or corm vegetable.

[001839] In embodiment 1465 provided herein is the method of embodiment 1464 wherein the root, tuber or corm vegetable comprises carrot, potato, sweet potato, cassava, beets, ginger, horseradish, radish, ginseng, or turnip.

[001840] In embodiment 1466 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a stone fruit.

[001841] In embodiment 1467 provided herein is the method of embodiment 1466 wherein the stone fruit comprises apricot, cherry, nectarine, peach, plum, prune, or strawberry.

[001842] In embodiment 1468 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a grass.

[001843] In embodiment 1469 provided herein is the method of embodiment 1468 wherein the grass comprises grass for livestock feed.

[001844] In embodiment 1470 provided herein is the method of embodiment 1468 wherein the grass comprises turf grass.

[001845] In embodiment 1471 provided herein is the method of embodiment 1441 wherein the commercial crop comprises a tree.

[001846] In embodiment 1472 provided herein is the method of embodiment 1471 wherein the commercial crop comprises an evergreen tree.

[001847] In embodiment 1473 provided herein is the method of embodiment 1471 wherein the commercial crop comprises a deciduous tree.

[001848] In embodiment 1474 provided herein is the method of embodiment 1441 wherein the commercial crop comprises an herb or spice.

[001849] In embodiment 1475 provided herein is the method of embodiment 1441 wherein the commercial crop comprises an ornamental plant.

[001850] In embodiment 1476 provided herein is the method of embodiment 1475 wherein the ornamental plant comprises a flowering plant, a bush, or a shrub.

[001851] In embodiment 1477 provided herein is the method of embodiment 1441 wherein the commercial crop comprises an energy or raw material plant.

[001852] In embodiment 1478 provided herein is the method of embodiment 1477 wherein the energy or raw material plant comprises corn, canola, sugar cane, sunflower, safflower, Jatropha, castor, oil palm, coconut, wild flax, Pongam, olive, or flax.

[001853]

V. Equivalents

[001854] Throughout the description, where compositions are described as having, including, or comprising specific components, or where processes and methods are described as having, including, or comprising specific steps, it is contemplated that, additionally, there are compositions of the present invention that consist essentially of, or consist of, the recited components, and that there are processes and methods according to the present invention that consist essentially of, or consist of, the recited processing steps.

[001855] In the application, where an element or component is said to be included in and/or selected from a list of recited elements or components, it should be understood that the element or component can be any one of the recited elements or components, or the element or

component can be selected from a group consisting of two or more of the recited elements or components.

[001856] Further, it should be understood that elements and/or features of a composition or a method described herein can be combined in a variety of ways without departing from the spirit and scope of the present invention, whether explicit or implicit herein. For example, where reference is made to a particular compound, that compound can be used in various embodiments of compositions of the present invention and/or in methods of the present invention, unless otherwise understood from the context. In other words, within this application, embodiments have been described and depicted in a way that enables a clear and concise application to be written and drawn, but it is intended and will be appreciated that embodiments may be variously combined or separated without parting from the present teachings and invention(s). For example, it will be appreciated that all features described and depicted herein can be applicable to all aspects of the invention(s) described and depicted herein.

[001857] The terms "a" and "an" and "the" and similar references in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. For example, the term "a cell" includes a plurality of cells, including mixtures thereof. Where the plural form is used for compounds, salts, or the like, this is taken to mean also a single compound, salt, or the like.

[001858] It should be understood that the expression "at least one of" includes individually each of the recited objects after the expression and the various combinations of two or more of the recited objects unless otherwise understood from the context and use. The expression "and/or" in connection with three or more recited objects should be understood to have the same meaning unless otherwise understood from the context.

[001859] The use of the term "include," "includes," "including," "have," "has," "having," "contain," "contains," or "containing," including grammatical equivalents thereof, should be understood generally as open-ended and non-limiting, for example, not excluding additional unrecited elements or steps, unless otherwise specifically stated or understood from the context.

[001860] Where the use of the term "about" is before a quantitative value, the present invention also includes the specific quantitative value itself, unless specifically stated otherwise. As used herein, the term "about" refers to a ±10% variation from the nominal value unless otherwise indicated or inferred.

[001861] It should be understood that the order of steps order for performing certain actions is immaterial so long as the present invention remain operable. Moreover, two or more steps or actions may be conducted simultaneously.

[001862] The use of any and all examples, or exemplary language herein, for example, "such as" or "including," is intended merely to illustrate better the present invention and does not pose a limitation on the scope of the invention unless claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the present invention.

[001863] The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting on the invention described herein. Scope of the invention is thus indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are intended to be embraced therein.

CLAIMS

WHAT IS CLAIMED IS:

1. A composition comprising one or more *Streptomyces* microbes, wherein the one or more *Streptomyces* microbes comprise a 16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5 identical, or 100% identical, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to a nucleic acid sequence to one or more of SEQ ID NOs: 68-109 and 120-196.

2. The composition of claim 1 comprising microbes of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, yet even more preferably 10-30 different *Streptomyces* strains.

3. The composition of claim 1 or claim 2 further comprising one or more non-*Streptomyces* microbes.

4. The composition of any one of the previous claims comprising one or more *Pseudomonas* microbes.

5. The composition of any one of the previous claims comprising one or more *Microvirga* microbes.

6. The composition of any one of the previous claims comprising one or more *Micrococcus* microbes.

7. The composition of any one of the previous claims comprising one or more *Paenibacillus* microbes

8. The composition of any one of the previous claims comprising one or more *Aureimonas* microbes.

9. The composition of any one of the previous claims comprising one or more *Bradyrhizobium* microbes.

10. The composition of any one of the previous claims comprising one or more *Rhodococcus* microbes.

11. The composition of any one of the previous claims comprising one or more *Amycolatopsis* microbes.

12. The composition of any one of the previous claims comprising one or more *Lysinibacillus* microbes.

13. The composition of any one of the previous claims wherein two or more of the microbes are heterologous to each othe

14. A composition comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, or 60 and/or not more than 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 25, 30, 35, 40, 50, 60, 70, 80, or 100, preferably 2-100, more preferably 5-100, even more preferably 5-80, still more preferably 5-40, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, further preferably 10-30, different *Streptomyces* microbes.

