

MICROBIAL COMPOSITIONS AND METHODS

CROSS-REFERENCE TO RELATED APPLICATIONS

5 [0001] This application claims priority to U.S. Provisional Application No. 63/547,326, filed November 3, 2023, U.S. Provisional Application No. 63/599,944, filed November 16, 2023, U.S. Provisional Application No. 63/674,021, filed July 22, 2024, and U.S. Provisional Application No. 63/648,580, filed May 16, 2024, the contents of which are incorporated herein by reference in their entireties.

SEQUENCE LISTING

10 [0002] The instant application contains a Sequence Listing which has been submitted electronically in .XML format and is hereby incorporated by reference in its entirety. Said .XML copy, created on October 29, 2024, is named OATH-015_PCT2_SL.xml and is 1,102,911 bytes in size. The sequence listing contained in this .XML file is part of the specification and is hereby incorporated by reference herein in its entirety.

15

BACKGROUND

[0003] 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.

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INCORPORATION BY REFERENCE

[0004] 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.

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BRIEF DESCRIPTION OF THE DRAWINGS

[0005] 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:

30

[0006] Figure 1a shows a method of preparation of a microbial composition from individual microbial stocks.

[0007] Figure 1b shows a method of growth and treatment of a microbial stock.

- [0008] Figure 1c shows a method of preparation of a microbial composition.
- [0009] Figure 1d shows a method of combining one or more microbes and one or more heterologous components.
- [0010] Figure 2 shows the topography of a Maximum-Likelihood phylogenetic tree displaying 195 ribotype gene signatures representing the OSL probiotic culture collection.
- [0011] Figure 3 shows water holding capacity of soil samples.
- [0012] Figure 4 shows turf resulting from treated (right) and untreated (left) seeds.
- [0013] Figure 5 shows a box and whiskers chart of increased biomass in treated plants.
- [0014] Figure 6 shows common bean root biomass, in plants growing in soil treated with a microbial consortium and untreated.
- [0015] Figure 7 shows common bean shoot biomass, in plants growing in soil treated with a microbial consortium and untreated.
- [0016] Figure 8 shows common bean pod biomass, in plants growing in soil treated with a microbial consortium and untreated.
- [0017] Figure 9 shows grain biomass, in plants growing in soil treated with a microbial consortium and untreated.
- [0018] Figure 10 shows soil water content in soil in which almond trees were grown, soil treated with a microbial consortium and untreated.
- [0019] Figure 11 shows stem water potential in almond trees growing in soil treated with a microbial consortium and untreated.
- [0020] Figure 12 shows soil bulk density in soil in which almond trees were grown, soil treated with a microbial consortium and untreated.
- [0021] Figure 13 shows streaking pattern of agar plates streaked for purity determination.
- [0022] Figure 14 shows landscape inoculation of plates for solid state fermentation of microbes.

DETAILED DESCRIPTION

I. Compositions and methods

A. Microbes

- [0023] 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.

[0024] 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.

[0025] 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. In certain embodiments, the compositions and/or methods comprise one or more fungi. In certain embodiments, the compositions and/or methods comprise one or more bacteria and one or more fungi.

[0026] 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 include microbes belonging to the genus of *Streptomyces*. The microbe can be any suitable species of *Streptomyces*, including but not limited to *Streptomyces achromogenes*, *Streptomyces albogriseolus*, *Streptomyces antibioticus*, *Streptomyces bacillari*, *Streptomyces bikiniensis*, *Streptomyces bobili*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces echinatus*, *Streptomyces eurythermus*, *Streptomyces globosus*, *Streptomyces griseocaurantiacus*, *Streptomyces griseofuscus*, *Streptomyces griseoincarnatus*, *Streptomyces griseoruber*, *Streptomyces griseoviridis*, *Streptomyces kurssanovii*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces musisoli*, *Streptomyces nigra*, *Streptomyces nigrescens*, *Streptomyces olivaceus*, *Streptomyces rochei*, *Streptomyces sennicomposti*, *Streptomyces sp000721605*, *Streptomyces sp019049245*, and/or *Streptomyces toxytricini*, *Streptomyces achromogenes*,

Streptomyces albobogrusolus, *Streptomyces antibioticus*, *Streptomyces bacillari*, *Streptomyces bikiniensis*, *Streptomyces bobili*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces echinatus*, *Streptomyces eurythermus*, *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces griseofuscus*, *Streptomyces griseoincarnatus*, *Streptomyces griseoruber*,
 5 *Streptomyces griseoviridis*, *Streptomyces kurssanovii*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces musisoli*, *Streptomyces nigra*, *Streptomyces nigrescens*, *Streptomyces olivaceus*, *Streptomyces rochei*, *Streptomyces sennicomposti*, *Streptomyces sp000721605*, *Streptomyces sp019049245*, and/or *Streptomyces toxytricini*. In many cases, a species may be represented by more than one different strain; see Table 2A for strains of the above species, and
 10 SEQ ID NOs for 16S rRNA sequence or sequences associated with each strain, as well as ATCC deposit number in which the strain may be found. In some embodiments, a microbial composition of the present disclosure includes some or all of the microbes in the microbial consortia deposited with the American Type Culture Collection (ATCC) on October 30, 2024 and assigned deposit numbers PTA127834-127850. As used herein, a “16S rRNA sequence” or
 15 the like includes a RNA sequence for 16S rRNA or a nucleotide gene sequence for the 16S rRNA, as will be clear from context.

[0027] In certain embodiments, provided are compositions comprising microbes of one or more non-*Streptomyces* genera. In certain embodiments, provides are compositions comprising microbes of one or more species and/or strains of *Streptomyces* and microbes of one or more
 20 microbes of non-*Streptomyces* genera. In certain embodiments, the one or more non-*Streptomyces* genera comprise one or more of *Pseudomonas*, *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillis*, *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola_A*, *Neorhizobium*, *Nocardia*, *Nocardioideis*,
 25 *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, or *Zhihengliuella* or a combination thereof. In certain embodiments, provided are compositions comprising microbes of one or more species and/or strains of *Streptomyces* and microbes of the taxonomic class Bacilli, such as microbes of one or more genera including
 30 *Paenibacillus*, *Lysinibacillis*, *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, *Peribacillus*, and/or *Pristimantibacillus*. In many cases, a species may be represented by more than one different strain; see Table 2A for strains of the above species, and SEQ ID NOs for 16S rRNA sequence or sequences associated with each strain, as well as ATCC deposit number in which the strain may be found. In some embodiments, a microbial composition of the present disclosure includes some or all of the microbes in the microbial consortia deposited with the American Type Culture
 35 Collection (ATCC) on October 30, 2024 and assigned deposit numbers PTA127834-127850.

[0028] 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 and Table 2A.

Table 1 16S rRNA genetic sequences

SEQ ID NO	Genus/Species	Strain #
1	<i>Lysinibacillus capsici</i>	162
2	<i>Lysinibacillus capsici</i>	161
3	<i>Lysinibacillus capsici</i>	159
4	<i>Lysinibacillus capsici</i>	150
5	<i>Lysinibacillus capsici</i>	155
6	<i>Lysinibacillus capsici</i>	174
7	<i>Lysinibacillus capsici</i>	166
8	<i>Lysinibacillus capsici</i>	160
9	<i>Lysinibacillus capsici</i>	163
10	<i>Paenibacillus cellulositrophicus</i> A	56
11	<i>Paenibacillus cellulositrophicus</i> A	59
12	<i>Paenibacillus cellulositrophicus</i> A	62
13	<i>Paenibacillus cellulositrophicus</i> A	41
14	<i>Paenibacillus cellulositrophicus</i> A	67
15	<i>Paenibacillus cellulositrophicus</i> A	49
16	<i>Paenibacillus cellulositrophicus</i> A	65
17	<i>Paenibacillus illinoisensis</i>	206
18	<i>Aureimonas</i> A sp001425485	199
19	<i>Aureimonas</i> A sp001425485	112
20	<i>Aureimonas</i> A sp001425485	86
21	<i>Aureimonas</i> A sp001425485	87
22	<i>Bradyrhizobium elkanii</i>	209
23	<i>Bradyrhizobium elkanii</i>	191
24	<i>Bradyrhizobium elkanii</i>	136
25	<i>Bradyrhizobium elkanii</i>	182
26	<i>Bradyrhizobium elkanii</i>	188
27	<i>Bradyrhizobium elkanii</i>	145
28	<i>Bradyrhizobium elkanii</i>	121
29	<i>Bradyrhizobium elkanii</i>	144
30	<i>Bradyrhizobium elkanii</i>	115
31	<i>Bradyrhizobium denitrificans</i>	133
32	<i>Bradyrhizobium denitrificans</i>	122
33	<i>Bradyrhizobium denitrificans</i>	130
34	<i>Bradyrhizobium denitrificans</i>	193
35	<i>Bradyrhizobium denitrificans</i>	97
36	<i>Bradyrhizobium denitrificans</i>	181
37	<i>Bradyrhizobium denitrificans</i>	186
38	<i>Microvirga</i> sp OATH 1	21
39	<i>Pseudomonas poae</i>	14
40	<i>Pseudomonas</i> sp OATH 2	30
41	<i>Pseudomonas</i> sp OATH 3	33

SEQ ID NO	Genus/Species	Strain #
42	<i>Pseudomonas</i> sp OATH6	44
43	<i>Pseudomonas</i> poae	76
44	<i>Pseudomonas</i> sp OATH 16	77
45	<i>Pseudomonas</i> sp OATH 14	69
46	<i>Pseudomonas</i> azotoformans	158
47	<i>Pseudomonas</i> azotoformans	180
48	<i>Pseudomonas</i> azotoformans	167
49	<i>Pseudomonas</i> azotoformans	156
50	<i>Pseudomonas</i> azotoformans	24
51	<i>Pseudomonas</i> fluorescens	82
52	<i>Pseudomonas</i> fluorescens	80
53	<i>Pseudomonas</i> E sp002836515	42
54	<i>Pseudomonas</i> sp OATH 53	147
55	<i>Pseudomonas</i> sp OATH 56	165
56	<i>Pseudomonas</i> E sp003253735	200
57	<i>Pseudomonas</i> E sp003253735	207
58	<i>Pseudomonas</i> straminea	152
59	<i>Pseudomonas</i> sp OATH 55	164
60	<i>Pseudomonas</i> koreensis	52
61	<i>Pseudomonas</i> koreensis	70
62	<i>Pseudomonas</i> sp OATH 45	134
63	<i>Pseudomonas</i> sp OATH 51	142
64	<i>Pseudomonas</i> koreensis	28
65	<i>Pseudomonas</i> koreensis	61
66	<i>Pseudomonas</i> sp OATH 15	71
67	<i>Pseudomonas</i> sp OATH 4	39
68	<i>Streptomyces</i> violaceorectus	114
69	<i>Streptomyces</i> sp OATH 38	110
70	<i>Streptomyces</i> sp OATH 40	116
71	<i>Streptomyces</i> rochei	123
72	<i>Streptomyces</i> labedae	113
73	<i>Streptomyces</i> rochei	189
74	<i>Streptomyces</i> griseoincarnatus	102
75	<i>Streptomyces</i> griseoincarnatus	23
76	<i>Streptomyces</i> griseoincarnatus	202
77	<i>Streptomyces</i> griseoincarnatus	75
78	<i>Streptomyces</i> griseoincarnatus	74
79	<i>Streptomyces</i> nigra	73
80	<i>Streptomyces</i> sp OATH 8	48
81	<i>Streptomyces</i> sp OATH 12	60
82	<i>Streptomyces</i> sp OATH 22	90
83		
84	<i>Streptomyces</i> sp001509795	72
85	<i>Streptomyces</i> flavoviridis	81
86	<i>Streptomyces</i> sp OATH 41	117

SEQ ID NO	Genus/Species	Strain #
87	<i>Streptomyces</i> flavoviridis	27
88	<i>Streptomyces</i> fimbriatus	11
89	<i>Streptomyces</i> rochei	16
90	<i>Streptomyces</i> rochei	19
91	<i>Streptomyces</i> rochei	125
92	<i>Streptomyces</i> misionensis	127
93	<i>Streptomyces</i> misionensis	129
94	<i>Streptomyces</i> misionensis	128
95	<i>Streptomyces</i> misionensis	55
96	<i>Streptomyces</i> misionensis	37
97	<i>Streptomyces</i> misionensis	35
98	<i>Streptomyces</i> misionensis	131
99	<i>Streptomyces</i> misionensis	3
100	<i>Streptomyces</i> misionensis	36
101	<i>Streptomyces</i> misionensis	47
102	<i>Streptomyces</i> griseoviridis A	184
103	<i>Streptomyces</i> griseoviridis A	50
104	<i>Streptomyces</i> griseoviridis A	66
105	<i>Streptomyces</i> griseofuscus	2
106	<i>Streptomyces</i> sp OATH 10	54
107	<i>Streptomyces</i> griseofuscus	135
108	<i>Streptomyces</i> misionensis	17
109	<i>Streptomyces</i> misionensis	53
110	<i>Amycolatopsis</i> lurida	149
111	<i>Amycolatopsis</i> OATH 54	153
112	<i>Amycolatopsis</i> lurida	194
113	<i>Amycolatopsis</i> lurida	151
114	<i>Amycolatopsis</i> lurida	168
115	<i>Amycolatopsis</i> lurida	154
116	<i>Rhodococcus</i> qingshengii	187
117	<i>Rhodococcus</i> erythropolis	146
118	<i>Micrococcus</i> luteus	32
119	<i>Micrococcus</i> luteus	43
120	<i>Streptomyces</i> sp OATH 44	126
121	<i>Streptomyces</i> sp OATH 66	210
122	<i>Streptomyces</i> sp OATH 63	204
123	<i>Streptomyces</i> sp OATH 52	143
124	<i>Streptomyces</i> sp OATH B	5
125	<i>Streptomyces</i> sp OATH 57	170
126	<i>Streptomyces</i> sp OATH 49	140
127	<i>Streptomyces</i> sp OATH G	34
128	<i>Streptomyces</i> sp OATH 7	46
129	<i>Streptomyces</i> sp OATH 5	40
130	<i>Streptomyces</i> sp OATH 9	51
131	<i>Streptomyces</i> sp OATH 13	68

SEQ ID NO	Genus/Species	Strain #
132	<i>Streptomyces</i> sp OATH 46	137
133	<i>Streptomyces</i> sp OATH 12	63
134	<i>Streptomyces</i> lydicus	45
135	<i>Streptomyces</i> lydicus	203
136	<i>Streptomyces</i> lydicus	78
137	<i>Streptomyces</i> sp OATH 17	79
138	<i>Streptomyces</i> sp OATH D	7
139	<i>Streptomyces</i> sp OATH 50	141
140	<i>Streptomyces</i> sp OATH 26	94
141	<i>Streptomyces</i> griseoaurantiacus	26
142	<i>Streptomyces</i> griseoaurantiacus	18
143	<i>Streptomyces</i> sp OATH 65	208
144	<i>Streptomyces</i> sp OATH 27	57
145	<i>Streptomyces</i> sp OATH 61	197
146	<i>Streptomyces</i> sp AOTH 58	173
147	<i>Streptomyces</i> sp OATH A	4
148	<i>Streptomyces</i> sp OATH E	10
149	<i>Streptomyces</i> sp OATH 62	201
150	<i>Streptomyces</i> sp OATH 20	85
151	<i>Streptomyces</i> sp OATH 30	99
152	<i>Streptomyces</i> OATH 28	96
153	<i>Streptomyces</i> sp OATH 64	205
154	<i>Streptomyces</i> sp OATH F	13
155	<i>Streptomyces</i> sp OATH 22	89
156	<i>Streptomyces</i> sp OATH 44	132
157	<i>Streptomyces</i> sp OATH 43	124
158	<i>Streptomyces</i> sp OATH 59	179
159	<i>Streptomyces</i> sp900105755	25
160	<i>Streptomyces</i> sp900105755	20
161	<i>Streptomyces</i> sp900105755	196
162	<i>Streptomyces</i> sp OATH 11	58
163	<i>Streptomyces</i> sp OATH 19	84
164	<i>Streptomyces</i> sp OATH 36	108
165	<i>Streptomyces</i> sp OATH 47	138
166	<i>Streptomyces</i> sp OATH 48	139
167	<i>Streptomyces</i> sp OATH C	6
168	<i>Streptomyces</i> antibioticus B	22
169	<i>Streptomyces</i> antibioticus B	185
170	<i>Streptomyces</i> globosus	120
171	<i>Streptomyces</i> globosus	198
172	<i>Streptomyces</i> globosus	119
173	<i>Streptomyces</i> globosus	31
174	<i>Streptomyces</i> globosus	1
175	<i>Streptomyces</i> globosus	183
176	<i>Streptomyces</i> globosus	157

SEQ ID NO	Genus/Species	Strain #
177	<i>Streptomyces globosus</i>	176
178	<i>Streptomyces globosus</i>	178
179	<i>Streptomyces globosus</i>	175
180	<i>Streptomyces globosus</i>	177
181	<i>Streptomyces globosus</i>	172
182	<i>Streptomyces globosus</i>	171
183	<i>Streptomyces globosus</i>	169
184	<i>Streptomyces bikiniensis</i>	12
185	<i>Streptomyces</i> sp OATH 32	101
186	<i>Streptomyces</i> sp OATH 39	111
187	<i>Streptomyces</i> sp OAT 37	109
188	<i>Streptomyces</i> sp OATH 31	100
189	<i>Streptomyces</i> sp OATH 60	190
190	<i>Streptomyces</i> sp OATH 42	118
191	<i>Streptomyces cavourensis</i>	64
192	<i>Streptomyces bacillaris</i>	15
193	<i>Streptomyces</i> sp OATH 23	91
194	<i>Streptomyces bacillaris</i>	29
195	<i>Streptomyces cavourensis</i>	38
196	<i>Streptomyces bacillaris</i>	211

[0029] In certain embodiments provided herein, a composition or method utilizes one or more microbes. Any suitable microbes may be used.

[0030] Certain of the microbes described in this Application were deposited with the American Type Culture Collection (ATCC, Manassas, Va.) on November 15, 2022, and October 30, 2024, and assigned the deposit numbers shown in Table 2 and Table 2A, respectively. 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.

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

Designation	ATCC No.
9	PTA-127375
10	PTA-127376
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

Designation	ATCC No.
42	PTA-127408
43	PTA-127409
44	PTA-127410
45	PTA-127411
46	PTA-127412
47	PTA-127413

Table 2A 16s rRNA Genetic Sequences and ATCC deposit numbers for selected microbes

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH00011	197	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH00021	216	<i>Streptomyces</i>	<i>echinatu</i>	PTA-127836
OATH00031	228	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00071	273	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00072	282	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00081	292	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00101	207	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00102	304, 305	<i>Psuedomonas E</i>	<i>paracanis</i>	PTA-127844
OATH00103	208	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127849
OATH00143	345	<i>Microbacterium</i>	<i>oxydans</i>	PTA-127834
OATH00144	209	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127841
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00224	210	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00241	212	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00242	346	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00243	347	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00264	349	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00301	218	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00321	222	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127836

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH00322	224	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00323	223	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00331	225	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00342	356	<i>Microbacterium</i>	<i>resistens</i> (81%)	PTA-127834
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00351	358	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00352	226, 227, 360	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00353	229	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00354	359	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00371	361	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00372	362	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00373	230	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127837
OATH00373	363	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127837
OATH00374	231	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00374	364	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00375	233	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00376	232	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00381	235	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00382	234	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00383	365	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00384	366	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00402	238	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00403	237	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00404	240	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00412	367, 368, 369	<i>Streptomyces</i>	<i>griseoincarnatus</i>	
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00424	370	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00425	242	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00442	246	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00443	371, 372	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00492	248	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00493	374	<i>Microbacterium</i>	sp002979655	
OATH00521	249	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127837
OATH00522	375	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127836
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00564	376	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00581	377	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH00591	255	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00592	379	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00593	380	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00601	256	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH00641	260	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00651	383	<i>Streptomyces</i>	<i>misionensis</i>	
OATH00661	262, 263	<i>Streptomyces</i>	<i>chartreusis</i>	PTA-127837
OATH00662	384	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127836
OATH00663	385	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127836
OATH00681	386	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127836
OATH00691	264	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00692	265, 266	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00701	387	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00702	206	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00702	388	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00711	267	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00741	268	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00742	390	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00743	389	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00753	269	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00762	391	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00802	392	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00811	393	<i>Paenibacillus</i>	<i>cellulositrophicus</i>	PTA-127848
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00851	272	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00871	274	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00881	275	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00901	276	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00912	259, 258	<i>Streptomyces</i>	<i>globosus</i>	PTA-127844
OATH00913	382	<i>Streptomyces</i>	<i>nigrescens</i>	PTA-127840
OATH00921	398	<i>Streptomyces</i>	<i>griseoincarnatus</i>	
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01002	278	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127837
OATH01003	279	<i>Lysinibacillus</i>	<i>capsici</i>	PTA-127847
OATH01021	301	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01022	302	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01071	303	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01091	280	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH01101	306	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127835
OATH01102	307	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127835
OATH01112	281	<i>Psuedomonas E</i>	<i>paracarnis</i>	PTA-127849

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH01121	308	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127835
OATH01141	283	<i>Streptomyces</i>	<i>griseoviridis</i>	PTA-127841
OATH01142	309	<i>Streptomyces</i>	<i>griseoviridis</i>	PTA-127841
OATH01181	313, 311, 310, 314, 312	<i>Stenotrophomonas</i>	<i>geniculata</i>	PTA-127849
OATH01182	284	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01183	285	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01201	286	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01241	287	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01242	317	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01243	319	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127835
OATH01244	316	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01245	318	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127835
OATH01246	288	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127837
OATH01247	315	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127835
OATH01251	320	<i>Streptomyces</i>	<i>murinus</i>	PTA-127835
OATH01252	289	<i>Bacillus</i>	<i>haynesii</i>	PTA-127847
OATH01253	321	<i>Streptomyces</i>	<i>murinus</i>	PTA-127836
OATH01254	322	<i>Streptomyces</i>	<i>griseofuscus</i>	PTA-127836
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01262	291	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01263	323	<i>Paenibacillus</i>	<i>cellulositrophicus</i>	PTA-127848
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01272	324	<i>Pristimantibacillus</i>	<i>undefined</i>	PTA-127848
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01281	294	<i>Aneurinibacillus</i>	<i>aneurinityticus</i>	PTA-127839
OATH01281	327	<i>Aneurinibacillus</i>	<i>aneurinityticus</i>	PTA-127839
OATH01283	329	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01285	328	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01291	295	<i>Bacillus</i>	<i>licheniformis</i>	PTA-127847
OATH01292	331	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01302	298	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01303	299	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01304	332	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01305	333	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01306	334	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01311	335	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01312	336	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01313	338	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01314	337	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01315	339	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01316	340	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH01331	341	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01352	344	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01363	300	<i>Brevibacillus</i>	<i>panacihumi</i>	PTA-127848
OATH01371	199	<i>Paenibacillus</i>	<i>cellulolyticus</i>	PTA-127848
OATH01382	201	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01383	200	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH01411	203	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH01412	204, 205	<i>Streptomyces</i>	<i>murinus</i>	PTA-127849
OATH01431	459	<i>Pseudomonas_K</i>	<i>oryzae</i>	PTA-127849
OATH01441	479	<i>Bacillus_A</i>	<i>thuringiensis_K</i>	PTA-127847
OATH01451	480, 481	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01461	482	<i>Pseudomonas_K</i>	<i>oryzae</i>	PTA-127849
OATH01471	484, 483	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01481	485, 486	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01491	487	<i>Bacillus</i>	<i>safensis</i>	PTA-127848
OATH01501	488	<i>Cupriavidus</i>	<i>laharis</i>	PTA-127850
OATH01511	444	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01521	445, 446	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01531	447	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01541	448	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01551	449, 450	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01561	451	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01571	452	<i>Arthrobacter</i>	<i>siccitolerans</i>	PTA-127834
OATH01581	453, 454	<i>Priestia</i>	<i>megaterium</i>	
OATH01591	455	<i>Arthrobacter</i>	<i>nitrophenolicus</i>	PTA-127834
OATH01601	457, 458, 456	<i>Pseudomonas</i>	<i>delhiensis</i>	PTA-127849
OATH01611	460, 461	<i>Bacillus</i>	<i>safensis</i>	PTA-127847
OATH01621	462	<i>Bacillus</i>	<i>inaquosorum</i>	PTA-127847
OATH01631	463	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01641	464, 465	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01651	466	<i>Pseudomonas</i>	<i>delhiensis</i>	PTA-127849
OATH01661	467	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127849
OATH01671	468, 469	<i>Arthrobacter</i>	<i>pascens</i>	PTA-127834
OATH01681	470	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01691	471	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127850
OATH01701	472	<i>Zhihenghuella</i>	sp031178195_(90%)	PTA-127849
OATH01711	474, 473	<i>Arthrobacter</i>	sp019977195	PTA-127834
OATH01721	475	<i>Arthrobacter</i>	sp021129155_(94.97%)	PTA-127834
OATH01731	476	<i>Arthrobacter</i>	sp021129155	PTA-127834
OATH01741	477	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127850
OATH01751	478	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01761	412	<i>Nonomuraea</i>	<i>rhodomycinica</i>	PTA-127849

USID#	SEQ ID No(s)	Genus	species	Deposit #
OATH01771	424	<i>Nocardia</i>	<i>farcinica</i>	PTA-127849
OATH01781	436	<i>Kocuria</i>	<i>turfanensis</i>	PTA-127849
OATH01791	439	<i>Stutzerimonas</i>	<i>stutzeri</i> <i>Al</i>	PTA-127850
OATH01801	440	<i>Caldimonas</i>	<i>mangrovi</i> (87.99%)	PTA-127850
OATH01811	441	<i>Arthrobacter</i>	<i>phenanthrenivorans</i>	PTA-127834
OATH01821	442	<i>Terrimonas</i>	<i>undefined</i> (97%)	PTA-127850
OATH01831	443	<i>Kocuria</i>	<i>polaris</i> <i>A</i> (91%)	PTA-127849
OATH01841	402, 401	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01851	403	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127837
OATH01861	404	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01871	405	<i>Kocuria</i>	<i>polaris</i> <i>A</i> (91%)	PTA-127849
OATH01881	406	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH01891	407	<i>Arthrobacter</i>	sp006715285 (955%)	PTA-127834
OATH01901	408	<i>Kocuria</i>	<i>polaris</i> <i>A</i> (91%)	PTA-127849
OATH01911	409	<i>Actinoplanes</i>	<i>aureus</i> (88%)	PTA-127849
OATH01921	410	<i>Neorhizobium</i>	<i>petrolearium</i> (85%)	PTA-127850
OATH01931	411	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01941	413	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01951	414	<i>Streptomyces</i>	<i>nigra</i>	PTA-127844
OATH01961	415, 416	<i>Bacillus</i>	<i>inaquosorum</i>	PTA-127847
OATH01971	417	<i>Microvirga</i>	sp022346925 (95%)	PTA-127848
OATH01981	418	<i>Agromyces</i>	sp031178025 (89%)	
OATH01991	419	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH02001	420	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH02011	421	<i>Microbispora</i>	sp014161445	PTA-127849
OATH02021	422	<i>Erythrobacter</i>	sp006542605 (92%)	PTA-127850
OATH02031	423	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127838
OATH02041	425	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127838
OATH02051	426	<i>Streptomyces</i>	<i>bobili</i>	PTA-127839
OATH02061	428, 427	<i>Streptomyces</i>	<i>griseoruber</i> (95%)	PTA-127834
OATH02071	429	<i>Streptomyces</i>	sp000721605	PTA-127846
OATH02081	430	<i>Streptomyces</i>	<i>kurssanovii</i> (95%)	PTA-127835
OATH02091	431	<i>Streptomyces</i>	sp019049245 (91%)	PTA-127835
OATH02101	432	<i>Allosphingosinice lla</i>	sp011320075 (95%)	PTA-127850
OATH02111	433	<i>Mycetocola</i> <i>A</i>	<i>miduensis</i> (95%)	PTA-127849
OATH02121	434	<i>Nocardioides</i>	<i>undefined</i> (96%)	PTA-127849
OATH02131	435	<i>Bacillus</i>	<i>paralicheniformis</i>	PTA-127847
OATH02141	437	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH02151	438	<i>Bacillus</i>	<i>paralicheniformis</i>	PTA-127847

[0031] As shown in Example 32, the original 140 stocks (ATCC deposit #s PTA-127367 through PTA-127413 as shown in Table 2 and Oath-maintained deposits O-46 through O-140) were sequenced using PacBio full length 16S RNA gene sequencing. Once the results were ready

16S sequences were identified using GenBank's data base and sequence homology searches. 99% sequence identity was used as the threshold value to add a species name to each 16S gene. The outcome of this analyses showed that multiple of the original 140 stocks comprised more than one microbial species. A new set of internal stocks was developed comprising single microbial isolates. Literature and conventional microbiology knowledge were used to select correct phenotypes for further sequencing evaluation. If there were any unknown phenotypes they were also sent for 16S sequencing. The effort resulted in the production of the isolates shown in **Table 32 (Example 32)**, reproduced below. **Table 32** shows the updated isolate (ID# and taxonomic prediction) information as well as its corresponding designation from **Table 1** (Strain # and Genus/Species). The matches are represented with BLAST comparisons of the 16S rRNA sequences. BLAST values (% identity and alignment length) are shown under the alignment info. Using Tables 1, 2, 2A, and 32, deposit numbers, 16S rRNA genetic sequences, and genus and species designations of the bacteria deposited with ATCC on November 15, 2022 may be matched with those deposited on October 30, 2024.

Table 32: isolate correlation matrix

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Align ment lengt h
OATH 00011	<i>Streptomyces toxytricini</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00021	<i>Streptomyces echinatu</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00031	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1448
OATH 00041	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448
OATH 00051	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00052	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00053	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00071	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00072	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00081	<i>Streptomyces rochei</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00091	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448
OATH 00101	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces</i> sp900105755	100	1218
OATH 00102	<i>Pseudomonas E paracanis</i>	197	<i>Streptomyces</i> sp. OATH_61	100	623
OATH 00102	<i>Pseudomonas E paracanis</i>	10	<i>Streptomyces</i> sp. OATH_E	100	876

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00103	<i>Streptomyces sennicomposti</i>	24	<i>Pseudomonas azotoformans</i>	100	1459
OATH 00143	<i>Microbacterium oxydans</i>	99	<i>Streptomyces</i> sp. OATH_30	93.814	1455
OATH 00144	<i>Streptomyces griseoincarnatus</i>	23	<i>Streptomyces griseoincarnatus</i>	100	1450
OATH 00223	<i>Streptomyces misionensis</i>	17	<i>Streptomyces misionensis</i>	100	1447
OATH 00224	<i>Microbacterium paraoxydans</i>	99	<i>Streptomyces</i> sp. OATH_30	92.995	1456
OATH 00241	<i>Streptomyces sennicomposti</i>	4	<i>Streptomyces</i> sp. OATH_A	100	1448
OATH 00242	<i>Streptomyces sennicomposti</i>	57	<i>Streptomyces</i> sp. OATH_27	100	912
OATH 00243	<i>Streptomyces sennicomposti</i>	57	<i>Streptomyces</i> sp. OATH_27	100	912
OATH 00252	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00253	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00261	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00262	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00263	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00264	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00291	<i>Streptomyces griseoaurantiacus</i>	18	<i>Streptomyces griseoaurantiacus</i>	100	1446
OATH 00292	<i>Streptomyces griseoaurantiacus</i>	18	<i>Streptomyces griseoaurantiacus</i>	100	1446
OATH 00301	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 00312	<i>Streptomyces bacillari</i>	15	<i>Streptomyces bacillaris</i>	100	1450
OATH 00313	<i>Streptomyces bacillari</i>	15	<i>Streptomyces bacillaris</i>	100	1450
OATH 00321	<i>Streptomyces griseoincarnatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00322	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00323	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00331	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00342	<i>Microbacterium resistens</i>	99	<i>Streptomyces</i> sp. OATH_30	92.376	1456
OATH 00343	<i>Streptomyces achromogenes</i>	68	<i>Streptomyces</i> sp. OATH_13	100	1275
OATH 00351	<i>Streptomyces olivaceus</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00352	<i>Streptomyces olivaceus</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00352	<i>Streptomyces olivaceus</i>	174	<i>Lysinibacillus capsici</i>	93.659	410

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00353	<i>Streptomyces rochei</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00354	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00371	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00372	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00373	<i>Streptomyces antibioticus</i>	5	<i>Streptomyces sp. OATH B</i>	100	1449
OATH 00374	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00375	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00376	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00381	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces sp900105755</i>	99.507	1218
OATH 00382	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00383	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	99.517	1448
OATH 00384	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	99.102	1448
OATH 00392	<i>Streptomyces bacillari</i>	64	<i>Streptomyces cavourensis</i>	100	1276
OATH 00402	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	99.033	1448
OATH 00403	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	100	1217
OATH 00404	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	99.033	1448
OATH 00412	<i>Streptomyces griseoincarnatus</i>	129	<i>Streptomyces misionensis</i>	100	688
OATH 00412	<i>Streptomyces griseoincarnatus</i>	139	<i>Streptomyces sp. OATH 48</i>	100	432
OATH 00412	<i>Streptomyces griseoincarnatus</i>	170	<i>Streptomyces sp. OATH 57</i>	100	832
OATH 00413	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00421	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00422	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00423	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00424	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00425	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00442	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	100	1217
OATH 00443	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH E</i>	100	631
OATH 00443	<i>Streptomyces sennicomposti</i>	197	<i>Streptomyces sp. OATH 61</i>	100	623

