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DESCRIPTION

Description

TECHNICAL FIELD

[0001] The present invention belongs to the field of human and/or animal nutrition and health. The present invention, which is defined by the claims, particularly relates to a yeast product for use as a prebiotic agent, and a composition comprising it. It also relates to the non-therapeutic use of a yeast product, and a composition comprising it, as a prebiotic agent. The yeast product, and the composition comprising it, stimulate the growth of bacteria of the *Bacteroidetes* phylum in the mammal gut microbiota, independently from the initial microbial composition of the donor and enterotype.

TECHNICAL BACKGROUND

[0002] Non-digestible oligosaccharides (NDOs) resist digestion and absorption in the human small intestine, so that they are completely or partially fermented in the large intestine. These carbohydrates help to maintain regularity of colonic functioning and may contribute to human health by reducing the risk of chronic diseases. A lot of NODs are considered to be prebiotic agents.

[0003] The activity of a prebiotic agent on the mammal gut microbiota, particularly the human gut microbiota, can be evaluated on the basis of the growth of health-promoting bacteria such as Lactobacilli and Bifidobacteria, the decrease in intestinal pathogens and the increase or decrease in production of health-related bacterial metabolites. The latter include for instance straight short-chain fatty acids (SCFAs), such as acetate, propionate and butyrate, which are generally believed to be positive for colonic health, while ammonia and branched SCFAs are regarded as risk factors for colon carcinogenesis.

[0004] However, Lactobacilli and Bifidobacteria are two genera only constituting a minor group within the gut microbiome, particularly the human gut microbiota. They have received a lot of attention due to the initial definition of a prebiotic compound that mentioned that prebiotic compounds should selectively be fermented by specific bacterial groups including Bifidobacteria and Lactobacilli, thus resulting in potential health-promoting effects. As a result of this narrow definition, many of the initial studies focusing on prebiotic effects of novel fibres have been applying a targeted approach focusing on these two groups, thus neglecting the potential effect of prebiotics on a large amount of other gut microorganisms.

[0005] The gut microbiota comprises a huge diversity of microorganisms. For example, bacteria of the phyla *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* are present in the gut microbiota. The growth of some of these bacteria has proven beneficial, as they would promote a healthy fermentation and particularly increase the production of short chain fatty acids (SCFAs) such as acetate, propionate and butyrate.

[0006] Compositions comprising cell wall material from yeast and their uses are disclosed in e.g., US 2017/080015 A1 and WO 2005/021015 A1.

[0007] There is therefore a need for providing new prebiotic agents suitable for stimulating mammal gut microbiota, and particularly for stimulating the growth of bacteria of the *Bacteroidetes* phylum.

SUMMARY OF THE INVENTION

[0008] It is a first object of the invention, which is defined by the claims, to provide a yeast product, or a composition comprising it, for use as a prebiotic agent for stimulating the growth of bacteria of the *Bacteroidetes* phylum, in the mammal gut microbiota; wherein the yeast product comprises a soluble sub-fraction of the walls of yeast cells or a fraction thereof. According to the invention, said soluble sub-fraction is obtained by submitting whole yeast cells to a disruption treatment, separating a soluble fraction from an insoluble fraction, then treating the insoluble fraction with ribonucleases and glucanases, before separating a protein-rich insoluble sub-fraction from a soluble sub-fraction; or by submitting whole yeast cells to a disruption treatment, then treating the mixture obtained with ribonucleases and glucanases, before separating a protein-rich insoluble sub-fraction from a soluble sub-fraction.

[0009] In some embodiments, the yeast product, or a composition comprising it, is selected from the group consisting of the genera *Saccharomyces*, *Pichia*, *Candida*, *Kluyveromyces*, *Yarrowia* and/or *Wickehomomyces*; preferably wherein the yeast is selected from the group consisting of the species *Saccharomyces cerevisiae*, *Pichia jadinii*, *Kluyveromyces marxianus*; more preferably wherein the yeast is *Saccharomyces cerevisiae*.

[0010] In some embodiments, the bacteria of the *Bacteroidetes* phylum are bacteria of the *Bacteroidia* class; preferably bacteria of the *Bacteroidales* order; more preferably bacteria of the *Bacteroidaceae* family; still more preferably bacteria of the *Bacteroides* genus; most preferably *Bacteroides ovatus* spp.