15. The composition of claim 14 further comprising one or more non-*Streptomyces* microbes.

16. The composition of claim 14 or claim 15 wherein two or more of the microbes are heterologous to each other.

17. The composition of claim 15 or claim 16 wherein the one or more non-*Streptomyces* microbes comprise a *Pseudomonas*, *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

18. The composition of claim 15 or claim 16 wherein the one or more non-*Streptomyces* microbes comprise a *Pseudomonas*, *Microvirga*, *Micrococcus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

19. The composition of claim 15 or claim 16 wherein the one or more non-*Streptomyces* microbes comprise a *Microvirga*, *Micrococcus*, *Paenibacillus*, *Aureimonas*, *Bradyrhizobium*, *Rhodococcus*, *Amycolatopsis*, or *Lysinibacillis* microbe, or a combination thereof.

20. The composition of claim 17 or claim 18 wherein the one or more non-*Streptomyces* microbes comprise one or more *Pseudomonas* microbes.

21. The composition of any one of claims 17 through 20 comprising a *Microvirga* microbe.

22. The composition of any one of claims 17 through 21 wherein the one or more non-*Streptomyces* microbes comprise one or more *Micrococcus* microbes.

23. The composition of any one of claims 17 through 22 wherein the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes.

24. The composition of any one of claims 17 through 23 wherein the one or more non-*Streptomyces* microbes comprise one or more *Aureimonas* microbes.

25. The composition of any one of claims 17 through 24 wherein the one or more non-*Streptomyces* microbes comprise one or more *Bradyrhyzobium* microbes.

26. The composition of any one of claims 17 through 25 wherein the one or more non-*Streptomyces* microbes comprise one or more *Rhodococcus* microbes.

27. The composition of any one of claims 17 through 26 wherein the one or more non-*Streptomyces* microbes comprise one or more *Amycolatopsis* microbes.

28. The composition of any one of claims 17 through 27 wherein the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes.

29. A composition comprising *Streptomyces* spp. microbes and at least one, two, three, four, five, 6, or 7 and/or not more than one, two, three, four, five, 6, 7, or 8, preferably 2-8, more preferably 2-6, yet more preferably 3-8, such as 2, 3, 4, 5, 6, 7, 8, or 8 additional microbes selected from the group consisting of *Pseudomonas* spp., *Microvirga* spp., *Paenibacillus* spp., *Aureimonas* spp., *Bradyrhizobium* spp., *Rhodococcus* spp., *Amycolatopsis* spp., and *Lysinibacillis* spp.

30. The composition of claim [0028] comprising at least 2, 3, 5, 7, 10, 12, 15, 20, 30, 40, or 50 and/or not more than 3, 5, 7, 10, 12, 15, 20, 30, 40, 50, 60, 80, or 100 different *Streptomyces* microbes, for example 2-100 different *Streptomyces* microbes.

31. The composition of claim [0028] or claim 30 comprising *Pseudomonas* spp. microbes.

32. The composition of claim 31 comprising at least 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16 or 18 and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, 20 or 24 different *Pseudomonas* microbes, for example 2-24 different *Pseudomonas* microbes.

33. The composition any one of claims [0028] through 32 comprising *Microvirga* spp. microbes.

34. The composition any one of claims [0028] through 33 comprising *Micrococcus* spp. microbes.

35. The composition of claim 34 comprising at least 2, 3, 4, 5 and/or not more than 3, 4, 5, or 6 different *Micrococcus* microbes, for example 2-6 different *Micrococcus* microbes.

36. The composition of any one of claims [0028] through 35 comprising *Paenibacillus* spp. microbes.

37. The composition of claim 36 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Paenibacillus* microbes, for example 2-10 different *Paenibacillus* microbes.

38. The composition of any one of claims [0028] through 37 comprising *Aureimonas* spp. microbes.

39. The composition of claim 38 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Aureimonas* microbes, for example 2-10 different *Aureimonas* microbes.

40. The composition of any one of claims [0028] through 39 comprising *Bradyrhizobium* spp. microbes.

41. The composition of claim 40 comprising at least 2, 3, 4, 5, 6, 7, 8, 10, 12, or 14 and/or not more than 3, 4, 5, 6, 7, 8, 10, 12, 14, or 16 different *Bradyrhyzobium* microbes, for example 2-16 different *Bradyrhyzobium* microbes.

42. The composition of any one of claims [0028] through 41 comprising *Rhodococcus* spp. microbes.

43. The composition of claim 42 comprising at least 2 different *Rhodococcus* microbes.

44. The composition of any one of claims [0028] through 43 comprising *Amycolatopsis* spp. microbes.

45. The composition of claim 44 comprising at least 2, 3, 4, or 5 and/or not more than 3, 4, 5, or 6 different *Amycolatopsis* microbes, for example 2-6 different *Amycolatopsis* microbes.

46. The composition of any one of claims [0028] through 45 comprising *Lysinibacillis* spp. microbes.

47. The composition of claim 46 comprising at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Lysinibacillus* microbes, for example 2-10 different *Lysinibacillus* microbes.

48. A composition comprising one or more *Streptomyces* mirobes and at least one non-*Streptomyces* microbe, wherein the non-*Streptomyces* microbe is a nitrogen-fixing microbe.

49. The composition of claim [0029] comprising at least 2, 3, 5, 7, 10, 12, 15, 20, 30, 40, or 50 and/or not more than 3, 5, 7, 10, 12, 15, 20, 30, 40, 50, 60, 80, or 100 different *Streptomyces* strains, for example 2-100 different *Streptomyces* microbes.