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00483	<i>Microbacterium paraoxydans</i>	99	<i>Streptomyces</i> sp. OATH_30	93.814	1455
OATH 00491	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00492	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00493	<i>Microbacterium</i> sp002979655	99	<i>Streptomyces</i> sp. OATH_30	93.814	1455
OATH 00521	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00522	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00562	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00563	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00564	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00571	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00581	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 00591	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00592	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces</i> sp900105755	100	1218
OATH 00593	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.448	1448
OATH 00601	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00641	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1448
OATH 00651	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00661	<i>Streptomyces chartreusis</i>	174	<i>Lysinibacillus capsici</i>	87.705	488
OATH 00661	<i>Streptomyces chartreusis</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00662	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00663	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00681	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00691	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.507	1218
OATH 00692	<i>Streptomyces sennicomposti</i>	180	<i>Pseudomonas azotoformans</i>	87.013	462
OATH 00692	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00701	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00702	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00711	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00741	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00742	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00743	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00753	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.448	1448
OATH 00762	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00801	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00802	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00811	<i>Paenibacillus cellulositrophicus</i>	59	<i>Paenibacillus cellulositrophicus</i> A	100	1266
OATH 00823	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00851	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00871	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.931	1448
OATH 00881	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00891	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00892	<i>Lysinibacillus sphaericus</i>	129	<i>Streptomyces misionensis</i>	98.243	569
OATH 00892	<i>Lysinibacillus sphaericus</i>	162	<i>Lysinibacillus capsici</i>	98.711	1474
OATH 00892	<i>Lysinibacillus sphaericus</i>	170	<i>Streptomyces</i> sp. OATH_57	99.685	634
OATH 00901	<i>Streptomyces sennicomposti</i>	4	<i>Streptomyces</i> sp. OATH_A	100	1448
OATH 00912	<i>Streptomyces globosus</i>	45	<i>Streptomyces lydicus</i>	100	1451
OATH 00912	<i>Streptomyces globosus</i>	174	<i>Lysinibacillus capsici</i>	81.481	108
OATH 00913	<i>Streptomyces nigrescens</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00921	<i>Streptomyces griseoincarnatus</i>	23	<i>Streptomyces griseoincarnatus</i>	100	1450
OATH 00923	<i>Rhodococcus erythropolis</i>	146	<i>Rhodococcus erythropolis</i>	100	1440
OATH 00961	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01002	<i>Streptomyces misionensis</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01003	<i>Lysinibacillus capsici</i>	174	<i>Lysinibacillus capsici</i>	100	1279
OATH 01021	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01022	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01071	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01091	<i>Streptomyces toxytricini</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01101	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 01102	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 01112	<i>Pseudomonas E paracanis</i>	156	<i>Pseudomonas azotoformans</i>	100	1459
OATH 01121	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01141	<i>Streptomyces griseoviridis</i>	50	<i>Streptomyces griseoviridis</i> A	100	1447
OATH 01142	<i>Streptomyces griseoviridis</i>	66	<i>Streptomyces griseoviridis</i> A	100	1447
OATH 01181	<i>Stenotrophomonas geniculata</i>	197	<i>Streptomyces</i> sp. OATH_61	100	460
OATH 01181	<i>Stenotrophomonas geniculata</i>	170	<i>Streptomyces</i> sp. OATH_57	100	742
OATH 01181	<i>Stenotrophomonas geniculata</i>	211	<i>Streptomyces bacillaris</i>	100	20
OATH 01181	<i>Stenotrophomonas geniculata</i>	183	<i>Streptomyces globosus</i>	80.769	104
OATH 01181	<i>Stenotrophomonas geniculata</i>	193	<i>Bradyrhizobium denitrificans</i>	78.409	88
OATH 01182	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 01183	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 01201	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 01241	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01242	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01243	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01244	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01245	<i>Streptomyces griseoincarnatus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01246	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01247	<i>Streptomyces misionensis</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01251	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01252	<i>Bacillus haynesii</i>	166	<i>Lysinibacillus capsici</i>	94.164	1268
OATH 01253	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01254	<i>Streptomyces griseofuscus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01261	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01262	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01263	<i>Paenibacillus cellulositrophicus</i>	59	<i>Paenibacillus cellulositrophicus</i> A	100	1266
OATH 01271	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01272	<i>Pristimantibacillus undefined</i>	65	<i>Paenibacillus cellulositrophicus</i> A	96.921	1234
OATH 01273	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01281	<i>Aneurinibacillus aneurinilyticus</i>	155	<i>Lysinibacillus capsici</i>	88.784	1480
OATH 01283	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01285	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01291	<i>Bacillus licheniformis</i>	163	<i>Lysinibacillus capsici</i>	91.87	1476
OATH 01292	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01293	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01294	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01301	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01302	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01303	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01304	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01305	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01306	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01311	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01312	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01313	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01314	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01315	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01316	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01331	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 01341	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01351	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01352	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01363	<i>Brevibacillus panacihumi</i>	174	<i>Lysinibacillus capsici</i>	91.424	1271

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01371	<i>Paenibacillus cellulositrophicus</i>	59	<i>Paenibacillus cellulositrophicus</i> A	100	1266
OATH 01382	<i>Bacillus velizensis</i>	162	<i>Lysinibacillus capsici</i>	92.333	1226
OATH 01383	<i>Bacillus velizensis</i>	162	<i>Lysinibacillus capsici</i>	91.667	1476
OATH 01401	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448
OATH 01411	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01412	<i>Streptomyces murinus</i>	80	<i>Pseudomonas fluorescens</i>	86.429	420
OATH 01412	<i>Streptomyces murinus</i>	111	<i>Streptomyces</i> sp. OATH_39	89.011	1456
OATH 01431	<i>Pseudomonas_K oryzae</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01441	<i>Bacillus_A thuringiensis_K</i>	174	<i>Lysinibacillus capsici</i>	94.266	1273
OATH 01451	<i>Priestia aryabhattai</i>	160	<i>Lysinibacillus capsici</i>	89.931	437
OATH 01451	<i>Priestia aryabhattai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017
OATH 01461	<i>Pseudomonas_K oryzae</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01471	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.701	1019
OATH 01471	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.146	529
OATH 01481	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.189	523
OATH 01481	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.706	1020
OATH 01491	<i>Bacillus safensis</i>	162	<i>Lysinibacillus capsici</i>	92.417	1477
OATH 01501	<i>Cupriavidus laharis</i>	28	<i>Pseudomonas koreensis</i>	82.787	1464
OATH 01511	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01521	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.189	523
OATH 01521	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.706	1020
OATH 01531	<i>Priestia aryabhattai</i>	160	<i>Lysinibacillus capsici</i>	92.886	1476
OATH 01541	<i>Priestia aryabhattai</i>	160	<i>Lysinibacillus capsici</i>	93.055	1411
OATH 01551	<i>Priestia aryabhattai</i>	160	<i>Lysinibacillus capsici</i>	89.931	437
OATH 01551	<i>Priestia aryabhattai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017
OATH 01561	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.745	1231
OATH 01571	<i>Arthrobacter siccitolerans</i>	32	<i>Micrococcus luteus</i>	96.508	1260
OATH 01581	<i>Priestia megaterium</i>	160	<i>Lysinibacillus capsici</i>	89.931	437

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01581	<i>Priestia megaterium</i>	174	<i>Lysinibacillus capsici</i>	94.834	755
OATH 01591	<i>Arthrobacter nitrophenolicus</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01601	<i>Pseudomonas delhiensis</i>	163	<i>Lysinibacillus capsici</i>	91.604	667
OATH 01601	<i>Pseudomonas delhiensis</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01601	<i>Pseudomonas delhiensis</i>	174	<i>Lysinibacillus capsici</i>	94.137	614
OATH 01611	<i>Bacillus safensis</i>	166	<i>Lysinibacillus capsici</i>	91.785	353
OATH 01611	<i>Bacillus safensis</i>	162	<i>Lysinibacillus capsici</i>	92.959	1051
OATH 01621	<i>Bacillus inaquosorum</i>	166	<i>Lysinibacillus capsici</i>	93.853	1269
OATH 01631	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01641	<i>Bacillus_l endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.783	442
OATH 01641	<i>Bacillus_l endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.701	1019
OATH 01651	<i>Pseudomonas delhiensis</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01661	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.234	1478
OATH 01671	<i>Arthrobacter pascens</i>	32	<i>Micrococcus luteus</i>	98.305	354
OATH 01671	<i>Arthrobacter pascens</i>	32	<i>Micrococcus luteus</i>	95.387	1084
OATH 01681	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01691	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.542	1409
OATH 01701	<i>Zhihengliuella sp031178195</i>	32	<i>Micrococcus luteus</i>	95.73	1452
OATH 01711	<i>Arthrobacter sp019977195</i>	32	<i>Micrococcus luteus</i>	95.772	1017
OATH 01711	<i>Arthrobacter sp019977195</i>	43	<i>Micrococcus luteus</i>	94.622	502
OATH 01721	<i>Arthrobacter sp021129155</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01731	<i>Arthrobacter sp021129155</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01741	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.234	1478
OATH 01751	<i>Bacillus subtilis</i>	174	<i>Lysinibacillus capsici</i>	94.672	976
OATH 01761	<i>Nonomuraea rhodomycinica</i>	50	<i>Streptomyces griseoviridis A</i>	89.931	1450
OATH 01771	<i>Nocardia farcinica</i>	146	<i>Rhodococcus erythropolis</i>	96.53	1441
OATH 01781	<i>Kocuria turfanensis</i>	32	<i>Micrococcus luteus</i>	94.345	1450
OATH 01791	<i>Stutzerimonas stutzeri_A1</i>	71	<i>Pseudomonas sp. OATH_15</i>	97.944	1459

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01801	<i>Caldimonas mangrovi</i>	167	<i>Pseudomonas azotoformans</i>	83.424	1466
OATH 01811	<i>Arthrobacter phenanthrenivorans</i>	32	<i>Micrococcus luteus</i>	96.066	1449
OATH 01821	<i>Terrimonas undefined</i>	145	<i>Bradyrhizobium elkanii</i>	74.859	1420
OATH 01831	<i>Kocunia polaris_A</i>	32	<i>Micrococcus luteus</i>	95.379	1450
OATH 01841	<i>Priestia aryabhatai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017
OATH 01841	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	90.038	532
OATH 01851	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 01861	<i>Neorhizobium flavum</i>	21	<i>Microvirga sp. OATH_1</i>	90.149	1411
OATH 01871	<i>Kocunia polaris_A</i>	146	<i>Rhodococcus erythropolis</i>	91.69	1444
OATH 01881	<i>Bacillus spizizenii</i>	155	<i>Lysinibacillus capsici</i>	91.875	1477
OATH 01891	<i>Arthrobacter sp006715285</i>	32	<i>Micrococcus luteus</i>	95.58	1448
OATH 01901	<i>Kocunia polaris_A</i>	32	<i>Micrococcus luteus</i>	95.379	1450
OATH 01911	<i>Actinoplanes aureus</i>	146	<i>Rhodococcus erythropolis</i>	91.407	1443
OATH 01921	<i>Neorhizobium petrolearium</i>	145	<i>Bradyrhizobium elkanii</i>	90.709	1410
OATH 01931	<i>Neorhizobium flavum</i>	21	<i>Microvirga sp. OATH_1</i>	90.149	1411
OATH 01941	<i>Neorhizobium flavum</i>	21	<i>Microvirga sp. OATH_1</i>	90.149	1411
OATH 01951	<i>Streptomyces nigra</i>	72	<i>Streptomyces sp001509795</i>	99.838	1232
OATH 01961	<i>Bacillus inaquosorum</i>	155	<i>Lysinibacillus capsici</i>	88.785	535
OATH 01961	<i>Bacillus inaquosorum</i>	166	<i>Lysinibacillus capsici</i>	93.996	1016
OATH 01971	<i>Microvirga sp022346925</i>	21	<i>Microvirga sp. OATH_1</i>	97.871	1409
OATH 01981	<i>Agromyces sp031178025</i>	32	<i>Micrococcus luteus</i>	91.758	1456
OATH 01991	<i>Bacillus spizizenii</i>	166	<i>Lysinibacillus capsici</i>	93.127	1295
OATH 02001	<i>Bacillus spizizenii</i>	166	<i>Lysinibacillus capsici</i>	93.127	1295
OATH 02011	<i>Microbispora sp014161445</i>	96	<i>Streptomyces OATH_28</i>	90.809	1458
OATH 02021	<i>Erythrobacter sp006542605</i>	21	<i>Microvirga sp. OATH_1</i>	86.803	1417
OATH 02031	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 02041	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 02051	<i>Streptomyces bobilli</i>	6	<i>Streptomyces sp. OATH_C</i>	98.689	1449

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 02061	<i>Streptomyces griseoruber</i>	197	<i>Streptomyces</i> sp. OATH_61	99.104	558
OATH 02061	<i>Streptomyces griseoruber</i>	17	<i>Streptomyces misionensis</i>	97.933	629
OATH 02071	<i>Streptomyces</i> sp000721605	73	<i>Streptomyces nigra</i>	98.896	1449
OATH 02081	<i>Streptomyces kurssanovii</i>	64	<i>Streptomyces cavourensis</i>	98.414	1450
OATH 02091	<i>Streptomyces</i> sp019049245	6	<i>Streptomyces</i> sp. OATH_C	98.896	1449
OATH 02101	<i>Allosphingosinicella</i> sp011320075	21	<i>Microvirga</i> sp. OATH_1	87.8	1418
OATH 02111	<i>Mycetocola_A miduensis</i>	99	<i>Streptomyces</i> sp. OATH_30	91.736	1452
OATH 02121	<i>Nocardioides</i> sp.	146	<i>Rhodococcus erythropolis</i>	91.967	1444
OATH 02131	<i>Bacillus paralicheniformis</i>	166	<i>Lysinibacillus capsici</i>	93.601	1047
OATH 02141	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 02151	<i>Bacillus paralicheniformis</i>	163	<i>Lysinibacillus capsici</i>	92.005	1476

[0032] 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.

[0033] This deposit of the aforementioned bacteria will be maintained in the ATCC or other depository that conforms to the Budapest Treaty, which are 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.

- [0034] In certain embodiments, fungi are used, e.g., separately, or in addition to the *Streptomyces* and/or other bacteria. The term “mycorrhiza” or “mycorrhizal fungus or fungi,” as used herein includes a fungal cell associated with a root of a plant. The mycorrhizal fungus can be an endomycorrhizal fungus or an ectomycorrhizal fungus. The mycorrhizal fungus can be an Arbuscular endomycorrhizal fungus, Ericoid endomycorrhizal fungus, Arbutoid endomycorrhizal fungus, Monotropoid endomycorrhizal fungus, orchidaceous endomycorrhizal fungus, or ectendomycorrhizal fungus, or other suitable fungus. In certain embodiments, the mycorrhizal fungus comprises any one of the mycorrhizal fungi 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. In embodiments disclosed herein, any suitable fungi may be used. Certain embodiments comprise fungi of one or more of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, *Sebacina*, *Alternaria*, *Beauveria*, *Cladosporeum*, *Claroideoglomus*, *Funneliformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*, *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, *Trichoderma*, *Mucor*, and/or *Phanerochaete* genera. Certain embodiments comprise fungi of one or more of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, *Sebacina*, *Alternaria*, *Beauveria*, *Cladosporeum*, *Claroideoglomus*, *Funneliformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*, *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, and/or *Trichoderma* genera.

B. Compositions comprising one or more microbes

1. Microbial compositions
- [0035] Provided herein are microbial compositions.
- [0036] 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 strains of *Streptomyces* microbes. Any suitable microbe microbes, such as those described herein, such as those described in Table 2A, 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 one or more genera comprising *Pseudomonas*,
5 *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*, *Allophingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola_A*, *Neorhizobium*, *Nocardia*, *Nocardioideis*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*. In certain embodiments,
10 the in one or more non-*Streptomyces* microbes comprise one or more *Pseudomonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microvirga* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-
15 *Streptomyces* microbes comprise one or more *Rhodococcus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Actinoplanes* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one
20 or more *Agromyces* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Allophingosinicella* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Aneurinibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Arthrobacter*
25 microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Bacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Brevibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Caldimonas* microbes ; additionally or
30 alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Cupriavidus* microbes ; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Erythrobacter* microbes ; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Kocuria* microbes ; additionally or alternatively, in certain embodiments the one or
35 more non-*Streptomyces* microbes comprise one or more *Microbacterium* microbes; additionally

or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microbispora* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Mycetocola* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Neorhizobium* microbes; additionally or alternatively, in certain
5 embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nocardia* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nocardioides* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one
10 or more *Nonomuraea* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Peribacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Priestia* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Pristimantibacillus* microbes; additionally or
15 alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stenotrophomonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stutzerimonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Terrimonas* microbes; additionally or alternatively, in certain
20 embodiments the one or more non-*Streptomyces* microbes comprise one or more *Zhihengliuella* microbes. In certain embodiments the composition comprises one or more of the microbes of Table 2A. In certain embodiments, the one or more microbes, e.g., *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, such as at least 95%, preferably at least 96%, more preferably
25 at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 68-109, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437. In certain embodiments the one or more microbes, e.g.,
30 *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, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 197, 198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280,
35 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-

392, 394, 398, 403, 414, 423, 425-431, and/or 437. In certain embodiments, each microbe is present in a concentration of at least 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or 10^{10} CFU/gm and/or not more than 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} or 10^{11} CFU/gm, preferably 10^5 to 10^{10} CFU/gm, more preferably 10^6 to 10^{10} CFU/gm, yet more preferably 10^7 to 10^{10} CFU/gm, even more preferably 10^6 to 10^{10}

5 CFU/gm.

[0037] 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, such as at least 95%, 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, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437. In certain embodiments, the one or more *Streptomyces* microbes comprise a 16S

15 rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5 identical, or 100% identical, such as at least 95%, 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: 197, 198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-

20 322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437. In certain embodiments the composition comprises 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 5-80, even more preferably 5-40, still more preferably

25 5-30, 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, each microbe is present in a concentration of at least 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or 10^{10} CFU/gm and/or not more than 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} or 10^{11} CFU/gm, preferably 10^5 to 10^{10} CFU/gm, more preferably 10^6 to 10^{10} CFU/gm, yet more preferably 10^7 to 10^{10} CFU/gm, even more preferably

30 10^6 to 10^{10} CFU/gm. 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 one or more genera comprising *Pseudomonas*,

35 *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*,

Allosphingosinicella, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola* *A*, *Neorhizobium*, *Nocardia*, *Nocardioideis*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*. In certain embodiments,

5 the in one or more non-*Streptomyces* microbes comprise one or more *Pseudomonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microvirga* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-

10 *Streptomyces* microbes comprise one or more *Rhodococcus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Actinoplanes* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one

15 or more *Agromyces* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Allosphingosinicella* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Aneurinibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Arthrobacter*

20 microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Bacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Brevibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Caldimonas* microbes ; additionally or

25 alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Cupriavidus* microbes ; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Erythrobacter* microbes ; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Kocuria* microbes ; additionally or alternatively, in certain embodiments the one or

30 more non-*Streptomyces* microbes comprise one or more *Microbacterium* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microbispora* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Mycetocola* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes

35 comprise one or more *Neorhizobium* microbes; additionally or alternatively, in certain

embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nocardia* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nocardioides* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nonomuraea* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Peribacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Priestia* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Pristimantibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stenotrophomonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stutzerimonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Terrimonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Zhihengliuella* microbes. In certain embodiments, the composition comprises one or more of the microbes of Table 2A. One or more of the microbes may be heterologous to one or more other microbes.

[0038] In certain embodiments, provided herein is a composition comprising *Streptomyces* spp. microbes and cells of at least one, two, three, four, five, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 20, 22, 25, 27, 30, or 32 and/or not more than one, two, three, four, five, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 20, 22, 25, 27, 30, 32, or 35 preferably 2-35, more preferably 3-35, yet more preferably 5-35, even yet more preferably 5-20, still more preferably 5-15, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 additional microbial species selected from the group consisting of *Pseudomonas* spp., *Microvirga* spp., *Paenibacillus* spp., *Rhodococcus* spp., *Lysinibacillus* spp., *Actinoplanes* spp., *Agromyces* spp., *Allosphingosinicella* spp., *Aneurinibacillus* spp., *Arthrobacter* spp., *Bacillus* spp., *Brevibacillus* spp., *Caldimonas* spp., *Cupriavidus* spp., *Erythrobacter* spp., *Kocuria* spp., *Microbacterium* spp., *Microbispora* spp., *Mycetocola* spp., *Neorhizobium* spp., *Nocardia* spp., *Nocardioides* spp., *Nonomuraea* spp., *Peribacillus* spp., *Priestia* spp., *Pristimantibacillus* spp., *Stenotrophomonas* spp., *Stutzerimonas* spp., *Terrimonas* spp., and *Zhihengliuella* spp. In certain embodiments, the composition comprises microbes of 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* strains, or 2-40, or 2-30. In certain embodiments, the one or more non-*Streptomyces* microbes comprise one or more *Pseudomonas* microbes, such as 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* strains, for example 2-24 different *Pseudomonas* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microvirga* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes, such as at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Paenibacillus* species, for example 2-10 different *Paenibacillus* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Rhodococcus* microbes, such as at least 1, or at least 2 different *Rhodococcus* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes, such as at least 1, 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Lysinibacillus* strains, for example 1-10, preferably 1-5, more preferably 1, or 2, different *Lysinibacillus* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Actinoplanes* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Agromyces* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Allosphingosinicella* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Aneurinibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Arthrobacter* microbes, such as at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Arthrobacter* strains, for example 2-10 different *Arthrobacter* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Bacillus* microbes, such as at least 1, 2, 3, 4, 5, 6, or 7 and/or not more than 2, 3, 4, 5, 6, 7, 8, or 10 different *Bacillus* strains, for example 1-10, preferably 2-10 different *Bacillus* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Brevibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Caldimonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Cupriavidus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Erythrobacter* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Kocuria* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microbacterium* microbes, such as at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6 different *Microbacterium* strains, for example 1-6, preferably 1-4, different *Microbacterium*

strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Microbispora* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Mycetocola* microbes; additionally or alternatively, in certain embodiments the one or more non-

5 *Streptomyces* microbes comprise one or more *Neorhizobium* microbes, such as microbes of 1, or microbes of 2, different *Neorhizobium* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nocardia* microbes, such as microbes of 1, or microbes of 2, different *Nocardia* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one

10 or more *Nocardioides* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Nonomuraea* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Peribacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Priestia* microbes microbes of 1, or

15 microbes of 2, different *Priestia* strains; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Pristimantibacillus* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stenotrophomonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Stutzerimonas*

20 microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Terrimonas* microbes; additionally or alternatively, in certain embodiments the one or more non-*Streptomyces* microbes comprise one or more *Zhihengliuella* microbes. In certain embodiments, the composition comprises one or more of the microbes of Table 2A. In certain embodiments, the one or more microbes, e.g.,

25 *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, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 68-109, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-

30 278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437. In certain embodiments, the one or more microbes, e.g., *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, such as at least 95%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%,

35 still more preferably at least 99%, yet still more preferably at least 99.5% identical to a nucleic

acid sequence of one or more of SEQ ID NOs: 197, 198 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437.

[0039] In certain embodiments, compositions provided herein comprise nitrogen-fixing
 5 bacteria. In certain embodiments, provided is a composition comprising microbes of one or more *Streptomyces* species and microbes 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 microbes of one or more of *Pseudomonas* spp., *Microvirga* spp., *Bradyrhizobium* spp., *Aureimonas* spp., *Paenibacillus* spp., and/or *Lysinibacillus* spp. In
 10 certain embodiments the nitrogen-fixing non-*Streptomyces* species comprise microbes of one or more of *Cupriavidus*, *Neorhizobium*, *Paenibacillus*, *Pseudomonas*, *Bacillus*, *Arthrobacter*, and/or *Lysinibacillus*. In certain embodiments the composition comprises microbes of *Pseudomonas* spp. In certain embodiments the composition comprises microbes of *Microvirga* spp. In certain embodiments the composition comprises microbes of *Aureimonas* spp. In certain
 15 embodiments the composition comprises microbes of *Paenibacillus* spp. In certain embodiments the composition comprises microbes of *Bradyrhizobium* spp. In certain embodiments the composition comprises microbes of *Lysinibacillus* spp. In certain embodiments the composition comprises microbes of *Bacillus* spp. In certain embodiments the composition comprises microbes of *Brevibacillus* spp. In certain embodiments the composition comprises microbes of
 20 *Aneurinibacillus* spp.

[0040] 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, and/or one or more microbes of one or more of ATCC deposits PTA-127834-127850.

[0041] In embodiments including one or more *Streptomyces* microbes, any suitable
 25 *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,
 30 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.

[0042] In embodiments including one or more *Streptomyces* microbes, *Streptomyces*
 35 microbes comprise microbes of *Streptomyces achromogenes*, such as microbes of one or more

Streptomyces achromogenes strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, or 15 *Streptomyces achromogenes* strains, such as 1-15, preferably 1-12, more preferably 1-10, even more preferably 2-15, still more preferably 2-12. In certain embodiments, one or more *Streptomyces achromogenes* microbes comprise a first

5 microbe of a first *Streptomyces achromogenes* strain. In certain embodiments, one or more *Streptomyces achromogenes* microbes comprise a second microbe of a second *Streptomyces achromogenes* strain, different from the first strain. In certain embodiments, one or more *Streptomyces achromogenes* microbes comprise a third microbe of a third *Streptomyces achromogenes* strain, different from the first and second strains. In certain embodiments, one or

10 more *Streptomyces achromogenes* microbes comprise a fourth microbe of a fourth *Streptomyces achromogenes* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces achromogenes* strain, such as the strain designated OATH00343, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces achromogenes* strain, such as the strain designated OATH00601 are used.

15 Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces achromogenes* strain, such as the strain designated OATH00701, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces achromogenes* strain, such as the strain designated OATH00702 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces achromogenes* strain, such as the strain

20 designated OATH01021, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces achromogenes* strain, such as the strain designated OATH01022 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces achromogenes* strain, such as the strain designated OATH01071 are used. Alternatively or additionally, in certain embodiments, microbes of an eighth *Streptomyces*

25 *achromogenes* strain, such as the strain designated OATH01242 are used. Alternatively or additionally, in certain embodiments, microbes of a ninth *Streptomyces achromogenes* strain, such as the strain designated OATH01244 are used. Alternatively or additionally, in certain embodiments, microbes of a tenth *Streptomyces achromogenes* strain, such as the strain designated OATH01261 are used. Alternatively or additionally, in certain embodiments,

30 microbes of an eleventh *Streptomyces achromogenes* strain, such as the strain designated OATH01262 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces achromogenes* 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, such as at least 95%, preferably at

35 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 one or more sequences for each strain as designated in Table 2A.

[0043] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces albogriseolus*, such as microbes of one or more *Streptomyces albogriseolus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces albogriseolus* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces albogriseolus* microbes comprise a first microbe of a first *Streptomyces albogriseolus* strain. In certain embodiments, one or more *Streptomyces albogriseolus* microbes comprise a second microbe of a second *Streptomyces albogriseolus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces albogriseolus* microbes comprise a third microbe of a third *Streptomyces albogriseolus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces albogriseolus* microbes comprise a fourth microbe of a fourth *Streptomyces albogriseolus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces albogriseolus* strain, such as the strain designated OATH01851, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces albogriseolus* strain, such as the strain designated OATH02031, are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces albogriseolus* strain, such as the strain designated OATH02041, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces albogriseolus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0044] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces antibioticus*, such as microbes of one or more *Streptomyces antibioticus* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, or 8 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, or 12 *Streptomyces antibioticus* strains, such as 1-12, preferably 1-10, more preferably 1-8, even more preferably 2-12, still more preferably 2-10. In certain embodiments, one or more *Streptomyces antibioticus* microbes comprise a first microbe of a first *Streptomyces antibioticus* strain. In certain embodiments, one or more *Streptomyces antibioticus* microbes comprise a second microbe of a second *Streptomyces antibioticus* strain, different from the first strain. In certain embodiments, one or more

Streptomyces antibioticus microbes comprise a third microbe of a third *Streptomyces antibioticus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces antibioticus* microbes comprise a fourth microbe of a fourth *Streptomyces antibioticus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces antibioticus* strain, such as the strain designated OATH00354, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces antibioticus* strain, such as the strain designated OATH00371 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces antibioticus* strain, such as the strain designated OATH00372, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces antibioticus* strain, such as the strain designated OATH00373 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces antibioticus* strain, such as the strain designated OATH00374, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces antibioticus* strain, such as the strain designated OATH00375 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces antibioticus* strain, such as the strain OATH00376 designated are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces antibioticus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0045] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces bacillari*, such as microbes of one or more *Streptomyces bacillari* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces bacillari* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces bacillari* microbes comprise a first microbe of a first *Streptomyces bacillari* strain. In certain embodiments, one or more *Streptomyces bacillari* microbes comprise a second microbe of a second *Streptomyces bacillari* strain, different from the first strain. In certain embodiments, one or more *Streptomyces bacillari* microbes comprise a third microbe of a third *Streptomyces bacillari* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces bacillari* microbes comprise a fourth microbe of a fourth *Streptomyces bacillari* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces bacillari* strain, such as the strain

designated OATH00312, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces bacillari* strain, such as the strain designated OATH00313 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces bacillari* strain, such as the strain designated OATH00392, are used. 16S rRNA sequences and
5 ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces bacillari* 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, such as at least 95%, 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
10 99.5% identity to one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0046] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces bikiniensis*, such as microbes of one or more *Streptomyces bikiniensis* strains, e.g., at least 1, 2, 3, or 4 and/or not
15 more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces bikiniensis* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces bikiniensis* microbes comprise a first microbe of a first *Streptomyces bikiniensis* strain. In certain embodiments, one or more *Streptomyces bikiniensis* microbes comprise a second microbe of a second *Streptomyces bikiniensis* strain, different from the first strain. In certain embodiments, one or more
20 *Streptomyces bikiniensis* microbes comprise a third microbe of a third *Streptomyces bikiniensis* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces bikiniensis* microbes comprise a fourth microbe of a fourth *Streptomyces bikiniensis* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces bikiniensis* strain, such as the strain designated OATH00041,
25 are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces bikiniensis* strain, such as the strain designated OATH00091 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces bikiniensis* strain, such as the strain designated OATH01401, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain
30 embodiments, microbe or microbes of *Streptomyces bikiniensis* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more
35 sequences for each strain as designated in Table 2A.

[0047] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces echinatus*, such as microbes of one or more *Streptomyces echinatus* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, or 8 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, or 12 *Streptomyces echinatus* strains, such as 1-12, preferably 1-10, more preferably 1-8, even more preferably 2-12, still more preferably 2-10. In certain embodiments, one or more *Streptomyces echinatus* microbes comprise a first microbe of a first *Streptomyces echinatus* strain. In certain embodiments, one or more *Streptomyces echinatus* microbes comprise a second microbe of a second *Streptomyces echinatus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces echinatus* microbes comprise a third microbe of a third *Streptomyces echinatus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces echinatus* microbes comprise a fourth microbe of a fourth *Streptomyces echinatus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces echinatus* strain, such as the strain designated OATH00021, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces echinatus* strain, such as the strain designated OATH00322 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces echinatus* strain, such as the strain designated OATH00323, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces echinatus* strain, such as the strain designated OATH00522 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces echinatus* strain, such as the strain designated OATH00663, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces echinatus* strain, such as the strain designated OATH00851 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces echinatus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0048] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces bobili*, such as microbes of one or more *Streptomyces bobili* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces bobili* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces bobili* microbes comprise a first microbe of a first *Streptomyces bobili* strain. In certain embodiments, one or more *Streptomyces bobili* microbes

comprise a second microbe of a second *Streptomyces bobili* strain, different from the first strain. In certain embodiments, one or more *Streptomyces bobili* microbes comprise a third microbe of a third *Streptomyces bobili* strain, different from the first and second strains. In certain embodiments, microbes of a first *Streptomyces bobili* strain, such as the strain designated

5 OATH02051, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces bobili* 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, such as at least 95%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least
10 99%, yet still more preferably at least 99.5% identity to one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0049] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces chartreusis*, such as microbes of one or more *Streptomyces chartreusis* strains, e.g., at least 1, 2, 3, or 4 and/or not
15 more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces chartreusis* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces chartreusis* microbes comprise a first microbe of a first *Streptomyces chartreusis* strain. In certain embodiments, one or more *Streptomyces chartreusis* microbes comprise a second microbe of a second *Streptomyces chartreusis* strain, different from the first strain. In certain embodiments, one or more
20 *Streptomyces chartreusis* microbes comprise a third microbe of a third *Streptomyces chartreusis* strain, different from the first and second strains. In certain embodiments, microbes of a first *Streptomyces chartreusis* strain, such as the strain designated OATH00661, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces chartreusis* strains have a 16S rRNA
25 gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100% identity, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A..

30 [0050] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces eurythermus*, such as microbes of one or more *Streptomyces eurythermus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces eurythermus* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces eurythermus* microbes
35 comprise a first microbe of a first *Streptomyces eurythermus* strain. In certain embodiments, one

or more *Streptomyces eurythermus* microbes comprise a second microbe of a second *Streptomyces eurythermus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces eurythermus* microbes comprise a third microbe of a third *Streptomyces eurythermus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces eurythermus* microbes comprise a fourth microbe of a fourth *Streptomyces eurythermus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces eurythermus* strain, such as the strain designated OATH01121, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces eurythermus* strain, such as the strain designated OATH01243 are used.

Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces eurythermus* strain, such as the strain designated OATH01246, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces eurythermus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0051] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces globosus*, such as microbes of one or more *Streptomyces globosus* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, or 25 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, or 30 *Streptomyces globosus* strains, such as 1-30, preferably 1-27, more preferably 1-25, even more preferably 2-30, still more preferably 2-27. In certain embodiments, one or more *Streptomyces globosus* microbes comprise a first microbe of a first *Streptomyces globosus* strain. In certain embodiments, one or more *Streptomyces globosus* microbes comprise a second microbe of a second *Streptomyces globosus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces globosus* microbes comprise a third microbe of a third *Streptomyces globosus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces globosus* microbes comprise a fourth microbe of a fourth *Streptomyces globosus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces globosus* strain, such as the strain designated OATH00801, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces globosus* strain, such as the strain designated OATH00802 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces globosus* strain, such as

the strain designated OATH00912, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces globosus* strain, such as the strain designated OATH01271 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces globosus* strain, such as the strain designated OATH01273, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces globosus* strain, such as the strain designated OATH01283 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces globosus* strain, such as the strain OATH01285 designated are used. Alternatively or additionally, in certain embodiments, microbes of an eighth *Streptomyces globosus* strain, such as the strain designated OATH01292 are used. Alternatively or additionally, in certain embodiments, microbes of a ninth *Streptomyces globosus* strain, such as the strain designated OATH01293 are used. Alternatively or additionally, in certain embodiments, microbes of a tenth *Streptomyces globosus* strain, such as the strain designated OATH01294 are used. Alternatively or additionally, in certain embodiments, microbes of an eleventh *Streptomyces globosus* strain, such as the strain designated OATH01301 are used. Alternatively or additionally, in certain embodiments, microbes of a twelfth *Streptomyces globosus* strain, such as the strain designated OATH01302 are used. Alternatively or additionally, in certain embodiments, microbes of a thirteenth *Streptomyces globosus* strain, such as the strain designated OATH01303 are used. Alternatively or additionally, in certain embodiments, microbes of a fourteenth *Streptomyces globosus* strain, such as the strain designated OATH01304 are used. Alternatively or additionally, in certain embodiments, microbes of a fifteenth *Streptomyces globosus* strain, such as the strain designated OATH01305 are used. Alternatively or additionally, in certain embodiments, microbes of a sixteenth *Streptomyces globosus* strain, such as the strain designated OATH01306 are used. Alternatively or additionally, in certain embodiments, microbes of an seventeenth *Streptomyces globosus* strain, such as the strain designated OATH01311 are used. Alternatively or additionally, in certain embodiments, microbes of an eighteenth *Streptomyces globosus* strain, such as the strain designated OATH01312 are used. Alternatively or additionally, in certain embodiments, microbes of a nineteenth *Streptomyces globosus* strain, such as the strain designated OATH01313 are used. Alternatively or additionally, in certain embodiments, microbes of a twentieth *Streptomyces globosus* strain, such as the strain designated OATH01314 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-first *Streptomyces globosus* strain, such as the strain designated OATH01315 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-second *Streptomyces globosus* strain, such as the strain designated OATH01316 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-third *Streptomyces globosus* strain, such as the strain

designated OATH01341 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-fourth *Streptomyces globosus* strain, such as the strain designated OATH01351 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-fifth *Streptomyces globosus* strain, such as the strain designated OATH01352 are used.

