acidilacti, P. argentenicus, P. claussenii or a combinations thereof.

[0011a] In one example, there is provided a composition of a non-milk food comprising mammalian milk oligosaccharides (MMO) from a human, bovine or caprine source, or the MMO comprises HMO, BMO, BCO, GMO, GOS, FOS, or combinations thereof.

[0011b] In another example, there is provided a composition described herein, comprising a non-milk food and a bacterial culture, wherein the bacterial culture comprises commensal bacteria, the commensal bacteria optionally selected from the species of *Lactobacillus*, *Bifidobacterium*, *Pediococcus* and combinations thereof.

[0011c] In one aspect, the present disclosure refers to a composition comprising a non-milk weaning food and human milk oligosaccharides (HMO), wherein the non-milk weaning food comprises dietary fiber selected from vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof, wherein microbial breakdown of said vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof releases particular free sugar monomers (FSM) extracellularly, said composition further comprises a bacterial culture, wherein the bacterial culture is genetically predisposed to metabolize the particular FSM, and the bacterial culture comprises a bacteria selected from the species of *Lactobacillus*, *Bifidobacterium*, *Pediococcus*, and combinations thereof.

[0011d] In another aspect, the present disclosure refers to the use of a composition as described herein in the manufacture of a medicament for increasing gut microbiome complexity in an infant having a gut microbiome comprising greater than 20% of a single genus of bacteria.

[0011e] In another aspect, the present disclosure refers to the use of the composition as described herein and a bacterial culture in the manufacture of a medicament for combination therapy to increase gut microbiome complexity in a human in need thereof, wherein the composition is in a dry powder form, wherein the bacterial culture comprises bacteria from the genus *Bifidobacterium*, *Lactobacillus*, or combinations thereof, wherein the weaning food comprises carbohydrates which release free sugar monomers that are preferred for consumption by said bacteria.

~~**[0011f]** In another aspect, the present disclosure refers to a method for weaning an infant, said infant having an initial gut microbiome dominated by bacteria particularly adapted to grow on human milk oligosaccharides (HMO), said gut microbiome stabilized by consuming a pre-weaning diet comprising HMO as at least 50% to at least 90% of total dietary fiber in said pre-weaning diet, said method comprising the steps of (a) supplementing the pre-weaning diet with a non-milk weaning food comprising a first non-HMO dietary fiber, wherein the first non-HMO~~

~~dietary fiber constitutes no more than 10% of total dietary fiber in the infant's diet; and (b) after beginning to supplement according to step (a), supplementing the pre-weaning diet with a second non-milk weaning food comprising a second non-HMO dietary fiber, wherein HMO constitutes at least 50% of total dietary fiber in the infant's diet; and (c) further supplementing the infant's diet with additional non-milk weaning foods comprising non-HMO dietary fiber until no more than 10% of total dietary fiber in the infant's diet is made up of HMO, and wherein the non-milk weaning food comprises non-HMO dietary fiber selected from vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof.~~

[0012] Non-milk food, if it contains any dietary fiber, does not provide MMO as the majority of the dietary fiber. Infant formula as marketed today would be considered a non-milk food for the purposes of this disclosure, since it does not include MMO. Preferably, the non-milk food composition contributes a controlled portion of dietary fiber to adapt to the bacterial culture. For example, the non-milk food can contribute about 50%, less than 50%, less than 40%, less than 30%, less than 20%, less than 15%, less than 10%, less than 5%, less than 2.5%, less than 1%, less than 0.5% by weight of the total dietary fiber in the diet, depending on the phase of weaning. In some examples, the non-milk food can contribute more than 50%, more than 55%, more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 95%, more than 99% of the dietary fiber by weight in the composition. Fiber is described herein in grams and their percentages are described herein as percent by weight.

[0013] Preferably, the milk source of the MMO is from a human, bovine, ovine, equine, or caprine source. Preferably, the MMO contributes a controlled portion of dietary fiber. For example, the MMO can contribute more than 50%, more than 55%, more than 60%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 95%, more than 99% by weight of the dietary fiber in the composition, depending on the phase of weaning. In some examples, the non-milk food can contribute about 50%, less than 50%, less than 40%, less than 30%, less than 20%, less than 15%, less than 10%, less than 5%, less than 2.5%, less than 1%, less than 0.5% by weight of the dietary fiber in the composition, depending on the phase of weaning.

[0014] In one example, the non-milk food can contribute about 50%, less than 50%, less than 40%, less than 30%, less than 20%, less than 15%, less than 10%, less than 5%, less than

CLAIMS

1. A composition comprising a non-milk weaning food and human milk oligosaccharides (HMO), wherein the non-milk weaning food comprises dietary fiber selected from vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof, ~~.~~

~~**2.** The composition of claim 1,~~ wherein microbial breakdown of said vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof releases particular free sugar monomers (FSM) extracellularly, said composition further comprises a bacterial culture, wherein the bacterial culture is genetically predisposed to metabolize the particular FSM, and the bacterial culture comprises a bacteria selected from the species of *Lactobacillus*, *Bifidobacterium*, *Pediococcus*, and combinations thereof.

~~**3**~~**2.** The composition of claim 1, wherein the dietary fiber of the composition is at least 10% to 70% HMO.

~~**4**~~**3.** The composition of claim ~~2~~1, wherein the bacterial culture is provided in a dose from 10^7 - 10^{12} cfu.