50. The composition of claim [0029] or claim 49 wherein the nitrogen-fixing, non-*Streptomyces* microbe comprises a *Pseudomonas* spp., *Microvirga* spp., *Bradyrhyizobium* spp., *Aureimonas* spp., *Paenibacillus* spp., and/or *Lysinibacillus* spp. microbe.

51. The composition of claim 50 comprising one or more *Pseudomonas* spp. microbe.

52. The composition of claim [0029] or 49 wherein the nitrogen-fixing, non-*Streptomyces* microbe comprises a *Microvirga* spp., *Bradyrhyizobium* spp., *Aureimonas* spp., *Paenibacillus* spp., and/or *Lysinibacillus* spp. microbe.

53. The composition of any one of claims [0029] through 52 comprising one or more *Microvirga* spp. microbe.

54. The composition of any one of claims [0029] through 53 comprising one or more *Micrococcus* spp. microbe.

55. The composition of any one of claims [0029] through 54 comprising one or more *Paenibacillus* spp. microbe.

56. The composition of any one of claims [0029] through 55 comprising one or more *Aureimonas* spp. microbe.

57. The composition of any one of claims [0029] through 56 comprising one or more *Bradyrhyzobium* spp. microbe.

58. The composition of any one of claims [0029] through 57 comprising one or more *Lysinibacillus* spp. microbe.

59. The composition of any one of the previous claims wherein the one or more *Streptomyces* microbes comprise one or more of *Streptomyces antibioticus* B, *Streptomyces bacillaris*, *Streptomyces bikiniensis*, *Streptomyces cavourensis*, *Streptomyces fimbriatus*, *Streptomyces*

flavoviridis, *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces griseofuscus*, *Streptomyces griseoincarnatus*, *Streptomyces griseoviridis* A, *Streptomyces labedae*, *Streptomyces lydicus*, *Streptomyces misionensis*, *Streptomyces nigra*, *Streptomyces rochei*, *Streptomyces* sp. OATH_5, *Streptomyces* sp. OATH_7, *Streptomyces* sp. OATH_8, *Streptomyces* sp. OATH_9, *Streptomyces* sp. OATH_10, *Streptomyces* sp. OATH_11, *Streptomyces* sp. OATH_12, *Streptomyces* sp. OATH_13, *Streptomyces* sp. OATH_17, *Streptomyces* sp. OATH_19, *Streptomyces* sp. OATH_20, *Streptomyces* sp. OATH_22A, *Streptomyces* sp. OATH_22B, *Streptomyces* sp. OATH_23, *Streptomyces* sp. OATH_26, *Streptomyces* sp. OATH_27, *Streptomyces* sp. OATH_28, *Streptomyces* sp. OATH_30, *Streptomyces* sp. OATH_31, *Streptomyces* sp. OATH_34, *Streptomyces* sp. OATH_36, *Streptomyces* sp. OATH_37, *Streptomyces* sp. OATH_38, *Streptomyces* sp. OATH_39, *Streptomyces* sp. OATH_40, *Streptomyces* sp. OATH_41, *Streptomyces* sp. OATH_42, *Streptomyces* sp. OATH_43, *Streptomyces* sp. OATH_44, *Streptomyces* sp. OATH_46, *Streptomyces* sp. OATH_47, *Streptomyces* sp. OATH_48, *Streptomyces* sp. OATH_49, *Streptomyces* sp. OATH_50, *Streptomyces* sp. OATH_52, *Streptomyces* sp. OATH_57, *Streptomyces* sp. OATH_58, *Streptomyces* sp. OATH_59, *Streptomyces* sp. OATH_60, *Streptomyces* sp. OATH_61, *Streptomyces* sp. OATH_62, *Streptomyces* sp. OATH_63, *Streptomyces* sp. OATH_64, *Streptomyces* sp. OATH_65, *Streptomyces* sp. OATH_66, *Streptomyces* sp. OATH_A, *Streptomyces* sp. OATH_B, *Streptomyces* sp. OATH_C, *Streptomyces* sp. OATH_D, *Streptomyces* sp. OATH_E, *Streptomyces* sp. OATH_F, *Streptomyces* sp. OATH_G, *Streptomyces* sp001509795, *Streptomyces* sp900105755, and/or *Streptomyces violaceorectus*.

60. The composition of any one of the previous claims comprising the one or more *Streptomyces* microbes comprise one or more of *Streptomyces* sp. OATH_5, *Streptomyces* sp. OATH_7, *Streptomyces* sp. OATH_8, *Streptomyces* sp. OATH_9, *Streptomyces* sp. OATH_10, *Streptomyces* sp. OATH_11, *Streptomyces* sp. OATH_12, *Streptomyces* sp. OATH_13, *Streptomyces* sp. OATH_17, *Streptomyces* sp. OATH_19, *Streptomyces* sp. OATH_20, *Streptomyces* sp. OATH_22A, *Streptomyces* sp. OATH_22B, *Streptomyces* sp. OATH_23, *Streptomyces* sp. OATH_26, *Streptomyces* sp. OATH_27, *Streptomyces* sp. OATH_28, *Streptomyces* sp. OATH_30, *Streptomyces* sp. OATH_31, *Streptomyces* sp. OATH_34, *Streptomyces* sp. OATH_36, *Streptomyces* sp. OATH_37, *Streptomyces* sp. OATH_38, *Streptomyces* sp. OATH_39, *Streptomyces* sp. OATH_40, *Streptomyces* sp. OATH_41, *Streptomyces* sp. OATH_42, *Streptomyces* sp. OATH_43, *Streptomyces* sp. OATH_44, *Streptomyces* sp. OATH_46, *Streptomyces* sp. OATH_47, *Streptomyces* sp. OATH_48,

Streptomyces sp. OATH_49, *Streptomyces* sp. OATH_50, *Streptomyces* sp. OATH_52, *Streptomyces* sp. OATH_57, *Streptomyces* sp. OATH_58, *Streptomyces* sp. OATH_59, *Streptomyces* sp. OATH_60, *Streptomyces* sp. OATH_61, *Streptomyces* sp. OATH_62, *Streptomyces* sp. OATH_63, *Streptomyces* sp. OATH_64, *Streptomyces* sp. OATH_65, *Streptomyces* sp. OATH_66, *Streptomyces* sp. OATH_A, *Streptomyces* sp. OATH_B, *Streptomyces* sp. OATH_C, *Streptomyces* sp. OATH_D, *Streptomyces* sp. OATH_E, *Streptomyces* sp. OATH_F, *Streptomyces* sp. OATH_G.