- 5 Alternatively or additionally, in certain embodiments, microbes of a twenty-sixth *Streptomyces globosus* strain, such as the strain designated OATH02141 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces globosus* 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
10 100% identity, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

- [0052] Additionally or alternatively, in embodiments including one or more *Streptomyces*
15 microbes, *Streptomyces* microbes comprise microbes of *Streptomyces misionensis*, such as microbes of one or more *Streptomyces misionensis* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, or 25 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, or 30 *Streptomyces misionensis* strains, such as 1-30, preferably 1-27, more preferably 1-25, even more preferably 2-30, still more preferably 2-27. In certain embodiments, one or more
20 *Streptomyces misionensis* microbes comprise a first microbe of a first *Streptomyces misionensis* strain. In certain embodiments, one or more *Streptomyces misionensis* microbes comprise a second microbe of a second *Streptomyces misionensis* strain, different from the first strain. In certain embodiments, one or more *Streptomyces misionensis* microbes comprise a third microbe of a third *Streptomyces misionensis* strain, different from the first and second strains. In certain
25 embodiments, one or more *Streptomyces misionensis* microbes comprise a fourth microbe of a fourth *Streptomyces misionensis* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces misionensis* strain, such as the strain designated OATH00223, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces misionensis* strain, such as the strain designated OATH00252
30 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces misionensis* strain, such as the strain designated OATH00253, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces misionensis* strain, such as the strain designated OATH00331 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces misionensis* strain, such as the strain designated
35 OATH00382, are used. Alternatively or additionally, in certain embodiments, microbes of a

sixth *Streptomyces misionensis* strain, such as the strain designated OATH00413 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces misionensis* strain, such as the strain OATH00421 designated are used. Alternatively or additionally, in certain embodiments, microbes of an eighth *Streptomyces misionensis* strain, such as the strain designated OATH00423 are used. Alternatively or additionally, in certain
5 embodiments, microbes of a ninth *Streptomyces misionensis* strain, such as the strain designated OATH00424 are used. Alternatively or additionally, in certain embodiments, microbes of a tenth *Streptomyces misionensis* strain, such as the strain designated OATH00425 are used. Alternatively or additionally, in certain embodiments, microbes of an eleventh *Streptomyces*
10 *misionensis* strain, such as the strain designated OATH00491 are used. Alternatively or additionally, in certain embodiments, microbes of a twelfth *Streptomyces misionensis* strain, such as the strain designated OATH00492 are used. Alternatively or additionally, in certain embodiments, microbes of a thirteenth *Streptomyces misionensis* strain, such as the strain designated OATH00571 are used. Alternatively or additionally, in certain embodiments,
15 microbes of a fourteenth *Streptomyces misionensis* strain, such as the strain designated OATH00651 are used. Alternatively or additionally, in certain embodiments, microbes of a fifteenth *Streptomyces misionensis* strain, such as the strain designated OATH00741 are used. Alternatively or additionally, in certain embodiments, microbes of a sixteenth *Streptomyces misionensis* strain, such as the strain designated OATH00742 are used. Alternatively or
20 additionally, in certain embodiments, microbes of a seventeenth *Streptomyces misionensis* strain, such as the strain designated OATH00743 are used. Alternatively or additionally, in certain embodiments, microbes of an eighteenth *Streptomyces misionensis* strain, such as the strain designated OATH00891 are used. Alternatively or additionally, in certain embodiments, microbes of a nineteenth *Streptomyces misionensis* strain, such as the strain designated
25 OATH00961 are used. Alternatively or additionally, in certain embodiments, microbes of a twentieth *Streptomyces misionensis* strain, such as the strain designated OATH01002 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-first *Streptomyces misionensis* strain, such as the strain designated OATH01241 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-second *Streptomyces misionensis*
30 strain, such as the strain designated OATH01247 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-third *Streptomyces misionensis* strain, such as the strain designated OATH01411 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-fourth *Streptomyces misionensis* strain, such as the strain designated OATH00422 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain
35 are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces*

misionensis 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0053] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces murinus*, such as microbes of one or more *Streptomyces murinus* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, or 15 *Streptomyces murinus* strains, such as 1-15, preferably 1-12, more preferably 1-10, even more preferably 2-15, still more preferably 2-12. In certain embodiments, one or more *Streptomyces murinus* microbes comprise a first microbe of a first *Streptomyces murinus* strain. In certain embodiments, one or more *Streptomyces murinus* microbes comprise a second microbe of a second *Streptomyces murinus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces murinus* microbes comprise a third microbe of a third *Streptomyces murinus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces murinus* microbes comprise a fourth microbe of a fourth *Streptomyces murinus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces murinus* strain, such as the strain designated OATH00261, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces murinus* strain, such as the strain designated OATH00262 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces murinus* strain, such as the strain designated OATH00263, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces murinus* strain, such as the strain designated OATH00264 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces murinus* strain, such as the strain designated OATH00562, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces murinus* strain, such as the strain designated OATH00563 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces murinus* strain, such as the strain OATH00564 designated are used. Alternatively or additionally, in certain embodiments, microbes of an eighth *Streptomyces murinus* strain, such as the strain designated OATH00823 are used. Alternatively or additionally, in certain embodiments, microbes of a ninth *Streptomyces murinus* strain, such as the strain designated OATH00881 are used. Alternatively or additionally, in certain embodiments, microbes of a tenth *Streptomyces murinus* strain, such as the strain designated OATH01251 are used. Alternatively

or additionally, in certain embodiments, microbes of an eleventh *Streptomyces murinus* strain, such as the strain designated OATH01253 are used. Alternatively or additionally, in certain embodiments, microbes of an twelfth *Streptomyces murinus* strain, such as the strain designated OATH01412 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces murinus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0054] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces musisoli*, such as microbes of one or more *Streptomyces musisoli* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces musisoli* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces musisoli* microbes comprise a first microbe of a first *Streptomyces musisoli* strain. In certain embodiments, one or more *Streptomyces musisoli* microbes comprise a second microbe of a second *Streptomyces musisoli* strain, different from the first strain. In certain embodiments, one or more *Streptomyces musisoli* microbes comprise a third microbe of a third *Streptomyces musisoli* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces musisoli* microbes comprise a fourth microbe of a fourth *Streptomyces musisoli* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces musisoli* strain, such as the strain designated OATH00521, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces musisoli* strain, such as the strain designated OATH00662 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces musisoli* strain, such as the strain designated OATH00681, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces musisoli* strain, such as the strain designated OATH01101, are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces musisoli* strain, such as the strain designated OATH01102, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces musisoli* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0055] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces sennicomposti*, such as microbes of one or more *Streptomyces sennicomposti* strains, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, or 30 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, 22, 25, 27, 30, or 35 *Streptomyces sennicomposti* strains, such as 1-35, preferably 1-32, more preferably 1-30, even more preferably 2-35, still more preferably 2-32. In certain embodiments, one or more *Streptomyces sennicomposti* microbes comprise a first microbe of a first *Streptomyces sennicomposti* strain. In certain embodiments, one or more *Streptomyces sennicomposti* microbes comprise a second microbe of a second *Streptomyces sennicomposti* strain, different from the first strain. In certain embodiments, one or more *Streptomyces sennicomposti* microbes comprise a third microbe of a third *Streptomyces sennicomposti* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces sennicomposti* microbes comprise a fourth microbe of a fourth *Streptomyces sennicomposti* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces sennicomposti* strain, such as the strain designated OATH00031, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces sennicomposti* strain, such as the strain designated OATH00071 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces sennicomposti* strain, such as the strain designated OATH00072, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces sennicomposti* strain, such as the strain designated OATH00101 are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces sennicomposti* strain, such as the strain designated OATH00103, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces sennicomposti* strain, such as the strain designated OATH00241 are used. Alternatively or additionally, in certain embodiments, microbes of a seventh *Streptomyces sennicomposti* strain, such as the strain OATH00242 designated are used. Alternatively or additionally, in certain embodiments, microbes of an eighth *Streptomyces sennicomposti* strain, such as the strain designated OATH00243 are used. Alternatively or additionally, in certain embodiments, microbes of a ninth *Streptomyces sennicomposti* strain, such as the strain designated OATH00424 are used. Alternatively or additionally, in certain embodiments, microbes of a tenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00301 are used. Alternatively or additionally, in certain embodiments, microbes of an

eleventh *Streptomyces sennicomposti* strain, such as the strain designated OATH00381 are used. Alternatively or additionally, in certain embodiments, microbes of a twelfth *Streptomyces sennicomposti* strain, such as the strain designated OATH00383 are used. Alternatively or additionally, in certain embodiments, microbes of a thirteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00384 are used. Alternatively or additionally, in certain embodiments, microbes of a fourteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00402 are used. Alternatively or additionally, in certain embodiments, microbes of a fifteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00403 are used. Alternatively or additionally, in certain embodiments, microbes of a sixteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00404 are used. Alternatively or additionally, in certain embodiments, microbes of a seventeenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00442 are used. Alternatively or additionally, in certain embodiments, microbes of an eighteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00443 are used. Alternatively or additionally, in certain embodiments, microbes of a nineteenth *Streptomyces sennicomposti* strain, such as the strain designated OATH00581 are used. Alternatively or additionally, in certain embodiments, microbes of a twentieth *Streptomyces sennicomposti* strain, such as the strain designated OATH00591 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-first *Streptomyces sennicomposti* strain, such as the strain designated OATH00592 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-second *Streptomyces sennicomposti* strain, such as the strain designated OATH00593 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-third *Streptomyces sennicomposti* strain, such as the strain designated OATH00641 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-fourth *Streptomyces sennicomposti* strain, such as the strain designated OATH00691 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-fifth *Streptomyces sennicomposti* strain, such as the strain designated OATH00692 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-sixth *Streptomyces sennicomposti* strain, such as the strain designated OATH00711 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-seventh *Streptomyces sennicomposti* strain, such as the strain designated OATH00753 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-eighth *Streptomyces sennicomposti* strain, such as the strain designated OATH00871 are used. Alternatively or additionally, in certain embodiments, microbes of a twenty-ninth *Streptomyces sennicomposti* strain, such as the strain designated OATH00901 are used. Alternatively or additionally, in certain embodiments, microbes of a thirtieth *Streptomyces*

sennicomposti strain, such as the strain designated OATH01182 are used. Alternatively or additionally, in certain embodiments, microbes of a thirty-first *Streptomyces sennicomposti* strain, such as the strain designated OATH01183 are used. Alternatively or additionally, in certain embodiments, microbes of a thirty-second *Streptomyces sennicomposti* strain, such as the strain designated OATH01201 are used. Alternatively or additionally, in certain embodiments, microbes of a thirty-third *Streptomyces sennicomposti* strain, such as the strain designated OATH01331 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces sennicomposti* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0056] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces rochei*, such as microbes of one or more *Streptomyces rochei* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces rochei* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces rochei* microbes comprise a first microbe of a first *Streptomyces rochei* strain. In certain embodiments, one or more *Streptomyces rochei* microbes comprise a second microbe of a second *Streptomyces rochei* strain, different from the first strain. In certain embodiments, one or more *Streptomyces rochei* microbes comprise a third microbe of a third *Streptomyces rochei* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces rochei* microbes comprise a fourth microbe of a fourth *Streptomyces rochei* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces rochei* strain, such as the strain designated OATH00051, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces rochei* strain, such as the strain designated OATH00052 are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces rochei* strain, such as the strain designated OATH00053, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces rochei* strain, such as the strain designated OATH0081, are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces rochei* strain, such as the strain designated OATH00353, are used. Alternatively or additionally, in certain embodiments, microbes of a sixth *Streptomyces rochei* strain, such as the strain designated OATH00762, are used. 16S rRNA sequences and

ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces rochei* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0057] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces griseoaurantiacus*, such as microbes of one or more *Streptomyces griseoaurantiacus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces griseoaurantiacus* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces griseoaurantiacus* microbes comprise a first microbe of a first *Streptomyces griseoaurantiacus* strain. In certain embodiments, one or more *Streptomyces griseoaurantiacus* microbes comprise a second microbe of a second *Streptomyces griseoaurantiacus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces griseoaurantiacus* microbes comprise a third microbe of a third *Streptomyces griseoaurantiacus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces griseoaurantiacus* microbes comprise a fourth microbe of a fourth *Streptomyces griseoaurantiacus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces griseoaurantiacus* strain, such as the strain designated OATH00291, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces griseoaurantiacus* strain, such as the strain designated OATH00292 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces griseoaurantiacus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0058] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces griseoincarnatus*, such as microbes of one or more *Streptomyces griseoincarnatus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces griseoincarnatus* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces griseoincarnatus*

microbes comprise a first microbe of a first *Streptomyces griseoincarnatus* strain. In certain embodiments, one or more *Streptomyces griseoincarnatus* microbes comprise a second microbe of a second *Streptomyces griseoincarnatus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces griseoincarnatus* microbes comprise a third microbe of a third *Streptomyces griseoincarnatus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces griseoincarnatus* microbes comprise a fourth microbe of a fourth *Streptomyces griseoincarnatus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces griseoincarnatus* strain, such as the strain designated OATH00144 are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces griseoincarnatus* strain, such as the strain designated OATH00321, are used. Alternatively or additionally, in certain embodiments, microbes of a third *Streptomyces griseoincarnatus* strain, such as the strain designated OATH00412, are used. Alternatively or additionally, in certain embodiments, microbes of a fourth *Streptomyces griseoincarnatus* strain, such as the strain designated OATH00921, are used. Alternatively or additionally, in certain embodiments, microbes of a fifth *Streptomyces griseoincarnatus* strain, such as the strain designated OATH01245, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces griseoincarnatus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0059] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces griseoviridis*, such as microbes of one or more *Streptomyces griseoviridis* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces griseoviridis* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces griseoviridis* microbes comprise a first microbe of a first *Streptomyces griseoviridis* strain. In certain embodiments, one or more *Streptomyces griseoviridis* microbes comprise a second microbe of a second *Streptomyces griseoviridis* strain, different from the first strain. In certain embodiments, one or more *Streptomyces griseoviridis* microbes comprise a third microbe of a third *Streptomyces griseoviridis* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces griseoviridis* microbes comprise a fourth microbe of a fourth *Streptomyces griseoviridis* strain, different from the first, second, and third strains. In certain embodiments,

microbes of a first *Streptomyces griseoviridis* strain, such as the strain designated OATH01141, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces griseoviridis* strain, such as the strain designated OATH01142 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces griseoviridis* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0060] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces olivaceus*, such as microbes of one or more *Streptomyces olivaceus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces olivaceus* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces olivaceus* microbes comprise a first microbe of a first *Streptomyces olivaceus* strain. In certain embodiments, one or more *Streptomyces olivaceus* microbes comprise a second microbe of a second *Streptomyces olivaceus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces olivaceus* microbes comprise a third microbe of a third *Streptomyces olivaceus* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces olivaceus* microbes comprise a fourth microbe of a fourth *Streptomyces olivaceus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces olivaceus* strain, such as the strain designated OATH00351, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces olivaceus* strain, such as the strain designated OATH00352 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces olivaceus* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0061] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces toxytricini*, such as microbes of one or more *Streptomyces toxytricini* strains, e.g., at least 1, 2, 3, or 4 and/or not

more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces toxytricini* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces toxytricini* microbes comprise a first microbe of a first *Streptomyces toxytricini* strain. In certain embodiments, one or more *Streptomyces toxytricini* microbes comprise a second microbe of a second *Streptomyces toxytricini* strain, different from the first strain. In certain embodiments, one or more *Streptomyces toxytricini* microbes comprise a third microbe of a third *Streptomyces toxytricini* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces toxytricini* microbes comprise a fourth microbe of a fourth *Streptomyces toxytricini* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces toxytricini* strain, such as the strain designated OATH00011, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Streptomyces toxytricini* strain, such as the strain designated OATH01091 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces toxytricini* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0062] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces griseoruber*, such as microbes of one or more *Streptomyces griseoruber* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces griseoruber* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces griseoruber* microbes comprise a first microbe of a first *Streptomyces griseoruber* strain. In certain embodiments, one or more *Streptomyces griseoruber* microbes comprise a second microbe of a second *Streptomyces griseoruber* strain, different from the first strain. In certain embodiments, one or more *Streptomyces griseoruber* microbes comprise a third microbe of a third *Streptomyces griseoruber* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces griseoruber* microbes comprise a fourth microbe of a fourth *Streptomyces griseoruber* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces griseoruber* strain, such as the strain designated OATH02061, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces griseoruber* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

5 [0063] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces kurssanovii*, such as microbes of one or more *Streptomyces kurssanovii* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces kurssanovii* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces kurssanovii* microbes comprise
10 a first microbe of a first *Streptomyces kurssanovii* strain. In certain embodiments, one or more *Streptomyces kurssanovii* microbes comprise a second microbe of a second *Streptomyces kurssanovii* strain, different from the first strain. In certain embodiments, one or more *Streptomyces kurssanovii* microbes comprise a third microbe of a third *Streptomyces kurssanovii* strain, different from the first and second strains. In certain embodiments, one or more
15 *Streptomyces kurssanovii* microbes comprise a fourth microbe of a fourth *Streptomyces kurssanovii* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces kurssanovii* strain, such as the strain designated OATH02081, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces kurssanovii* strains
20 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

25 [0064] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces griseofuscus*, such as microbes of one or more *Streptomyces griseofuscus* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces griseofuscus* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces griseofuscus* microbes
30 comprise a first microbe of a first *Streptomyces griseofuscus* strain. In certain embodiments, one or more *Streptomyces griseofuscus* microbes comprise a second microbe of a second *Streptomyces griseofuscus* strain, different from the first strain. In certain embodiments, one or more *Streptomyces griseofuscus* microbes comprise a third microbe of a third *Streptomyces griseofuscus* strain, different from the first and second strains. In certain embodiments, one or
35 more *Streptomyces griseofuscus* microbes comprise a fourth microbe of a fourth *Streptomyces*

- griseofuscus* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces griseofuscus* strain, such as the strain designated OATH01254, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces griseofuscus* strains
- 5 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.
- 10 [0065] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces nigra*, such as microbes of one or more *Streptomyces nigra* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces nigra* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces nigra* microbes comprise a first microbe of a first
- 15 *Streptomyces nigra* strain. In certain embodiments, one or more *Streptomyces nigra* microbes comprise a second microbe of a second *Streptomyces nigra* strain, different from the first strain. In certain embodiments, one or more *Streptomyces nigra* microbes comprise a third microbe of a third *Streptomyces nigra* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces nigra* microbes comprise a fourth microbe of a fourth
- 20 *Streptomyces nigra* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces nigra* strain, such as the strain designated OATH01951, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces nigra* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96,
- 25 97, 98, 99, or 99.55 identity, or 100% identity, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.
- [0066] Additionally or alternatively, in embodiments including one or more *Streptomyces* microbes, *Streptomyces* microbes comprise microbes of *Streptomyces nigrescens*, such as
- 30 microbes of one or more *Streptomyces nigrescens* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces nigrescens* strains, such as 1-8, preferably 1-7, more preferably 1-5 In certain embodiments, one or more *Streptomyces nigrescens* microbes comprise a first microbe of a first *Streptomyces nigrescens* strain. In certain embodiments, one or more
- 35 *Streptomyces nigrescens* microbes comprise a second microbe of a second *Streptomyces*

nigrescens strain, different from the first strain. In certain embodiments, one or more *Streptomyces nigrescens* microbes comprise a third microbe of a third *Streptomyces nigrescens* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces nigrescens* microbes comprise a fourth microbe of a fourth *Streptomyces*
 5 *nigrescens* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces nigrescens* strain, such as the strain designated OATH00913, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces nigrescens* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98,
 10 99, or 99.55 identity, or 100% identity, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0067] Additionally or alternatively, in embodiments including one or more *Streptomyces*
 15 microbes, *Streptomyces* microbes comprise microbes of *Streptomyces sp000721605*, such as microbes of one or more *Streptomyces sp000721605* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces sp000721605* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces sp000721605* microbes comprise a first microbe of a first *Streptomyces sp000721605* strain. In certain embodiments, one
 20 or more *Streptomyces sp000721605* microbes comprise a second microbe of a second *Streptomyces sp000721605* strain, different from the first strain. In certain embodiments, one or more *Streptomyces sp000721605* microbes comprise a third microbe of a third *Streptomyces sp000721605* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces sp000721605* microbes comprise a fourth microbe of a fourth *Streptomyces*
 25 *sp000721605* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces sp000721605* strain, such as the strain designated OATH02071, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces sp000721605* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96, 97, 98,
 30 99, or 99.55 identity, or 100% identity, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0068] Additionally or alternatively, in embodiments including one or more *Streptomyces*
 35 microbes, *Streptomyces* microbes comprise microbes of *Streptomyces sp019049245*, such as

microbes of one or more *Streptomyces sp019049245* strains, e.g., at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, 5, 6, 7, or 8 *Streptomyces sp019049245* strains, such as 1-8, preferably 1-7, more preferably 1-5. In certain embodiments, one or more *Streptomyces sp019049245* microbes comprise a first microbe of a first *Streptomyces sp019049245* strain. In certain embodiments, one or more *Streptomyces sp019049245* microbes comprise a second microbe of a second *Streptomyces sp019049245* strain, different from the first strain. In certain embodiments, one or more *Streptomyces sp019049245* microbes comprise a third microbe of a third *Streptomyces sp019049245* strain, different from the first and second strains. In certain embodiments, one or more *Streptomyces sp019049245* microbes comprise a fourth microbe of a fourth *Streptomyces sp019049245* strain, different from the first, second, and third strains. In certain embodiments, microbes of a first *Streptomyces sp019049245* strain, such as the strain designated OATH02091, are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Streptomyces sp019049245* 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0069] 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 one or more of *Pseudomonas*, *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola*, *Neorhizobium*, *Nocardia*, *Nocardioideis*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*.

[0070] In embodiments including microbes of one or more *Pseudomonas* strains, any suitable species and/or strain(s) of *Pseudomonas* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, 4, 5, or 6 and/or not more than 2, 3, 4, 5, 6, or 7, preferably 1-7, more preferably 1-5, even more preferably 1-3, such as 1, or 2, *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, microbes of a first *Pseudomonas E paracarnis* strain, such as the strain designated OATH00102, are used. Alternatively or additionally, in certain embodiments, microbes of a

second *Pseudomonas E paracarnis* strain, such as the strain designated OATH01112 are used. Alternatively or additionally, in certain embodiments, microbes of a first *Pseudomonas delhiensis* strain, such as the strain designated OATH01601, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Pseudomonas delhiensis* strain, such as the strain designated OATH01651 are used. Alternatively or additionally, in certain embodiments, microbes of a first *Pseudomonas_K oryzae* strain, such as the strain designated OATH01461, are used. Alternatively or additionally, in certain embodiments, microbes of a second *Pseudomonas_K oryzae* strain, such as the strain designated OATH01431 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0071] 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* sp022346925, such as the strain designated OATH01971. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0072] 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, or 5 and/or not more than 2, 3, 4, 5, or 6 *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, microbes of a first *Paenibacillus cellulositrophicus* strain, such as the strain designated as OATH00811, are used. Alternatively or additionally, in certain embodiments, microbes of a

second *Paenibacillus cellulositrophicus* strain, designated as OATH01263 are used.

Alternatively or additionally, in certain embodiments, microbes of a third *Paenibacillus cellulositrophicus* strain, designated as OATH01371 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments,

- 5 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each
- 10 strain as designated in Table 2A.

- [0073] 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 1, 2, 3, or 4, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6 *Rhodococcus* strains are used. In certain embodiments, one or more *Rhodococcus* microbes comprise a first microbe of a first
- 15 *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, microbes of *Rhodococcus* strains comprise microbes of one or more of *Rhodococcus erythropolis* strains, such as *Rhodococcus erythropolis* designation OATH00923 are used. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown
- 20 in Table 2A. 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, such as at least 95%, 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 one or more sequences for each strain as designated in Table
- 25 2A to one or more sequences for each strain as designated in Table 2A.

- [0074] In embodiments including microbes of one or more *Lysinibacillus* strains, any suitable strain(s) of *Lysinibacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 *Lysinibacillus* strains are used. In certain embodiments, one or more *Lysinibacillus* microbes comprise a first microbe of a first
- 30 *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, microbes of *Lysinibacillus* strains comprise microbes of *Lysinibacillus capsici*, such as *Lysinibacillus capsici* designation OATH01003, are used. Alternatively or additionally, in certain embodiments, microbes of *Lysinibacillus* strains comprise microbes of *Lysinibacillus*
- 35 *sphaericus*, such as *Lysinibacillus sphaericus* designation OATH00892, are used. 16S rRNA

sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0075] In embodiments including microbes of one or more *Bacillus* strains, any suitable strain(s) of *Bacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 15, 17, 20, or 22 and/or not more than 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 15, 17, 20, 22, 25, or 30 *Bacillus* strains are used. In certain embodiments, one or more *Bacillus* microbes comprise a first microbe of a first *Bacillus* strain. In certain embodiments, one or more *Bacillus* microbes comprise a second microbe of a second *Bacillus* strain, different from the first strain. In certain embodiments, one or more *Bacillus* microbes comprise a third microbe of a third *Bacillus* strain, different from the first and second strains. In certain embodiments, one or more *Bacillus* microbes comprise a fourth microbe of a fourth *Bacillus* strain, different from the first, second, and third strains. In certain embodiments, one or more *Bacillus* microbes comprise a fifth microbe of a fifth *Bacillus* strain, different from the first, second, third, and fourth strains. In certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus haynesii* such as *Bacillus haynesii* designation OATH01252 are used. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus inaquosorum* such as *Bacillus inaquosorum* designation OATH01621, and/or *Bacillus inaquosorum* designation OATH01961, are used. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus licheniformis* such as *Bacillus licheniformis* designation OATH01291. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus paralicheniformis* such as *Bacillus paralicheniformis* designation OATH02131 and/or *Bacillus paralicheniformis* designation OATH02151. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus safensis* such as *Bacillus safensis* designation OATH01491, and/or *Bacillus safensis* designation OATH01611. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus spizizenii* such as *Bacillus spizizenii* designation OATH01881, *Bacillus spizizenii* designation OATH01991, and/or *Bacillus spizizenii* designation OATH02001. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus subtilis* such as *Bacillus subtilis* designation OATH01511, *Bacillus subtilis* designation OATH01561, *Bacillus*

subtilis designation OATH01631 *Bacillus subtilis* designation OATH01681 and/or *Bacillus subtilis* designation OATH01751. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus velizensis* such as *Bacillus velizensis* designation OATH01382, and/or *Bacillus velizensis* designation OATH01383. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus_A thuringiensis_K* such as *Bacillus_A thuringiensis_K* designation OATH01441. Alternatively or additionally, in certain embodiments, microbes of *Bacillus* strains comprise microbes of *Bacillus_I endophytica_A* such as *Bacillus_I endophytica_A* designation OATH01471, *Bacillus_I endophytica_A* designation OATH01481, *Bacillus_I endophytica_A* designation OATH01521, and/or *Bacillus_I endophytica_A* designation OATH01641. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Bacillus* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0076] In embodiments including microbes of one or more *Aneurinibacillus* strains, any suitable strain(s) of *Aneurinibacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, or 3 and/or not more than 2, 3, or 4 *Aneurinibacillus* strains are used. In certain embodiments, one or more *Aneurinibacillus* microbes comprise a first microbe of a first *Aneurinibacillus* strain. In certain embodiments, one or more *Aneurinibacillus* microbes comprise a second microbe of a second *Aneurinibacillus* strain, different from the first strain. In certain embodiments, microbes of *Aneurinibacillus* strains comprise microbes of *Aneurinibacillus aneurinilyticus*, such as *Aneurinibacillus aneurinilyticus* designation OATH01281. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Aneurinibacillus* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0077] In embodiments including microbes of one or more *Brevibacillus* strains, any suitable strain(s) of *Brevibacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 *Brevibacillus* strains are used. In certain embodiments,

one or more *Brevibacillus* microbes comprise a first microbe of a first *Brevibacillus* strain. In certain embodiments, one or more *Brevibacillus* microbes comprise a second microbe of a second *Brevibacillus* strain, different from the first strain. In certain embodiments, microbes of *Brevibacillus* strains comprise microbes of *Brevibacillus panacihumi*, such as *Brevibacillus* 5 *panacihumi* designation OATH01363. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Brevibacillus* 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%, such as at least 95%, such as at least 95%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still 10 more preferably at least 99%, yet still more preferably at least 99.5% identity to one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0078] In embodiments including microbes of one or more *Caldimonas* strains, any suitable strain(s) of *Caldimonas* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, 15 or 4 and/or not more than 2, 3, 4, or 5 *Caldimonas* strains are used. In certain embodiments, one or more *Caldimonas* microbes comprise a first microbe of a first *Caldimonas* strain. In certain embodiments, one or more *Caldimonas* microbes comprise a second microbe of a second *Caldimonas* strain, different from the first strain. In certain embodiments, microbes of *Caldimonas* strains comprise microbes of *Caldimonas* such as *Caldimonas mangrovi* designation 20 OATH01801. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Caldimonas* 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%, such as at least 95%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more 25 preferably at least 99.5% identity to one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0079] In embodiments including microbes of one or more *Actinoplanes* strains, any suitable strain(s) of *Actinoplanes* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more 30 *Actinoplanes* microbes comprise a first microbe of a first *Actinoplanes* strain. In certain embodiments, one or more *Actinoplanes* microbes comprise a second microbe of a second *Actinoplanes* strain, different from the first strain. In certain embodiments, microbes of *Actinoplanes* strains comprise microbes of *Actinoplanes aureus*, such as *Actinoplanes aureus* designation OATH01911. 16S rRNA sequences and ATCC Deposit numbers including each 35 strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Actinoplanes*

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%, such as at least 95%, 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 one or more sequences for each strain as

5 designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0080] In embodiments including microbes of one or more *Agromyces* strains, any suitable strain(s) of *Agromyces* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Agromyces* microbes comprise a first microbe of a first *Agromyces* strain. In certain

10 embodiments, one or more *Agromyces* microbes comprise a second microbe of a second *Agromyces* strain, different from the first strain. In certain embodiments, microbes of *Agromyces* strains comprise microbes of *Agromyces* sp031178025, such as *Agromyces* sp031178025 designation OATH01981. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Agromyces* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

20 [0081] In embodiments including microbes of one or more *Allospingosinicella* strains, any suitable strain(s) of *Allospingosinicella* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Allospingosinicella* microbes comprise a first microbe of a first *Allospingosinicella* strain. In certain embodiments, one or more *Allospingosinicella* microbes comprise a second microbe of a second *Allospingosinicella* strain, different from the first strain. In certain embodiments, microbes of *Allospingosinicella* strains comprise microbes of *Allospingosinicella* sp011320075, such as *Allospingosinicella* sp011320075 designation OATH02101. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Allospingosinicella* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0082] In embodiments including microbes of one or more *Arthrobacter* strains, any suitable strain(s) of *Arthrobacter* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, 4, 5, 6, or 7 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 strains are used. In certain embodiments, one or more *Arthrobacter* microbes comprise a first microbe of a first

5 *Arthrobacter* strain. In certain embodiments, one or more *Arthrobacter* microbes comprise a second microbe of a second *Arthrobacter* strain, different from the first strain. In certain embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter nitrophenolicus*, such as *Arthrobacter nitrophenolicus* designation OATH01591. Alternatively or additionally, in certain embodiments, microbes of *Arthrobacter* strains comprise microbes of

10 *Arthrobacter pascens* such as *Arthrobacter pascens* designation OATH01671. Alternatively or additionally, in certain embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter phenanthrenivorans* such as *Arthrobacter phenanthrenivorans* designation OATH01811. Alternatively or additionally, in certain embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter siccitolerans* such as *Arthrobacter siccitolerans*

15 designation OATH01571. Alternatively or additionally, in certain embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter sp006715285* such as *Arthrobacter sp006715285* designation OATH01891. Alternatively or additionally, in certain embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter sp019977195* such as *Arthrobacter sp019977195* designation OATH01711. Alternatively or additionally, in certain

20 embodiments, microbes of *Arthrobacter* strains comprise microbes of *Arthrobacter sp021129155* such as *Arthrobacter sp021129155* designation OATH01731 and/or *Arthrobacter sp021129155* designation OATH01721. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Arthrobacter* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80, 85, 90, 95, 96,

25 97, 98, 99, or 99.5% identity, or 100%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0083] In embodiments including microbes of one or more *Cupriavidus* strains, any suitable strain(s) of *Cupriavidus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Cupriavidus* microbes comprise a first microbe of a first *Cupriavidus* strain. In certain

30 embodiments, one or more *Cupriavidus* microbes comprise a second microbe of a second *Cupriavidus* strain, different from the first strain. In certain embodiments, microbes of *Cupriavidus* strains comprise microbes of *Cupriavidus laharis*, such as *Cupriavidus laharis*

35

designation OATH01501. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Cupriavidus* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0084] In embodiments including microbes of one or more *Erythrobacter* strains, any suitable strain(s) of *Erythrobacter* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Erythrobacter* microbes comprise a first microbe of a first *Erythrobacter* strain. In certain embodiments, one or more *Erythrobacter* microbes comprise a second microbe of a second *Erythrobacter* strain, different from the first strain. In certain embodiments, microbes of *Erythrobacter* strains comprise microbes of *Erythrobacter* sp006542605, such as *Erythrobacter* sp006542605 designation OATH2021. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Erythrobacter* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0085] In embodiments including microbes of one or more *Kocuria* strains, any suitable strain(s) of *Kocuria* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Kocuria* microbes comprise a first microbe of a first *Kocuria* strain. In certain embodiments, one or more *Kocuria* microbes comprise a second microbe of a second *Kocuria* strain, different from the first strain. In certain embodiments, microbes of *Kocuria* strains comprise microbes of *Kocuria polaris*_A, such as *Kocuria polaris*_A designation OATH01831, *Kocuria polaris*_A designation OATH01871, and/or *Kocuria polaris*_A designation OATH01901. Alternatively or additionally, in certain embodiments, microbes of *Kocuria* strains comprise microbes of *Kocuria turfanensis* such as *Kocuria turfanensis* designation OATH01781. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Kocuria* 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%,

such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

- 5 [0086] In embodiments including microbes of one or more *Microbacterium* strains, any suitable strain(s) of *Microbacterium* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Microbacterium* microbes comprise a first microbe of a first *Microbacterium* strain. In certain embodiments, one or more *Microbacterium* microbes comprise a second microbe of a
- 10 second *Microbacterium* strain, different from the first strain. In certain embodiments, microbes of *Microbacterium* strains comprise microbes of *Microbacterium oxydans*, such as *Microbacterium oxydans* designation OATH00143 . Alternatively or additionally, in certain embodiments, microbes of *Microbacterium* strains comprise microbes of *Microbacterium paraoxydans* such as *Microbacterium paraoxydans* designation OATH00224 and/or
- 15 *Microbacterium paraoxydans* designation OATH00483 . Alternatively or additionally, in certain embodiments, microbes of *Microbacterium* strains comprise microbes of *Microbacterium resistens* such as *Microbacterium resistens* designation OATH00342 . Alternatively or additionally, in certain embodiments, microbes of *Microbacterium* strains comprise microbes of *Microbacterium sp002979655* such as *Microbacterium sp002979655* designation OATH00493
- 20 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Microbacterium* 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%, such as at least 95%, 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
- 25 least 99.5% identity to one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

- [0087] In embodiments including microbes of one or more *Microbispora* strains, any suitable strain(s) of *Microbispora* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Microbispora* microbes comprise a first microbe of a first *Microbispora* strain. In certain
- 30 embodiments, one or more *Microbispora* microbes comprise a second microbe of a second *Microbispora* strain, different from the first strain. In certain embodiments, microbes of *Microbispora* strains comprise microbes of *Microbispora sp014161445*, such as *Microbispora sp014161445* designation OATH02011 . 16S rRNA sequences and ATCC Deposit numbers
- 35 including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of

Microbispora 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0088] In embodiments including microbes of one or more *Mycetocola* strains, any suitable strain(s) of *Mycetocola* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Mycetocola* microbes comprise a first microbe of a first *Mycetocola* strain. In certain embodiments, one or more *Mycetocola* microbes comprise a second microbe of a second *Mycetocola* strain, different from the first strain. In certain embodiments, microbes of *Mycetocola* strains comprise microbes of *Mycetocola* *A miduiensis* such as *Mycetocola* *A miduiensis* designation OATH02111. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Mycetocola* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0089] In embodiments including microbes of one or more *Neorhizobium* strains, any suitable strain(s) of *Neorhizobium* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Neorhizobium* microbes comprise a first microbe of a first *Neorhizobium* strain. In certain embodiments, one or more *Neorhizobium* microbes comprise a second microbe of a second *Neorhizobium* strain, different from the first strain. In certain embodiments, microbes of *Neorhizobium* strains comprise microbes of *Neorhizobium flavum*, such as *Neorhizobium flavum* designation OATH01861, *Neorhizobium flavum* designation OATH01931, and/or *Neorhizobium flavum* designation OATH01941. Alternatively or additionally, in certain embodiments, microbes of *Neorhizobium* strains comprise microbes of *Neorhizobium petrolearium* such as *Neorhizobium petrolearium* designation OATH01921. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Neorhizobium* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0090] In embodiments including microbes of one or more *Nocardia* strains, any suitable strain(s) of *Nocardia* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Nocardia* microbes comprise a first microbe of a first *Nocardia* strain. In certain embodiments, one or more *Nocardia* microbes comprise a second microbe of a second *Nocardia* strain, different from the first strain. In certain embodiments, microbes of *Nocardia* strains comprise microbes of *Nocardia farcinica*, such as *Nocardia farcinica* designation OATH01771. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Nocardia* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0091] In embodiments including microbes of one or more *Nocardioides* strains, any suitable strain(s) of *Nocardioides* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Nocardioides* microbes comprise a first microbe of a first *Nocardioides* strain. In certain embodiments, one or more *Nocardioides* microbes comprise a second microbe of a second *Nocardioides* strain, different from the first strain. In certain embodiments, microbes of *Nocardioides* strains comprise microbes of *Nocardioides strain* designation OATH02121. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Nocardioides* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0092] In embodiments including microbes of one or more *Nonomuraea* strains, any suitable strain(s) of *Nonomuraea* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Nonomuraea* microbes comprise a first microbe of a first *Nonomuraea* strain. In certain

embodiments, one or more *Nonomuraea* microbes comprise a second microbe of a second *Nonomuraea* strain, different from the first strain. In certain embodiments, microbes of *Nonomuraea* strains comprise microbes of *Nonomuraea rhodomycinica*, such as *Nonomuraea rhodomycinica* designation OATH01761 . 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Nonomuraea* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0093] In embodiments including microbes of one or more *Peribacillus* strains, any suitable strain(s) of *Peribacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Peribacillus* microbes comprise a first microbe of a first *Peribacillus* strain. In certain embodiments, one or more *Peribacillus* microbes comprise a second microbe of a second *Peribacillus* strain, different from the first strain. In certain embodiments, microbes of *Peribacillus* strains comprise microbes of *Peribacillus frigiditolerans* _A, such as *Peribacillus frigiditolerans* _A designation OATH01661 , *Peribacillus frigiditolerans* _A designation OATH01691 ., and/or *Peribacillus frigiditolerans* _A designation OATH01741 . 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Peribacillus* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0094] In embodiments including microbes of one or more *Priestia* strains, any suitable strain(s) of *Priestia* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Priestia* microbes comprise a first microbe of a first *Priestia* strain. In certain embodiments, one or more *Priestia* microbes comprise a second microbe of a second *Priestia* strain, different from the first strain. In certain embodiments, microbes of *Priestia* strains comprise microbes of *Priestia aryabhattai*, such as *Priestia aryabhattai* designation OATH01451 , *Priestia aryabhattai* designation OATH01531 , *Priestia aryabhattai* designation OATH01541, *Priestia aryabhattai*

designation OATH01841, and/or *Priestia aryabhattai* designation OATH01551. Alternatively or additionally, in certain embodiments, microbes of *Priestia* strains comprise microbes of *Priestia megaterium* such as *Priestia megaterium* designation OATH01581. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain

5 embodiments, microbe or microbes of *Priestia* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for
10 each strain as designated in Table 2A.