~~**5**~~**4.** The composition of claim ~~2~~1, wherein the *Bifidobacteria* is selected from *B. longum* subsp *longum*, *B. longum* subsp *infantis*, *B. breve*, *B. pseudocatanulatum*, *B. bifidum*, *B. adolescentis*, *B. pseudolongum*, *and B. animalis*, wherein the *Lactobacillus* is selected from *L. crispatus*, *L. casei*, *L. silivarius*, *L. reuteri*, and *L. plantarum*, and wherein the *Pediococcus* is selected from *P. pentosaceus*, *P. stilesii*, *P. acidilacti*, *P. argentenicus*, and *P. claussenii*.

~~**6**~~**5.** The composition of claim 1, wherein the non-milk weaning food comprises

vegetable fiber comprising complex oligosaccharides from fruits, vegetables, or combinations thereof and/or

meat fiber comprising complex oligosaccharides from meat, eggs, or combinations thereof and/or

fish fiber comprising complex oligosaccharides from fish, shellfish, or combinations thereof and/or

cereal fiber comprising complex oligosaccharides from grains, nuts, seeds or combinations thereof and/or

combinations thereof.

~~7~~**6.** Use of a composition according to claim 1 in the manufacture of a medicament for increasing gut microbiome complexity in an infant having a gut microbiome comprising greater than 20% of a single genus of bacteria.

~~8~~**7.** The use of claim ~~7~~6, wherein the infant is a human.

~~9~~**8.** The use of claim ~~7~~6, wherein the HMO are added to the food such that they represent at least ~~10~~20% to at least 70% of total daily dietary fiber being consumed by the infant.

~~10~~**9.** The use of claim ~~7~~6, wherein the single genus of bacteria comprises *Bifidobacterium longum* subsp. *infantis*.

~~11~~**10.** The composition of claim 1, wherein the non-milk weaning food comprises meat, fish, eggs, shellfish, fruits, vegetables, grains, nuts, seeds, dairy, barley, corn, hummus, lentils, oats, rice, wheat, avocado, beetroot, broccoli, squash, carrots, green beans, peas, potatoes, cassava, sweet potatoes, pumpkin, apples, bananas, plantains, blueberries, mango, peach, pear, papaya, watermelon, cheese, or combinations thereof.

~~12~~**11.** The composition of claim ~~11~~10, wherein the composition comprises bacterial culture and weaning food in a ratio of from 10^6 - 10^{11} cfu of bacterial culture to 100 g of weaning food.

~~13~~**12.** The composition of claim 1, wherein the HMO comprises one or more of neutral HMOs, acidic HMOs, and/or fucosylated oligosaccharides.

~~14~~**13.** The composition of claim ~~13~~12, wherein the HMO comprises one or more of neutral HMOs, acidic HMOs, and fucosylated oligosaccharides, which may be selected from lacto-N-

tetraose (LNT), lacto-N-neotetraose (LNnT), lacto-N-hexaose, 2-fucosyllactose (2FL), 3-fucosyllactose (3FL), difucosyllactose, lacto-N-fucopentaoses I, II, III, and V, sialyllacto-N-tetraose, 3' and 6' sialyllactose (6SL), and 3'-sialyllactosamine, 6'- sialyllactosamine, and 3'-sialyl-3-fucosyllactose.

~~15~~14. The composition of claim 1, wherein the HMO comprises oligosaccharides that provide selective growth of *B. longum* subsp. *infantis*.

~~16~~15. Use of the composition of claim 1 and a bacterial culture in the manufacture of a medicament for combination therapy to increase gut microbiome complexity in a human in need thereof, wherein the composition is in a dry powder form, wherein the bacterial culture comprises bacteria from the genus *Bifidobacterium, Lactobacillus*, or combinations thereof, wherein the weaning food comprises carbohydrates which release free sugar monomers that are preferred for consumption by said bacteria.

~~17. A method for weaning an infant, said infant having an initial gut microbiome dominated by bacteria particularly adapted to grow on human milk oligosaccharides (HMO), said gut microbiome stabilized by consuming a pre-weaning diet comprising HMO as at least 50% to at least 90% of total dietary fiber in said pre-weaning diet, said method comprising the steps of~~

~~(a) supplementing the pre-weaning diet with a non-milk weaning food comprising a first non-HMO dietary fiber, wherein the first non-HMO dietary fiber constitutes no more than 10% of total dietary fiber in the infant's diet; and~~

~~(b) after beginning to supplement according to step (a), supplementing the pre-weaning diet with a second non-milk weaning food comprising a second non-HMO dietary fiber, wherein HMO constitutes at least 50% of total dietary fiber in the infant's diet; and~~

~~(c) further supplementing the infant's diet with additional non-milk weaning foods comprising non-HMO dietary fiber until no more than 10% of total dietary fiber in the infant's diet is made up of HMO, and~~

~~wherein the non-milk weaning food comprises non-HMO dietary fiber selected from vegetable fiber and/or meat fiber and/or fish fiber and/or cereal fiber and/or combinations thereof.~~

~~**18.** The method of claim 17, wherein microbial breakdown of the first non-HMO dietary fiber releases particular free sugar monomers (FSM) extracellularly, while administering to the infant a first bacteria which prefer the particular FSM as a carbon source for growth, wherein microbial breakdown of the second non-HMO dietary fiber releases a second particular FSM extracellularly, while administering to the infant a second bacteria which prefer the second particular FSM as a carbon source for growth.~~

~~**19.** The method of claim 17, wherein the infant having an initial gut microbiome has 10^8cfu/g stool or greater of one species of bacteria.~~

~~**20.** The method of claim 17, wherein the initial gut microbiome has greater than 20% of a single genus of bacteria.~~

~~**21.** The method of claim 20, wherein the single genus is *Bifidobacterium*.~~