[0011] In some embodiments, the yeast product increases the ratio of the bacteria of the *Bacteroidetes* phylum versus the bacteria of the *Firmicutes* phylum in the mammal gut microbiota.

[0012] In some embodiments, the prebiotic agent is selected from the group consisting of

deactivated whole yeasts, yeast cell walls, fractions of the yeast cell walls, or mixtures thereof; preferably the prebiotic agent is selected from the group consisting of yeast cell walls, their fractions, or mixtures thereof.

[0013] In some embodiments, the disruption treatment is a thermal plasmolysis.

[0014] In some embodiments, the yeast product has a β -glucan content (expressed as equivalent mass of glucose) from 15 to 50% by mass on a dry matter basis; and/or a mannan content (expressed as equivalent mass of mannose) from 10 to 40% by mass on a dry matter basis

[0015] In some embodiments, the yeast product does not stimulate the growth of bacteria of the *Bifidobacterium* genus; preferably bacteria of the *Bifidobacteriaceae* family; more preferably bacteria of the *Bifidobacteriales* order.

[0016] In some embodiments, the yeast product does not stimulate the growth of bacteria of the *Lactobacillus* genus; preferably bacteria of the *Lactobacillaceae* family; more preferably bacteria of the *Lactobacillales* order.

[0017] In some embodiments, the yeast product, or the composition comprising it, is administered orally; preferably wherein the yeast product, or the composition comprising it, is administered orally at a daily dose from 500mg to 15g; preferably wherein the yeast product, or the composition comprising it, is administered orally at a daily dose from 500mg to 5g in up to 10 takings.

[0018] In some embodiments, the composition is formulated as a gum, a tablet, a capsule, a pill, a powder, granules or a suspension.

[0019] The above yeast product, or a composition comprising it, may also be for use for preventing or limiting gut pathologies such as diarrheas and irritable bowel syndrome, for stimulating immunity, for regulating glycemia and/or lipidemia, for treating or limiting metabolic disorders associated to obesity.

[0020] It is a third object of the invention to provide the non-therapeutic use of the yeast product defined above, or a composition comprising it, as defined herein, as a prebiotic agent for stimulating the growth of bacteria of the *Bacteroidetes* phylum in the mammal gut microbiota; wherein the yeast product is the above-defined soluble sub-fraction of the walls of yeast cells or a fraction thereof.

[0021] In some embodiments, the composition is a foodstuff or a food supplement; preferably a dairy product, a fruit-based product, a drink, a solid foodstuff or a food supplement.

[0022] The present invention, which is defined by the claims, makes it possible to address the need of the prior art. In particular, the invention provides a yeast product, or a composition

comprising it, for stimulating the growth of bacteria of the *Bacteroidetes* phylum in the mammal gut microbiota. By "*stimulating the growth*" is meant increasing the population of bacteria of the *Bacteroidetes* phylum in the mammal gut microbiota and/or increasing its relative abundance versus other bacteria.

[0023] The yeast product comprises the walls of yeast cells or a fraction thereof. The yeast product, or the composition comprising it, is therefore suitable for use as a prebiotic agent. By "*prebiotic agent*" is meant a non-digestible or non-fully digestible food product that beneficially affects the host by selectively stimulating the growth and/or activity of one or a limited number of beneficial bacteria in the colon, thereby improving host health. Prebiotic agents differ from probiotic agents in that the prebiotic agent is not a living organism.

[0024] The inventors have shown that yeast, especially *Saccharomyces cerevisiae* or its derivatives, regulates the gut microbiota, particularly by stimulating the growth of bacteria of the *Bacteroidetes* phylum, such as bacteria of the *Bacteroides* genus. It has therefore been demonstrated that yeast products have a prebiotic potential on the gut microbiota, by positively and selectively impacting both its metabolism and its composition. This prebiotic potential is particularly beneficial for preventing or limiting gut pathologies such as diarrheas and irritable bowel syndrome, for stimulating immunity, for regulating glycemia and/or lipidemia, for treating or limiting metabolic disorders associated to obesity (e.g. glucose tolerance and fatty liver disease).