[0095] In embodiments including microbes of one or more *Pristimantibacillus* strains, any suitable strain(s) of *Pristimantibacillus* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Pristimantibacillus* microbes comprise a first microbe of a first *Pristimantibacillus*
15 strain. In certain embodiments, one or more *Pristimantibacillus* microbes comprise a second microbe of a second *Pristimantibacillus* strain, different from the first strain. In certain embodiments, microbes of *Pristimantibacillus* strains comprise microbes of *Pristimantibacillus* strain designation OATH01272. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of
20 *Pristimantibacillus* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table
25 2A.

[0096] In embodiments including microbes of one or more *Stenotrophomonas* strains, any suitable strain(s) of *Stenotrophomonas* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Stenotrophomonas* microbes comprise a first microbe of a first *Stenotrophomonas*
30 strain. In certain embodiments, one or more *Stenotrophomonas* microbes comprise a second microbe of a second *Stenotrophomonas* strain, different from the first strain. In certain embodiments, microbes of *Stenotrophomonas* strains comprise microbes of *Stenotrophomonas geniculata*, such as *Stenotrophomonas geniculata* designation OATH01181. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In
35 certain embodiments, microbe or microbes of *Stenotrophomonas* 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%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A.

5 [0097] In embodiments including microbes of one or more *Zhihengliuella* strains, any suitable strain(s) of *Zhihengliuella* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Zhihengliuella* microbes comprise a first microbe of a first *Zhihengliuella* strain. In certain embodiments, one or more *Zhihengliuella* microbes comprise a second microbe of a
10 second *Zhihengliuella* strain, different from the first strain. In certain embodiments, microbes of *Zhihengliuella* strains comprise microbes of *Zhihengliuella* sp031178195, such as *Zhihengliuella* sp031178195 designation OATH01701. 16S rRNA sequences and ATCC Deposit numbers including each strain are as shown in Table 2A. In certain embodiments, microbe or microbes of *Zhihengliuella* strains have a 16S rRNA gene nucleotide sequence or sequences with at least 80,
15 85, 90, 95, 96, 97, 98, 99, or 99.55 identity, or 100%, such as at least 95%, 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A..

20 [0098] In embodiments including microbes of one or more *Stutzerimonas* strains, any suitable strain(s) of *Stutzerimonas* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3, or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Stutzerimonas* microbes comprise a first microbe of a first *Stutzerimonas* strain. In certain embodiments, one or more *Stutzerimonas* microbes comprise a second microbe of a
25 second *Stutzerimonas* strain, different from the first strain. In certain embodiments, microbes of *Stutzerimonas* strains comprise microbes of *Stutzerimonas stutzeri*_AI, such as *Stutzerimonas stutzeri*_AI designation OATH01791. In certain embodiments, microbe or microbes of *Stutzerimonas* 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%, such as at least 95%, preferably at least
30 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 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[0099] In embodiments including microbes of one or more *Terrimonas* strains, any suitable
35 strain(s) of *Terrimonas* may be used. In certain embodiments, cells (microbes) of at least 1, 2, 3,

or 4 and/or not more than 2, 3, 4, or 5 strains are used. In certain embodiments, one or more *Terrimonas* microbes comprise a first microbe of a first *Terrimonas* strain. In certain embodiments, one or more *Terrimonas* microbes comprise a second microbe of a second *Terrimonas* strain, different from the first strain. In certain embodiments, microbes of

5 _____ strains comprise microbes of *Terrimonas* designation OATH01821 . In certain embodiments, microbe or microbes of *Terrimonas* 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%, such as at least 95%, 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
10 one or more sequences for each strain as designated in Table 2A to one or more sequences for each strain as designated in Table 2A.

[00100] In certain embodiments, provided is a composition comprising microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can include one or more strains of the species *Streptomyces griseoincarnatus*, *Streptomyces misionensis*, *Streptomyces*
15 *murinus*, *Streptomyces echinatu*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, *Streptomyces chartreusis*, *Streptomyces globosus*, *Streptomyces achromogenes*, and/or *Streptomyces eurythermus*. *Microbacterium* can include one or more strains of the species *Microbacterium paraoxydans* . *Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. The composition can comprise one or more of the bacteria of Table 33, Example 36. The composition may
20 further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00921 comprising a 16S rRNA sequence of SEQ ID No. 398. The composition may further comprise one or more microbes of the genera *Bacillus*, *Brevibacillus*, *Lysinibacillus*, and/or *Paenibacillus*. Exemplary
25 species include but are not limited to *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus sphaericus*, and *Paenibacillus cellulositrophicus*. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00101] In certain embodiments, provided is a composition comprising microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can
30 include one or more strains of the species *Streptomyces griseoincarnatus*, *Streptomyces griseoaurantiacus*, *Streptomyces rochei*, *Streptomyces bikiniensis*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, and/or *Streptomyces achromogenes*. *Lysinibacillus* can include one or more strains of the species *Lysinibacillus sphaericus*. *Microbacterium* can include one or more strains of the species *Microbacterium*
35 *paraoxydans*. *Rhodococcus* can include one or more strains of the species *Rhodococcus*

erythropolis. The composition can comprise one or more of the bacteria of Table 34, Example 37. The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces* 5 *griseoincarnatus* OATH00921 comprising a 16S rRNA sequence of SEQ ID No. 398 and/or *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369. The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus* 10 *licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, and *Paenibacillus cellulositrophicus*. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00102] In certain embodiments, provided is a composition comprising microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can 15 include one or more strains of the species *Streptomyces misionensis*, *Streptomyces bacillari*, *Streptomyces achromogenes*, and/or *Streptomyces globosus*. *Lysinibacillus* can include one or more strains of the species *Lysinibacillus sphaericus*. *Microbacterium* can include one or more strains of the species *Microbacterium paraoxydans*. *Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. The composition can comprise one or more of 20 the bacteria of Table 37, Example 40. The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus* 25 *aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Paenibacillus cellulositrophicus*. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00103] In certain embodiments, provided is a composition comprising microbes from the genera *Bacillus*, *Lysinibacillus*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can include one 30 or more strains of the species *Streptomyces misionensis*, *Streptomyces bacillari*, *Streptomyces achromogenes*, *Streptomyces globosus*, *Streptomyces antibioticus*, *Streptomyces bikiniensis*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces griseoaurantiacus*, *Streptomyces murinus*, *Streptomyces musisoli*, *Streptomyces olivaceus*, *Streptomyces sennicompusti*, and/or *Streptomyces toxytricini*. *Bacillus* can include one or more strains of the species *Bacillus velezensis*. 35 *Lysinibacillus* can include one or more strains of the species *Lysinibacillus sphaericus*.

- Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. The composition can comprise one or more of the bacteria of Table 38, Example 41. The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of
- 5 SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369. The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Brevibacillus*, *Microbacterium*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*,
- 10 *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Microbacterium azadirachtae*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, and *Streptomyces griseostramineus*. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.
- [00104] In certain embodiments, provided is a composition comprising microbes from the
- 15 genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can include one or more strains of the species *Streptomyces achromogenes*, *Streptomyces bacillari*, *Streptomyces globosus*, *Streptomyces misionensis*, and/or *Streptomyces rochei*. *Lysinibacillus* can include one or more strains of the species *Lysinibacillus sphaericus*. *Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. *Microbacterium* can
- 20 include one or more strains of the species *Microbacterium paraoxydans*. The composition can comprise one or more of the bacteria of Table 40, Example 43. The composition may further comprise one or more microbes of the genera *Bacillus*, *Paenibacillus*, *Pisolithus*, *Rhizopogon*, and/or *Scleroderma*. Exemplary species include but are not limited to *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Paenibacillus cellulositrophicus*, *Pisolithus tinctorius*,
- 25 *Rhizopogon luteolus*, and *Scleroderma citrinum*. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein, for example, ectomycorrhizal fungi such as one or more of ectomycorrhizal fungi of one more genera of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, and/or *Sebacina*, as described further herein.
- 30 [00105] In certain embodiments, provided is a composition comprising microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*. *Microbacterium* can include one or more strains of the species *Microbacterium paraoxydans*. *Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. *Streptomyces* can include one or more strains of the species *Streptomyces achromogenes*, *Streptomyces bacillari*, *Streptomyces bikiniensis*
- 35 *Streptomyces globosus*, *Streptomyces griseoincarnatus*, *Streptomyces misionensis*, *Streptomyces*

murinus, and/or *Streptomyces rochei*. The composition can comprise one or more of the bacteria of Table 41, Example 44. The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. In certain embodiments the composition

5 comprises one or more fungi, such as one or more of the fungi disclosed herein, for example, ectomycorrhizal fungi such as one or more of ectomycorrhizal fungi of one more genera of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, and/or *Sebacina*, as described further herein.

[00106] In certain embodiments, provided is a composition comprising microbes from the

10 genera *Bacillus*, *Lysinibacillus*, *Microbacterium*, *Neorhizobium*, *Peribacillus*, *Priestia*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. *Streptomyces* can include one or more strains of the species *Streptomyces nigrescens*, *Streptomyces nigra*, *Streptomyces bobili*, *Streptomyces albogriseolus*, *Streptomyces globosus*, *Streptomyces griseoincarnatus*, *Streptomyces griseoaurantiacus*, *Streptomyces rochei*, *Streptomyces bikiniensis*, *Streptomyces misionensis*,

15 *Streptomyces murinus*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, and/or *Streptomyces achromogenes*. *Bacillus* can include one or more strains of the species *Bacillus spizizenii* and/or *Bacillus paralicheniformis*. *Lysinibacillus* can include one or more strains of the species *Lysinibacillus sphaericus*. *Microbacterium* can include one or more strains of the species *Microbacterium paraoxydans*. *Neorhizobium* can include one or more strains of the species

20 *Neorhizobium flavum*. *Peribacillus* can include one or more strains of the species *Peribacillus frigoritolerans*_A. *Priestia* can include one or more strains of the species *Priestia aryabhatai*. *Pseudomonas* can include one or more strains of the species *Pseudomonas paracanis*. *Rhodococcus* can include one or more strains of the species *Rhodococcus erythropolis*. The composition can comprise one or more of the bacteria of Table 35, Example 38. The composition

25 may further comprise one or more microbes of the genera *Aneurinibacillus*, *Brevibacillus*, *Glomus*, *Paenibacillus*, *Pisolithus*, and/or *Rhizopogon*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Glomus aggregatum*, *Glomus etunicatum*, *Glomus intraradices*, *Glomus mosseae*, *Lysinibacillus capsici*, *Neorhizobium flavum*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Peribacillus frigoritolerans*, *Pisolithus tinctorius*, *Priestia aryabhatai*, *Priestia megaterium*, *Rhizopogon amylopogon*, *Rhizopogon fulvigleba*, *Rhizopogon luteolus*, *Rhizopogon villosulus*, and *Streptomyces nigrescens*. In certain

30 embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

- [00107] In certain embodiments, provided is a composition comprising microbes from the genera *Aneurinibacillus*, *Microbacterium*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. *Aneurinibacillus* can comprise one or more strains of the species *Aneurinibacillus aneurinilyticus*. *Microbacterium* can comprise one or more strains of the species
- 5 *Microbacterium paraoxydans*. *Pseudomonas* can comprise one or more strains of the species *Pseudomonas paracanis*. *Rhodococcus* can comprise one or more strains of the species *Rhodococcus erythropolis*. *Streptomyces* can comprise one or more strains of the species *Streptomyces achromogenes*, *Streptomyces antibioticus*, *Streptomyces bacillari*, *Streptomyces bikiniensis*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces echinatus*,
- 10 *Streptomyces eurythermus*, *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces musisoli*, *Streptomyces olivaceus*, *Streptomyces rochei*, *Streptomyces sennicomposti*, and/or *Streptomyces toxytricini*. The composition can comprise one or more of the bacteria of Table 42, Example 45. The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a
- 15 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369. The composition may further comprise one or more microbes of the genera *Bacillus*, *Lysinibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Bacillus licheniformis*, *Bacillus velezensis*, *Lysinibacillus capsici*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, and *Streptomyces griseostramineus*. In certain
- 20 embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein. In certain embodiments, provided is a composition comprising microbes from the genera *Aneurinibacillus*, *Bacillus*, *Microbacterium*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. *Aneurinibacillus* can comprise one or more strains of the species *Aneurinibacillus aneurinilyticus*. *Bacillus* can comprise one or more strains of the species *Bacillus velezensis*.
- 25 *Microbacterium* can comprise one or more strains of the species *Microbacterium paraoxydans*. *Pseudomonas* can comprise one or more strains of the species *Pseudomonas paracanis*. *Rhodococcus* can comprise one or more strains of the species *Rhodococcus erythropolis*. *Streptomyces* can comprise one or more strains of the species *Streptomyces achromogenes*, *Streptomyces antibioticus*, *Streptomyces bacillari*, *Streptomyces bikiniensis*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces echinatus*, *Streptomyces eurythermus*,
- 30 *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces musisoli*, *Streptomyces olivaceus*, *Streptomyces rochei*, *Streptomyces sennicomposti*, and/or *Streptomyces toxytricini*. The composition can comprise one or more of the bacteria of Table 43, Example 46. The composition may further comprise one or
- 35 more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for

example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369. The composition may further comprise one or more microbes of the genera *Brevibacillus*, *Lysinibacillus*, *Microbacterium*, and/or

- 5 *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Lysinibacillus sphaericus*, *Microbacterium azadirachtae*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, *Streptomyces griseoincarnatus*, and *Streptomyces griseostramineus*. In certain
10 embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00108] In certain embodiments, provided herein is a composition comprising bacteria of the genus *Streptomyces* and bacteria of the class Bacilli, e.g., bacteria of one or more of *Aneurinibacillus*, e.g., one or more strains of the species *Aneurinibacillus aneurinilyticus*;

- 15 *Bacillus*, e.g., one or more strains of the species *Bacillus_I endophytica_A*, *Bacillus haynesii*, *Bacillus inaqosorum*, *Bacillus licheniformis*, *Bacillus paralicheniformis*, *Bacillus safensis*, *Bacillus spizizenii*, *Bacillus subtilis*, *Bacillus_A thuringiensis_K*, and/or *Bacillus velezensis*; *Brevibacillus*, such as one or more strains of the species *Brevibacillus panacihumi*; *Lysinibacillus*, such as one or more strains of the species *Lysinibacillus sphaericus* and/or
20 *Lysinibacillus capsica*; *Paenibacillus*, such as one or more strains of the species *Paenibacillus cellulositrophicus*; *Peribacillus*, such as one or more strains of the species *Peribacillus frigoritolerans_A*; and/or *Pristimantibacillus*. In certain embodiments, the composition comprises one or more of the *Streptomyces* species or strains of the species as shown in Table 2A and one or more of the Bacilli genera, species or strains of the species as shown in Table 2A. In
25 certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00109] In certain embodiments, provided is a composition comprising bacteria from one or more of genera *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Arthrobacter*, *Bacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbispora*, *Microvirga*, *Mycetocola*,
30 *Neorhizobium*, *Nocardia*, *Nocardioides*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pseudomonas*, *Streptomyces*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*, such as one or more of the strains of Table 44, Example 47. In certain embodiments, one or more or all of these bacteria may be free-living nitrogen-fixing bacteria. In certain embodiments the composition comprises one or more fungi, such as one or more of the fungi disclosed herein.

[00110] In certain embodiments, provided herein is a composition comprising one or more bacteria from one or more of ATCC deposit numbers PTA-127834-PTA-127850, as shown in Table 2A, e.g., one or more bacteria of ATCC deposit number PTA-127834, and/or one or more bacteria of ATCC deposit number PTA-127835, and/or one or more bacteria of ATCC deposit number PTA-127836, and/or one or more bacteria of ATCC deposit number PTA-127837, and/or one or more bacteria of ATCC deposit number PTA-127838, and/or one or more bacteria of ATCC deposit number PTA-127839, and/or one or more bacteria of ATCC deposit number PTA-127840, and/or one or more bacteria of ATCC deposit number PTA-127841, and/or one or more bacteria of ATCC deposit number PTA-127842, and/or one or more bacteria of ATCC deposit number PTA-127843, and/or one or more bacteria of ATCC deposit number PTA-127844, and/or one or more bacteria of ATCC deposit number PTA-127845, and/or one or more bacteria of ATCC deposit number PTA-127846, and/or one or more bacteria of ATCC deposit number PTA-127847, and/or one or more bacteria of ATCC deposit number PTA-127848, and/or one or more bacteria of ATCC deposit number PTA-127849, and/or one or more bacteria of ATCC deposit number PTA-127850. In certain embodiments, the composition comprises one or more bacteria of the genus *Microbacterium* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Rhodococcus* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Arthrobacter* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Aneurinibacillus* from ATCC deposit number PTA-127839 and/or the composition comprises one or more bacteria of the genus *Pseudomonas* from ATCC deposit number PTA-127844 and/or the composition comprises one or more bacteria of the genus *Bacillus* from ATCC deposit number PTA-127847 and/or the composition comprises one or more bacteria of the genus *Paenibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Pristimantibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Brevibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Paenibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the *Bacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Microvirga* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Pseudomonas* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Peribacillus* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Zhihengliuella* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nonomuraea* from

ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nocardia* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Kocuria* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Actinoplanes* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Microbispora* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Mycetocola* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nocardioides* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Priestia* from ATCC deposit number PTA-127850 and/or the the composition comprises one or more bacteria of the genus *Cupriavidus* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Peribacillus* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Stutzerimonas* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Caldimonas* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Terrimonas* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Neorhizobium* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Erythrobacter* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Allophosphoricella* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127835 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127836 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127837 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127838 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127839 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127840 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127841 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127842 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127843 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127844 and/or the composition

comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127845 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127846 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127849. Details for each bacterial species and strains, and associated 16S rRNA sequences and unique designations may be found in Table 2A.

[00111] In certain embodiments, a mixture of motile and non-motile microbes is used, such as motile and non-motile microbes of the bacteria described herein. The ratio of motile to non-motile bacteria may be any suitable ratio, such as at least 0.01-10, 0.05-10, 0.1-10, 0.2-10, 0.5-10, 0.7-10, 1-2, 1-5, or 1-10, 1-10, and/or not more than 0.05-10, 0.1-10, 0.2-10, 0.5-10, 0.7-10, 1-2, 1-5, or 1-10, 1-10, or 1-20, motile-non-motile bacteria.

Fungi.

[00112] In certain embodiments, compositions provided herein comprise one or more fungal microbes. In certain embodiments, compositions provided herein comprise one or more bacterial microbes and one or more fungal microbes. A composition may comprise a composition comprising bacterial microbes as described above in this section I.B.1 and one or more fungal microbes, as described below.

[00113] Any suitable fungi may be used. In certain embodiments, provided is a composition comprising fungi of one or more of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, *Sebacina*, *Alternaria*, *Beauveria*, *Cladosporium*, *Claroideoglomus*, *Funneliformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*, *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, *Trichoderma*, *Mucor*, and/or *Phanerochaete* genera. In certain embodiments, provided is a composition comprising fungi of one or more of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, *Sebacina*, *Alternaria*, *Beauveria*, *Cladosporium*, *Claroideoglomus*, *Funneliformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*, *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, and/or *Trichoderma* genera. In certain embodiments, provided is a composition comprising fungi of one or more of *Glomus*, *Rhizopogon*, and/or *Scleroderma* genera, such as *Glomus aggregatum*, *Glomus etunicatum*, *Glomus intradices*, *Glomus mosseae*, *Rhizopogon amylopogon*, *Rhizopogon fulvigleba*, *Rhizopogon luteolus*, *Rhizopogon villosulus*, *Scleroderma cepa*, and/or *Scleroderma citrinum*.

[00114] In certain embodiments, provides are compositions comprising ectomycorrhizal fungi. In certain embodiments, provided is a composition comprising ectomycorrhizal fungi of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, or 15 different

genera, preferably 1-15, more preferably 1-10, even more preferably 1-9, yet more preferably 1-8 different genera. In certain embodiments, a composition comprises ectomycorrhizal fungi of one more genera of *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, and/or *Sebacina*. The composition may further
 5 comprise bacteria, such as one or more of the bacteria described herein, e.g., *Streptomyces* and/or one or more genera comprising *Pseudomonas*, *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola_A*, *Neorhizobium*, *Nocardia*, *Nocardioidea*, *Nonomuraea*,
 10 *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*. A composition may further comprise bacteria, such as a combinations of bacteria are as described above in this section I.B.1.

[00115] Additionally or alternatively, a composition may comprise endomycorrhizal fungi. In certain embodiments, provided is a composition comprising endomycorrhizal fungi of at least 1,
 15 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, or 15 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, or 20 different genera, preferably 1-20, more preferably 1-17, even more preferably 1-15, yet more preferably 2-15 different genera. In certain embodiments, a composition comprises ectomycorrhizal fungi of one more genera of *Alternaria*, *Beauveria*, *Cladospodium*, *Claroideoglomus*, *Funneliformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*,
 20 *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, and/or *Trichoderma*. The composition may further comprise bacteria, such as one or more of the bacteria described herein, e.g., *Streptomyces* and/or one or more genera comprising *Pseudomonas*, *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*,
 25 *Kocuria*, *Microbacterium*, *Microbispora*, *Mycetocola_A*, *Neorhizobium*, *Nocardia*, *Nocardioidea*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*. A composition may further comprise bacteria, such as a combinations of bacteria are as described above in this section I.B.1.

[00116] In compositions comprising fungi of the genus *Aspergillus*, any suitable species may
 30 be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Aspergillus*. In certain embodiments, a composition comprises *Aspergillus flavus* and/or *Aspergillus niger*.

[00117] In compositions comprising fungi of the genus *Chaetomium*, any suitable species may
 35 be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or

not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Chaetomium*.

[00118] In compositions comprising fungi of the genus *Coniothyrium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5
5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Coniothyrium*. In certain embodiments, a composition comprises *Coniothyrium minitans*.

[00119] In compositions comprising fungi of the genus *Lecanicillium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5
10 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Lecanicillium*.

[00120] In compositions comprising fungi of the genus *Paecilomyces*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5
15 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Paecilomyces*. In certain embodiments, a composition comprises *Paecilomyces lilacinus*.

[00121] In compositions comprising fungi of the genus *Penicillium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or
20 not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Penicillium*. In certain embodiments, a composition comprises *Penicillium bilaiae*, *Penicillium bilaii*, and/or *Penicillium oxalicum*.

[00122] In compositions comprising fungi of the genus *Phlebia*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or
25 not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Phlebia*. In certain embodiments, a composition comprises *Phlebia gigantea*.

[00123] In compositions comprising fungi of the genus *Rhizopogon*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or
30 not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Rhizopogon*. In certain embodiments, a composition comprises *Rhizopogon amylopogon*, *Rhizopogon fulvigleba*, *Rhizopogon luteolus*, and/or *Rhizopogon villosullus*.

[00124] In compositions comprising fungi of the genus *Scleroderma*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or
35 not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such

as 1, or 2, different species of *Scleroderma*. In certain embodiments, a composition comprises *Scleroderma cepa* and/or *Scleroderma citrinum*.

[00125] In compositions comprising fungi of the genus *Sebacina*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Sebacina*. In certain embodiments, a composition comprises *Sebacina vermifera*.

[00126] In compositions comprising fungi of the genus *Alternaria*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Alternaria*. In certain embodiments, a composition comprises *Alternaria alternata*.

[00127] In compositions comprising fungi of the genus *Beauveria*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Beauveria*. In certain embodiments, a composition comprises *Beauveria bassiana*.

[00128] In compositions comprising fungi of the genus *Cladosporium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Cladosporium*. In certain embodiments, a composition comprises *Cladosporium tenuissimum*.

[00129] In compositions comprising fungi of the genus *Claroideoglossum*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Claroideoglossum*. In certain embodiments, a composition comprises *Claroideoglossum etunicatum*.

[00130] In compositions comprising fungi of the genus *Funneliformis*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Funneliformis*. In certain embodiments, a composition comprises *Funneliformis mosseae*.

[00131] In compositions comprising fungi of the genus *Glomus*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such

as 1, or 2, different species of *Glomus*. In certain embodiments, a composition comprises *Glomus aggregatum*, *Glomus etunicatum*, *Glomus intraradices*, and/or *Glomus mosseae*.

[00132] In compositions comprising fungi of the genus *Laccaria*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Laccaria*. In certain embodiments, a composition comprises *Laccaria laccata*.

[00133] In compositions comprising fungi of the genus *Lecanicillium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Lecanicillium*.

[00134] In compositions comprising fungi of the genus *Metarhizium*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Metarhizium*. In certain embodiments, a composition comprises *Metarhizium anisopliae*.

[00135] In compositions comprising fungi of the genus *Piriformospora*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Piriformospora*.

[00136] In compositions comprising fungi of the genus *Pisolithus*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Pisolithus*. In certain embodiments, a composition comprises *Pisolithus tinctorius*.

[00137] In compositions comprising fungi of the genus *Rhizophagus*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Rhizophagus*. In certain embodiments, a composition comprises *Rhizophagus intraradices* and/or *Rhizophagus irregularis*.

[00138] In compositions comprising fungi of the genus *Serendipita*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Serendipita*. In certain embodiments, a composition comprises *Serendipita indica*.

[00139] In compositions comprising fungi of the genus *Talaromyces*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Talaromyces*. In certain embodiments, a composition comprises
5 *Talaromyces flavus*.

[00140] In compositions comprising fungi of the genus *Trichoderma*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Trichoderma*. In certain embodiments, a composition
10 comprises *Trichoderma asperellum*, *Trichoderma atrobrunneum*, *Trichoderma atroviride*, *Trichoderma harzianum*, and/or *Trichoderma viride*.

[00141] In compositions comprising fungi of the genus *Phanerochaete*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Phanerochaete*. In certain embodiments, a composition
15 comprises *Phanerochaete chrysosporium*.

[00142] In compositions comprising fungi of the genus *Mucor*, any suitable species may be used. In certain embodiments, a composition comprises fungi of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6, preferably 1-6, more preferably 1-4, still more preferably 1-3, such as 1, or 2, different species of *Mucor*.
20

[00143] 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 2, and/or one or more microbes of deposits designation OATH-1 to OATH-140. Deposits may be referred to herein by ATCC number, by
25 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 2,
30 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
35 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

[illegible]

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.

[00144] 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.

[00145] 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.

[00146] 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.

[00147] 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^{11} even more preferably 10^5 to 10^{11} , yet more preferably 10^8 to 10^{11} , still more preferably 10^9 to 10^{11} . In certain embodiments a composition comprises at least 10^8 CFU/gm. In certain embodiments a composition comprises at least 10^9 CFU/gm. In certain embodiments a composition comprises at least 10^9 CFU/gm. In certain embodiments a composition comprises at least 10^{10} CFU/gm. 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} ,

10¹¹, 10¹², 10¹³, or 10¹⁴, and/or not more than 10⁵, 10⁷, 10⁸, 10⁹, 10¹⁰, 10¹¹, 10¹², 10¹³, 10¹⁴, or 10¹⁵ CFU/gm of composition, preferably 10⁶ to 10¹⁵, more preferably 10⁷ to 10¹⁴, even more preferably 10⁷ to 10¹³, yet more preferably 10⁷ to 10¹¹, even yet more preferably 10⁸ to 10¹¹ 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.

[00148] 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 microorganisms 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 and/or one or more microbes of ATCC Nos. 127834-127850 has been growing.

2. Dry compositions

[00149] In certain embodiments a composition, such as a composition comprising one of the compositions comprising bacteria and/or fungi, e.g., a composition of section I.B.1, 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.

- 10 [00150] 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.
- 15 [00151] In certain embodiments, provided herein are compositions comprising a plurality of particles wherein each particle comprises a composition comprising one or more microbes, e.g., one or more bacteria and/or one or more fungi, as described herein. 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
- 20 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
- 25 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,
- 30 250, 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.

[00152] 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 μm 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 μm ,
5 preferably 0.2-40 μm , more preferably 0.5-20 μm , even more preferably 1-20 μm , still more preferably 1-15 μm , yet more preferably 2-15 μm , even still more preferably 2-12 μm .

[00153] 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,
10 900, 1000, 1500, 2000, 3000, 4000, 5000, or 7000 μm 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 μm , or even larger, such as 200-10,000, preferably 500-5000, more preferably 1000-10,000 μm . 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
15 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.

[00154] Certain particulate compositions are dry compositions. Certain particulate
20 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

[00155] 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
25 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
30 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.

[00156] In certain embodiments, provided is a delayed release composition comprising a plurality of particles, each of which comprises a composition comprising microbes, e.g., one or more bacteria and/or one or more fungi, as described herein, 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 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.
[00157] Provided herein are compositions comprising microbes, such as a composition as described above, e.g., one or more bacteria and/or one or more fungi, as described herein, 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.

[00158] 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, alkyl naphthalenesulfonates such as dibutyl naphthalenesulfonate, or C.sub.14-16 olefin sulfonates), alkyl-, alkylaryl- and

arylsulfates or salts thereof (such as sodium, potassium or calcium salts of tridecyl 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 (Agasco), 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, Plytargent B, Renex 600, Solar NO, Sterox, Serfonic N, T-DET-N, Tergitol NP, Triton N, IGEPAL CA-630, Nonident P-40, Pluronic.

[00159] 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%.

[00160] 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. In certain embodiments, a composition comprises polyethylene glycol (PEG). In certain embodiments, a composition comprises PEG and glycerol. The composition comprising PEG may be solid or liquid, depending on the molecular weight of the PEG.

[00161] 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%.

[00162] 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%.

[00163] 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.
- 5
- 10 [00164] 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.
- 15
- [00165] 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
- 20
- 25 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
- 30
- [00166] 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.

[00167]

6. Compositions comprising additional microbes.

[00168] 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
5 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
10 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

[00169] 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
15 "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
20 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
25 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,
30 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, such as tree seedlings to be used for reforestation or upforestation, such as seedlings of a conifer such as pine, or oak, or beech. 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,
- 5 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
- 10 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
- 15 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.
- [00170] In certain embodiments, the commercial crop is corn (maize).
- 20 [00171] In certain embodiments, the commercial crop is soy.
- [00172] In certain embodiments, the commercial crop is rice (e.g., dry grown rice).
- [00173] In certain embodiments, the commercial crop is wheat.
- [00174] In certain embodiments, the commercial crop is barley.
- [00175] In certain embodiments, the commercial crop is sorghum.
- 25 [00176] In certain embodiments, the commercial crop is oat.
- [00177] In certain embodiments, the commercial crop is rye.
- [00178] In certain embodiments, the commercial crop is sugar cane.
8. Plants or plant parts and one or more microbes (optionally with soil).
- [00179] In certain embodiments, provided are compositions that comprise a plant or plant part
- 30 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.
- [00180] 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%,
5 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
10 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
15 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
20 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
25 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
30 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
35 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
5 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
10 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
15 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
20 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
25 the energy or raw material plant is for use in producing a biofuel. In certain embodiments, the
plant is a corn plant. In certain embodiments, the plant is a rice plant. In certain embodiments,
the plant is a soy plant. In certain embodiments, the plant is a wheat plant. In certain
embodiments, the plant is a barley plant. In certain embodiments, the plant is an oat plant. In
certain embodiments, the plant is a rye plant. In certain embodiments, the plant is a sugar cane
30 plant. In certain embodiments, the plant is a sorghum plant. 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
35 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 0.1%, 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/m³ of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³, 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/m³ 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 nematocide, e.g., synthetic nematocide. 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.

[00181] 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 microbes 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. 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 B₁ (thiamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B₂ (riboflavin) density. In certain embodiments the increased vitamin density comprises increased vitamin B₃ (niacin, nicotinic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₅ (pantothenic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₆ (pyridoxal, pyridoxine, or pyridoxamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B₇ (biotin) density. In certain embodiments the increased vitamin density comprises increased vitamin B₉ (folic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₁₂ 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 I.B.10.

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

[00182] 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 commercial crop is a corn plant. In certain embodiments, the commercial crop is a rice plant. In certain embodiments, the commercial crop is a soy plant. In certain embodiments, the commercial crop is a wheat plant. In certain embodiments, the commercial crop is a barley plant. In certain embodiments, the commercial crop is an oat plant. In certain embodiments, the commercial crop is a rye plant. In certain embodiments, the commercial crop is a sugar cane plant. In certain embodiments, the commercial crop is a sorghum plant. 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%,
 5 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
 10 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/m³ of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³, 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/m³ of soil. In certain
 15 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,
 20 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,
 25 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.

30 10. Plants

[00183] 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
- 5 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
- 10 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
- 15 the energy or raw material plant is for use in producing a biofuel. In certain embodiments a plant is a hemp plant.
- [00184] In certain embodiments, the commercial crop is corn (maize).
- [00185] In certain embodiments, the commercial crop is soy.
- [00186] In certain embodiments, the commercial crop is rice (e.g., dry grown rice).
- 20 [00187] In certain embodiments, the commercial crop is wheat.
- [00188] In certain embodiments, the commercial crop is barley.
- [00189] In certain embodiments, the commercial crop is sorghum.
- [00190] In certain embodiments, the commercial crop is oat.
- [00191] In certain embodiments, the commercial crop is rye.
- 25 [00192] In certain embodiments, the commercial crop is sugar cane.