61. The composition of any one of the previous claims wherein the one or more *Streptomyces* microbes have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 68-109 and 120-196.

62. The composition of any one of claims 4-13, 17-47, or 50-61 wherein the one or more *Pseudomonas* microbes comprise a first *Pseudomonas* strain.

63. The composition of claim 62 wherein the one or more *Pseudomonas* microbes comprise a second *Pseudomonas* strain, wherein the second *Pseudomonas* strain is different from the first *Pseudomonas* strain.

64. The composition of claim 63 wherein the one or more *Pseudomonas* microbes comprise a third *Pseudomonas* strain, wherein the third *Pseudomonas* strain is different from the first and second *Pseudomonas* strains.

65. The composition of claim 64 wherein the one or more *Pseudomonas* microbes comprise a fourth *Pseudomonas* strain, wherein the fourth *Pseudomonas* strain is different from the first, second, and third *Pseudomonas* strains.

66. The composition of claim 65 wherein the one or more *Pseudomonas* microbes comprise a fifth *Pseudomonas* strain, wherein the fifth *Pseudomonas* strain is different from the first, second, third, and fourth *Pseudomonas* strains.

67. The composition of any one of claims 62 through 66 wherein the first, second, third, fourth, and/or fifth *Pseudomonas* strains comprise one or more of *Pseudomonas* E sp003253735,

Pseudomonas fluorescens, *Pseudomonas koreensis*, *Pseudomonas poae*, *Pseudomonas* sp. OATH_2, *Pseudomonas* sp. OATH_3, *Pseudomonas* sp. OATH_4, *Pseudomonas* sp. OATH_6, *Pseudomonas* sp. OATH_14, *Pseudomonas* sp. OATH_15, *Pseudomonas* sp. OATH_16, *Pseudomonas* sp. OATH_45 *Pseudomonas* sp. OATH_51 *Pseudomonas* sp. OATH_53, *Pseudomonas* sp. OATH_55, *Pseudomonas* sp. OATH_56, *Pseudomonas* sp.002836515, and/or *Pseudomonas straminea*.

68. The composition of any one of claims 62 through 67 wherein the first, second, third, fourth, and/or fifth *Pseudomonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 39-67.

69. The composition of any one of claims 5-13, 21-28, 33-47 or 53-61 wherein the *Microvirga* microbe comprises a first *Microvirga* strain comprising *Microvirga* sp. OATH1.

70. The composition of claim 69 wherein the first *Microvirga* strain has a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to SEQ ID NO: 38.

71. The composition of any one of claims 6-13, 22-28, 34-47 or 54-61 wherein the one or more *Micrococcus* microbes comprise a first *Micrococcus* strain.

72. The composition of claim 71 wherein the one or more *Micrococcus* microbes comprise a second *Micrococcus* strain, wherein the second *Micrococcus* strain is different from the first strain.

73. The composition of claim 71 or claim 72 wherein the first or second *Micrococcus* strains comprise *Micrococcus luteus*.

74. The composition of any one of claims 71 through 73 wherein the first and/or second *Micrococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80,

85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 118-119.

75. The composition of any one of claims 7-13, 17, 19-28, 36-47, or 55-61 wherein the one or more *Paenibacillus* microbes comprise a first *Paenibacillus* strain.

76. The composition of claim 75 wherein the one or more *Paenibacillus* microbes comprise second *Paenibacillus* strain, wherein the second *Paenibacillus* strain is different from the first *Paenibacillus* strain.

77. The composition of claim 76 wherein the one or more *Paenibacillus* microbes comprise a third *Paenibacillus* strain, wherein the third *Paenibacillus* strain is different from the first and second *Paenibacillus* strains.

78. The composition of claim 77 wherein the one or more *Paenibacillus* microbes comprise a fourth *Paenibacillus* strain, wherein the fourth *Paenibacillus* strain is different from the first, second, and third *Paenibacillus* strains.

79. The composition of claim 78 wherein the one or more *Paenibacillus* microbes comprise a fifth *Paenibacillus* strain, wherein the fifth *Paenibacillus* strain is different from the first, second, third, and fourth *Paenibacillus* strains.

80. The composition of any one of claims 75 through 79 wherein the first, second, third, fourth, and/or fifth *Paenibacillus* strains comprise *Paenibacillus cellulositrophicus* A and/or *Paenibacillus illinoisensis*.

81. The composition of any one of claims 75 through 80 wherein the first, second, third, fourth, and/or fifth *Paenibacillus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 10-17.

82. The composition of any one of claims 8-13, 24-28, 38-47 or 56-61 wherein the one or more *Aureimonas* microbes comprise a first *Aureimonas* strain.

83. The composition of claim 82 wherein the one or more *Aureimonas* microbes comprise a second *Aureimonas* strain, wherein the second *Aureimonas* strain is different from the first *Aureimonas* strain.

84. The composition of claim 83 wherein the one or more *Aureimonas* microbes comprise a third *Aureimonas* strain, wherein the third *Aureimonas* strain is different from the first and second *Aureimonas* strains.

85. The composition of claim 84 wherein the one or more *Aureimonas* microbes comprise a fourth *Aureimonas* strain, wherein the fourth *Aureimonas* strain is different from the first, second, and third *Aureimonas* strains.

86. The composition of any one of claims 82 through 85 wherein the first, second, third, and/or fourth *Aureimonas* strains comprise *Aureimonas* A sp001425485.

87. The composition of any one of claims 82 through 86 wherein the first, second, third, and/or fourth *Aureimonas* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 18-21.

