example, Dodd *et al.* (*Nature*, 2007, 551: 648-652) have proposed FMT as a therapeutic to modulate the levels of aromatic amino acid metabolites in the serum of gnotobiotic mice, which affect intestinal permeability and systemic immunity. In further examples, administration of bacterial compositions have also been proposed as a method for treating *Clostridium difficile* infection, ulcerative colitis, cholestatic disease, and hyperoxaluria.

As a modality for treating various diseases and/or conditions, there is a need for microbial compositions comprising a plurality of microbial species having improved therapeutic efficacy and an ability to efficiently engraft in a host, grow, and metabolize pathogenic substrates to non-pathogenic metabolic products within the various biological niches of the gastrointestinal tract and within the diverse gastrointestinal environments of different individuals. Furthermore, there is an unmet need for a treatment of diseases using a complex microbial community that can engraft and function symbiotically in the human gastrointestinal tract to degradation of a disease-associated metabolic substrate.

SUMMARY OF THE INVENTION

In one aspect, provided herein is a composition comprising: (a) a consortium comprising

(i) *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorirosoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae sp. FBI00191*, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, *Lachnospiraceae sp. FBI00290*, or a functional equivalent thereof; or

(ii) FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102,

FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

(b) a consortium comprising

(i) *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae sp. FBI00097*, *Gordonibacter pamelaeae*, *Bacteroides uniformis*, *Gordonibacter pamelaeae*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae sp. FBI00233*, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof; or

(ii) FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

(c) a consortium comprising

(i) *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*,

Clostridium bolteae, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof; or

(ii) FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof;

(d) a consortium comprising

(i) *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes sp. FBI00180*, *Bacteroides coprocola*, *Alistipes sp. FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof; or

(ii) FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof; or

(e) a combination thereof.

In another aspect, provided herein is a microbial consortium comprising microbial strains set forth in Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, Table 12, Table 13, Table 14, Table 15, Table 16, Table 17, Table 18, Table 19, Table 22, or a functional equivalent thereof, optionally wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

In another aspect, provided herein is a method of manufacturing the composition as described herein, the method comprising:

(a) obtaining a first consortium comprising

(i) *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorirosoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium*

adolescentis, Bifidobacterium catenulatum, Lactobacillus rogosae, Bacteroides faecis, Bacteroides finegoldii, Clostridiaceae sp. FBI00191, Ruminococcus faecis, Lachnoclostridium pacaense, Clostridium bolteae, Longicatena caecimuris, Eggerthella lenta, Blautia massiliensis, Bacteroides xylanisolvens, Bacteroides vulgatus, Megasphaera massiliensis, Butyricimonas faecihominis, Eisenbergiella tayi, Acidaminococcus intestini, Emergencia timonensis, Bifidobacterium pseudocatenulatum, Eubacterium hallii, Anaerofustis stercorihominis, Eubacterium ventriosum, Blautia hydrogenotrophica, Lachnospiraceae sp. FBI00290, or a functional equivalent thereof; or

(ii) FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

(b) obtaining a second consortium comprising

(i) *Acutalibacter timonensis, Alistipes onderdonkii, Bacteroides uniformis, Eubacterium rectale, Alistipes timonensis, Bacteroides kribbi, Coprococcus eutactus, Bilophila wadsworthia, Bacteroides caccae, Alistipes shahii, Parasutterella excrementihominis, Paraprevotella clara, Sutterella wadsworthensis, Sutterella massiliensis, Porphyromonas asaccharolytica, Ruminococcus bromii, Monoglobus pectinilyticus, Ruminococcaceae sp. FBI00097, Gordonibacter pamelaeae, Bacteroides uniformis, Gordonibacter pamelaeae, Bacteroides fragilis, Phascolarctobacterium faecium, Monoglobus pectinilyticus, Clostridium aldenense, Ruthenibacterium lactatiformans, Bacteroides ovatus, Bifidobacterium bifidum, Anaerotruncus massiliensis, Clostridium aldenense, Sutterella wadsworthensis, Catabacter hongkongensis, Alistipes senegalensis, Ruminococcaceae sp. FBI00233, Alistipes shahii, Dielma fastidiosa, Eubacterium siraeum, Faecalibacterium prausnitzii, Turicibacter sanguinis, Eubacterium rectale, Bacteroides caccae, Methanobrevibacter smithii, Barnesiella intestinihominis, Alistipes onderdonkii, Methanobrevibacter smithii,* or a functional equivalent thereof; or

(ii) FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224,

FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

(c) obtaining a third consortium comprising

(i) *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof; or

(ii) FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof

(d) obtaining a fourth consortium comprising

(i) *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes sp. FBI00180*, *Bacteroides coprocola*, *Alistipes sp. FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof; or

(ii) FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof; and

(e) blending the first consortium, the second consortium, the third consortium, and the fourth to thereby obtain the composition.

In another aspect, provided herein is the composition as described herein for use in treating hyperoxaluria, reducing the risk of developing hyperoxaluria, and/or reducing urinary oxalate in a subject in need thereof.

In another aspect, provided herein is use of the composition as described herein in the manufacture of a medicament for treating hyperoxaluria, reducing the risk of developing

hyperoxaluria, and/or reducing urinary oxalate in a subject in need thereof, wherein a first dose of the composition as described herein is to be administered.

The present disclosure relates to compositions and methods for reducing oxalate in a subject. In certain non-limiting embodiments, the present disclosure provides a composition comprising at least 1 oxalate-metabolizing microbial strain. In certain embodiments, the at least one strain expresses an enzyme selected from a formyl-CoA transferase, an oxalate-formate antiporter, and an oxalyl-CoA decarboxylase. In certain embodiments, the at least 1 oxalate-metabolizing microbial strain is from the *Oxalobacter* genus.

In certain embodiments, the composition comprises at least 3 oxalate-metabolizing microbial strains. In certain embodiments, the at least 3 oxalate-metabolizing microbial strains are different strains of the same species. In certain embodiments, the at least 3 oxalate-metabolizing microbial strains are different strains of different species.

In certain embodiments, the species is *Oxalobacter formigenes (O. formigenes),* and optionally wherein the number of oxalate-metabolizing microbial strains is 3 or more.

In certain embodiments:

a) at least one strain is a low pH tolerance strain;

b) at least one strain is a high oxalate tolerance strain; and/or

c) at least one strain is a high growth rate strain.

In certain non-limiting embodiments, the present disclosure provides a composition comprising at least 2 Oxalobacter formigenes (O. formigenes) strains, wherein each of the strains comprises one or more of the following functions: a) a low pH tolerance strain; b) a high oxalate tolerance strain; and/or c) a high growth rate strain.