11. Compositions comprising soil

- [00193] 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
- 30 certain embodiments, microbes are those of one of the microbial compositions provided herein, e.g., comprising bacteria and/or fungi, such as 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.
- [00194] 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.

[00195] 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..

10 [00196] 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-
15 1.85 g/cm³ dry weight of soil.

[00197] 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
20 more preferably 35-55%.

[00198] 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,
25 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.

[00199] Alternatively 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/m³ of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³, 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
30 kg/m³ 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%.

[00200] 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
 5 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.

[00201] 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,
 10 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,
 15 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.

[00202] 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.
 20 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
 25 above established standards for organic farming in the area in which soil and/or plants are
 30 situated.

C. Methods

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

[00203] In certain embodiments, provided herein is a method comprising applying a microbial composition, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., 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

10⁹ to 10¹⁴, yet more preferably 10¹⁰ to 10¹³, still more preferably 10¹⁰ to 10¹² 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

5 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

10 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

15 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

20 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

25 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

30 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

35 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 embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum.

[00204] 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 at 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 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 I.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

10⁹-10¹³ cfu/acre, even more preferably 10¹⁰-10¹² 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 comprises 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. In certain embodiments, the method comprises 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 comprises 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.

[00205] In certain embodiments, a composition is applied to soil and/or plants by means of a portable, refillable apparatus comprising a tank to hold the composition and a system for spraying the composition from the tank to the soil and/or plants. The weight of the apparatus is such that, when full, it can be carried and utilized by one person, e.g., not more than 80, 70, 60, 50, 40, 30, or 20 pounds when full.

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

[00206] 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, e.g., comprising bacteria and/or fungi, such as 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., 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 corn vegetable. In certain embodiments, the root, tuber, or corn 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 cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. 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
 [00207] In certain embodiments, provided herein is a method comprising contacting surfaces
 25 of a populations of seeds, seedlings, or other plant propagules with a microbial composition such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., or a derivative produced from the composition. The method results in one or more microbes of the microbial composition associated with the seeds,
 30 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

5 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

10 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,

15 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,

20 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,

25 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

30 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

35 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 corn vegetable. In certain embodiments, the root, tuber, or corn 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 embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum.

4. Aerial application

[00208] 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. Any suitable composition may be used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., or a derivative

thereof. 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

- 5 [00209] 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, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., or a derivative
- 10 thereof. 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
- 15 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,
- 20 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
- 25 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
- 30 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.

[00210] 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.

10 [00211] 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/m³ and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³/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/m³/year compared to reference soil. Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are not cannabis plants. In certain cases, the

plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course. In certain cases, the method further comprises applying one or more soil amendments to the soil, e.g., as described herein, e.g., in some cases, performing one or more tests on soil and/or plants to determine which/how much amendment to use.

[00212] 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. Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

[00213] 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 cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum.

[00214] 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 economically valuable attribute can comprise 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, the increased nutrient density comprises increased protein content, increased mineral content, increased
5 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, and/or horses. In certain
10 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, e.g., corn. 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
15 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
20 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.

[00215] 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
25 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.

[00216] 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
30 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 benefit

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.

[00217] 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
5 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
10 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
15 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
20 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
25 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
30 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 the plants are trees. In certain embodiments the financial benefit comprises a financial benefit realized from animals that eat the plants.

[00218] 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, such as a composition comprising bacteria and/or fungi, , such as compositions described herein, including but not limited to, in sections 5 I.B.1-6, for example section I.B.1, or I.B.5, or I.B.6., or a derivative produced from the composition. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein, e.g., methods including more than one application of a microbial composition or derivative thereof. In certain embodiments, a delayed-release composition is used. In certain embodiments, aerial delivery, e.g., by one or more unmanned 10 vehicles is used, for example as described herein.

[00219] Any suitable area of land may be used. In certain embodiments, 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 15 hectares, yet more preferably 10M to 1B hectares, still more preferably 50M to 1B hectares.

[00220] 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 20 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 25 comprises increasing root biomass, or a component of root biomass.

[00221] 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.

[00222] In certain embodiments, the method further comprises improving one or more soil 30 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 35 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.

[00223] 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 described above.

[00224] 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.

- 5 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.

[00225] 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.

- 10 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
- 15 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
- 20 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
- 25 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
- 30 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
- 35 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

- [00226] 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.
- [00227] 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.
- [00228] 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.
- [00229] 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.
- [00230] 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.
- [00231] 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.
- [00232] 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.
- [00233] In certain embodiments, provided herein is use of the composition as disclosed herein in preventing or reducing flooding.
- [00234] 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.

[00235] 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.

5 [00236] 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.

[00237] 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.

10 [00238] In certain embodiments, provided herein is use of the composition as disclosed herein in reducing carbon footprint for raising livestock.

[00239] In certain embodiments, provided herein is use of the composition as disclosed herein in increasing oil production of a plant not cannabis.

15 [00240] In certain embodiments, provided herein is use of the composition as disclosed herein in regenerating degraded soil.

7. Modulating soil characteristics

[00241] 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
20 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,
25 bioavailability of one or more plant nutrients in the soil, and/or carbon content of the soil.

[00242] 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
30 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.

[00243] 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 5 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 10 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.

[00244] In certain embodiments provided is a method for converting one or more plant 15 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 20 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 25 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 30 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 35 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.

[00245] 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/cm³ 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/m³ of soil and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³, 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/m³ 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.

[00246] 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*.

[00247] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., 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.

[00248] Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

8. Reducing water use

[00249] 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
5 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
10 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,
15 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
20 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.

[00250] 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
25 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
30 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.

[00251] 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*.

[00252] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., 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.

[00253] Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild

grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

9. Obtaining economic benefit

- 5 [00254] 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, hectares, 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
- 10 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
- 15 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
- 20 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
- 25 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,
- 30 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
5 that eat the plants. The plants may be any suitable plants, such as those described herein.

10. Repair and regeneration

[00255] 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
10 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
15 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
20 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.

[00256] 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
25 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.

[00257] 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.

[00258] 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.

[00259] 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*.

[00260] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., 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.

[00261] Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

11. Nutrients

[00262] 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.

- 5 [00263] 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/or the plants; and (ii) providing conditions
- 10 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,
- 15 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,
- 20 400, 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
- 25 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
- 30 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 B₁ (thiamine) density. In
- 35 certain embodiments the increased vitamin density comprises increased vitamin B₂ (riboflavin)

density. In certain embodiments the increased vitamin density comprises increased vitamin B₃ (niacin, nicotinic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₅ (pantothenic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₆ (pyridoxal, pyridoxine, or pyridoxamine) density. In certain embodiments the increased vitamin density comprises increased vitamin B₇ (biotin) density. In certain embodiments the increased vitamin density comprises increased vitamin B₉ (folic acid) density. In certain embodiments the increased vitamin density comprises increased vitamin B₁₂ 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.

[00264] 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 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).

[00265] 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.

[00266] 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*.

[00267] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., 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.

[00268] 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. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain

embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

12. Conversion to organic farming

- 5 [00269] 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
- 10 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,
- 15 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
- 20 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.

- [00270] 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
- 25 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
- 30 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.

[00271] 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.

[00272] 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.

[00273] 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*.

[00274] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as 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., or a derivative thereof. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein, including more than one application of a microbial composition or derivative thereof. 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.

[00275] 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. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum.

13. Economic benefit

[00276] 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
 5 entity and each of the other entities, and communicates information comprising the apportionment to the first entity and/or each of the other entities.

[00277] In certain embodiments a microbial composition as described herein is used, such as a microbial composition as disclosed herein, e.g., comprising bacteria and/or fungi, such as compositions described herein, including but not limited to, in sections I.B.1-6, for example
 10 section I.B.1, or I.B.5, or I.B.6., 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.

[00278] The plants in the soil may be any suitable plants, such as plants described herein, e.g.
 15 one or more of those described in Section I.B.10. In certain cases, the plants are a commercial crop. In certain embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the
 20 commercial crop is rye. In certain embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

14. Trees

25 [00279] 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
 30 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 improved 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.

[00280] 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.

[00281] 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.

[00282] 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

[00283] 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, such as a composition comprising bacteria and/or fungi, , such as 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., or a derivative produced from the composition. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein, e.g., methods including more than one application of a microbial composition or derivative thereof. 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.

[00284] A tree may be any suitable tree, such as a tree as disclosed herein, for example in Section I.B.10. In certain embodiments, the tree is a conifer, e.g., pine. In certain embodiments, the tree is an oak. In certain embodiments, the tree is a beech tree.

[00285] 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

5 [00286] 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.

[00287] In certain embodiments provided herein is a method for increasing biomass of plants
10 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; 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
15 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
20 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
25 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%.

[00288] 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, such as a composition comprising bacteria
30 and/or fungi, , such as 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., or a derivative produced from the composition. Any suitable protocol may be used to apply the microbial composition or derivative thereof, such as the methods described herein, e.g., methods including more than one application of a microbial composition or derivative thereof. 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.

[00289] Plants growing in the soil can include any of the plants described herein, e.g., plants described in section I.B.10 herein. In certain cases, the plants are a commercial crop. In certain 5 embodiments, the commercial crop is corn. In certain embodiments, the commercial crop is rice. In certain embodiments, the commercial crop is soy. In certain embodiments, the commercial crop is wheat. In certain embodiments, the commercial crop is barley. In certain embodiments, the commercial crop is oat. In certain embodiments, the commercial crop is rye. In certain 10 embodiments, the commercial crop is sugar cane. In certain embodiments, the commercial crop is sorghum. In some cases, the plants are uncultivated plants, such as plants on pastureland, wild grasslands, or forests. In certain cases, the plants are turf plants, e.g., turf of a sporting surface, such as a golf course.

16. Production methods

[00290] Microbial compositions as disclosed herein can be produced using any suitable 15 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 20 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 25 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 30 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
- 5 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.
- 10 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
- 15 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.
- [00291] In preferred embodiments, the methods as disclosed herein are performed aseptically.
- 20 [00292] 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.
- [00293] In certain embodiments, a growth medium (*e.g.*, solid or liquid medium) is inoculated
- 25 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,
- 30 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%.
- [00294] 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
- 35 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.

10 [00295] In certain embodiments, microbes grown on the solid medium are removed from the medium and used to produce one or more of the microbial compositions described herein. An exemplary protocol for such procedures is provided in Example 33.

[00296] 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.

20 [00297] 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 (OD₆₀₀), 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.

[00298] 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.

[00299] 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.

[00300] 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 μ m, for example, 0.2-300 μ m, and/or not more than 2, 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, or 300 μ m, for example, 0.2-300 μ m. 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 μ m, for example, 0.2-300 μ m, preferably 120-240 μ m, more preferably 160-220 μ m. 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 μ m, for example, 0.2-300 μ m, preferably 20-100 μ m, more preferably 40-80 μ m. 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
5 in a collection vessel. Additionally or alternatively, the microbes can be spray dried and/or lyophilized.

[00301] 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
10 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%.

[00302] In certain embodiments, the dried microbes are then processed into a powder. In
15 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 μm 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 μm , for example 20-500 μm , preferably 90-270 μm , more preferably 140-220 μm , even more preferably 160-200 μm , still more preferably 170-190 μm .
20 Any suitable technique can be used to process the dried first population of microbes to the desired median particle size, for example blending.

[00303] 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
25 (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,
30 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,
35 100, 110, 120, 130, 140, or 150 stocks.

[00304] 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.

[00305] 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%.

[00306] 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%.

[00307] 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 concentrated 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.

[00308] 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.

[00309] 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.

[00310] 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.

[00311] 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.

[00312] 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 grown 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 (OD₆₀₀), 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.

[00313] 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.

[00314] 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, or one or more microbes from one or more of ATCC Nos. 127834-127850, and providing suitable conditions for one or more microbes to grow.

[00315] In certain embodiments, the first stock can be, but is not required to be, pure.

[00316] 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
5 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
10 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
15 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
20 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
25 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
30 embodiments, the first population comprises Streptomyces designation 45. In certain
embodiments, the first population comprises any one of the microbes in Streptomyces
designation 46.

[00317] In certain embodiments, the heterologous medium comprises a solid medium. In
certain embodiments, the solid medium comprises agar. In certain embodiments, the
35 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
5 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
10 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
15 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
20 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.

[00318] 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
25 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%.

30 [00319] 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
35 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.

[00320] In certain embodiments, the method further comprises concentrating the one or more microbes after growing. In certain embodiments, concentrating comprises filtering. In certain 5 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 μm , for example, 0.2-300 μm . In certain embodiments, the first 10 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 μm , for example, 0.2-300 μm , preferably 120-240 μm , more preferably 160-220 μm . 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 μm , for example, 0.2-300 μm , preferably 20-100 μm , more preferably 40-80 μm . 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.

[00321] 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, 25 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%.

[00322] 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 30 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 35

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%.

[00323] In certain embodiments, the dried microbes are processed to a powder.

[00324] 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., vacuum sealing under nitrogen.

[00325] 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** or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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**, or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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, or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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

5 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

10 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,

15 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

20 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 μm 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 μm , for example 20-500 μm , preferably 90-270 μm , more preferably 140-220 μm , even more preferably 160-200 μm , still more preferably 170-190 μm , and/or a mean particle size of at least 20, 30, 40, 50, 60, 70,

25 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 250, 370, 300, or 400 μm 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 μm , for example 20-500 μm , preferably 90-270 μm , more preferably 140-220 μm , even more preferably 160-200 μm , still more preferably 170-190 μm . In certain embodiments, the microbes comprises a viability of at least 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} ,

30 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

- [00326] 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 or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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 or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, and a heterologous growth medium.
- [00327] 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

[illegible]

[illegible]

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

5 Streptomyces designation O-140.

[00328] In certain embodiments, the heterologous medium comprises a solid medium.

[00329] 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

10 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

15 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

20 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,

25 600, 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

30 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

35 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.

[00330] 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, 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%.

[00331] In certain embodiments, provided herein is a composition comprising one or more of Streptomyces deposited as ATCC Nos. as shown in **Table 2** or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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
5 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
10 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
15 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
20 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
25 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
30 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
35 embodiments, the composition comprises Streptomyces designation O-69. In certain

[illegible]

[illegible]

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.

[00332] 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 one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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 one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, or Streptomyces Designation O-46- O-140 has been growing.

[00333] 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.

[00334] 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.

[00335] 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.

[00336] 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 μm 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 μm , for example 20-500 μm , preferably 90-270 μm , more preferably 140-220 μm , even more preferably 160-200 μm , still more preferably 170-190 μm . 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.

[00337] 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

5 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

10 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

15 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

20 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

25 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

30 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.

[00338] In certain embodiments, the composition comprises one or more agriculturally

35 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 10 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, 15 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%.

[00339] In certain embodiments, the composition is a solid composition.

20 [00340] In certain embodiments, the composition is a liquid composition.

[00341] 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 25 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%.

[00342] In certain embodiments, the composition comprises one or more materials that protect 30 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 35 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.

[00343] 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%.

[00344] 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.

[00345] 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.

[00346] 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 μm 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.

[00347] In certain embodiments, the composition comprises 10-20 of Streptomyces designation 1-45 (deposited as ATCC Nos. PTA-127367-127413, respectively) or one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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.

[00348] 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 one or more microbes from one or more of ATCC Nos. 127834-127850, as shown in Table 2A, 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. Fungi can be as described herein.

III. Examples

Example 1: Preparation of microbial composition

[00349] 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.

[00350] 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 μ m). 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

5 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.

[00351] 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.

[00352] 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.

[00353] 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

[00354] 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.

[00355] 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

[00356] 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

[00357] 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.

[00358] 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.

[00359] Soil bulk density and soil moisture content were determined for each soil sample as follows.

[00360] 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

[00361] 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

[00362] 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

[00363] 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 of 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

15 **[00364]** 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.

[00365] The following data was compiled over the course of 112 days after treatment of soil
20 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
25 soil moisture reader for percentages in the top six inches of soil.

[00366] 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

5 [00367] 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.

[00368] 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.

[00369] 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.

5 **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**

[00370] 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).

10 [00371] 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
15 microbes.

[00372] 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
20 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
25 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
30 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

[00373] 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

[00374] 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.

[00375] 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

[00376] 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

[00377] 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.

[00378] 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

[00379] 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).

[00380] 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.

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

[00381] 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.

15 [00382] 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.

[00383] 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

[00384] 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

[00385] 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.

[00386] Four plots of turf and shrubs were treated with the composition comprising a plurality of different microbes.

Table 12: Beneficial microbe measurements per gram of soil

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

[00387] 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).

[00388] 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

[00389] 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.

[00390] 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

[00391] 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.

[00392] 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

[00393] 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.

[00394] 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

[00395] 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.

[00396] 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

[00397] 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.

[00398] 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).

5 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

[00399] 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).

[00400] 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

[00401] 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.

[00402] 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 aurally 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.

[00403] 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

[00404] 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.

[00405] 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.

[00406] 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

[00407] 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.

[00408] 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

5 [00409] 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

10 [00410] 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.

15 [00411] 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

25

[00412] 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

[00413] 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.

[00414] 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

[00415] 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

[00416] 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.

[00417] 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

5 [00418] 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

10 [00419] 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.

15 [00420] 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
20 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.

25 [00421] 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%
30 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

[00422] 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.

[00423] 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

[00424] 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.

[00425] 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

[00426] 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.

- [00427] 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

- [00428] 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.
- [00429] 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.
- [00430] 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

- [00431] 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.
- [00432] 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%.

- [00433] 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

- [00434] 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.
- [00435] 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.
- [00436] 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

- [00437] 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.
- [00438] 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/barnmap>). 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.

[00439] Figure 2 shows the topography of a Maximum-Likelihood phylogenetic tree displaying 195 ribotype gene signatures representing the OSL probiotic culture collection. Ten genera are presented with *Streptomyces* 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) *Amicycolatopsis*, (9) *Rhodococcus*, (10) *Micrococcus*, and (11) *Streptomyces*. 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
- 5 *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
- 10 *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
- 15 (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),
- 20 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
- 25 *Streptomyces* sp OATH 61 (SEQ ID NO: 145), 173 *Streptomyces* sp OATH 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
- 30 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
- 35 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).

[00440] *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.

[00441] Consortia signatures of carbon sequestration: CO₂ 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 CO₂ 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 CO₂ sequestration and a long-term solution of storing carbon in soil.

[00442] 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.

[00443] 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.

[00444] 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.

[00445] 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

[00446] 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.

[00447] 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 destructively harvested and evaluated for root and shoot biomass.

[00448] 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%

[00449] 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

[00450] 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.

[00451] 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

[00452] 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.

[00453] 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

5 [00454] 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.

[00455] 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,
10 carotene, shell firmness, porosity, translucency, blemish, and yield were measured.

[00456] 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:
15 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
20 plants, the average rating was lower than 2, which implies acceptable trace to moderate porosity for both treatments.

[00457] 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
25 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.

30 [00458] 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

[00459] 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.

[00460] 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.

[00461] 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

[00462] 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.

[00463] 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.

[00464] 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

[00465] 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.

[00466] 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.

[00467] 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 nearest 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.

[00468] 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.

5

[00469] 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.

10

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

[00470] 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.

15

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

[00471] 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.

[00472] 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.

[00473] 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

[00474] 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.

[00475] 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.

[00476] 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

[00477] 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

[00478] 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.

[00479] 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.

[00480] 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.

5 [00481] 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.

10 [00482] 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.

15 [00483] 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 had 181% higher fine root weight on average, and 3x treated plants had 282% higher fine root weight than untreated plants.

[00484] 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.

20 [00485] 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.

25 [00486] 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.

30 [00487] 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.

- [00488] 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.
- [00489] 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.
- [00490] 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

- [00491] 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

[00492] 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

[00493] 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

Example 32: Conversion from mixed strain stocks to single strain stocks

[00494] This example demonstrates the production of single strain isolates from mixed strain isolates.

[00495] The original 140 stocks (ATCC deposit #s PTA-127367 through PTA-127413 as shown in Table 2 and Oath-maintained deposits O-46 through O-140) were sequenced using PacBio full length 16S RNA gene sequencing. Once the results were ready 16S sequences were identified using GenBank’s data base and sequence homology searches. 99% sequence identity was used as the threshold value to add a species name to each 16S gene. The outcome of this analyses showed that multiple of the original 140 stocks comprised more than one microbial species.

[00496] A new set of internal stocks was developed comprising single microbial isolates. Literature and conventional microbiology knowledge were used to select correct phenotypes for further sequencing evaluation. If there were any unknown phenotypes they were also sent for 16S sequencing. The effort resulted in the production of the isolates shown in **Table 32**.

- 5 [00497] **Table 32** shows the updated isolate (ID# and taxonomic prediction) information as well as its corresponding designation from **Table 1** (Strain # and Genus/Species). The matches are represented with BLAST comparisons of the 16S rRNA sequences. BLAST values (% identity and alignment length) are shown under the alignment info.

- [00498] Isolated bacterial colonies were subjected to DNA extraction and full genome
10 sequencing using an Illumina platform. Genomes were assembled using a de Bruijn graph assembler. 16S RNA genes were extracted from genomes by using sequence alignments of reference 16S genes obtained from a database. 16S genes from target genomes were extracted and searched in GenBank for its closest species match using the The Basic Local Alignment Search Tool Blastn. Species names from Blastn searches were added to 16S sequences that
15 showed >98% positive ID in output alignment. The highest percentage positive ID match was chosen as the species designation. For 16S genes that had no full species name matches; these were abbreviated as “sp. OATH_1” etc. For example: *Streptomyces* sp. OATH_1, *Streptomyces* sp. OATH_2 etc.

20

Table 32: isolate correlation matrix

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00011	<i>Streptomyces toxytricini</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00021	<i>Streptomyces echinatu</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00031	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1448
OATH 00041	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448
OATH 00051	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00052	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00053	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00071	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00072	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00081	<i>Streptomyces rochei</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00091	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00101	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces sp900105755</i>	100	1218
OATH 00102	<i>Pseudomonas E paracanis</i>	197	<i>Streptomyces sp. OATH_61</i>	100	623
OATH 00102	<i>Pseudomonas E paracanis</i>	10	<i>Streptomyces sp. OATH_E</i>	100	876
OATH 00103	<i>Streptomyces sennicomposti</i>	24	<i>Pseudomonas azotoformans</i>	100	1459
OATH 00143	<i>Microbacterium oxydans</i>	99	<i>Streptomyces sp. OATH_30</i>	93.814	1455
OATH 00144	<i>Streptomyces griseoincarnatus</i>	23	<i>Streptomyces griseoincarnatus</i>	100	1450
OATH 00223	<i>Streptomyces misionensis</i>	17	<i>Streptomyces misionensis</i>	100	1447
OATH 00224	<i>Microbacterium paraoxydans</i>	99	<i>Streptomyces sp. OATH_30</i>	92.995	1456
OATH 00241	<i>Streptomyces sennicomposti</i>	4	<i>Streptomyces sp. OATH_A</i>	100	1448
OATH 00242	<i>Streptomyces sennicomposti</i>	57	<i>Streptomyces sp. OATH_27</i>	100	912
OATH 00243	<i>Streptomyces sennicomposti</i>	57	<i>Streptomyces sp. OATH_27</i>	100	912
OATH 00252	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00253	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00261	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00262	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00263	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00264	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00291	<i>Streptomyces griseoaurantiacus</i>	18	<i>Streptomyces griseoaurantiacus</i>	100	1446
OATH 00292	<i>Streptomyces griseoaurantiacus</i>	18	<i>Streptomyces griseoaurantiacus</i>	100	1446
OATH 00301	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	100	1217
OATH 00312	<i>Streptomyces bacillari</i>	15	<i>Streptomyces bacillaris</i>	100	1450
OATH 00313	<i>Streptomyces bacillari</i>	15	<i>Streptomyces bacillaris</i>	100	1450
OATH 00321	<i>Streptomyces griseoincarnatus</i>	6	<i>Streptomyces sp. OATH_C</i>	100	1448
OATH 00322	<i>Streptomyces echinatus</i>	6	<i>Streptomyces sp. OATH_C</i>	100	1448
OATH 00323	<i>Streptomyces echinatus</i>	6	<i>Streptomyces sp. OATH_C</i>	100	1448
OATH 00331	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00342	<i>Microbacterium resistens</i>	99	<i>Streptomyces sp. OATH_30</i>	92.376	1456
OATH 00343	<i>Streptomyces achromogenes</i>	68	<i>Streptomyces sp. OATH_13</i>	100	1275
OATH 00351	<i>Streptomyces olivaceus</i>	11	<i>Streptomyces fimbriatus</i>	100	1453

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00352	<i>Streptomyces olivaceus</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00352	<i>Streptomyces olivaceus</i>	174	<i>Lysinibacillus capsici</i>	93.659	410
OATH 00353	<i>Streptomyces rochei</i>	11	<i>Streptomyces fimbriatus</i>	100	1453
OATH 00354	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00371	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00372	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00373	<i>Streptomyces antibioticus</i>	5	<i>Streptomyces sp. OATH_B</i>	100	1449
OATH 00374	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00375	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00376	<i>Streptomyces antibioticus</i>	22	<i>Streptomyces antibioticus B</i>	100	1448
OATH 00381	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces sp900105755</i>	99.507	1218
OATH 00382	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00383	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	99.517	1448
OATH 00384	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	99.102	1448
OATH 00392	<i>Streptomyces bacillari</i>	64	<i>Streptomyces cavourensis</i>	100	1276
OATH 00402	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	99.033	1448
OATH 00403	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	100	1217
OATH 00404	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	99.033	1448
OATH 00412	<i>Streptomyces griseoincarnatus</i>	129	<i>Streptomyces misionensis</i>	100	688
OATH 00412	<i>Streptomyces griseoincarnatus</i>	139	<i>Streptomyces sp. OATH_48</i>	100	432
OATH 00412	<i>Streptomyces griseoincarnatus</i>	170	<i>Streptomyces sp. OATH_57</i>	100	832
OATH 00413	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00421	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00422	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00423	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00424	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00425	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00442	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	100	1217
OATH 00443	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	100	631

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00443	<i>Streptomyces sennicomposti</i>	197	<i>Streptomyces</i> sp. OATH_61	100	623
OATH 00483	<i>Microbacterium paraoxydans</i>	99	<i>Streptomyces</i> sp. OATH_30	93.814	1455
OATH 00491	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00492	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00493	<i>Microbacterium</i> sp002979655	99	<i>Streptomyces</i> sp. OATH_30	93.814	1455
OATH 00521	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00522	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00562	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00563	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00564	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00571	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00581	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 00591	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00592	<i>Streptomyces sennicomposti</i>	196	<i>Streptomyces</i> sp900105755	100	1218
OATH 00593	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.448	1448
OATH 00601	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00641	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1448
OATH 00651	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00661	<i>Streptomyces chartreusis</i>	174	<i>Lysinibacillus capsici</i>	87.705	488
OATH 00661	<i>Streptomyces chartreusis</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00662	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00663	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00681	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00691	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.507	1218
OATH 00692	<i>Streptomyces sennicomposti</i>	180	<i>Pseudomonas azotoformans</i>	87.013	462
OATH 00692	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 00701	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00702	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 00711	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 00741	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00742	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00743	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00753	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.448	1448
OATH 00762	<i>Streptomyces rochei</i>	16	<i>Streptomyces rochei</i>	100	1448
OATH 00801	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00802	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00811	<i>Paenibacillus cellulositrophicus</i>	59	<i>Paenibacillus cellulositrophicus</i> A	100	1266
OATH 00823	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00851	<i>Streptomyces echinatus</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 00871	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.931	1448
OATH 00881	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 00891	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 00892	<i>Lysinibacillus sphaericus</i>	129	<i>Streptomyces misionensis</i>	98.243	569
OATH 00892	<i>Lysinibacillus sphaericus</i>	162	<i>Lysinibacillus capsici</i>	98.711	1474
OATH 00892	<i>Lysinibacillus sphaericus</i>	170	<i>Streptomyces</i> sp. OATH_57	99.685	634
OATH 00901	<i>Streptomyces sennicomposti</i>	4	<i>Streptomyces</i> sp. OATH_A	100	1448
OATH 00912	<i>Streptomyces globosus</i>	45	<i>Streptomyces lydicus</i>	100	1451
OATH 00912	<i>Streptomyces globosus</i>	174	<i>Lysinibacillus capsici</i>	81.481	108
OATH 00913	<i>Streptomyces nigrescens</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 00921	<i>Streptomyces griseoincarnatus</i>	23	<i>Streptomyces griseoincarnatus</i>	100	1450
OATH 00923	<i>Rhodococcus erythropolis</i>	146	<i>Rhodococcus erythropolis</i>	100	1440
OATH 00961	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01002	<i>Streptomyces misionensis</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01003	<i>Lysinibacillus capsici</i>	174	<i>Lysinibacillus capsici</i>	100	1279
OATH 01021	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01022	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01071	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01091	<i>Streptomyces toxytricini</i>	1	<i>Streptomyces globosus</i>	100	1448

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01101	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 01102	<i>Streptomyces musisoli</i>	6	<i>Streptomyces</i> sp. OATH_C	100	1448
OATH 01112	<i>Pseudomonas E paracanis</i>	156	<i>Pseudomonas azotoformans</i>	100	1459
OATH 01121	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01141	<i>Streptomyces griseoviridis</i>	50	<i>Streptomyces griseoviridis</i> A	100	1447
OATH 01142	<i>Streptomyces griseoviridis</i>	66	<i>Streptomyces griseoviridis</i> A	100	1447
OATH 01181	<i>Stenotrophomonas geniculata</i>	197	<i>Streptomyces</i> sp. OATH_61	100	460
OATH 01181	<i>Stenotrophomonas geniculata</i>	170	<i>Streptomyces</i> sp. OATH_57	100	742
OATH 01181	<i>Stenotrophomonas geniculata</i>	211	<i>Streptomyces bacillaris</i>	100	20
OATH 01181	<i>Stenotrophomonas geniculata</i>	183	<i>Streptomyces globosus</i>	80.769	104
OATH 01181	<i>Stenotrophomonas geniculata</i>	193	<i>Bradyrhizobium denitrificans</i>	78.409	88
OATH 01182	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 01183	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	100	1217
OATH 01201	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces</i> sp. OATH_E	99.033	1448
OATH 01241	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01242	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01243	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01244	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01245	<i>Streptomyces griseoincarnatus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01246	<i>Streptomyces eurythermus</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01247	<i>Streptomyces misionensis</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01251	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01252	<i>Bacillus haynesii</i>	166	<i>Lysinibacillus capsici</i>	94.164	1268
OATH 01253	<i>Streptomyces murinus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01254	<i>Streptomyces griseofuscus</i>	2	<i>Streptomyces griseofuscus</i>	100	1447
OATH 01261	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01262	<i>Streptomyces achromogenes</i>	5	<i>Streptomyces</i> sp. OATH_B	100	1449
OATH 01263	<i>Paenibacillus cellulositrophicus</i>	59	<i>Paenibacillus cellulositrophicus</i> A	100	1266
OATH 01271	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01272	<i>Pristimantibacillus undefined</i>	65	<i>Paenibacillus cellulositrophicus A</i>	96.921	1234
OATH 01273	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01281	<i>Aneurinibacillus aneurinilyticus</i>	155	<i>Lysinibacillus capsici</i>	88.784	1480
OATH 01283	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01285	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01291	<i>Bacillus licheniformis</i>	163	<i>Lysinibacillus capsici</i>	91.87	1476
OATH 01292	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01293	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01294	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01301	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01302	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01303	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01304	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01305	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01306	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01311	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01312	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01313	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01314	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01315	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01316	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01331	<i>Streptomyces sennicomposti</i>	10	<i>Streptomyces sp. OATH_E</i>	100	1217
OATH 01341	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01351	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01352	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 01363	<i>Brevibacillus panacihumi</i>	174	<i>Lysinibacillus capsici</i>	91.424	1271
OATH 01371	<i>Paenibacillus cellulosytrophicus</i>	59	<i>Paenibacillus cellulositrophicus A</i>	100	1266
OATH 01382	<i>Bacillus velizensis</i>	162	<i>Lysinibacillus capsici</i>	92.333	1226
OATH 01383	<i>Bacillus velizensis</i>	162	<i>Lysinibacillus capsici</i>	91.667	1476

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01401	<i>Streptomyces bikiniensis</i>	12	<i>Streptomyces bikiniensis</i>	100	1448
OATH 01411	<i>Streptomyces misionensis</i>	3	<i>Streptomyces misionensis</i>	100	1447
OATH 01412	<i>Streptomyces murinus</i>	80	<i>Pseudomonas fluorescens</i>	86.429	420
OATH 01412	<i>Streptomyces murinus</i>	111	<i>Streptomyces</i> sp. OATH_39	89.011	1456
OATH 01431	<i>Pseudomonas_K oryzae</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01441	<i>Bacillus_A thuringiensis_K</i>	174	<i>Lysinibacillus capsici</i>	94.266	1273
OATH 01451	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	89.931	437
OATH 01451	<i>Priestia aryabhatai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017
OATH 01461	<i>Pseudomonas_K oryzae</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01471	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.701	1019
OATH 01471	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.146	529
OATH 01481	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.189	523
OATH 01481	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.706	1020
OATH 01491	<i>Bacillus safensis</i>	162	<i>Lysinibacillus capsici</i>	92.417	1477
OATH 01501	<i>Cupriavidus laharis</i>	28	<i>Pseudomonas koreensis</i>	82.787	1464
OATH 01511	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01521	<i>Bacillus_I endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.189	523
OATH 01521	<i>Bacillus_I endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.706	1020
OATH 01531	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	92.886	1476
OATH 01541	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	93.055	1411
OATH 01551	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	89.931	437
OATH 01551	<i>Priestia aryabhatai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017
OATH 01561	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.745	1231
OATH 01571	<i>Arthrobacter siccoltolerans</i>	32	<i>Micrococcus luteus</i>	96.508	1260
OATH 01581	<i>Priestia megaterium</i>	160	<i>Lysinibacillus capsici</i>	89.931	437
OATH 01581	<i>Priestia megaterium</i>	174	<i>Lysinibacillus capsici</i>	94.834	755
OATH 01591	<i>Arthrobacter nitrophenolicus</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01601	<i>Pseudomonas delhiensis</i>	163	<i>Lysinibacillus capsici</i>	91.604	667
OATH 01601	<i>Pseudomonas delhiensis</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01601	<i>Pseudomonas delhiensis</i>	174	<i>Lysinibacillus capsici</i>	94.137	614
OATH 01611	<i>Bacillus safensis</i>	166	<i>Lysinibacillus capsici</i>	91.785	353
OATH 01611	<i>Bacillus safensis</i>	162	<i>Lysinibacillus capsici</i>	92.959	1051
OATH 01621	<i>Bacillus inaquosorum</i>	166	<i>Lysinibacillus capsici</i>	93.853	1269
OATH 01631	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01641	<i>Bacillus_l endophytica_A</i>	163	<i>Lysinibacillus capsici</i>	87.783	442
OATH 01641	<i>Bacillus_l endophytica_A</i>	174	<i>Lysinibacillus capsici</i>	94.701	1019
OATH 01651	<i>Pseudomonas delhiensis</i>	82	<i>Pseudomonas fluorescens</i>	94.884	1466
OATH 01661	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.234	1478
OATH 01671	<i>Arthrobacter pascens</i>	32	<i>Micrococcus luteus</i>	98.305	354
OATH 01671	<i>Arthrobacter pascens</i>	32	<i>Micrococcus luteus</i>	95.387	1084
OATH 01681	<i>Bacillus subtilis</i>	166	<i>Lysinibacillus capsici</i>	93.75	1216
OATH 01691	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.542	1409
OATH 01701	<i>Zhihengliuella sp031178195</i>	32	<i>Micrococcus luteus</i>	95.73	1452
OATH 01711	<i>Arthrobacter sp019977195</i>	32	<i>Micrococcus luteus</i>	95.772	1017
OATH 01711	<i>Arthrobacter sp019977195</i>	43	<i>Micrococcus luteus</i>	94.622	502
OATH 01721	<i>Arthrobacter sp021129155</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01731	<i>Arthrobacter sp021129155</i>	32	<i>Micrococcus luteus</i>	95.859	1449
OATH 01741	<i>Peribacillus frigoritolerans_A</i>	155	<i>Lysinibacillus capsici</i>	93.234	1478
OATH 01751	<i>Bacillus subtilis</i>	174	<i>Lysinibacillus capsici</i>	94.672	976
OATH 01761	<i>Nonomuraea rhodomycinica</i>	50	<i>Streptomyces griseoviridis A</i>	89.931	1450
OATH 01771	<i>Nocardia farcinica</i>	146	<i>Rhodococcus erythropolis</i>	96.53	1441
OATH 01781	<i>Kocuria turfanaensis</i>	32	<i>Micrococcus luteus</i>	94.345	1450
OATH 01791	<i>Stutzerimonas stutzeri_A1</i>	71	<i>Pseudomonas sp. OATH_15</i>	97.944	1459
OATH 01801	<i>Caldimonas mangrovi</i>	167	<i>Pseudomonas azotoformans</i>	83.424	1466
OATH 01811	<i>Arthrobacter phenanthrenivorans</i>	32	<i>Micrococcus luteus</i>	96.066	1449
OATH 01821	<i>Terrimonas undefined</i>	145	<i>Bradyrhizobium elkanii</i>	74.859	1420
OATH 01831	<i>Kocuria polaris_A</i>	32	<i>Micrococcus luteus</i>	95.379	1450
OATH 01841	<i>Priestia aryabhatai</i>	174	<i>Lysinibacillus capsici</i>	94.592	1017