DESCRIPTION OF EMBODIMENTS

[0025] The invention will now be described in more detail without limitation in the following description.

[0026] In a first aspect, the present invention relates to a yeast product as defined by the claims, or a composition comprising it, for use as a prebiotic agent for stimulating the growth of bacteria of the *Bacteroidetes* phylum, in the mammal gut microbiota. In a second aspect, the present invention relates to the non-therapeutic use of a yeast product as defined by the claims, or a composition comprising it, for use as a prebiotic agent for stimulating the growth of bacteria of *Bacteroidetes* phylum in the mammal gut microbiota.

[0027] In some embodiments, the mammal is a human.

[0028] In other embodiments, the mammal is an animal.

[0029] The therapeutic and non-therapeutic uses of the yeast product depend on the subject to whom or which it is administered.

[0030] If the subject is healthy, the yeast product may be administered for maintaining the well-being of the subject and for facilitating the functioning of the gastrointestinal tract. The yeast

product may be used non-therapeutically e.g. as a food supplement, e.g. for preserving digestive comfort.

[0031] If the subject is affected or is at a risk of being affected by gastrointestinal disorders or any related condition, the yeast product may be administered for preventing, treating or limiting such disorders, and for restoring or preserving the normal functioning of the gastrointestinal tract. The yeast product may then be used therapeutically and be formulated as a pharmaceutical composition.

[0032] The yeast product comprises the walls of yeast cells or a fraction thereof. The inventors have shown that yeast cell walls or fractions thereof are particularly advantageous.

[0033] The yeast may be selected from the group consisting of the genera *Saccharomyces*, *Pichia*, *Candida*, *Kluyveromyces*, *Yarrowia* and/or *Wickehomomyces*; preferably from the group consisting of the species *Saccharomyces cerevisiae*, *Pichia jadinii*, *Kluyveromyces marxianus*. More preferably, the yeast is *Saccharomyces cerevisiae* spp.

[0034] The yeast may in particular be baker's yeast and/or brewer's yeast.

[0035] Yeast comprises a cytoplasm surrounded by a cell membrane. The cytoplasm comprises intracellular compartments, including the nucleus, mitochondrion and Golgi. The cell membrane is surrounded by the cell wall. The space in-between the cell membrane and the cell wall forms the periplasma.

[0036] The yeast product may be selected from the group consisting of deactivated whole yeast, yeast cell walls, fractions of yeast cell walls, or mixtures thereof.

[0037] The yeast product such as the yeast cell walls is obtained using conventional disruption treatments. Upon application of a disruption treatment, an insoluble fraction of yeast cells is obtained, which comprises the yeast cell walls. The disruption treatment may be a biochemical treatment and/or a mechanical treatment. The mechanical disruption may be obtained using glass beads, pressurized homogenization, ultrasounds or microwaves. The biochemical treatment may be selected from the group consisting of autolysis, thermal plasmolysis, enzymatic hydrolysis, osmotic shock and/or repeated cycles of freezing-thawing.

[0038] Lynside[®] Wall Basic is an example of commercially available yeast cell wall product suitable for implementing the claimed invention. Lynside[®] Wall Basic comprises from about 20% to about 29% β -1,3/1,6-glucans, from about 18% to about 25% mannans, and has a dry matter of at least 94%, by total weight of the product. The nutrient content of Lynside[®] Wall Basic is as follows: from about 10.0% to about 31.2% of protein, from about 10% to about 25% of lipids, from about 38% of total carbohydrate and from about 3% to about 9% of ash, by total weight of the product.

[0039] Methods for obtaining yeast cell walls or fractions thereof are known. For example, European application EP2170359, PCT application WO2005/021015 and PCT application WO2009/013357 disclose yeast products comprised of yeast cell walls, comprising specific total glucan and mannan dry matter content by weight, and a specific glycogen dry matter content by weight.

[0040] In one embodiment, the yeast product may be a soluble sub-fraction obtained by submitting whole yeast cells to a thermal plasmolysis, then treating the mixture obtained with ribonucleases and glucanases, before separating the protein-rich insoluble sub-fraction from the soluble sub-fraction.