88. The composition of any one of claims 9-13, 25-28, 40-47 or 57-61 wherein the one or more *Bradyrhizobium* microbes comprise a first *Bradyrhizobium* strain.

89. The composition of claim 88 wherein the one or more *Bradyrhizobium* microbes a second *Bradyrhizobium* strain, wherein the second *Bradyrhizobium* strain is different from the first *Bradyrhizobium* strain.

90. The composition of claim 89 wherein the one or more *Bradyrhizobium* microbes comprise third *Bradyrhizobium* strain, wherein the third *Bradyrhizobium* strain is different from the first and second *Bradyrhizobium* strains.

91. The composition of claim 90 wherein the one or more *Bradyrhizobium* microbes comprise a fourth *Bradyrhizobium* strain, wherein the fourth *Bradyrhizobium* strain is different from the first, second, and third *Bradyrhizobium* strains.

92. The composition of claim 91 wherein the one or more *Bradyrhizobium* microbes comprise a fifth *Bradyrhizobium* strain, wherein the fifth *Bradyrhizobium* strain is different from the first, second, third, and fourth *Bradyrhizobium* strains.

93. The composition of any one of claims 88 through 92 wherein first, second, third, fourth, and/or fifth *Bradyrhizobium* stains comprise *Bradyrhizobium denitrificans* and/or *Bradyrhizobium elkanii*.

94. The composition of any one of claims 88 through 93 wherein the first, second, third, fourth, and/or fifth *Bradyrhyzobium* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 22-37.

95. The composition of any one of claims 10-13, 26-28, 42-47 or 59-61 wherein the one or more *Rhodococcus* microbes comprise a first *Rhodococcus* strain.

96. The composition of claim 95 wherein the one or more *Rhodococcus* microbes comprise a second *Rhodococcus* strain, wherein the second *Rhodococcus* strain is different from the first *Rhodococcus* strain.

97. The composition of claim 95 or 96 wherein the first and/or second *Rhodococcus* strains comprise *Rhodococcus erythropoli* and/or *Rhodococcus qingshengii*.

98. The composition of any one of claims 95 through 97 wherein first and/or second *Rhodococcus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 116-117..

99. The composition of any one of claims 11-13, 27-28, 44-47 or 59-61 wherein the one or more *Amycolatopsis* microbes comprise a first *Amycolatopsis* strain.

100. The composition of claim 99 wherein the one or more *Amycolatopsis* microbes comprise a second *Amycolatopsis* strain, wherein the second *Amycolatopsis* strains is different from the first *Amycolatopsis* strain.

101. The composition of claim 100 wherein the one or more *Amycolatopsis* microbes comprise a third *Amycolatopsis* strain, wherein the third *Amycolatopsis* strains is different from the first and second *Amycolatopsis* strains.

102. The composition of claim 101 wherein the one or more *Amycolatopsis* microbes comprise a fourth *Amycolatopsis* strain, wherein the fourth *Amycolatopsis* strains is different from the first, second, and third *Amycolatopsis* strains.

103. The composition of claim 102 wherein the one or more *Amycolatopsis* microbes comprise a fifth *Amycolatopsis* strain, wherein the fifth *Amycolatopsis* strains is different from the first, second, third, and fourth *Amycolatopsis* strains.

104. The composition of any one of claims 99-103 wherein the first, second, third, fourth, and/or fifth *Amycolatopsis* strains comprise *Amycolatopsis lurida* and/or *Amycolatopsis*_OATH_54.

105. The composition of any one of claims 99-104 wherein the first, second, third, fourth, and/or fifth *Amycolatopsis* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 110-115.

106. The composition of any one of claims 12-13, 28, 46-47 or 58-61 wherein the one or more *Lysinibacillus* microbes comprise a first *Lysinibacillus* strain.

107. The composition of claim 106 wherein the one or more *Lysinibacillus* microbes comprise a second *Lysinibacillus* strain, wherein the second *Lysinibacillus* strain is different from the first *Lysinibacillus* strain.

108. The composition of claim 107 wherein the one or more *Lysinibacillus* microbes comprise a third *Lysinibacillus* strain, wherein the third *Lysinibacillus* strain is different from the first and second *Lysinibacillus* strains.

109. The composition of claim 108 wherein the one or more *Lysinibacillus* microbes comprise a fourth *Lysinibacillus* strain, wherein the fourth *Lysinibacillus* strain is different from the first, second, and third *Lysinibacillus* strains.

110. The composition of claim 109 wherein the one or more *Lysinibacillus* microbes comprise a fifth *Lysinibacillus* strain, wherein the fifth *Lysinibacillus* strain is different from the first, second, third, and fourth *Lysinibacillus* strains.

111. The composition of any one of claims 106 through 110 wherein the first, second, third, fourth, and/or fifth *Lysinibacillus* strains comprise *Lysinibacillus capsici*.

112. The composition of any one of claims 106 through 111 wherein the first, second, third, fourth, and/or fifth *Lysinibacillus* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to any one of SEQ ID NOs: 1-9.

113. A composition comprising one or more microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2.

114. The composition of any one of the previous claims comprising one or more microbes of ATCC deposits designated 1-45, deposited as ATCC Nos. PTA-127367-127413, respectively, as shown in Table 2.

115. The composition of any one of the previous claims further comprising a liquid medium in which the one or more microbes are distributed.

116. A composition comprising a plurality of particles, wherein each particle comprises a composition of any one of claims 1 through 115.

117. A delayed release composition comprising a plurality of particles, wherein the particles comprises one or more microbes, and wherein the plurality of particles comprises a first population of particles wherein each particle of the first population comprises one or more first components configured to confine at least a portion of the microbes to the particles, and wherein the one or more first components are such that the one or more first components lose sufficient integrity upon exposure to one or more environmental triggers that at least a portion of the confined microbes are released from the particles.

118. The composition of any one of the previous claims further comprising one or more agriculturally acceptable adjuvants.