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 01841	<i>Priestia aryabhatai</i>	160	<i>Lysinibacillus capsici</i>	90.038	532
OATH 01851	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 01861	<i>Neorhizobium flavum</i>	21	<i>Microvirga</i> sp. OATH_1	90.149	1411
OATH 01871	<i>Kocuria polaris_A</i>	146	<i>Rhodococcus erythropolis</i>	91.69	1444
OATH 01881	<i>Bacillus spizizenii</i>	155	<i>Lysinibacillus capsici</i>	91.875	1477
OATH 01891	<i>Arthrobacter</i> sp006715285	32	<i>Micrococcus luteus</i>	95.58	1448
OATH 01901	<i>Kocuria polaris_A</i>	32	<i>Micrococcus luteus</i>	95.379	1450
OATH 01911	<i>Actinoplanes aureus</i>	146	<i>Rhodococcus erythropolis</i>	91.407	1443
OATH 01921	<i>Neorhizobium petrolearium</i>	145	<i>Bradyrhizobium elkanii</i>	90.709	1410
OATH 01931	<i>Neorhizobium flavum</i>	21	<i>Microvirga</i> sp. OATH_1	90.149	1411
OATH 01941	<i>Neorhizobium flavum</i>	21	<i>Microvirga</i> sp. OATH_1	90.149	1411
OATH 01951	<i>Streptomyces nigra</i>	72	<i>Streptomyces</i> sp001509795	99.838	1232
OATH 01961	<i>Bacillus inaquosorum</i>	155	<i>Lysinibacillus capsici</i>	88.785	535
OATH 01961	<i>Bacillus inaquosorum</i>	166	<i>Lysinibacillus capsici</i>	93.996	1016
OATH 01971	<i>Microvirga</i> sp022346925	21	<i>Microvirga</i> sp. OATH_1	97.871	1409
OATH 01981	<i>Agromyces</i> sp031178025	32	<i>Micrococcus luteus</i>	91.758	1456
OATH 01991	<i>Bacillus spizizenii</i>	166	<i>Lysinibacillus capsici</i>	93.127	1295
OATH 02001	<i>Bacillus spizizenii</i>	166	<i>Lysinibacillus capsici</i>	93.127	1295
OATH 02011	<i>Microbispora</i> sp014161445	96	<i>Streptomyces</i> OATH_28	90.809	1458
OATH 02021	<i>Erythrobacter</i> sp006542605	21	<i>Microvirga</i> sp. OATH_1	86.803	1417
OATH 02031	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 02041	<i>Streptomyces albogriseolus</i>	73	<i>Streptomyces nigra</i>	99.379	1449
OATH 02051	<i>Streptomyces boblii</i>	6	<i>Streptomyces</i> sp. OATH_C	98.689	1449
OATH 02061	<i>Streptomyces griseoruber</i>	197	<i>Streptomyces</i> sp. OATH_61	99.104	558
OATH 02061	<i>Streptomyces griseoruber</i>	17	<i>Streptomyces misionensis</i>	97.933	629
OATH 02071	<i>Streptomyces</i> sp000721605	73	<i>Streptomyces nigra</i>	98.896	1449
OATH 02081	<i>Streptomyces kurssanovii</i>	64	<i>Streptomyces cavourensis</i>	98.414	1450
OATH 02091	<i>Streptomyces</i> sp019049245	6	<i>Streptomyces</i> sp. OATH_C	98.896	1449
OATH 02101	<i>Allosphingosinicella</i> sp011320075	21	<i>Microvirga</i> sp. OATH_1	87.8	1418

Updated isolate		Designation from Table 1		Alignment info.	
ID#	BestTaxa	Strain #	Genus/Species	% identity	Alignment length
OATH 02111	<i>Mycetocola_A miduiensis</i>	99	<i>Streptomyces sp. OATH_30</i>	91.736	1452
OATH 02121	<i>Nocardioides sp.</i>	146	<i>Rhodococcus erythropolis</i>	91.967	1444
OATH 02131	<i>Bacillus paralicheniformis</i>	166	<i>Lysinibacillus capsici</i>	93.601	1047
OATH 02141	<i>Streptomyces globosus</i>	1	<i>Streptomyces globosus</i>	100	1448
OATH 02151	<i>Bacillus paralicheniformis</i>	163	<i>Lysinibacillus capsici</i>	92.005	1476

[00499] These same protocols can be followed to convert mixed strain ATCC deposits into single strain isolates if desired.

5 Example 33: Exemplary production protocol

[00500] This example demonstrates a protocol for production (e.g., culturing, inoculating, incubating, and collection of microbial biomass) of one or more microbes as disclosed herein using solid-state fermentation.

[00501] Solid-state fermentation is a process in which microorganisms grow on solid substrates alternatively to liquid mediums. In this procedure, solid media, such as agar-based culture mediums, serve as the foundation for microbial growth. By integrating core microbiological techniques and principles, this SOP has been developed to optimize solid-state fermentation processes, ensuring precision and consistency in microbial cultivation. This approach enhances the efficiency and scalability of microbial production for various applications.

[00502] Definitions and Abbreviations used include (1) ISP-3: International Streptomyces Project-3 Medium; (2) DI: distilled; (3) BSC: biological safety cabinet; and (4) SSF: solid state fermentation.

[00503] The following materials, consumables, and equipment are recommended:

[00504] Reagents: (1) ISP-3 (Himedia, M358); (2) DI water; (3) 70% Ethyl Alcohol (Sigma-Aldrich, 65350-M); (4) Glucose Broth Media; (5) Dextrose; (6) Yeast Extract; (7) Peptone; (8) Calcium Chloride Dihydrate

[00505] Consumables: (1) Sterile Swabs; (2) 10 µL Sterile inoculating Loops; (3) Autoclave Indicator Tape; (4) 5 mL Serological Pipettes; (5) 14 mL Sterile culture tubes; (6) Large weigh boats; (7) Scalpels; (8) 50 mL conical tubes; and (9) 2 mL microcentrifuge tubes

[00506] Equipment: (1) Autoclave; (2) BSC (LABCONCO, Model 302319101); (3) Three-tier Shaking incubator (aniCell, Model NB-206CXXL); (4) Incubator (walk-in incubator); (5) High-

speed Grinder (Vevor, Model 1000); (6) Analytical Balance (LACHOI, Model JT103D); and (7) Large Sheet Trays 18" x 26"

5 [00507] The following safety measures should be taken: (1) wear a lab coat; (2) use appropriately sized gloves; (3) wear safety glasses; (4) wear an N-95 respirator for at least the grinding step.

[00508] ISP-3 agar plate preparation: 19 g of ISP-3 medium was combined with 500 mL of DI water and autoclave at 121°C for 15 minutes. Plates are then poured and allowed to cool to room temperature prior to use.

10 [00509] Glucose Broth Medium: 10 g of ISP-3 medium, 4 g of Yeast Extract, 4 g of Peptone, and 0.5 g Calcium Chloride Dihydrate are combined with 500 mL of DI water and autoclaved at 121°C for 15 minutes. The solution was then cooled to room temperature before use.

[00510] Sterilize work surfaces: (1) all interior surfaces of the Biological Safety Cabinet (BSC) are sprayed with a 10% bleach solution with at least a 10 minute contact time; (2) surfaces are then rinsed by spraying with deionized (DI) water and dried with paper towels; (3) all
15 surfaces are sprayed with 70% Ethyl Alcohol and allowed to sit for 10 minutes; (4) a second application of 70% Ethyl Alcohol was then applied and dried by wiping with paper towels; (5) the BSC was then closed and UV irradiated using the integrated UV light for 15 minutes to complete sterilization.

[00511] Material preparation: (1) a 14 mL sterile culture tube was labeled with the
20 corresponding ID and date of inoculation for each isolate to be processed. A control tube containing 3 mL was also prepared as a negative control; (2) the exterior of the glucose broth media was disinfected by spraying it with 70% Ethyl Alcohol. The bottle was then wiped down with paper towels and placed inside the sterilized BSC; (3) all necessary supplies (uninoculated broths, sterile swabs, loops, and trash setup) are placed into the BSC and exposed to UV light for
25 15 minutes.

[00512] Reviving glycerol stocks: (1) all working stock cultures are stored in 20% glycerol in the - 80°C freezer. Glycerol stocks were plated every three production to produce fresh working stock plates; (2) a cool box in the - 80°C freezer was used to retrieve working stock cultures in batches of 8 to 10 to reduce freeze/thaw cycles; (3) the exterior of the cool box was sprayed with
30 70% Ethyl Alcohol before placing it in the sterilized BSC; (4) using aseptic technique, the glycerol stock was opened and the entire volume was transferred into a labeled 3 mL glucose culture tube using a sterile 10 µL inoculation loop. The 3 mL tube was then gently mixed to create a homogenous mixture; (5) the cap on the newly inoculated broth tube was loosely closed to allow aeration and secured in place for incubation; (6) the process was repeated for all glycerol

working stocks to create seed cultures for all isolate; and (7) after inoculation, the seed cultures were placed in the shaking incubator at incubated at 28°C with mixing at 240 rpm for two nights.

[00513] Preparing sterility plates and working stock plates: (1) the BSC was sterilized as described herein; (2) After the two night incubation, all seed cultures were removed. Turbidity of cultures were observed and reported (T for "Turbid", NG for "No Growth"). If no turbidity was observed, the culture was incubated for an additional 24 hours; (3) For each isolate ID, one ISP-3 Agar plate was labeled with the isolate ID, date of inoculation and "Purity". A negative control plate was also prepared for the negative control broth; (4) a sterile cotton swab was dipped into the turbid culture and inoculated onto the corresponding ISP-3 agar plate in the primary quadrant with saturated swab; (5) a sterile inoculation loop (10 µl or 1 µl) was used to streak purity for isolation as shown in **Figure 13**; (6) the process was repeated for each seed culture; (7) all seed cultures were paced back in the shaking incubator and the purity plates were placed in a 28°C incubator to continue incubation; and (8) the strains used in process were recorded.

[00514] Isolation of production plates: (1) turbidity and purity plate results were recorded for each seed culture tube; (2) If the plate looked clean (e.g., single colony type and consistent with individual isolated growth morphology), the 3 mL seed culture was deemed ready to be used for scale up to production plate inoculation; (3) If there was no observed growth on the purity plate, it was determined if further incubation was needed before moving forward. The decision was made considering each isolate's growth rate and the growth rate of common laboratory contaminants. No growth on the purity plate and a turbid liquid culture was considered clean; (4) broths that had no growth after one overnight incubation but are now turbid by the second overnight incubation were reincubated for another overnight incubation to grow mature cultures for working stock plates; (5) The BSC was sterilized using the steps detailed herein, the exterior of culture plate sleeves were sterilized by spraying with 70% Ethyl Alcohol, wiped dry and placed in the BSC; (7) all other supplies to be used were placed in the BSC and UV irradiated for 15 minutes. No bacterial cultures were introduced into the BSC during this step; (8) plate sleeves and gloves were sprayed with 70% Ethyl Alcohol and allowed to dry before handling; (9) the turbid culture tubes were brought into the sterile BSC and eighty ISP-3 plates were inoculated for each isolate; (10) plates were separated into sets of 10 and every 10th plate was labeled with the strain number, date, and tech initials; (11) plated we inoculated in sets of 5 by dipping a sterile swab into the seed culture, making a single streak down the middle of each plate, and covering until all 5 plates are inoculated; (12) Once all 5 plates were inoculated with the single streak using the same swab, plates were then swabbed with the landscaping technique as shown in **Figure 14**; (13) the process was repeated until completion; (14) once al plate were inoculated, the inoculated plates were placed in a walk-in incubator room, organized by strain number and

incubated; (15) plated were regularly checked during incubation progress, paying special attention to plates with little or no growth or contamination signs. Production was repeated or adjusted as necessary (e.g., starting new cultures, inoculating more plates, etc.).

[00515] Harvesting biomass: (1) Once plates reached the designated incubation time and were
5 inspected for purity, results and date of harvest/scraping were recorded; (2) plates that appeared considerably different than the others for a given isolate were considered contaminated. Any unusual colonies or growth that differ from all other plates of a given isolate were also be considered contaminated. Contaminated plates were discarded and recorded; (3) The BSC was sterilized using the steps detailed herein; (4) all materials to be used were gathered (scalpels,
10 small tray, parchment paper and dextrose); (5) 50 g of dextrose was added to each tray on parchment paper, placed in the BSC, and UV irradiated for 15 mins; (6) after sterilization, production plates to be harvested were brought into the BSC; (7) a scalpel was used to scrape the bacterial biomass from agar onto the sterile metal tray containing 50g of dextrose; (8) some of the isolates worked with grow into the agar and needed a little more pressure with the scalpel to
15 be removed. Agar collection was minimized; (9) the process was repeated for each isolate ready to be harvested, ensuring the bacteria was thoroughly mixed with the dextrose; (10) each tray of microbes and dextrose was weighed, and the weight was recorded.

[00516] Drying: (1) Each tray was wrapped with sterilized blue autoclave paper; (2) all folds/
overlaps in the paper were closed/sealed to protect biomass from potential contamination from
20 outside air; (3) the blue paper was ensured to not be in direct contact with microbes; (4) the covered tray was placed onto the drying rack and the drying rack was covered with a plastic cover.

[00517] Grinding: (1) drying was considered complete after at least one week and the mixture no longer felt sticky. This was checked by hand with a clean set of sterilized gloves; (2) once
25 biomass and dextrose reached the appropriate drying consistency, product grinding began; (3) With the grinder unplugged, it was sterilized thoroughly with 70% Ethyl Alcohol, wiped down with paper towels, and allowed to air dry for at least 15 minutes before adding mixture; (4) dried mixture was transferred from the tray to the grinder and the was closed lid tightly. When ready, the grinder was plugged into the power outlet; (5) grinding was completed avoiding repetitive
30 grinding steps to prevent heat build up; (6) when the grinding was complete, consistency was checked; if chunks were present, grinding continued. Once a homogeneous powder was achieved, the powder was carefully transferred into an opaque 32 oz black bag; (7) the outside of the 32 oz bag was clearly labeled with the Production batch number and date; (8) the grinder was cleaned with distilled water, wiped thoroughly, then resterilized; (9) 0.5 g of the powder was
35 weighed into a 2 mL microcentrifuge tube labeled with batch number and date for quality

control; (10) the 0.5 g microcentrifuge sample was the combined with 1 mL of Zymo DNA/RNA shield and thoroughly homogenized to ensure complete coverage of our concentrate with the solution. This sample was submitted for sequencing as soon as possible; (11) 3 additional replicate samples were weighed, each containing 0.5 g of concentrate. The concentrate of each replicate was placed into its own 50 mL non-vented conical tube labeled with batch number and date. These were used for CFU determination of the current batch in replicates of 3; (12) CFUs were then counted.

Example 34: Influence of application of a composition comprising a plurality of different microbes in improving yield, root biomass, seed pod biomass, and plant biomass in common bean

- [00518] This example demonstrates a significant increase in common bean yield, root biomass, seed pod biomass, and plant biomass following treatment with a composition comprising a plurality of different microbes.
- [00519] The composition comprising a plurality of different microorganisms comprised isolates of the *Paenibacillus*, *Rhodococcus*, and *Streptomyces* genera, including isolates of *Paenibacillus cellulositrophicus*, *Rhodococcus qingshengii*, *Streptomyces ansochromogenes*, *Streptomyces antibioticus*, *Streptomyces avermitilis*, *Streptomyces diastatochromogenes*, *Streptomyces fragilis*, *Streptomyces fumigatiscleroticus*, *Streptomyces griseoaurantiacus*, *Streptomyces misionensis*, *Streptomyces nogalater*, *Streptomyces padanus*, *Streptomyces violaceorectus*, *Streptomyces violaceus*, and *Streptomyces violaceusniger*. The microorganisms were grown and formulated into the composition as described in Example 33.
- [00520] The composition was applied to an already established field of common beans (*Phaseolus vulgaris*) on November 15th. The total field area was four hectares. Two hectares were left untreated and served as an untreated control (see next page). A second application was applied on December 1st. There were approximately 133,333 plants per hectare. Diammonium phosphate (DAP) 18-46-0 and manure was added during planting. Easygrow 27-10-16 was added as a foliar fertilizer during the season. The dosage rate per application was 10Bn CFUs per acre. The composition comprising a plurality of different microbes was mixed with Sea minerals and diluted in water. Back pack sprayers were used to apply the composition comprising a plurality of different microbes to the crops. The top diseases in the farm were Anthracnose, Early & Late Blight, Bean Rust, and Leaf Spot. The plants were harvested and all measurements recorded in mid-January the following year.
- [00521] Root biomass was 50-56% higher for crops treated with the composition comprising a plurality of different microbes than for untreated control crops. Data is shown in Figure 6. As

shown in **Figure 6** (right), root fresh weight (FW) averaged 4.2 g for crops treated with the composition comprising a plurality of different microbes as compared to 2.7 g for untreated control crops ($P=0.0019$). As shown in **Figure 6** (left), root dry weight (DW) averaged 1.5 g for crops treated with the composition comprising a plurality of different microbes as compared to 1.0 for untreated control crops ($P=0.0015$).

[00522] Shoot biomass was 10-15% higher for crops treated with the composition comprising a plurality of different microbes than for untreated control crops. Data is shown in **Figure 7**. As shown in **Figure 7** (right), shoot biomass fresh weight averaged 7.4 g for crops treated with the composition comprising a plurality of different microbes as compared to 6.7 g for untreated control plants ($P=0.0728$). As shown in **Figure 7** (left), shoot biomass dry weight averaged 5.0 g for crops treated with the composition comprising a plurality of different microbes as compared to 4.3 g for untreated control crops ($P=0.3374$).

[00523] Pod biomass was 32-40% higher for crops treated with the composition comprising a plurality of different microbes than for untreated control crops. Data is shown in **Figure 8**. As shown in **Figure 8** (right), pod biomass fresh weight averaged 7.5 g for crops treated with the composition comprising a plurality of different microbes as compared to 5.7 g for untreated control plants ($P=0.0002$). As shown in **Figure 8** (left), pod biomass dry weight averaged 6.3 g for crops treated with the composition comprising a plurality of different microbes as compared to 4.5 g for untreated control plants ($P<0.0001$).

[00524] Grain biomass was 40-45% higher for crops treated with the composition comprising a plurality of different microbes than for untreated control crops. Data is shown in **Figure 9**. As shown in **Figure 9** (right), grain biomass fresh weight averaged 23.5 g for crops treated with the composition comprising a plurality of different microbes as compared to 16.2 g for untreated control plants ($P<0.0001$). As shown in **Figure 9** (left), grain biomass dry weight averaged 22.0 g for crops treated with the composition comprising a plurality of different microbes as compared to 15.7 g for untreated control plants ($P<0.0001$).

[00525] Yield per hectare was estimated by using the approximate 133,333 plants per hectare and the per-plant yield (i.e., grain biomass) mean value (FW: 23.5 g treated and 16.2 g non-treated; as shown in **Figure 9**). It was estimated that a total of 3.1 tonnes of bean grains were produced in the treated areas, while 2.2 tonnes were produced in non-treated areas, corresponding to a 45% increase in yield per hectare.

[00526] This example demonstrates a significant and positive effect on the growth of common beans following only two treatments of the composition comprising a plurality of different microbes. The composition comprising a plurality of different microbes delivered a rapid (1) 40-45% increase in yield per hectare, (2) a rapid 50-56% increase in root biomass, (3) a 10-15%

increase in shoot biomass, and (4) a 32-40% increase in seed pod biomass, in only 45 days.

These results demonstrate that the composition comprising a plurality of different microbes have a great capacity to not only increase yield (food) by 45%, but also crucial soil health parameters, such as soil structure and soil carbon. Increased plant root growth helps prevent soil erosion as well as sequestering carbon from the atmosphere (40% of plant root biomass derives from plant photosynthesis)

Example 35: Influence of soil application of a composition comprising a plurality of different microbes in improving soil health, nutrient availability, tree nutrient and water status, fruit set, and nut retention in almond

[00527] This example demonstrates a positive improvement in soil bulk density, soil water holding capacity, and stem water potential following treatment with a composition comprising a plurality of different microbes.

[00528] The composition comprising a plurality of different microorganisms comprised isolates of the *Microbacterium*, *Rhodococcus*, and *Streptomyces* genera, including isolates of *Microbacterium* sp. 002979655, *Rhodococcus qingshengii*, *Streptomyces antibioticus*_B, *Streptomyces bacillaris*, *Streptomyces bikiniensis*, *Streptomyces broussonetiae*, *Streptomyces chartreusis*, *Streptomyces diastatochromogenes*, *Streptomyces eurythermus*, *Streptomyces globosus*, *Streptomyces griseoaurantiacus*, *Streptomyces griseofuscus*, *Streptomyces griseoincarnatus*, *Streptomyces griseostramineus*, *Streptomyces griseoviridis*_A, *Streptomyces libani*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces puniscabiei*, *Streptomyces rochei*, *Streptomyces sennicomposti*, *Streptomyces seoulensis*_A, *Streptomyces toxytricini*, and *Streptomyces yatensis*. The microorganisms were grown and formulated into the composition as described in Example 33.

[00529] Three blocks of almond tree stands were treated with a composition comprising a plurality of different microbes. Three additional blocks were maintained as untreated controls. The irrigation was lowfrequency drip irrigation as grower standard. All practices will were grower/industry standard practices.

[00530] Pre-treatment composite soil samples were collected from each block at 0-18 inches depth using Auger. Just before soil probiotics were added, baseline samples were placed in airtight bags and sent for analysis including soil physical (bulk density and water holding capacity, pH) and soil chemical properties (total carbon, inorganic, carbon, macro- and micronutrients). Soil samples were also sent for analysis of microbiome function and diversity.

[00531] Nonpareil trees on one side of irrigation riser and their two neighboring trees were treated as one experimental unit and product was injected using a gasoline powered injection

pump. To do so, the composition comprising a plurality of different microbes was added to 30 gallons water and 10 gallons solution was injected through drip irrigation to each row. After injection, a further 2-3 hours of irrigation water was applied to incorporate product into the soil. The gasoline powdered injection pump was used to provide enough pressure to uniformly apply the composition in the irrigation line. The composition was applied at days 0, 30, 60, 90, and 120 post-bloom.

[00532] Samples were collected to measure soil water content, soil bulk density, and soil pH at days 0, 30, 60 90, 120, and at harvest.

[00533] Samples were collected to measure soil macro and micronutrients at days 0, 60, and 120.

[00534] Samples were collected to measure soil microbial community composition at days 0, 30, and 120. Taxonomic diversity was measured.

[00535] Leaf samples were collected at day 120. Leaf samples were dried at 60 C, ground, and analyzed for N, P, K, S, Ca, Mg, B, Zn, Mn, Fe, and Cu concentration.

[00536] Fruit samples were collected at harvest. Almond kernel size and crackout percentage was measured. 200 nuts were collected from three trees in each replicated treatment at harvest. Nut weight was recorded after drying. Kernels were separated, weighed, and crackout percentage was determined.

[00537] Stem water potential was measured at days 90, 120, and harvest. Stem water potential was measured to assess the influence of the composition comprising a plurality of different microbes on improving soil water holding capacity and increasing water availability, thereby reducing water stress in trees. Mid-day stem water potential was determined for two trees in each replicated treatment before irrigation cycle. Leaves were covered with aluminum bags for an hour, removed, and tested inside pressure bomb.

[00538] As shown in **Figure 10**, soil water content was significantly higher in plots following treatment with the composition comprising a plurality of different microbes. Due to the higher soil water content, watering for treated crops was reduced by 17% on July 23rd. Even with reduced watering, treated crops show higher soil water content than untreated plots.

[00539] Stem water potential reflects plant stress levels if too high. As shown in **Figure 11**, trees treated with the composition comprising a plurality of different microbes shown a 13% decrease in stem water potential as compared to untreated trees ($P=0.019$). However, after watering was reduced with 17% in the just the plots treated with the composition comprising a plurality of different microbes, the stem water potential became similar to that of the untreated plots.

[00540] As shown in Figure 12, soil bulk density was significantly lower in plots treated with the composition comprising a plurality of different microbes as compared to untreated plots.

[00541] This example demonstrates a positive improvement in soil bulk density, soil water holding capacity, and stem water potential following only a single treatment with a composition comprising a plurality of different microbes.

Example 36: Exemplary composition comprising a plurality of different microbes

[00542] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops, grass, and trees. The composition comprises microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes are as shown in Table 33, below.

Table 33 Microbes in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00144	209	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00021	216	<i>Streptomyces</i>	<i>echinatu</i>	PTA-127836
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00641	260	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00661	262, 263	<i>Streptomyces</i>	<i>chartreusis</i>	PTA-127837
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00881	275	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH01201	286	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01241	287	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01242	317	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01245	318	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127835
OATH01243	319	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127835
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01285	328	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01283	329	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00264	349	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00581	377	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00802	392	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834

[00543] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00921 comprising a 16S rRNA sequence of SEQ ID No. 398.

- 5 [00544] The composition may further comprise one or more microbes of the genera *Bacillus*, *Brevibacillus*, *Lysinibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus sphaericus*, and *Paenibacillus cellulositrophicus*.

10 **Example 37: Exemplary composition comprising a plurality of different microbes for treating crops**

[00545] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops and grass. The composition comprises microbes from the genera *Lysinibacillus*,
15 *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 34, below.

- [00546] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a
20 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00921 comprising a 16S rRNA sequence of SEQ ID No. 398 and/or *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369.

Table 34 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00031	228	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127845
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00071	273	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127846
OATH00072	282	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00101	207	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127845
OATH00144	209	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127841
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00241	212	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127845
OATH00242	346	<i>Streptomyces</i>	<i>sennicompoti</i>	PTA-127844

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00243	347	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00264	349	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00321	222	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127836
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01245	318	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127835
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839

[00547] The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*,

Bacillus velezensis, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, and *Paenibacillus cellulositrophicus*.

Example 38: Exemplary composition comprising a plurality of different microbes

- 5 [00548] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example grass. The composition comprises fungal and bacterial microbes from the genera *Bacillus*, *Lysinibacillus*, *Microbacterium*, *Neorhizobium*, *Peribacillus*, *Priestia*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for
- 10 example in Example 33. Microbes used in the composition are shown in Table 35, below

Table 35 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00031	228	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00071	273	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00072	282	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00101	207	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00102	304, 305	<i>Pseudomonas</i> _E	<i>paracanis</i>	PTA-127844
OATH00144	209	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127841
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00241	212	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00242	346	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00243	347	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127844
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00264	349	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00321	222	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127836
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00913	382	<i>Streptomyces</i>	<i>nigrescens</i>	PTA-127840
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01112	281	<i>Pseudomonas</i>	<i>paracarnis</i>	PTA-127849
OATH01245	318	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127835
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH01451	480, 481	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01661	467	<i>Peribacillus</i>	<i>frigortolerans_A</i>	PTA-127849
OATH01691	471	<i>Peribacillus</i>	<i>frigortolerans_A</i>	PTA-127850
OATH01741	477	<i>Peribacillus</i>	<i>frigortolerans_A</i>	PTA-127850
OATH01841	402, 401	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01851	403	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127837
OATH01861	404	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01951	414	<i>Streptomyces</i>	<i>nigra</i>	PTA-127844
OATH01991	419	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH02051	426	<i>Streptomyces</i>	<i>bobili</i>	PTA-127839
OATH02131	435	<i>Bacillus</i>	<i>paralicheniformis</i>	PTA-127847

[00549] The composition may further comprise one or more microbes of the genera

Aneurinibacillus, *Brevibacillus*, *Glomus*, *Paenibacillus*, *Pisolithus*, and/or *Rhizopogon*.

Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus*

- 5 *haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Glomus aggregatum*, *Glomus etunicatum*, *Glomus intraradices*, *Glomus mosseae*, *Lysinibacillus capsici*, *Neorhizobium flavum*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Peribacillus*

frigoritolerans, *Pisolithus tinctorius*, *Priestia aryabhattai*, *Priestia megaterium*, *Rhizopogon amylopogon*, *Rhizopogon fulvigleba*, *Rhizopogon luteolus*, *Rhizopogon villosulus*, and *Streptomyces nigrescens*.

5 **Example 39: exemplary composition comprising a plurality of different microbes for the treatment of crops, for example soy beans**

[00550] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops, such as soybeans, and grass. The composition comprises microbes from the
10 genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 36, below.

Table 36 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840

- [00551] The composition may further comprise one or more microbes of the genera *Bacillus*, *Glomus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Glomus aggregatum*, *Glomus etunicatum*,
 5 *Glomus intraradices*, *Glomus mosseae*, *Paenibacillus cellulositrophicus*.

Example 40: Exemplary composition comprising a plurality of different microbes

- [00552] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for
 10 example crops and grass. The composition comprises microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 37, below.

Table 37 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840

[00553] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374.

[00554] The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Paenibacillus cellulositrophicus*.

Example 41: Exemplary composition comprising a plurality of different microbes for the treatment of crops

[00555] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops and grass. The composition comprises microbes from the genera *Bacillus*, *Lysinibacillus*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 38, below.

[00556] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369.

Table 38 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00011	197	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH00021	216	<i>Streptomyces</i>	<i>echinatu</i>	PTA-127836
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00081	292	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00103	208	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127849
OATH00241	212	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00322	224	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00351	358	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00352	226, 227, 360	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00353	229	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00371	361	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00373	230	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127837
OATH00375	233	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00492	248	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00601	256	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH00661	262, 263	<i>Streptomyces</i>	<i>chartreusis</i>	PTA-127837
OATH00741	268	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00851	272	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01002	278	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127837
OATH01091	280	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH01102	307	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127835
OATH01201	286	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01241	287	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01242	317	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01253	321	<i>Streptomyces</i>	<i>murinus</i>	PTA-127836
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01262	291	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01283	329	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01292	331	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01302	298	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01303	299	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01312	336	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01313	338	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01352	344	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01382	201	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839

[00557] The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Brevibacillus*, *Microbacterium*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Microbacterium azadirachtae*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, and *Streptomyces griseostramineus*.

Example 42: Exemplary composition comprising a plurality of different microbes

[00558] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops and grass. The composition comprises microbes from the genera *Bacillus*, *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 39, below.

Table 39 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH01253	321	<i>Streptomyces</i>	<i>murinus</i>	PTA-127836
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01382	201	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01383	200	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848

[00559] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374.

- [00560] The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Brevibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Microbacterium azadirachtae*,
 5 *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, and *Paenibacillus thailandensis*.

Example 43: Exemplary composition comprising a plurality of different microbes for the treatment of trees, for example forest trees

- [00561] This example provides an exemplary composition comprising a plurality of different
 10 microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example trees. The composition comprises microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 40, below.

15 **Table 40 Microbes used in exemplary microbial composition**

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00491	373	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00571	254	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00891	394	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00892	396, 395, 397	<i>Lysinibacillus</i>	<i>sphaericus</i>	PTA-127847
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840

[00562] The composition may further comprise one or more microbes of the genera *Bacillus*, *Paenibacillus*, *Pisolithus*, *Rhizopogon*, and/or *Scleroderma*. Exemplary species include but are not limited to *Bacillus haynesii*, *Bacillus licheniformis*, *Bacillus velezensis*, *Paenibacillus* 5 *cellulositrophicus*, *Pisolithus tinctorius*, *Rhizopogon luteolus*, and *Scleroderma citrinum*.

Example 44: Exemplary composition comprising a plurality of different microbes for the treatment of trees, for example forest trees

[00563] This example provides an exemplary composition comprising a plurality of different 10 microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example trees. The composition comprises microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 41, below.

Table 41 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00052	261	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00144	209	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127841
OATH00223	211	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00264	349	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00321	222	<i>Streptomyces</i>	<i>griseoincarnatus</i>	PTA-127836
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00491	373	Streptomyces	misionensis	PTA-127841
OATH00562	252	Streptomyces	murinus	PTA-127843
OATH00563	253	Streptomyces	murinus	PTA-127843
OATH00823	271	Streptomyces	murinus	PTA-127843
OATH00923	399	Rhodococcus	erythropolis	PTA-127834
OATH00961	277	Streptomyces	misionensis	PTA-127843
OATH01261	290	Streptomyces	achromogenes	PTA-127837
OATH01271	326	Streptomyces	globosus	PTA-127839
OATH01273	293	Streptomyces	globosus	PTA-127841
OATH01301	297	Streptomyces	globosus	PTA-127841
OATH01341	342	Streptomyces	globosus	PTA-127840
OATH01401	202	Streptomyces	bikiniensis	PTA-127839

[00564] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374.

- 5 [00565] The composition may further comprise one or more microbes of the genera *Aneurinibacillus*, *Bacillus*, *Brevibacillus*, *Lysinibacillus*, *Paenibacillus*, *Pisolithus*, and/or *Rhizopogon*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus licheniformis*, *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Lysinibacillus sphaericus*, *Paenibacillus cellulositrophicus*, *Pisolithus tinctorius*, *Rhizopogon amylopogon*, *Rhizopogon fulvigleba*, *Rhizopogon luteolus*, and *Rhizopogon villosulus*.
- 10

Example 45: Exemplary composition comprising a plurality of different microbes

- [00566] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops and grass. The composition comprises microbes from the genera *Aneurinibacillus*, *Microbacterium*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 42, below.
- 15

Table 42 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00011	197	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH00021	216	<i>Streptomyces</i>	<i>echinatu</i>	PTA-127836
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00081	292	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00102	304, 305	<i>Psuedomonas_E</i>	<i>paracanis</i>	PTA-127844
OATH00103	208	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127849
OATH00241	212	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00322	224	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00351	358	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00352	226, 227, 360	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00371	361	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00373	230	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127837
OATH00375	233	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00492	248	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00601	256	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH00661	262, 263	<i>Streptomyces</i>	<i>chartreusis</i>	PTA-127837
OATH00741	268	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00851	272	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01091	280	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH01102	307	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127835
OATH01201	286	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01241	287	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01242	317	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01243	319	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127835
OATH01253	321	<i>Streptomyces</i>	<i>murinus</i>	PTA-127836
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01262	291	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01281	294	<i>Aneurinibacillus</i>	<i>aneurinilyticus</i>	PTA-127839
OATH01292	331	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01302	298	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01303	299	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01311	335	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01312	336	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01313	338	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01352	344	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839

[00567] The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369.