[0041] In one embodiment, the yeast product may be a soluble sub-fraction obtained by submitting whole yeast cells to a thermal plasmolysis, then separating the insoluble fraction from the soluble fraction, then treating the insoluble fraction obtained with ribonucleases and glucanases, before separating the protein-rich insoluble sub-fraction from the soluble sub-fraction.

[0042] Methods for obtaining such protein-rich insoluble sub-fractions are disclosed in the unpublished French application 1853748 filed on 27th April 2018.

[0043] The protein-rich insoluble sub-fraction comprises less than 3% of nucleotides and at least 72% of proteins. The final soluble sub-fraction comprises from 45 to 70% of carbohydrates by total weight of the soluble fraction. The carbohydrates comprise from 25 to 40% glucans and from 25 to 35% mannans by total weight of the carbohydrates. The soluble sub-fraction may also comprise nucleotides, when a treatment step with deaminases is carried out.

[0044] The thermal plasmolysis may be carried out at a temperature of at least 45°C, preferably between 70 and 95°C during a time period according to those skilled in the art, preferably from 30 sec to 4 h, still preferably from 1 min to 3 h, more preferably from 40 min to 2 h. The step of treatment with ribonucleases and glucanases may be carried out at a temperature between 40 and 65°C, preferably 60°C, and during a time period from 8 to 24 h; preferably 18 h.

[0045] The step of treatment with ribonucleases and glucanases may also be carried out in the presence of deaminases.

[0046] The step of separating the protein-rich insoluble sub-fraction from the soluble sub-fraction can be carried out in ethanol, a solvent or supercritical CO₂ in order to eliminate lipids and increase the proportion of proteins.

[0047] The preparation of the yeast product may comprise a drying step, such as spray-drying, vacuum-drying, fluidized-bed drying, drum-drying and/or freeze-drying.

[0048] In some embodiments, the yeast product is preferably free of yeast cell membrane, yeast cytoplasm and cellular compartments, their derivatives, or mixtures thereof.

[0049] The yeast product is not a yeast extract and does not comprise such a yeast extract. A yeast extract is the soluble fraction directly obtained by submitting whole yeast cells to a disruption treatment, such as a biochemical treatment and/or a mechanical treatment.

[0050] The yeast product is not a live whole yeast, such as instant dry yeast or active dry yeast.

[0051] Preferably, the yeast product comprises glucans.

[0052] The yeast product, and preferably the yeast cell walls or yeast cell wall derivative, may have a β -glucan content (expressed as equivalent mass of glucose) from 15 to 50%, preferably from 20 to 40%, more preferably from 20 to 30%, by mass on a dry matter basis.

[0053] Preferably, the glucan comprises β -1,3-glucans, β -1,6-glucans, or combinations thereof.

[0054] Preferably, the yeast product comprises mannans, either in a free form or in the form of mannoprotein complexes.

[0055] The yeast product, and preferably the yeast cell walls or yeast cell wall fraction, may have a mannan content (expressed as equivalent mass of mannose) from 10 to 40%, preferably from 15 to 30%, more preferably from 18 to 25%, by mass on a dry matter basis.

[0056] The yeast product, and preferably the yeast cell walls or yeast cell wall fraction may have a dry matter content of at least 90%, preferably of at least 95%, more preferably of 98%, by mass.

[0057] The prebiotic potential of the yeast product according to the invention may e.g. be assessed using an *in vitro* short-term model simulating the fermentation in the human proximal colon.

[0058] A suitable model is the continuous Simulator of the Human Microbial Ecosystem, known as SHIME[®], which has been used for many years and validated with *in vivo* parameters, and which consists of five sequential reactors modelling the stomach, the small intestine, and the three colon compartments (ascending, transverse and descending). Simplified versions have also been developed.

[0059] In vitro short-term simulation model allows establishing and testing representative microbial communities, which differ both in the composition and functionality in the different colon regions. The potential of a prebiotic agent on the metabolism of the gut microbiota may be assessed by monitoring and measuring different parameters relative to the overall microbial fermentation, the changes in microbial activity and the changes in the microbial community

composition.

[0060] The overall microbial fermentation may be monitored by measuring the pH and gas production. The changes in microbial activity may be assessed by comparing the kinetics in the production of bacterial metabolites (including SCFAs and lactate). The changes in the microbial community composition may be assessed by quantifying specific bacterial sequences (16S rRNA genes) through amplification (targeted qPCR and 16S-based Illumina sequencing).