119. A population of seeds, seedlings, or other plant propagules comprising at least 10, 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, or and/or not more than 12, 15, 17, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, or 120 different microbes, wherein at least 10, 20, 30, 40, 50, 60, 70, 80, 90, or 95%, or 100%, of the microbes are heterologous to the seeds, seedlings, or other plant propagules, wherein at least a portion of the microbes of the composition are associated with the seeds, seedlings, or other plant propagules.

120. A composition comprising soil in which plants are growing or have grown wherein the soil comprises at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, or 100 and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40, or 1-150, preferably 1-100, more preferably 2-80, even more preferably 2.

121. A composition comprising soil in which plants are growing or have grown wherein the soil comprises at least 1, 2, 5, 10, 15, 20, 30, 35, 40, or 45 different microbes comprising composition of any one of any one of claims 1 through 115.

122. A plant or plant part comprising one or more microbes of the composition of any one of any one of claims 1 through 115 disposed on or in the plant or plant part.

123. A composition comprising a population of plants wherein the plants or part of the plants comprises the microbe or microbes of the composition of any one of claims 1 through 115 disposed on or in the plant or plant part.

124. A method comprising applying the composition of any one of claims 1 through [00633], or a derivative thereof, to a plant, or a part thereof, and/or to soil or other growth medium in which the plant grows or will grow, in a first application.

125. A method comprising applying a composition comprising a plurality of microbes to an area comprising soil by aerial application.

126. A method comprising applying to a plant growth medium

(a) a plurality of microbes, and

(b) one or more macronutrients,

(c) one or more micronutrients, and/or

(d) one or more carbon sources,

wherein a composition and/or effective amount of (a), (b), (c) and/or (d) is determined at least in part by one or more results of a first test on one or more samples comprising growth medium to which the plurality of microbes is to be applied or has been applied and/or a component of a plant or plants growing in the growth medium.

127. A method comprising contacting a surface of a seed, seedling, or other plant propagule with a composition of any one of claims 1 through 115, or a derivative produced from the composition.

128. A method comprising contacting surfaces of a populations of seeds, seedlings, or other plant propagules with a composition of any one of claims 1 through 115, or a derivative produced from the composition.

129. Use of the composition of any one of claims 1 through 115 in reducing methane production in soil in which plants grow compared to before use of the composition.

130. Use of the composition of any one of claims 1 through 115 in coating a surface of seeds, seedlings, or other plant propagules with one or more microbes of the composition.

131. Use of the composition of any one of claims 1 through 115 in in increasing beneficial organisms in soil in which plants grow and to which composition applied, compared to without.

132. Use of the composition of any one of claims 1 through 115 in transitioning to organic farming in 3 years or less, or 2 years or less, or 1.5 years or less.

133. Use of the composition of any one of any one of claims 1 through 115 in improving soil density, soil water holding capacity, soil water retention capacity, in soil in which plants grow, compared to without.

134. Use of the composition of any one of claims 1 through 115 in increasing mycorrhizal fungi on or in roots of plant, compared to a reference plant

135. Use of the composition of any one of claims 1 through 115 in preventing or reducing flooding.

136. Use of the composition of any one of claims 1 through 115 in decreasing use of synthetic fertilizer, herbicide, and/or pesticide on plants or soil in which plants grow, compared to without.

137. Use of the composition of any one of claims 1 through 115 in increasing nutrient uptake by a plant grown in soil to which composition applied compared to without.

138. Use of the composition of any one of claims 1 through 115 in decreasing uptake of one or more toxins, e.g., heavy metals, by plants grown in soil comprising composition.

139. Use of the composition of any one of claims 1 through 115 in increasing plant nutrient density of a plant grown in soil to which composition applied compared to without.

140. Use of the composition of any one of claims 1 through 115 in reducing carbon footprint for raising livestock.

141. Use of the composition of any one of claims 1 through 115 in increasing oil production of a plant not cannabis.

142. Use of the composition of any one of claims 1 through 115 in regenerating degraded soil.

143. A method comprising combining a first population of microbes comprising microbes of any one of *Streptomyces* designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) as shown in Table 2 and a second population of microbes, different from the first.

144. A method of growing one or more microbes comprising inoculating a heterologous medium with a first population of microbes comprising microbes of the composition of any one of claims 1 through 115 and providing suitable conditions for one or more microbes to grow.

145. A composition comprising a pure population of microbes of the composition of any one of claims 1 through 115 and a heterologous growth medium.

146. A composition consisting essentially of a pure population of of microbes of the composition of a any one of claims 1 through 115 and a heterologous growth medium.

147. A method for enhancing a rate at which atmospheric carbon is converted to carbon products in soil in which plants are grown and/or in the plants comprising applying a composition comprising one or more microbes to the plants and/or soil,in a first application, wherein the rate is greater than that for reference soil and/or plants in which the plants are grown without the composition.

148. A method of increasing soil carbon content comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil in which the plants are grown or will be grown, and/or the plants, a first application of a composition comprising a plurality of different microbes; and

(ii) providing suitable conditions for the plants to grow in the soil for the period of time; thereby increasing soil carbon content.

149. A composition comprising soil and plants growing in the soil, wherein the plants comprise parts in the soil, *e.g.*, roots, and wherein the soil and plant parts comprise

(i) a carbon content of at least 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, or 35 kg/m^3 and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m^3, for example 0.5-40, preferably 2-

40, more preferably 5-40, even more preferably 7-35, yet more preferably 7-30, still more preferably 7-25 kg/m^3 of soil; and

(ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, or microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40.

150. A method of obtaining a carbon credit comprising allowing plants to grow in an area of soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and

(ii) providing conditions for the plants to grow in the soil;

(iii) determining the increase in soil carbon content over the period of time in the area of soil; and

(iv) based at least in part on (iii), obtaining a carbon credit.

151. A method of reducing soil methane production comprising allowing plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil in which the plants are grown or will be grown, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and

(ii) providing conditions for the plants to grow in the soil;thereby increasing decreasing soil methane production.