- [00568] The composition may further comprise one or more microbes of the genera *Bacillus*, *Lysinibacillus*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Bacillus licheniformis*, *Bacillus velezensis*, *Lysinibacillus capsici*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, and *Streptomyces griseostramineus*.

10 Example 46: Exemplary composition comprising a plurality of different microbes

- [00569] This example provides an exemplary composition comprising a plurality of different microbes for the treatment of soil in which plants are grown, plants, and/or plant parts, for example crops and grass. The composition comprises microbes from the genera *Aneurinibacillus*, *Bacillus*, *Microbacterium*, *Pseudomonas*, *Rhodococcus*, and *Streptomyces*. The composition may be produced as disclosed herein, for example in Example 33. Microbes used in the composition are shown in Table 43, below.

- [00570] The composition may further comprise one or more microbes of the genera *Microbacterium*, such as *Microbacterium* sp002979655, for example OATH00493 comprising a 16S rRNA sequence of SEQ ID No. 374. The composition may further comprise *Streptomyces griseoincarnatus* OATH00412 comprising a 16S rRNA sequence comprising SEQ ID NOs. 367, 368, and 369.

Table 43 Microbes used in exemplary microbial composition

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH00011	197	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846
OATH00021	216	<i>Streptomyces</i>	<i>echinatu</i>	PTA-127836
OATH00041	239	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00051	250	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00053	381	<i>Streptomyces</i>	<i>rochei</i>	PTA-127844
OATH00081	292	<i>Streptomyces</i>	<i>rochei</i>	PTA-127846
OATH00091	198	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839
OATH00102	304, 305	<i>Pseudomonas</i>	<i>paracanis</i>	PTA-127844
OATH00103	208	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127849
OATH00241	212	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127845
OATH00252	348	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127841
OATH00253	213	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00261	214	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00262	350	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00263	351	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00291	215	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00292	217	<i>Streptomyces</i>	<i>griseoaurantiacus</i>	PTA-127841
OATH00312	219	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00313	220	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00322	224	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00343	357	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127836
OATH00351	358	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00352	226, 227, 360	<i>Streptomyces</i>	<i>olivaceus</i>	PTA-127846
OATH00371	361	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00373	230	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127837
OATH00375	233	<i>Streptomyces</i>	<i>antibioticus</i>	PTA-127838
OATH00392	236	<i>Streptomyces</i>	<i>bacillari</i>	PTA-127838
OATH00413	241	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00421	243	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00422	244	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00423	245	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127842
OATH00483	247	<i>Microbacterium</i>	<i>paraoxydans</i>	PTA-127834
OATH00492	248	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00562	252	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00563	253	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00601	256	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH00661	262, 263	<i>Streptomyces</i>	<i>chartreusis</i>	PTA-127837
OATH00741	268	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH00801	270	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH00823	271	<i>Streptomyces</i>	<i>murinus</i>	PTA-127843
OATH00851	272	<i>Streptomyces</i>	<i>echinatus</i>	PTA-127837
OATH00923	399	<i>Rhodococcus</i>	<i>erythropolis</i>	PTA-127834
OATH00961	277	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01091	280	<i>Streptomyces</i>	<i>toxytricini</i>	PTA-127846

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01102	307	<i>Streptomyces</i>	<i>musisoli</i>	PTA-127835
OATH01201	286	<i>Streptomyces</i>	<i>sennicomposti</i>	PTA-127846
OATH01241	287	<i>Streptomyces</i>	<i>misionensis</i>	PTA-127843
OATH01242	317	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127835
OATH01243	319	<i>Streptomyces</i>	<i>eurythermus</i>	PTA-127835
OATH01253	321	<i>Streptomyces</i>	<i>murinus</i>	PTA-127836
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01261	290	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01262	291	<i>Streptomyces</i>	<i>achromogenes</i>	PTA-127837
OATH01271	326	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01273	293	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01281	294	<i>Aneurinibacillus</i>	<i>aneurinilyticus</i>	PTA-127839
OATH01292	331	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01293	296	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01294	330	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH01301	297	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01302	298	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01303	299	<i>Streptomyces</i>	<i>globosus</i>	PTA-127841
OATH01311	335	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01312	336	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01313	338	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01341	342	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01351	343	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01352	344	<i>Streptomyces</i>	<i>globosus</i>	PTA-127840
OATH01382	201	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01383	200	<i>Bacillus</i>	<i>velizensis</i>	PTA-127848
OATH01401	202	<i>Streptomyces</i>	<i>bikiniensis</i>	PTA-127839

[00571] The composition may further comprise one or more microbes of the genera *Brevibacillus*, *Lysinibacillus*, *Microbacterium*, and/or *Paenibacillus*. Exemplary species include but are not limited to *Aneurinibacillus aneurinilyticus*, *Bacillus haynesii*, *Bacillus licheniformis*,
5 *Bacillus velezensis*, *Brevibacillus panacihumi*, *Lysinibacillus capsici*, *Lysinibacillus sphaericus*, *Microbacterium azadirachtae*, *Microbacterium oxydans*, *Paenibacillus cellulositrophicus*, *Paenibacillus thailandensis*, *Streptomyces eurythermus*, *Streptomyces griseoincarnatus*, and *Streptomyces griseostramineus*.

10 Example 47: Isolation and characterization of soil bacteria

[00572] Soil Sample Collection and Preparation: (1) Collect approximately 1-2 grams of soil from the desired location; (2) Remove large debris (e.g., rocks, roots) by sieving or manually sorting through the soil.

[00573] Soil Suspension Preparation: (1) Add the soil sample to a sterile tube containing 9 mL of sterile saline solution (0.85% NaCl) or phosphate-buffered saline (PBS); (2) Vortex the tube for 2-3 minutes to release bacteria into the solution.

5 [00574] Serial Dilution: (1) Prepare a series of ten-fold serial dilutions by transferring 1 mL of the soil suspension into a tube with 9 mL of sterile saline; (2) Repeat the dilution for several steps (e.g., 10^{-3} to 10^{-6}) to obtain a range of bacterial concentrations.

[00575] Plating and Incubation: (1) Plate 100 μ L of each dilution onto nutrient agar or another general-purpose agar medium (e.g., LB agar); (2) Spread the inoculum evenly using a sterile spreader; (3) Incubate the plates at 25-30°C (ambient soil bacteria) or 37°C (for potentially
10 human-related microbes) for 24-48 hours.

[00576] Colony Selection: (1) After incubation, select well-isolated bacterial colonies of interest for further studies; (2) Streak each colony onto fresh agar plates to obtain pure cultures.

[00577] Preparation of Glycerol Stocks: (1) Culture Preparation; (1a) Inoculate a single, isolated colony into a tube containing 3-5 mL of liquid nutrient broth (e.g., LB broth); (1b)
15 Incubate the culture at an appropriate temperature (usually 25-37°C) with shaking until it reaches the exponential growth phase (OD₆₀₀ of ~0.5-1.0); (2) Mix with Glycerol; (2a) In a sterile cryovial, mix the bacterial culture with sterile glycerol to reach a final concentration of 15-20% glycerol; (2b) For example, mix 0.8 mL of bacterial culture with 0.2 mL of sterile glycerol (for 20% final concentration); (3) Storage; (3a) Gently mix the glycerol stock by inverting the
20 cryovial; (3b) Label the cryovial with the bacterial strain name, date, and any other necessary information; (3c) Store the glycerol stock at -80°C for long-term storage.

[00578] DNA Extraction (Soil Bacterial DNA Isolation): (1) Soil Sample Collection and Preparation; (1a) Collect soil samples (1-2 g) from the desired depth; (1b) Sieve the soil to remove large debris and homogenize it; (2) Cell Lysis; (2a) Add soil to a lysis buffer (containing
25 detergents, salts, and possibly proteinase K) to break open bacterial cell walls; (2b) Use mechanical disruption methods, such as bead beating, to further lyse cells and release DNA; (3) DNA Purification; (3a) Centrifuge the mixture to pellet debris and collect the supernatant containing DNA; (3b) Use a series of chemical washes and/or silica columns to purify DNA, removing proteins, polysaccharides, and inhibitors; (4) Elution; (4a) Elute the purified DNA with
30 a low-salt buffer or water; (4b) Quantify and assess purity (e.g., via spectrophotometer or fluorometer) to ensure a clean sample for sequencing.

[00579] DNA Library Preparation Protocol: (1) Fragmentation (If Needed) - Fragment DNA to a suitable length (e.g., 200-500 bp) if it isn't already fragmented, using either enzymatic treatment or mechanical shearing (e.g., sonication); (2) End Repair and A-Tailing - Treat
35 fragmented DNA to ensure blunt ends, then add adenine (A) overhangs at the 3' end to prepare

- for adapter ligation; (3) Adapter Ligation - Ligate sequencing adapters compatible with your sequencing platform to the DNA ends; (4) Size Selection and Cleanup; (4a) Perform size selection using beads or gel electrophoresis to target the desired DNA fragment length; (4b) Clean up the library to remove excess adapters and small DNA fragments; (5) PCR
- 5 Amplification (Optional) - Amplify the library to enrich for adapter-ligated fragments (depending on the input DNA quantity); (5) Quality Control - Quantify and assess library quality (using Bioanalyzer or similar) to ensure it meets sequencing requirements.

[00580] Exemplary Strains isolated and characterized using the above-mentioned protocol are
10 shown in Table 44, below:

Table 44 Exemplary strains isolated and characterized

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01431	459	<i>Pseudomonas_K</i>	<i>oryzae</i>	PTA-127849
OATH01441	479	<i>Bacillus_A</i>	<i>thuringiensis_K</i>	PTA-127847
OATH01451	480, 481	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01461	482	<i>Pseudomonas_K</i>	<i>oryzae</i>	PTA-127849
OATH01471	484, 483	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01481	485, 486	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01491	487	<i>Bacillus</i>	<i>safensis</i>	PTA-127848
OATH01501	488	<i>Cupriavidus</i>	<i>laharis</i>	PTA-127850
OATH01511	444	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01521	445, 446	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01531	447	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01541	448	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01551	449, 450	<i>Priestia</i>	<i>aryabhattai</i>	PTA-127850
OATH01561	451	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01571	452	<i>Arthrobacter</i>	<i>siccitolerans</i>	PTA-127834
OATH01591	455	<i>Arthrobacter</i>	<i>nitrophenolicus</i>	PTA-127834
OATH01601	457, 458, 456	<i>Pseudomonas</i>	<i>delhiensis</i>	PTA-127849
OATH01611	460, 461	<i>Bacillus</i>	<i>safensis</i>	PTA-127847
OATH01621	462	<i>Bacillus</i>	<i>inaquosorum</i>	PTA-127847
OATH01631	463	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01641	464, 465	<i>Bacillus_I</i>	<i>endophytica_A</i>	PTA-127847
OATH01651	466	<i>Pseudomonas</i>	<i>delhiensis</i>	PTA-127849
OATH01661	467	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127849
OATH01671	468, 469	<i>Arthrobacter</i>	<i>pascens</i>	PTA-127834
OATH01681	470	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01691	471	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127850
OATH01701	472	<i>Zhihengliuella</i>	sp031178195	PTA-127849
OATH01711	474, 473	<i>Arthrobacter</i>	sp019977195	PTA-127834
OATH01721	475	<i>Arthrobacter</i>	sp021129155	PTA-127834

USID	SEQ ID No(s)	Genus	Species	ATCC deposit #
OATH01731	476	<i>Arthrobacter</i>	sp021129155	PTA-127834
OATH01741	477	<i>Peribacillus</i>	<i>frigoritolerans_A</i>	PTA-127850
OATH01751	478	<i>Bacillus</i>	<i>subtilis</i>	PTA-127848
OATH01761	412	<i>Nonomuraea</i>	<i>rhodomycinica</i>	PTA-127849
OATH01771	424	<i>Nocardia</i>	<i>farcinica</i>	PTA-127849
OATH01781	436	<i>Kocuria</i>	<i>turfanensis</i>	PTA-127849
OATH01791	439	<i>Stutzerimonas</i>	<i>stutzeri_A1</i>	PTA-127850
OATH01801	440	<i>Caldimonas</i>	<i>mangrovi</i>	PTA-127850
OATH01811	441	<i>Arthrobacter</i>	<i>phenanthrenivorans</i>	PTA-127834
OATH01821	442	<i>Terrimonas</i>	<i>undefined</i>	PTA-127850
OATH01831	443	<i>Kocuria</i>	<i>polaris_A</i>	PTA-127849
OATH01841	402, 401	<i>Priestia</i>	<i>aryabhatai</i>	PTA-127850
OATH01851	403	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127837
OATH01861	404	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01871	405	<i>Kocuria</i>	<i>polaris_A</i>	PTA-127849
OATH01881	406	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH01891	407	<i>Arthrobacter</i>	sp006715285	PTA-127834
OATH01901	408	<i>Kocuria</i>	<i>polaris_A</i>	PTA-127849
OATH01911	409	<i>Actinoplanes</i>	<i>aureus</i>	PTA-127849
OATH01921	410	<i>Neorhizobium</i>	<i>petrolearium</i>	PTA-127850
OATH01931	411	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01941	413	<i>Neorhizobium</i>	<i>flavum</i>	PTA-127850
OATH01951	414	<i>Streptomyces</i>	<i>nigra</i>	PTA-127844
OATH01961	415, 416	<i>Bacillus</i>	<i>inaquosorum</i>	PTA-127847
OATH01971	417	<i>Microvirga</i>	sp022346925	PTA-127848
OATH01991	419	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH02001	420	<i>Bacillus</i>	<i>spizizenii</i>	PTA-127848
OATH02011	421	<i>Microbispora</i>	sp014161445	PTA-127849
OATH02021	422	<i>Erythrobacter</i>	sp006542605	PTA-127850
OATH02031	423	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127838
OATH02041	425	<i>Streptomyces</i>	<i>albogriseolus</i>	PTA-127838
OATH02051	426	<i>Streptomyces</i>	<i>bobili</i>	PTA-127839
OATH02061	428, 427	<i>Streptomyces</i>	<i>griseoruber</i>	PTA-127834
OATH02071	429	<i>Streptomyces</i>	sp000721605	PTA-127846
OATH02081	430	<i>Streptomyces</i>	<i>kurssanovii</i>	PTA-127835
OATH02091	431	<i>Streptomyces</i>	sp019049245	PTA-127835
OATH02101	432	<i>Allosphingosinicella</i>	sp011320075	PTA-127850
OATH02111	433	<i>Mycetocola_A</i>	<i>miduiensis</i>	PTA-127849
OATH02121	434	<i>Nocardioidea</i>	<i>undefined</i>	PTA-127849
OATH02131	435	<i>Bacillus</i>	<i>paralicheniformis</i>	PTA-127847
OATH02141	437	<i>Streptomyces</i>	<i>globosus</i>	PTA-127839
OATH02151	438	<i>Bacillus</i>	<i>paralicheniformis</i>	PTA-127847
OATH01581	453, 454	<i>Priestia</i>	<i>megaterium</i>	
OATH01981	418	<i>Agromyces</i>	sp031178025	

IV. Equivalents

[00581] 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
5 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.

[00582] 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
10 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.

[00583] 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
15 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
20 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.

[00584] The terms “a” and “an” and “the” and similar references in the context of describing
25 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.

[00585] It should be understood that the expression “at least one of” includes individually
30 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.

[00586] 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.

- 5 [00587] 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 $\pm 10\%$ variation from the nominal value unless otherwise indicated or inferred.

- [00588] It should be understood that the order of steps order for performing certain actions is
10 immaterial so long as the present invention remain operable. Moreover, two or more steps or actions may be conducted simultaneously.

- [00589] 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
15 be construed as indicating any non-claimed element as essential to the practice of the present invention.

- [00590] 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.
20 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
5 *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, such as at least 95%, 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% identical to a nucleic acid sequence of one or
more of SEQ ID NOs: 68-109, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-
10 278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-
377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437.
2. The composition of claim 1 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
15 identical, or 100% identical, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of 2SEQ ID NOs:
197, 198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-
299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414,
20 423, 425-431, and/or 437.
3. The composition of claim 1 or 2 wherein each microbe is present in a concentration of at
least 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or 10^{10} CFU/gm and/or not more than 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} or 10^{11}
CFU/gm, preferably 10^5 to 10^{10} CFU/gm, more preferably 10^6 to 10^{10} CFU/gm, yet more
25 preferably 10^7 to 10^{10} CFU/gm, even more preferably 10^6 to 10^{10} CFU/gm.
4. The composition of any previous claim 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,
30 preferably 2-100, more preferably 5-80, even more preferably 5-40, still more preferably 5-30,
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.
5. The composition of any previous claim further comprising one or more non-*Streptomyces*
35 microbes.

6. The composition of claim 5 comprising one or more *Pseudomonas* microbes.
7. The composition of claim 6 wherein the one or more *Pseudomonas* microbes comprise a
5 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 of one or more of SEQ ID NOs: 281, 304, 305, 456-
458, 459, 466, and/or 482.
- 10 8. The composition of any one of claims 5 through 7 comprising one or more *Microvirga*
microbes.
9. The composition of claim 8 wherein the one or more *Microvirga* microbes comprise a
15 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 of SEQ ID NO: 417.
- 20 10. The composition of any one of claims 5 through 9 comprising one or more *Paenibacillus*
microbes
11. The composition of claim 10 wherein the one or more *Paenibacillus* microbes comprise a
16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5
25 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 of one or more of SEQ ID NOs: 199, 323, and/or 393.
12. The composition of any one of claims 5 through 11 comprising one or more *Rhodococcus*
30 microbes.
13. The composition of claim 12 wherein the one or more *Rhodococcus* 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 of SEQ ID NO: 399.

14. The composition of any one of claims 5 through 13 comprising one or more
5 *Lysinibacillus* microbes.

15. The composition of claim 14 wherein the one or more *Lysinibacillus* 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
10 preferably at least 98%, still more preferably at least 99%, yet still more preferably at least
99.5% identity to a nucleic acid sequence of one or more of SEQ ID NOs: 279, and/or 395-397.

16. The composition of any one of claims 5 through 15 comprising *Actinoplanes* microbes.

15 17. The composition of claim 16 wherein the one or more *Actinoplanes* 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 of SEQ ID NO: 409.

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18. The composition of any one of claims 5 through 17 comprising *Agromyces* microbes.

19. The composition of claim 18 wherein the one or more *Agromyces* microbes comprise a
16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5
25 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 of SEQ ID NO: 418.

20. The composition of any one of claims 5 through 19 comprising *Allospingosinicella*
30 microbes.

21. The composition of claim 20 wherein the one or more *Allospingosinicella* 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 of SEQ ID NO: 432.

22. The composition of any one of claims 5 through 21 comprising *Aneurinibacillus* microbes.

23. The composition of claim 22 wherein the one or more *Aneurinibacillus* 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 of one or more of SEQ ID NOs: 294 and/or 327.

24. The composition of any one of claims 5 through 23 comprising *Arthrobacter* microbes.

25. The composition of claim 24 wherein the one or more *Arthrobacter* 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 of one or more of SEQ ID NOs: 407, 441, 452, 455, 468, 469, and/or 473-476.

26. The composition of any one of claims 5 through 25 comprising *Bacillus* microbes.

27. The composition of claim 26 wherein the one or more *Bacillus* 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 of one or more of SEQ ID NOs: 200, 201, 289, 295, 406, 415, 416, 419, 420, 435, 438, 444-446, 451, 460-465, 470, 478, 479, and/or 483-486.

28. The composition of any one of claims 5 through 27 comprising *Brevibacillus* microbes.

29. The composition of claim 28 wherein the one or more *Brevibacillus* 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 of SEQ ID NO: 300.

5 30. The composition of any one of claims 5 through 29 comprising *Caldimonas* microbes.

31. The composition of claim 30 wherein the one or more *Caldimonas* 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 of SEQ ID NO: 440.

32. The composition of any one of claims 5 through 31 comprising *Cupriavidus* microbes.

15 33. The composition of claim 32 wherein the one or more *Cupriavidus* 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 of SEQ ID NOs: 488.

20 34. The composition of any one of claims 5 through 33 comprising *Erythrobacter* microbes.

35. The composition of claim 34 wherein the one or more *Erythrobacter* 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 of SEQ ID NO: 422.

36. The composition of any one of claims 5 through 35 comprising *Kocuria* microbes.

30 37. The composition of claim 36 wherein the one or more *Kocuria* 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 of one or more of SEQ ID NOs: 405, 408, 436, and/or 443.

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38. The composition of any one of claims 5 through 37 comprising *Microbacterium* microbes.

39. The composition of claim 38 wherein the one or more *Microbacterium* microbes
5 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 of one or more of SEQ ID NOs: 210, 247, 345, 356, and/or 374.

10

40. The composition of any one of claims 5 through 39 comprising *Microbispora* microbes.

41. The composition of claim 40 wherein the one or more *Microbispora* microbes comprise a
16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5
15 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 of SEQ ID NO: 421.

42. The composition of any one of claims 5 through 41 comprising *Mycetocola* microbes.
20

43. The composition of claim 42 wherein the one or more *Mycetocola* 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
25 99.5% identity to a nucleic acid sequence of SEQ ID NO: 433.

44. The composition of any one of claims 5 through 43 comprising *Neorhizobium* microbes.

45. The composition of claim 44 wherein the one or more *Neorhizobium* microbes comprise a
16S rRNA gene nucleotide sequence that is at least 80, 85, 90, 95, 96, 97, 98, 99, or 99.5
30 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 of one or more of SEQ ID NOs: 404, 410, 411, and/or 413.

35

46. The composition of any one of claims 5 through 45 comprising *Nocardia* microbes.
47. The composition of claim 46 wherein the one or more *Nocardia* 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
5 100% 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 of SEQ ID NO: 424.
48. The composition of any one of claims 5 through 47 comprising *Nocardioides* microbes.
10
49. The composition of claim 48 wherein the one or more *Nocardioides* 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
15 99.5% identity to a nucleic acid sequence of SEQ ID NO: 434.
50. The composition of any one of claims 5 through 49 comprising *Nonomuraea* microbes.
51. The composition of claim 50 wherein the one or more *Nonomuraea* microbes comprise a
20 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 of SEQ ID NO: 412.
- 25 52. The composition of any one of claims 5 through 51 comprising *Peribacillus* microbes.
53. The composition of claim 52 wherein the one or more *Peribacillus* 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
30 preferably at least 98%, still more preferably at least 99%, yet still more preferably at least 99.5% identity to a nucleic acid sequence of one or more of SEQ ID NOs: 467, 471, and/or 477.
54. The composition of any one of claims 5 through 53 comprising *Priestia* microbes.

55. The composition of claim 54 wherein the one or more *Priestia* 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 of one or more of SEQ ID NOs: 401, 402, 447-450, 453, 454, 480, and/or 481.

56. The composition of any one of claims 5 through 55 comprising *Pristimantibacillus* microbes.

57. The composition of claim 56 wherein the one or more *Pristimantibacillus* 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 of SEQ ID NO: 324.

58. The composition of any one of claims 5 through 57 comprising *Stenotrophomonas* microbes.

59. The composition of claim 58 wherein the one or more *Stenotrophomonas* 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 of one or more of SEQ ID NOs: 310-314.

60. The composition of any one of claims 5 through 59 comprising *Stutzerimonas* microbes.

61. The composition of claim 60 wherein the one or more *Stutzerimonas* 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 of SEQ ID NO: 439.

62. The composition of any one of claims 5 through 61 comprising *Terrimonas* microbes.

63. The composition of claim 62 wherein the one or more *Terrimonas* 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 of SEQ ID NO: 442.

64. The composition of any one of claims 5 through 63 comprising *Zhihengliuella* microbes.

65. The composition of claim 64 wherein the one or more *Zhihengliuella* 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 of SEQ ID NO: 472.

66. The composition of any one of the previous claims wherein two or more of the microbes are heterologous to each other.

67. 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 5-80, even more preferably 5-40, still more preferably 5-30, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, yet even more preferably 10-30 different strains of *Streptomyces* microbes.

68. The composition of claim 67 wherein the strains of the *Streptomyces* microbes comprise 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 5-80, even more preferably 5-40, still more preferably 5-30, yet more preferably 10-80, still yet more preferably 10-70, even more preferably 10-60, yet even more preferably 10-30 different strains shown in Table 2A.

69. The composition of claim 67 or 68 further comprising one or more non-*Streptomyces* microbes.

70. The composition of any one of claims 67 through 69 wherein the one or more non-*Streptomyces* microbes comprise a *Pseudomonas*, *Microvirga*, *Paenibacillus*, *Rhodococcus*, *Lysinibacillus*, *Actinoplanes*, *Agromyces*, *Allosphingosinicella*, *Aneurinibacillus*, *Arthrobacter*, *Bacillus*, *Brevibacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbacterium*,
5 *Microbispora*, *Mycetocola*, *Neorhizobium*, *Nocardia*, *Nocardioidea*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pristimantibacillus*, *Stenotrophomonas*, *Stutzerimonas*, *Terrimonas*, or *Zhihengliuella* microbe, or a combination thereof.

71. The composition of claim 70 wherein the one or more non-*Streptomyces* microbes
10 comprise one or more *Pseudomonas* microbes.

72. The composition of claim 70 or 71 comprising a *Microvirga* microbe.

73. The composition of any one of claims 70 through 72 wherein the one or more non-*Streptomyces* microbes comprise one or more *Paenibacillus* microbes.
15

74. The composition of any one of claims 70 through 73 wherein the one or more non-*Streptomyces* microbes comprise one or more *Rhodococcus* microbes.

75. The composition of any one of claims 70 through 74 wherein the one or more non-*Streptomyces* microbes comprise one or more *Lysinibacillus* microbes.
20

76. The composition of any one of claims 70 through 75 wherein the one or more non-*Streptomyces* microbes comprise one or more *Actinoplanes* microbes.
25

77. The composition of any one of claims 70 through 76 through wherein the one or more non-*Streptomyces* microbes comprise one or more *Agromyces* microbes.

78. The composition of any one of claims 70 through 77 wherein the one or more non-*Streptomyces* microbes comprise one or more *Allosphingosinicella* microbes.
30

79. The composition of any one of claims 70 through 78 wherein the one or more non-*Streptomyces* microbes comprise one or more *Aneurinibacillus* microbes.

80. The composition of any one of claims 70 through 79 wherein the one or more non-Streptomyces microbes comprise one or more *Arthrobacter* microbes.
81. The composition of any one of claims 70 through 80 wherein the one or more non-
5 Streptomyces microbes comprise one or more *Bacillus* microbes.
82. The composition of any one of claims 70 through 81 wherein the one or more non-Streptomyces microbes comprise one or more *Brevibacillus* microbes.
- 10 83. The composition of any one of claims 70 through 82 wherein the one or more non-Streptomyces microbes comprise one or more *Caldimonas* microbes.
84. The composition of any one of claims 70 through 83 wherein the one or more non-Streptomyces microbes comprise one or more *Cupriavidus* microbes.
15
85. The composition of any one of claims 70 through 84 wherein the one or more non-Streptomyces microbes comprise one or more *Erythrobacter* microbes.
86. The composition of any one of claims 70 through 85 wherein the one or more non-
20 Streptomyces microbes comprise one or more *Kocuria* microbes.
87. The composition of any one of claims 70 through 86 wherein the one or more non-Streptomyces microbes comprise one or more *Microbacterium* microbes.
- 25 88. The composition of any one of claims 70 through 87 wherein the one or more non-Streptomyces microbes comprise one or more *Microbispora* microbes.
89. The composition of any one of claims 70 through 88 wherein the one or more non-Streptomyces microbes comprise one or more *Mycetocola* microbes.
30
90. The composition of any one of claims 70 through 89 wherein the one or more non-Streptomyces microbes comprise one or more *Neorhizobium* microbes.
91. The composition of any one of claims 70 through 90 wherein the one or more non-
35 Streptomyces microbes comprise one or more *Nocardia* microbes.

92. The composition of any one of claims 70 through 91 wherein the one or more non-Streptomyces microbes comprise one or more *Nocardioides* microbes.
93. The composition of any one of claims 70 through 92 wherein the one or more non-
5 Streptomyces microbes comprise one or more *Nonomuraea* microbes.
94. The composition of any one of claims 70 through 93 wherein the one or more non-Streptomyces microbes comprise one or more *Peribacillus* microbes.
- 10 95. The composition of any one of claims 70 through 94 wherein the one or more non-Streptomyces microbes comprise one or more *Priestia* microbes.
96. The composition of any one of claims 70 through 95 wherein the one or more non-Streptomyces microbes comprise one or more *Pristimantibacillus* microbes.
15
97. The composition of any one of claims 70 through 96 wherein the one or more non-Streptomyces microbes comprise one or more *Stenotrophomonas* microbes.
98. The composition of any one of claims 70 through 97 wherein the one or more non-
20 Streptomyces microbes comprise one or more *Stutzerimonas* microbes.
99. The composition of any one of claims 70 through 98 wherein the one or more non-Streptomyces microbes comprise one or more *Terrimonas* microbes.
- 25 100. The composition of any one of claims 70 through 99 wherein the one or more non-Streptomyces microbes comprise one or more *Zhihengliuella* microbes.
101. The composition of any one of claims 67 through 100 comprising one or more of the microbes of Table 2A.
30
102. The composition of any one of claims 67 through 100 wherein the one or more 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, such as at least 95%, preferably at least 96%, more preferably at least 97%, even more preferably at least 98%, still more preferably at least 99%, yet still more
35 preferably at least 99.5% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 68-

109, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437 .

- 5 103. The composition of any one of claims 67 through 100 wherein the one or more 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, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of SEQ ID NOs:
- 10 197, 198 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437 .
- 15 104. A composition comprising *Streptomyces* spp. microbes and cells of at least one, two, three, four, five, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 20, 22, 25, 27, 30, or 32 and/or not more than one, two, three, four, five, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 20, 22, 25, 27, 30, 32, or 35 preferably 2-35, more preferably 3-35, yet more preferably 5-35, , even yet more preferably 5-20, still more preferably 5-15, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 additional microbial species selected
- 20 from the group consisting of *Pseudomonas* spp., *Microvirga* spp., *Paenibacillus* spp., *Rhodococcus* spp., *Lysinibacillus* spp., *Actinoplanes* spp., *Agromyces* spp., *Allospingosinicella* spp., *Aneurinibacillus* spp., *Arthrobacter* spp., *Bacillus* spp., , *Brevibacillus* spp., *Caldimonas* spp., *Cupriavidus* spp., *Erythrobacter* spp., *Kocuria* spp., *Microbacterium* spp., *Microbispora* spp., *Mycetocola* spp., *Neorhizobium* spp., *Nocardia* spp., *Nocardioides* spp., *Nonomuraea* spp.,
- 25 *Peribacillus* spp., *Priestia* spp., *Pristimantibacillus* spp., *Stenotrophomonas* spp., *Stutzerimonas* spp., *Terrimonas* spp., and *Zhihengliuella* spp.
105. The composition of claim 104 comprising microbes of 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
- 30 *Streptomyces* strains, for example 2-100 different *Streptomyces* strains.
106. The composition of claim 104 or claim 105 comprising *Pseudomonas* spp. microbes.

107. The composition of claim 106 comprising microbes of 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* species, for example 2-24 different *Pseudomonas* strains.
- 5 108. The composition any one of claims 104 through 107 comprising *Microvirga* spp. microbes.
109. The composition of any one of claims 104 through 108 comprising *Paenibacillus* spp. microbes.
- 10 110. The composition of claim 109 comprising microbes of at least 2, 3, 4, 5, 6, or 7 and/or not more than 3, 4, 5, 6, 7, 8, or 10 different *Paenibacillus* species, for example 2-10 different *Paenibacillus* strains.
- 15 111. The composition of any one of claims 104 through 110 comprising microbes g *Rhodococcus* spp. microbes.
112. The composition of claim 111 comprising microbes of at least 1, or at least 2 different *Rhodococcus* strains.
- 20 113. The composition of any one of claims 104 through 112 comprising microbes *Lysinibacillus* spp. microbes.
114. The composition of claim 113 comprising microbes of at least 1, 2, 3, 4, 5, 6, or 7 and/or 25 not more than 3, 4, 5, 6, 7, 8, or 10 different *Lysinibacillus* species, for example 1-10, preferably 1-5, more preferably 1, or 2, different *Lysinibacillus* strains.
115. The composition of any one of claims 104 through 114 comprising microbes *Actinoplanes* spp microbes.
- 30 116. The composition of any one of claims 104 through 115 comprising microbes *Agromyces* spp microbes.
117. The composition of any one of claims 104 through 116 comprising microbes 35 *Allospingosinicella* spp microbes.

118. The composition of any one of claims 104 through 117 comprising microbes
Aneurinibacillus spp microbes.
- 5 119. The composition of of any one of claims 104 through 118 comprising *Arthrobacter* spp
microbes.
120. The composition of claim 119 comprising microbes of at least 2, 3, 4, 5, 6, or 7 and/or not
more than 3, 4, 5, 6, 7, 8, or 10 different *Arthrobacter* species, for example 2-10 different
10 *Arthrobacter* strains.
121. The composition of of any one of claims 104 through 120 comprising *Bacillus* spp
microbes.
- 15 122. The composition of claim 121 comprising microbes of at least 1, 2, 3, 4, 5, 6, or 7 and/or
not more than 2, 3, 4, 5, 6, 7, 8, or 10 different *Bacillus* species, for example 1-10, preferably 2-
10 different *Bacillus* strains.
123. The composition of of any one of claims 104 through 122 comprising *Brevibacillus* spp
20 microbes.
124. The composition of of any one of claims 104 through 123 comprising *Caldimonas* spp
microbes.
- 25 125. The composition of of any one of claims 104 through 124 comprising *Cupriavidus* spp
microbes.
126. The composition of of any one of claims 104 through 125 comprising g *Erythrobacter*
spp microbes.
30
127. The composition of of any one of claims 104 through 126 comprising *Kocuria* spp
microbes.
128. The composition of of any one of claims 104 through 127 comprising *Microbacterium*
35 spp microbes.

129. The composition of claim 128 comprising microbes of at least 1, 2, 3, 4, or 5 and/or not more than 2, 3, 4, 5, or 6 different *Microbacterium* species, for example 1-6, preferably 1-4, different *Microbacterium* strains.

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130. The composition of any one of claims 104 through 129 comprising *Microbispora* spp microbes.

131. The composition of any one of claims 104 through 130 comprising *Mycetocola* spp
10 microbes.

132. The composition of any one of claims 104 through 131 comprising *Neorhizobium* spp microbes.

15 133. The composition of claim 132 comprising microbes of 1, or microbes of 2, different *Neorhizobium* strains.

134. The composition of any one of claims 104 through 133 comprising *Nocardia* spp
20 microbes.

135. The composition of claim 134 comprising microbes of 1, or microbes of 2, different *Nocardia* strains.

136. The composition of any one of claims 104 through 135 comprising *Nocardioides* spp
25 microbes.

137. The composition of any one of claims 104 through 136 comprising *Nonomuraea* spp microbes.

30 138. The composition of any one of claims 104 through 137 comprising *Peribacillus* spp microbes.

139. The composition of any one of claims 104 through 138 comprising *Priestia* spp microbes.

140. The composition of claim 139 comprising microbes of 1, or microbes of 2, different *Priestia* strains.

141. The composition of any one of claims 104 through 140 comprising *Pristimantibacillus* spp microbes.

142. The composition of any one of claims 104 through 141 comprising *Stenotrophomonas* spp microbes.

143. The composition of any one of claims 104 through 142 comprising *Stutzerimonas* spp microbes.

144. The composition of any one of claims 104 through 143 comprising *Terrimonas* spp microbes.

145. The of any one of claims 104 through 144 comprising *Zhihengliuella* spp microbes.

146. The composition of any one of claims 104 through 145 wherein the one or more 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, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 68-109, 120-198, 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437 .

147. The composition of any one of claims 104 through 145 wherein the one or more 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, such as at least 95%, 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% identical to a nucleic acid sequence of one or more of SEQ ID NOs: 197, 198 202-209, 211-220, 222-246, 248-250, 252-256, 258-278, 280, 282-288, 290-293, 296-299, 301-303, 306-322, 326, 328-344, 346-351, 357-373, 375-377, 379-392, 394, 398, 403, 414, 423, 425-431, and/or 437 .

