CLAIMS

1. A synthetic composition comprising a plurality of bacterial families and a plurality of particles, wherein the plurality of bacterial families is (i) a co-culture of at least two distinct bacterial families, having differing proliferative conditions, and (ii) comprising at least 30% bacterial families from an origin population of microbiota from which the bacterial families are derived or originated, wherein said plurality of bacterial families comprises at least one bacterial subset of bacteria in the form of biofilm and at least one bacterial subset of planktonic bacteria, and wherein said particles are suitable for biofilm formation.

2. The synthetic composition of claim 1, wherein at least a portion of the plurality of bacterial families originated from the origin population.

3. The synthetic composition of claim 1 or 2, comprising at least one bacterial subset of aerobic bacteria and at least one bacterial subset of anaerobic bacteria.

4. The synthetic composition of any one of claims 1-3, wherein said origin population of microbiota is selected from the group consisting of: a gut microbiota, a saliva microbiota, a skin microbiota, an oral microbiota, a bronchial microbiota, a vaginal microbiota, or a mixture thereof.

5. The synthetic composition of any one of claims 1-3, wherein said plurality of bacterial families is derived from one or more samples selected from the group consisting of: a faecal sample, a saliva sample, a skin sample, an oral sample, a bronchial sample, a vaginal sample, or a mixture thereof.

6. The synthetic composition of any one of claims 1-5, wherein said origin population of microbiota is derived from at least one origin.

7. The synthetic composition of any one of claims 1-6, wherein said plurality of bacterial families is derived from one or more healthy mammal, animal donor, bacterial strain, stored microbiota sample, bacterial colony, planktonic sample, and a biofilm.

8. The synthetic composition of any one of claims 1-7, further comprising a plurality of types of particles.

9. A method for obtaining a composition comprising a co-culture of at least two distinct bacterial families, having differing proliferative conditions, the method comprising the steps of:

a. providing a plurality of bacterial families comprising microbiota from at least one origin;

b. suspending said plurality of bacterial families to receive a bacterial families solution;

c. filtering the plurality of bacterial families solution thereby obtaining a filtrate comprising the plurality of bacterial families;

d. incubating the filtrate with one or more types of particles, and allowing the plurality of bacterial families to attach to the one or more types of particles;

e. dividing the plurality of bacterial families attached to the plurality of particles, into a plurality of bacterial solution subsets;

f. culturing each bacterial solution subset in a growth medium and under proliferative conditions suitable for the proliferative of the individual subset; and

g. removing the growth medium, and recombining the individual subsets;

thereby obtaining the composition comprising a co-culture of at least 2 distinct bacterial families, having differing proliferative conditions.

10. The method of claim 9, wherein said proliferative conditions are selected from the group consisting of: aerobic, anaerobic, and microaerophilic conditions.

11. The method of claim 9, wherein said proliferative conditions are selected from flow, shake, and static conditions.

12. The synthetic composition of claim 1, wherein said origin population of microbiota is the microbiota listed under any one of tables 1, 2, 9, and 11.

13. The method of claim 9, wherein said one or more types of particles comprises particles selected from the group consisting of: particles comprising cellulose fibers, cellulose particles, dicalcium phosphate particles (DCP), seeds, crushed seeds, grains, particles comprising bentonite clay, sand particles, white clay particles, agarose beads, and any combination thereof.

14. The synthetic composition of any one of claims 1-3, wherein said origin population of microbiota is soil microbiota.

15. The synthetic composition of any one of claims 1-3, wherein said plurality of bacterial families is derived from a soil sample.