152. A method of transferring atmospheric carbon to soil in which plants grow comprising

(i) applying a composition comprising a plurality of different microbes to the soil, plants, plant parts, and/or seed of the plants, wherein the composition is applied over an area of at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares; and

(ii) providing conditions suitable for growth of the plants for a period of time, thereby transferring atmospheric carbon to the soil to increase carbon content of the soil.

153. A method of reducing an overall carbon footprint for raising domesticated animals comprising feeding the animals, and/or allowing the animals to feed on, plants or parts of plants, wherein the plants have been or are growing in soil to which has been applied a composition comprising a plurality of different microbes, wherein the composition

(i) increases carbon dioxide transfer from atmosphere to soil thus increasing carbon content of the soil, compared to without the composition;

(ii) increases biomass of the plants in a given area, compared to without the composition, so that carbon produced per unit biomass of plants is decreased; and

(iii) increases nutrient density of the plants, compared to without the composition, so that less biomass of plants is used to produce a given amount of increase in economically valuable attribute of the domesticated animals

or a combination thereof, thus decreasing overall carbon footprint for raising the domesticated animals.

154. A method of obtaining carbon credit or other economic benefit comprising

(i) determining an increase in carbon content of soil in which plants grow after

(a) applying a composition comprising a plurality of different microbes to the soil, plants, plant parts, and/or seed of the plants, wherein the composition is applied over an area of at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares, and

(b) providing conditions suitable for growth of the plants for a period of time, thereby transferring atmospheric carbon to the soil to increase carbon content of the soil; and

(ii) obtaining the carbon credit and/or other economic benefit based, at least in part, on the increase in carbon content determined in (i).

155. A system comprising

(i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more second entities;

(ii) the second entity, or a plurality of second entities, that

(a) owns, controls, or otherwise has rights to land in an area of land on which plants grow and

(b) uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants

grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities,

wherein the area of land at least 1000, 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, or 500M hectares and/or not more than 10,000, 100,000, 1M, 10M, 50M, 100M, 250M, 500M, or 1B hectares, for example 1000 to 1B, preferably 10,000 to 1B, more preferably 100,000 to 1B, even more preferably 1M to 1B hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares;

(iii) an agreement between the first and second entities or between the first entity and each of the plurality of second entities that delineates an apportionment of the economic benefits between the first and second entities or between the first entity and each of the plurality of second entities; and

(iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines an apportionment between the first and second entities or between the first entity and each of the plurality of second entities and communicates information comprising the apportionment to the first and/or second entities.

156. A method of obtaining an economic benefit from land on which plants are grown, wherein the land comprises at least 10, 100, 1000, 10,000, 100,000, 1M, or 10M, hectacres, comprising

(i) obtaining and using one or more compositions comprising a microbial consortium, wherein

(a) the one or more compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity, or plurality of second entities that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity

(b) the second entity or plurality of second entities uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity or each of the plurality of second entities ;

(ii) determining a quantity of the one or more economic benefits; and

(iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities.

157. A method of reducing water use for growth and/or maintenance of plants in soil comprising allowing the plants to grow and/or be maintained in the soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil, the plants, a first application of a composition comprising a plurality of different microbes or a derivative thereof; and

(ii) providing suitable conditions for the plants to grow and/or be maintained in the soil for a period of time,;

thereby decreasing the amount of water necessary to produce a given amount of biomass from the plants and/or to maintain the plants in a desired state, compared to the amount of water necessary to produce the biomass and/or maintain the plants in a desired state for reference soil and plants, for the period of time.

158. A method of increasing water holding capacity of soil in which plants are grown comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes or a derivative thereof; and

(ii) providing suitable conditions for the plants to grow in the soil for a period of time;

thereby increasing the water holding capacity of the soil, for example, WHC compared to reference soil and plants.

159. A composition comprising soil in which plants are growing or have grown wherein the soil comprises

(i) a water holding capacity of at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt and/or not more than 25, 30, 35, 40, 45, 50, 55, 60, 65, or 70% wt/wt, for example, 20-70%, preferably 25-65%, more preferably 25-55%, yet more preferably 30-65%, still more preferably 35-65%, yet still more preferably 35-55%; and

(ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, or 100, and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40, or preferably 1-150, more preferably 1-100, even more preferably 1-70, yet more preferably 1-50.

160. A composition comprising soil in which plants are growing or have grown wherein the soil comprises

(i) an average density of at least 0.8, 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, or 1.70 and/or not more than 0.9, 1.0, 1.05, 1.10, 1.15, 1.20, 1.25, 1.30, 1.35, 1.40, 1.45, 1.50, 1.55, 1.60, 1.65, 1.70, 1.75, 1.80, 1.85, 1.90, or 1.95, for example, 1.0-1.90, preferably 1.05 to 1.85, more preferably 1.10 to 1.50, even more preferably 1.20-1.75, yet more preferably 1.35-1.70, still more preferably 1.55-1.85 g/cm3 dry weight of soil; and

(ii) at least 1, 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, or 100, and/or not more than 2, 5, 10, 15, 20, 30, 35, 40, 45, 50, 70, 100, or 150 different microbes that are heterologous to the soil and/or plants, for example, at least 1, preferably at least 5, more preferably at least 10, even more preferably at least 15, yet more preferably at least 25, still more preferably at least 40 or preferably 1-150, more preferably 1-100, even more preferably 1-70, yet more preferably 1-50

161. A method of modulating, e.g., improving, one or more characteristics of soil in which plants grow and/or are maintained, comprising allowing the plants to grow in the soil for a period of time, wherein the soil and/or plants have been treated by

(i) applying to the soil in which the plants are grown or will be grown and/or the plants, a first application of a composition comprising a plurality of different microbes; and

(ii) providing suitable conditions for the plants to grow in the soil for the period of time

thereby modulating, e.g,, improving the one or more characteristics compared to reference soil and plants.