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148. A composition comprising microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*.

149. The composition of claim 148 wherein *Streptomyces* comprise one or more strains of the species *Streptomyces griseoincarnatus*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces echinatu*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, *Streptomyces chartreusis*, *Streptomyces globosus*, *Streptomyces achromogenes*, and/or *Streptomyces eurythermus*.

150. The composition of claim 148 or 149 wherein *Microbacterium* comprises one or more strains of the species *Microbacterium paraoxydans*.

151. The composition of any one of claims claim 148 through 150 wherein *Rhodococcus* comprises one or more strains of the species *Rhodococcus erythropolis*.

152. The composition of any one of claims claim 148 through 151 comprising one or more of the bacteria of Table 33.

153. A composition comprising microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*.

154. The composition of claim 153 wherein the *Streptomyces* bacteria comprise one or more strains of the species *Streptomyces griseoincarnatus*, *Streptomyces griseoaurantiacus*, *Streptomyces rochei*, *Streptomyces bikiniensis*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, and/or *Streptomyces achromogenes*.

155. The composition of claim 153 or 154 wherein the *Lysinibacillus* bacteria comprise one or more strains of the species *Lysinibacillus sphaericus*.

156. The composition of any one of claims 153 through 155 wherein the *Microbacterium* bacteria comprise one or more strains of the species *Microbacterium paraoxydans*.

157. The composition of any one of claims 153 through 156 wherein the *Rhodococcus* bacteria comprise one or more strains of the species *Rhodococcus erythropolis*.

158. The composition of any one of claims 153 through 157 comprising one or more of the bacteria of Table 34.

5 159. A composition comprising microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*.

160. The composition of claim 159 wherein the *Lysinibacillus* bacteria comprise one or more strains of the species *Lysinibacillus sphaericus*.

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161. The composition of claim 159 or 160 wherein the *Microbacterium* bacteria comprise one or more strains of the species *Microbacterium paraoxydans*.

162. The composition of any one of claims 159 through 161 wherein the *Rhodococcus* bacteria
15 comprise one or more strains of the species *Rhodococcus erythropolis*.

163. The composition of any one of claims 159 through 162 wherein the *Streptomyces* bacteria comprise one or more strains of the species *Streptomyces misionensis*, *Streptomyces bacillari*, *Streptomyces achromogenes*, and/or *Streptomyces globosus*.

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164. The composition of any one of claims 159 through 163 comprising one or more of the bacteria of Table 37.

165. A composition comprising microbes from the genera *Bacillus*, *Lysinibacillus*,
25 *Rhodococcus*, and *Streptomyces*.

166. The composition of claim 165 wherein the *Lysinibacillus* bacteria comprise one or more strains of the species *Lysinibacillus sphaericus*.

167. The composition of claim 165 or 166 wherein the *Rhodococcus* bacteria comprise one or
30 more strains of the species *Rhodococcus erythropolis*.

168. The composition of any one of claims 165 through 167 wherein the *Bacillus* bacteria comprise one or more strains of the species *Bacillus velizensis*.

169. The composition of any one of claims 165 through 168 wherein the *Streptomyces* bacteria comprise one or more strains of the species *Streptomyces misionensis*, *Streptomyces bacillari*, *Streptomyces achromogenes*, *Streptomyces globosus*, *Streptomyces antibioticus*, *Streptomyces bikiniensis*, *Streptomyces chartreusis*, *Streptomyces echinatu*, *Streptomyces griseoaurantiacus*,
5 *Streptomyces murinus*, *Streptomyces mustoli*, *Streptomyces olivaceus*, *Streptomyces sennicomposti*, and/or *Streptomyces toxytricini*.

170. The composition of any one of claims 165 through 169 comprising one or more of the bacteria of Table 38.

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171. A composition comprising microbes from the genera *Lysinibacillus*, *Microbacterium*, *Rhodococcus*, and *Streptomyces*.

172. The composition of claim 171 wherein the *Lysinibacillus* bacteria comprise one or more
15 strains of the species *Lysinibacillus sphaericus*.

173. The composition of claim 171 or 172 wherein the *Rhodococcus* bacteria comprise one or more strains of the species *Rhodococcus erythropolis*.

20 174. The composition of any one of claims 171 through 173 wherein the *Microbacterium* bacteria comprise one or more strains of the species *Microbacterium paraoxydans*.

175. The composition of any one of claims 171 through 174 wherein the *Streptomyces* bacteria comprise one or more strains of the species *Streptomyces achromogenes*, *Streptomyces bacillari*,
25 *Streptomyces globosus*, *Streptomyces misionensis*, and/or *Streptomyces rochei*.

176. The composition of any one of claims 171 through 175 comprising one or more of the bacteria of Table 40.

30 177. A composition comprising microbes from the genera *Microbacterium*, *Rhodococcus*, and *Streptomyces*.

178. The composition of claim 177 wherein the *Rhodococcus* bacteria comprise one or more strains of the species *Rhodococcus erythropolis*.

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179. The composition of claim 177 or 178 wherein the *Microbacterium* bacteria comprise one or more strains of the species *Microbacterium paraoxydans*.

180. The composition of any one of claims 177 through 179 wherein the *Streptomyces* bacteria
5 comprise one or more strains of the species *Streptomyces achromogenes*, *Streptomyces bacillari*,
Streptomyces bikiniensis, *Streptomyces globosus*, *Streptomyces griseoincarnatus*, *Streptomyces*
misionensis, *Streptomyces murinus*, and/or *Streptomyces rochei*.

181. The composition of any one of claims 177 through 180 comprising one or more of the
10 bacteria of Table 41.

182. A composition comprising microbes from the genera *Bacillus*, *Lysinibacillus*,
Microbacterium, *Neorhizobium*, *Peribacillus*, *Priestia*, *Pseudomonas*, *Rhodococcus*, and
Streptomyces.

183. The composition of claim 182 wherein the *Rhodococcus* bacteria comprise one or more
15 strains of the species *Rhodococcus erythropolis*.

184. The composition of claim 182 or 183 wherein the *Microbacterium* bacteria comprise one
or more strains of the species *Microbacterium paraoxydans*.

20 185. The composition of any one of claims 182 through 184 wherein the *Bacillus* bacteria
comprise one or more strains of species *Bacillus spizizenii* and/or *Bacillus paralicheniformis*.

186. The composition of any one of claims 182 through 185 wherein the *Neorhizobium*
25 bacteria comprise one or more strains of species *Neorhizobium flavum*.

187. The composition of any one of claims 182 through 186 wherein the *Peribacillus* bacteria
comprise one or more strains of species *Peribacillus frigiditolerans* A.

30 188. The composition of any one of claims 182 through 187 wherein the *Priestia* bacteria
comprise one or more strains of species *Priestia aryabhattai*.

189. The composition of any one of claims 182 through 188 wherein the *Streptomyces* bacteria
comprise one or more strains of species *Streptomyces nigrescens*, *Streptomyces nigra*,
35 *Streptomyces bobili*, *Streptomyces albogriseolus*, *Streptomyces globosus*, *Streptomyces*

griseoincarnatus, *Streptomyces griseoaurantiacus*, *Streptomyces rochei*, *Streptomyces bikiniensis*, *Streptomyces misionensis*, *Streptomyces murinus*, *Streptomyces bacillari*, *Streptomyces sennicomposti*, and/or *Streptomyces achromogenes*.

5 190. The composition of any one of claims 182 through 189 comprising one or more of the bacteria of Table 35.

191. A composition comprising one or more of the bacteria of Table 42.

10 192. A composition comprising one or more of the bacteria of Table 43.

193. A composition comprising bacteria of the genus *Streptomyces* and bacteria of the class Bacilli.

15 194. The composition of claim 193 wherein the bacteria of the class Bacilli comprise bacteria of one or more of *Aneurinibacillus*, e.g., one or more strains of the species *Aneurinibacillus aneurinilyticus*; *Bacillus*, e.g., one or more strains of the species *Bacillus_I endophytica_A*, *Bacillus haynesii*, *Bacillus inaqosorum*, *Bacillus licheniformis*, *Bacillus paralicheniformis*, *Bacillus safensis*, *Bacillus spizizenii*, *Bacillus subtilis*, *Bacillus_A thuringiensis_K*, and/or
20 *Bacillus velizensis*; *Brevibacillus*, such as one or more strains of the species *Brevibacillus panacihumi*; *Lysinibacillus*, such as one or more strains of the species *Lysinibacillus sphaericus* and/or *Lysinibacillus capsica*; *Paenibacillus*, such as one or more strains of the species *Paenibacillus cellulositrophicus*; *Peribacillus*, such as one or more strains of the species *Peribacillus frigoritolerans_A*; and/or *Pristimantibacillus*.

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195. The composition of claim 193 or 194 comprising one or more of the *Streptomyces* species or strains of the species as shown in Table 2A and one or more of the Bacilli genera, species or strains of the species as shown in Table 2A.

30 196. A composition comprising bacteria from one or more of genera *Actinoplanes*, *Agromyces*, *Allospingosinicella*, *Arthrobacter*, *Bacillus*, *Caldimonas*, *Cupriavidus*, *Erythrobacter*, *Kocuria*, *Microbispora*, *Microvirga*, *Mycetocola*, *Neorhizobium*, *Nocardia*, *Nocardioides*, *Nonomuraea*, *Peribacillus*, *Priestia*, *Pseudomonas*, *Streptomyces*, *Stutzerimonas*, *Terrimonas*, and/or *Zhihengliuella*.

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197. The composition of claim 196 comprising one or more of the strains of Table 44.
198. The composition of claim 196 or 197 comprising free-living nitrogen-fixing bacteria.
- 5 199. The composition of any one of the previous claims comprising one or more microbes of ATCC deposits designated PTA-127834-127850 respectively, as shown in Table 2A.
200. A composition comprising one or more microbes of ATCC deposits designated Nos. PTA-127834-127850 respectively, as shown in Table 2A.
- 10 201. The composition of claim 199 or claim 200 comprising one or more bacteria of ATCC deposit number PTA-127834, and/or one or more bacteria of ATCC deposit number PTA-127835, and/or one or more bacteria of ATCC deposit number PTA-127836, and/or one or more bacteria of ATCC deposit number PTA-127837, and/or one or more bacteria of ATCC deposit number PTA-127838, and/or one or more bacteria of ATCC deposit number PTA-127839, and/or one or more bacteria of ATCC deposit number PTA-127840, and/or one or more bacteria of ATCC deposit number PTA-127841, and/or one or more bacteria of ATCC deposit number PTA-127842, and/or one or more bacteria of ATCC deposit number PTA-127843, and/or one or more bacteria of ATCC deposit number PTA-127844, and/or one or more bacteria of ATCC deposit number PTA-127845, and/or one or more bacteria of ATCC deposit number PTA-127846, and/or one or more bacteria of ATCC deposit number PTA-127847, and/or one or more bacteria of ATCC deposit number PTA-127848, and/or one or more bacteria of ATCC deposit number PTA-127849, and/or one or more bacteria of ATCC deposit number PTA-127850.
- 15 202. The composition of any one of claims 199 through 201 wherein the composition comprises one or more bacteria of the genus *Microbacterium* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Rhodococcus* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Arthrobacter* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Aneurinibacillus* from ATCC deposit number PTA-127839 and/or the composition comprises one or more bacteria of the genus *Psuedomonas* from ATCC deposit number PTA-127844 and/or the composition comprises one or more bacteria of the genus *Bacillus* from ATCC deposit number PTA-127847 and/or the composition comprises one or more bacteria of the genus *Paenibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Pristimantibacillus* from ATCC
- 25 30 35

deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Brevibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Paenibacillus* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the *Bacillus* from ATCC deposit number

5 PTA-127848 and/or the composition comprises one or more bacteria of the genus *Microvirga* from ATCC deposit number PTA-127848 and/or the composition comprises one or more bacteria of the genus *Psuedomonas* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Peribacillus* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus

10 *Zhihengliuella* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nonomuraea* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nocardia* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Kocuria* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of

15 the genus *Actinoplanes* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Microbispora* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Mycetocola* from ATCC deposit number PTA-127849 and/or the composition comprises one or more bacteria of the genus *Nocardioides* from ATCC deposit number PTA-127849 and/or the composition

20 comprises one or more bacteria of the genus *Priestia* from ATCC deposit number PTA-127850 and/or the the composition comprises one or more bacteria of the genus *Cupriavidus* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Peribacillus* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Shutzerimonas* from ATCC deposit number PTA-127850

25 and/or the composition comprises one or more bacteria of the genus *Caldimonas* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Terrimonas* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Neorhizobium* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Erythrobacter* from ATCC

30 deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Allospingosinicella* from ATCC deposit number PTA-127850 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127834 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127835 and/or the composition comprises one or more bacteria of

35 the genus *Streptomyces* from ATCC deposit number PTA-127836 and/or the composition

comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127837 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127838 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127839 and/or the composition
5 comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127840 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127841 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127842 and/or the composition
10 comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127843 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127844 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127845 and/or the composition
comprises one or more bacteria of the genus *Streptomyces* from ATCC deposit number PTA-127846 and/or the composition comprises one or more bacteria of the genus *Streptomyces* from
15 ATCC deposit number PTA-127849.

203. The composition of any one of the previous claims comprising one or more fungal microbes.

20 204. A composition comprising fungal microbes.

205. The composition of claim 203 or 204 wherein the fungal microbes comprise ectomycorrhizal fungi.

206. The composition of claim 205 wherein the fungal microbes comprise one or more of
25 *Aspergillus*, *Chaetomium*, *Coniothyrium*, *Paecilomyces*, *Penicillium*, *Phlebia*, *Rhizopogon*, *Scleroderma*, *Lecanicillium*, and/or *Sebacina* microbes.

207. The composition of claim 206 comprising one or more *Aspergillus* microbes.

208. The composition of claim 207 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Aspergillus*
30 microbes, for example 1-20 different *Aspergillus* microbes, preferably 1 to 16 different
208*Aspergillus* microbes, more preferably 1 to 10 different *Aspergillus* microbes, even more preferably 2 to 10 different *Aspergillus* microbes.

209. The composition of claim 207 or 208 wherein the *Aspergillus* microbes comprise *Aspergillus flavus*.
210. The composition of any one of claims 207 through 209 wherein the *Aspergillus* microbes comprise *Aspergillus niger*.
- 5 211. The composition of any one of claims 205 through 208 comprising one or more *Chaetomium* microbes.
212. The composition of claim 211 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Chaetomium* microbes, for example 1-20 different *Chaetomium* microbes, preferably 1 to 16 different
10 *Chaetomium* microbes, more preferably 1 to 10 different *Chaetomium* microbes, even more preferably 2 to 10 different *Chaetomium* microbes.
213. The composition of any one of claims 205 through 212 comprising one or more *Coniothyrium* microbes.
214. The composition of claim 213 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or
15 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Coniothyrium* microbes, for example 1-20 different *Coniothyrium* microbes, preferably 1 to 16 different *Coniothyrium* microbes, more preferably 1 to 10 different *Coniothyrium* microbes, even more preferably 2 to 10 different *Coniothyrium* microbes.
215. The composition of claim 213 or 214 wherein the *Coniothyrium* microbes comprise
20 *Coniothyrium minitans*.
216. The composition of any one of claims 205 through 215 comprising one or more *Lecanicillium* microbes.
217. The composition of claim 216 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Lecanicillium* microbes, for example 1-20 different *Lecanicillium* microbes, preferably 1 to 16 different
25 *Lecanicillium* microbes, more preferably 1 to 10 different *Lecanicillium* microbes, even more preferably 2 to 10 different *Lecanicillium* microbes.

218. The composition of any one of claims 205 through 217 comprising one or more *Paecilomyces* microbes.
219. The composition of claim 218 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Paecilomyces* microbes, for example 1-20 different *Paecilomyces* microbes, preferably 1 to 16 different *Paecilomyces* microbes, more preferably 1 to 10 different *Paecilomyces* microbes, even more preferably 2 to 10 different *Paecilomyces* microbes.
220. The composition of claim 219 wherein the *Paecilomyces* microbes comprise *Paecilomyces lilacinus*.
221. The composition of any one of claims 205 through 220 comprising one or more *Penicillium* microbes.
222. The composition of claim 221 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Penicillium* microbes, for example 1-20 different *Penicillium* microbes, preferably 1 to 16 different *Penicillium* microbes, more preferably 1 to 10 different *Penicillium* microbes, even more preferably 2 to 10 different *Penicillium* microbes.
223. The composition of claim 221 or 222 wherein the *Penicillium* microbes comprise *Penicillium bilaiae*.
224. The composition of any one of claims 221 through 223 wherein the *Penicillium* microbes comprise *Penicillium bilaii*.
225. The composition of any one of claims 221 through 224 wherein the *Penicillium* microbes comprise *Penicillium oxalicum*.
226. The composition of any one of claims 205 through 225 comprising one or more *Phlebia* microbes.
227. The composition of claim 226 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Phlebia* microbes, for example 1-20 different *Phlebia* microbes, preferably 1 to 16 different *Phlebia*

microbes, more preferably 1 to 10 different *Phlebia* microbes, even more preferably 2 to 10 different *Phlebia* microbes.

228. The composition of claim 226 or 227 wherein the *Phlebia* microbes comprise *Phlebia gigantea*.

5 229. The composition of any one of claims 205 through 228 comprising one or more *Rhizopogon* microbes.

230. The composition of claim 229 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Rhizopogon* microbes, for example 1-20 different *Rhizopogon* microbes, preferably 1 to 16 different
10 *Rhizopogon* microbes, more preferably 1 to 10 different *Rhizopogon* microbes, even more preferably 2 to 10 different *Rhizopogon* microbes.

231. The composition of claim 229 or 230 wherein the *Rhizopogon* microbes comprise *Rhizopogon amylopogon*.

232. The composition of any one of claims 229 through 231 wherein the *Rhizopogon* microbes
15 comprise *Rhizopogon fulvigleba*.

233. The composition of any one of claims 229 through 232 wherein the *Rhizopogon* microbes comprise *Rhizopogon luteolus*.

234. The composition of any one of claims 229 through 233 wherein the *Rhizopogon* microbes comprise *Rhizopogon villosullus*.

20 235. The composition of any one of claims 205 through 234 comprising one or more *Scleroderma* microbes.

236. The composition of claim 235 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Scleroderma* microbes, for example 1-20 different *Scleroderma* microbes, preferably 1 to 16 different
25 *Scleroderma* microbes, more preferably 1 to 10 different *Scleroderma* microbes, even more preferably 2 to 10 different *Scleroderma* microbes.

237. The composition of claim 235 or 236 wherein the *Scleroderma* microbes comprise *Scleroderma cepa*.

238. The composition of any one of claims 235 through 237 wherein the *Scleroderma* microbes comprise *Scleroderma citrinum*.
239. The composition of any one of claims 205 through 238 comprising one or more *Sebacina* microbes.
- 5 240. The composition of claim 239 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Sebacina* microbes, for example 1-20 different *Sebacina* microbes, preferably 1 to 16 different *Sebacina* microbes, more preferably 1 to 10 different *Sebacina* microbes, even more preferably 2 to 10 different *Sebacina* microbes.
- 10 241. The composition of claim 239 or 240 wherein the *Sebacina* microbes comprise *Sebacina vermifera*.
242. The composition of any one of claims 203 through 241 wherein the fungal microbes comprise endomycorrhizal fungi.
- 15 243. The composition of claim 242 wherein the fungi comprise fungi of one or more of the genera *Alternaria*, *Beauveria*, *Cladosporium*, *Claroideoglossum*, *Funnelformis*, *Glomus*, *Laccaria*, *Lecanicillium*, *Metarhizium*, *Piriformospora*, *Pisolithus*, *Rhizophagus*, *Serendipita*, *Talaromyces*, and/or *Trichoderma*.
244. The composition of claim 242 or 243 comprising one or more *Alternaria* microbes.
- 20 245. The composition of claim 244 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Alternaria* microbes, for example 1-20 different *Alternaria* microbes, preferably 1 to 16 different *Alternaria* microbes, more preferably 1 to 10 different *Alternaria* microbes, even more preferably 2 to 10 different *Alternaria* microbes.
- 25 246. The composition of claim 244 or 245 wherein the *Alternaria* microbes comprise *Alternaria alternata*.
247. The composition of any one of claims 242 through 246 comprising one or more *Beauveria* microbes.

248. The composition of claim 247 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Beauveria* microbes, for example 1-20 different *Beauveria* microbes, preferably 1 to 16 different *Beauveria* microbes, more preferably 1 to 10 different *Beauveria* microbes, even more preferably 2 to 10 different *Beauveria* microbes.
249. The composition of claim 247 or 248 wherein the *Beauveria* microbes comprise *Beauveria bassiana*.
250. The composition of any one of claims 242 through 249 comprising one or more *Cladosporium* microbes.
251. The composition of claim 250 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Cladosporium* microbes, for example 1-20 different *Cladosporium* microbes, preferably 1 to 16 different *Cladosporium* microbes, more preferably 1 to 10 different *Cladosporium* microbes, even more preferably 2 to 10 different *Cladosporium* microbes.
252. The composition of claim 250 or 251 wherein the *Cladosporium* microbes comprise *Cladosporium tenuissimum*.
253. The composition of any one of claims 242 through 252 comprising one or more *Claroideoglossus* microbes.
254. The composition of claim 253 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Claroideoglossus* microbes, for example 1-20 different *Claroideoglossus* microbes, preferably 1 to 16 different *Claroideoglossus* microbes, more preferably 1 to 10 different *Claroideoglossus* microbes, even more preferably 2 to 10 different *Claroideoglossus* microbes.
255. The composition of claim 253 or 254 wherein the *Claroideoglossus* microbes comprise *Claroideoglossus etunicatum*.
256. The composition of any one of claims 242 through 255 comprising one or more *Funneliformis* microbes.

257. The composition of claim 256 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Funneliformis* microbes, for example 1-20 different *Funneliformis* microbes, preferably 1 to 16 different *Funneliformis* microbes, more preferably 1 to 10 different *Funneliformis* microbes, even more preferably 2 to 10 different *Funneliformis* microbes.
258. The composition of claim 256 or 257 wherein the *Funneliformis* microbes comprise *Funneliformis mosseae*.
259. The composition of any one of claims 242 through 258 comprising one or more *Glomus* microbes.
260. The composition of claim 259 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Glomus* microbes, for example 1-20 different *Glomus* microbes, preferably 1 to 16 different *Glomus* microbes, more preferably 1 to 10 different *Glomus* microbes, even more preferably 2 to 10 different *Glomus* microbes.
261. The composition of claim 259 or 260 wherein the *Glomus* microbes comprise *Glomus aggregatum*.
262. The composition of any one of claims 259 through 261 wherein the *Glomus* microbes comprise *Glomus etunicatum*.
263. The composition of any one of claims 259 through 262 wherein the *Glomus* microbes comprise *Glomus intraradices*.
264. The composition of any one of claims 259 through 263 wherein the *Glomus* microbes comprise *Glomus mosseae*.
265. The composition of any one of claims 242 through 264 comprising one or more *Laccaria* microbes.
266. The composition of claim 265 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Laccaria* microbes, for example 1-20 different *Laccaria* microbes, preferably 1 to 16 different

Laccaria microbes, more preferably 1 to 10 different *Laccaria* microbes, even more preferably 2 to 10 different *Laccaria* microbes.

267. The composition of claim 265 or 266 wherein the *Laccaria* microbes comprise *Laccaria laccata*.

5 268. The composition of any one of claims 242 through 267 comprising one or more *Lecanicillium* microbes.

269. The composition of claim 268 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Lecanicillium* microbes, for example 1-20 different *Lecanicillium* microbes, preferably 1 to 16 different
10 *Lecanicillium* microbes, more preferably 1 to 10 different *Lecanicillium* microbes, even more preferably 2 to 10 different *Lecanicillium* microbes.

270. The composition of any one of claims 242 through 269 comprising one or more *Metarhizium* microbes.

271. The composition of claim 270 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Metarhizium* microbes, for example 1-20 different *Metarhizium* microbes, preferably 1 to 16 different
15 *Metarhizium* microbes, more preferably 1 to 10 different *Metarhizium* microbes, even more preferably 2 to 10 different *Metarhizium* microbes.

272. The composition of claim 270 or 271 wherein the *Metarhizium* microbes comprise
20 *Metarhizium anisopliae*.

273. The composition of any one of claims 242 through 272 comprising one or more *Piriformospora* microbes.

274. The composition of claim 273 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different
25 *Piriformospora* microbes, for example 1-20 different *Piriformospora* microbes, preferably 1 to 16 different *Piriformospora* microbes, more preferably 1 to 10 different *Piriformospora* microbes, even more preferably 2 to 10 different *Piriformospora* microbes.

275. The composition of claim 273 or 274 wherein the *Piriformospora* microbes comprise *Piriformospora indica*.
276. The composition of any one of claims 242 through 275 comprising one or more *Pisolithus* microbes.
- 5 277. The composition of claim 276 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Pisolithus* microbes, for example 1-20 different *Pisolithus* microbes, preferably 1 to 16 different *Pisolithus* microbes, more preferably 1 to 10 different *Pisolithus* microbes, even more preferably 2 to 10 different *Pisolithus* microbes.
- 10 278. The composition of claim 276 or 277 wherein the *Pisolithus* microbes comprise *Pisolithus tinctorius*.
279. The composition of any one of claims 242 through 278 comprising one or more *Rhizophagus* microbes.
- 15 280. The composition of claim 279 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Rhizophagus* microbes, for example 1-20 different *Rhizophagus* microbes, preferably 1 to 16 different *Rhizophagus* microbes, more preferably 1 to 10 different *Rhizophagus* microbes, even more preferably 2 to 10 different *Rhizophagus* microbes.
- 20 281. The composition of claim 279 or 280 wherein the *Rhizophagus* microbes comprise *Rhizophagus intraradices*.
282. The composition of any one of claims 279 through 281 wherein the *Rhizophagus* microbes comprise *Rhizophagus irregularis*.
283. The composition of any one of claims 242 through 282 comprising one or more *Serendipita* microbes.
- 25 284. The composition of claim 283 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Serendipita* microbes, for example 1-20 different *Serendipita* microbes, preferably 1 to 16 different

Serendipita microbes, more preferably 1 to 10 different *Serendipita* microbes, even more preferably 2 to 10 different *Serendipita* microbes.

285. The composition of claim 283 or 284 wherein the *Serendipita* microbes comprise *Serendipita indica*.

5 286. The composition of any one of claims 242 through 285 comprising one or more *Talaromyces* microbes.

287. The composition of claim 286 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Talaromyces* microbes, for example 1-20 different *Talaromyces* microbes, preferably 1 to 16 different
10 *Talaromyces* microbes, more preferably 1 to 10 different *Talaromyces* microbes, even more preferably 2 to 10 different *Talaromyces* microbes.

288. The composition of claim 286 or 287 wherein the *Talaromyces* microbes comprise *Talaromyces flavus*.

289. The composition of any one of claims 242 through 288 comprising one or more
15 *Trichoderma* microbes.

290. The composition of claim 289 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Trichoderma* microbes, for example 1-20 different *Trichoderma* microbes, preferably 1 to 16 different *Trichoderma* microbes, more preferably 1 to 10 different *Trichoderma* microbes, even more
20 preferably 2 to 10 different *Trichoderma* microbes.

291. The composition of claim 289 or 290 wherein the *Trichoderma* microbes comprise *Trichoderma asperellum*.

292. The composition of any one of claims 289 through 291 wherein the *Trichoderma* microbes comprise *Trichoderma atroviride*.

25 293. The composition of any one of claims 289 through 292 wherein the *Trichoderma* microbes comprise *Trichoderma atroviride*.

294. The composition of any one of claims 289 through 293 wherein the *Trichoderma* microbes comprise *Trichoderma harzianum*.

295. The composition of any one of claims 289 through 294 wherein the *Trichoderma* microbes comprise *Trichoderma viride*.
296. The composition of any one of claims 242 through 295 comprising one or more *Mucor* microbes.
- 5 297. The composition of claim 296 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Mucor* microbes, for example 1-20 different *Mucor* microbes, preferably 1 to 16 different *Mucor* microbes, more preferably 1 to 10 different *Mucor* microbes, even more preferably 2 to 10 different *Mucor* microbes.
- 10 298. The composition of claim 296 or 297 wherein the *Mucor* microbes comprise *Mucor circinelloides*.
299. The composition of any one of claims 242 through 298 comprising one or more *Phanerochaete* microbes.
300. The composition of claim 299 comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, or
15 18 and/or not more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 different *Phanerochaete* microbes, for example 1-20 different *Phanerochaete* microbes, preferably 1 to 16 different *Phanerochaete* microbes, more preferably 1 to 10 different *Phanerochaete* microbes, even more preferably 2 to 10 different *Phanerochaete* microbes.
301. The composition of claim 299 or 300 wherein the *Phanerochaete* microbes comprise
20 *Phanerochaete chrysosporium*.
302. The composition of any one of claims 242 through 301 wherein two or more of the fungal microbes are heterologous to each other.
303. A composition comprising a plurality of particles, wherein each particle comprises a composition of any one of claims 1 through 302
- 25 304. 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.

5 305. The composition of any one of the previous claims further comprising one or more agriculturally acceptable adjuvants.

306. The composition of claim 305 wherein the adjuvant comprises polyethylene glycol.

10 307. The composition of claim 305 wherein the adjuvant consists essentially of glucose.

308. 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, 15 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.

309. The population of claim 308 wherein the microbes comprise microbes of a composition
20 of any one of claims 1 through 302

310. 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
25 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.

30 311. The composition of claim 310 wherein the microbes comprise microbes of a composition of any one of claims 1 through 302

312. 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 of a
35 composition of any one of claims 1 through 302

313. A plant or plant part comprising one or more microbes of the composition of any one of any one of claims 1 through 302 disposed on or in the plant or plant part.
- 5 314. 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 302 disposed on or in the plant or plant part.
- 10 315. A method comprising applying the composition of any one of claims 1 through 302, 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.
316. A method comprising applying a composition comprising a plurality of microbes to an area comprising soil by aerial application.
- 15 317. 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
20 (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.
- 25 318. A method comprising contacting a surface of a seed, seedling, or other plant propagule with a composition of any one of claims 1 through 302, or a derivative produced from the composition.
- 30 319. 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 302, or a derivative produced from the composition.
- 35 320. Use of the composition of any one of claims 1 through 302 in reducing methane production in soil in which plants grow compared to before use of the composition.

321. Use of the composition of any one of claims 1 through 302 in coating a surface of seeds, seedlings, or other plant propagules with one or more microbes of the composition.
- 5 322. Use of the composition of any one of claims 1 through 302 in increasing beneficial organisms in soil in which plants grow and to which composition applied, compared to without.
- 10 323. Use of the composition of any one of claims 1 through 302 in transitioning to organic farming in 3 years or less, or 2 years or less, or 1.5 years or less.
- 15 324. Use of the composition of any one of claims 1 through 302 in improving soil density, soil water holding capacity, soil water retention capacity, in soil in which plants grow, compared to without.
325. Use of the composition of any one of claims 1 through 302 in increasing mycorrhizal fungi on or in roots of plant, compared to a reference plant
- 20 326. Use of the composition of any one of claims 1 through 302 in preventing or reducing flooding.
- 25 327. Use of the composition of any one of claims 1 through 302 in decreasing use of synthetic fertilizer, herbicide, and/or pesticide on plants or soil in which plants grow, compared to without.
- 30 328. Use of the composition of any one of claims 1 through 302 in increasing nutrient uptake by a plant grown in soil to which composition applied compared to without.
329. Use of the composition of any one of claims 1 through 302 in decreasing uptake of one or more toxins, e.g., heavy metals, by plants grown in soil comprising composition.
330. Use of the composition of any one of claims 1 through 302 in increasing plant nutrient density of a plant grown in soil to which composition applied compared to without.

331. Use of the composition of any one of claims 1 through 302 in reducing carbon footprint for raising livestock.

5 332. Use of the composition of any one of claims 1 through 302 in increasing oil production of a plant not cannabis.

333. Use of the composition of any one of claims 1 through 302 in regenerating degraded soil.

10

334. 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 302 and providing suitable conditions for one or more microbes to grow.

15

335. A composition comprising a pure population of microbes of the composition of any one of claims 1 through 302 and a heterologous growth medium.

20

336. A composition consisting essentially of a pure population of microbes of the composition of any one of claims 1 through 302 and a heterologous growth medium.

25

337. 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.

30

338. The method of claim 337 wherein the composition comprises a composition of any one of claims 1 through 302.

339. 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.

340. The method of claim 339 wherein the composition comprises a composition of any one of claims 1 through 302.

341. 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/m³ and/or not more than 0.5, 2, 3, 5, 7, 10, 12, 15, 20, 25, 30, 35 or 40 kg/m³, 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/m³ 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.

342. 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.

343. The method of claim 342 wherein the composition comprises a composition of any one of claims 1 through 302.

344. 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.

345. The method of claim 344 wherein the composition comprises a composition of any one of
5 claims 1 through 302.

346. 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
10 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,
15 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
20 domesticated animals.

347. The method of claim 346 wherein the composition comprises a composition of any one of claims 1 through 302.

25 348. 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
30 (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.

349. The method of claim 348 wherein the composition comprises a composition of any one of
5 claims 1 through 302.

350. 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

10 (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
15 reference soil and plants.

351. The method of claim 350 wherein the composition comprises a composition of any one of
claims 1 through 302.

20 352. 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
25 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
30 preferably 1-150, more preferably 1-100, even more preferably 1-70, yet more preferably 1-50.

353. The composition of claim 352 wherein the microbes comprise microbes of a composition
of any one of claims 1 through 302.

354. 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.
355. 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.
356. The method of claim 355 wherein the composition comprises a composition of any one of claims 1 through 302.
357. 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.
358. The method of claim 357 wherein the composition comprises a composition of any one of claims 1 through 302.

359. 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
5 (ii) providing suitable conditions for plants to grow in the soil for the period of time.
360. The method of claim 358 wherein the composition comprises a composition of any one of
claims 1 through 302.
- 10 361. 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
15 (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.
362. The method of claim 361 wherein the composition comprises a composition of any one of
claims 1 through 302.
20
363. 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
25 (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.
30
364. The method of claim 363 wherein the composition comprises a composition of any one of
claims 1 through 302.
365. A method for increasing uptake of one or more plant nutrients by plants grown in soil
35 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;
5 whereby plant nutrient uptake by the plants is increased.

366. The method of claim 365 wherein the composition comprises a composition of any one of claims 1 through 302.

10 367. 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
15 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.

20 368. The method of claim 367 wherein the composition comprises a composition of any one of claims 1 through 302.

369. A composition comprising a plant comprising
(i) an above-ground portion; and
25 (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.

30 370. 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
35 nutrients for the animal, that is greater than reference plant or plant part

371. A method to convert non-organic agricultural practice to organic agricultural practice comprising

5 (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

10 wherein after the period of time the non-organic agricultural practice has been converted to an organic agricultural practice.

372. The method of claim 371 wherein the composition comprises a composition of any one of claims 1 through 302.

15 373. 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;

20 (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.

25

374. The method of claim 373 wherein the composition comprises a composition of any one of claims 1 through 302.

375. A method of improving one or more characteristics of a tree rooted in soil comprising

30 (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.

376. The method of claim 375 wherein the composition comprises a composition of any one of claims 1 through 302.

5

377. 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.

10

378. The method of claim 377 wherein the composition comprises a composition of any one of claims 1 through 302.

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379. 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.

20

380. The kit of claim 379 wherein the composition comprising microbes comprises a composition of any one of claims 1 through 302.

25

381. A method comprising applying a composition comprising bacterial microbes and fungal microbes to a plurality of tree seedlings and/or growth medium in which the seedlings are located.

30

382. The method of claim 381 wherein the composition comprising bacterial microbes and fungal microbes comprises a composition of any one of claims 203 through 302.