162. A method of regenerating vegetation in a soil that has been partially or completely depleted of one or more types of vegetation and/or has reduced capacity to grow and/or maintain new vegetation, comprising

(i) applying to the soil, plants growing or to be grown in the soil, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and

(ii) providing suitable conditions for the plants to grow in the soil for a period of time.

163. A method of repairing damaged or degraded soil comprising

(i) applying to the soil a first application of a composition comprising a plurality of different microbes; and

(ii) providing suitable conditions for plants to grow in the soil for the period of time.

164. A method for decreasing or eliminating flooding on land that has experienced or is likely to experience flooding, wherein soil of the land has grown, is growing, or will grow plants, comprising

(i) applying to the soil, the plants, and/or seeds of the plants a first application of a composition comprising a plurality of different microbes; and

(ii) providing suitable conditions for the plants to grow in the soil for the period of time;

thereby decreasing or eliminating flooding on the land.

165. A method for increasing density of one or more nutrients in plants or plant parts, e.g., plants or plant parts to be consumed by animals, comprising

(i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/orthe plants, ; and

(ii) providing conditions suitable for growth of the plants for a period of time, e.g., a period of time sufficient for the plants or plant parts to be suitable for consumption by the animals;

thereby increasing density of the one or nutrients in the plants or plant parts compared to reference plants or plant parts.

166. A method for increasing uptake of one or more plant nutrients by plants grown in soil comprising

(i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/or the plants; and

(ii) providing conditions suitable for growth of the plants and proliferation and/or other actions of the microbes for a suitable duration for plant nutrient uptake to increase;

whereby plant nutrient uptake by the plants is increased.

167. A method for converting one or more plant nutrients in soil in which plants are grown from non-bioavailable to bioavailable form (i) applying a composition comprising a plurality of different microbes to the soil in which the plants are grown or will be grown and/orthe plants; and

(ii) providing conditions suitable for growth of the plants and proliferation and/or other actions of the microbes for a duration sufficient for the one or more plant nutrients in the soil to convert from non-bioavailable to bioavailable form;

whereby the one or more plant nutrients are converted from non-bioavailable to bioavailable form.

168. A composition comprising a plant comprising

(i) an above-ground portion; and

(ii) a below-ground portion, wherein the below-ground portion comprises roots of the plant and soil associated with the roots, wherein the below-ground portion comprises

(a) one or more microbes heterologous to the soil and/or plant; and

(b) a concentration of bio-available nutrient that is greater than reference plant and soil.

169. A composition comprising a plant, e.g. wherein the plant or part of the plant is for animal consumption, and soil in which the plant is growing, wherein

(i) the soil and/or roots of the plant in the soil comprise one or more microbes heterologous to the soil and/or plant; and

(ii) the plant or plant part comprises a density of one or more nutrients, e.g., one or more nutrients for the animal, that is greater than reference plant or plant part

170. A method to convert non-organic agricultural practice to organic agricultural practice comprising

(i) applying a composition comprising a plurality of microbes to plants, and/or to soil in which the plants grow or will grow, in a first application at a first time, wherein up to the first time the plants and soil were subject to non-organic farming practice;

(ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time

wherein after the period of time the non-organic agricultural practice has been converted to an organic agricultural practice.

171. A method for reducing concentration of a toxin in a soil, reducing uptake of the toxin by plants growing in the soil, and/or reducing a concentration of the toxin in the plants or plant parts, comprising

(i) applying a composition comprising a plurality of microbes to the plants, or parts thereof, and/or to the soil, in a first application;

(ii) providing conditions suitable for growth of the plants and proliferation and other actions of the microbes for a period of time

wherein after the period of time concentration of the toxin in the soil, uptake of the toxin by plants growing in the soil, and/or concentration of the toxin in the plants or plant parts is reduced compared to before the first application.

172. A system comprising

(i) a first entity that produces, distributes, or otherwise supplies one or more compositions comprising a plurality of different microbes to one or more other entities;

(ii) a second entity, or a third entity controlled directly or indirectly, at least in part, by the second entity, that obtains, directly or indirectly, the one or more compositions comprising a microbial consortium from the first entity, and uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable, in whole or in part, to the use of the one or more compositions, are achieved for the second entity;

(iii) an agreement between the first and second entities that delineates an apportionment of the economic benefits between the first and second entities; and

(iv) a processor that receives information regarding the agreement and information regarding the one or more economic benefits, determines the apportionment between the first and second entities, and communicates information comprising the apportionment to the first and/or second entities.

173. A method of obtaining an economic benefit from land on which plants are grown comprising

(i) obtaining and using one or more compositions comprising a plurality of different microbes, wherein

(a) the one or more compositions are supplied by a first entity that produces, distributes, or otherwise supplies the one or more compositions to a second entity that owns, controls, manages, or otherwise has rights to land in an area of land on which plants grow, or a third entity controlled directly or indirectly, at least in part, by the second entity, and

(b) the second entity uses the one or more compositions in a manner that comprises applying the one or more compositions to the plants, plant parts, seed of the plants, and/or soil in which the plants grow, whereby one or more economic benefits, attributable in whole or in part, to the use of the one or more compositions, are achieved for the second entity;

(ii) determining a quantity of the one or more economic benefits; and

(iii) apportioning the quantity of the one or more economic benefits between the first and second entities or between the first entity and each of the plurality of second entities.

174. A method of improving one or more characteristics of a tree rooted in soil comprising

(i) providing one or more nutrients to the soil in which the tree is rooted; and

(ii) providing a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil and/or the tree in a first application.

175. A method of revitalizing a dormant tree comprising applying to the soil in which the tree is rooted and/or the tree a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes to the soil in wherein the microbial composition the tree is rooted in a first application and allowing the tree to grow for a duration of time.

176. A kit comprising

(i) a composition comprising at least 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, or 150 and/or not more than 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 150, or 200 different microbes in a first package; and

(ii) a composition comprising at least 1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, or 200 and/or not more than 2, 3, 4, 5, 7, 10, 15, 20, 30, 40, 50, 100, 200 or 500 nutrients in a second package, different from the first.