[0061] Monitoring the pH during a colonic incubation provides a good indication of the production of SCFA, lactate. In general, a pH drop is observed during the first 24 h of incubation due to the formation of SCFA and lactate. This pH drop is often followed by a pH increase during the next 24 h of incubation due to proteolytic fermentation.

[0062] Gas production is a good measure for overall microbial activity, and thus speed of fermentation.

[0063] SCFA production results from carbohydrate metabolism in the colon and is related with various health effects. The most abundantly produced SCFAs consist of acetate, propionate and butyrate. Whereas acetate can be used as an energy source for the host and as a potential substrate for lipid synthesis in the body, propionate reduces cholesterol and fatty acid synthesis in the liver (beneficial effect on metabolic homeostasis). Butyrate on the other hand, is a major energy source for colonocytes and induces differentiation in these cells (related to cancer prevention) as well as a modulator of the immune response in the gut mucosa (related to an increase in regulatory T cells' number). The total SCFA levels are reflective of the overall fermentation of test ingredients.

[0064] In some embodiments, the yeast product of the present invention stimulates the growth of bacteria of the *Bacteroidetes* phylum in the mammal gut microbiota independently from the initial microbial composition of the donor and enterotype. The yeast product may stimulate the growth of bacteria of the *Bacteroidia* class; preferably bacteria of the *Bacteroidales* order; more preferably bacteria of the *Bacteroidaceae* family; still more preferably bacteria of the *Bacteroides* genus; most preferably *Bacteroides ovatus* spp.

[0065] In some embodiments, the yeast product does not stimulate the growth of bacteria of the *Bifidobacteriales* order; preferably bacteria of the *Bifidobacteriaceae* family; more preferably bacteria of the *Bifidobacterium* genus. Likewise, the yeast product may not stimulate the growth of bacteria of the *Lactobacillales* order; preferably bacteria of the *Lactobacillaceae* family; more preferably bacteria of the *Lactobacillus* genus.

[0066] In some embodiments, the yeast product increases the ratio of the bacteria of the *Bacteroidetes* phylum versus the bacteria of the *Firmicutes* phylum. It has been reported that the *Bacteroidetes* versus *Firmicutes* ratio is higher in lean subjects as compared to obese ones. Furthermore, increase in this ratio has been associated in prevention of obesity related disorders (weight gain, glucose intolerance or fatty liver disorders).

[0067] The yeast product may be administered orally. The yeast product may be administered at a daily effective dose, for example at a daily dose from 500mg to 15g. The daily effective dose may be administered up to ten takings, for example one, two, three, four or more takings. The yeast product may be administered as such or in a composition, in a form more suitable for oral administration.

[0068] The composition may be a pharmaceutical composition. The pharmaceutical composition may comprise any suitable pharmaceutically acceptable carrier or excipient. The pharmaceutical composition may further comprise one or more pharmaceutical active agents.

[0069] The composition may also be a foodstuff and/or food supplement. The composition may be a dairy product, a fruit-based product, a drink, a solid foodstuff or any other suitable edible product. The composition may be a nutraceutical composition, a dietary supplement or any other suitable food supplement.

[0070] The composition may be a liquid, a paste or a solid composition.

[0071] The composition may comprise one or more additional components. The additional components may be vitamins (for example A, C, D, E, K, B1, B2, B3, B5, B6, B8, B9, B12 or mixtures thereof), minerals (for example calcium, phosphorus, sodium, magnesium, iron or mixtures thereof).

[0072] The composition is preferably free of yeast extract.

[0073] The composition is preferably free of a live whole yeast, such as instant dry yeast or active dry yeast.

[0074] The yeast product may be formulated as a tablet, a capsule, a pill, a powder, a gum, granules or a suspension. If formulated as a powder or granules, the prebiotic agent, or the composition comprising it, may be packaged in a sachet or any suitable alternative packaging.

EXAMPLES

[0075] The following examples illustrate the invention without limiting it.

Example 1 - In vitro assessment of prebiotic potential of a yeast cell wall fraction

[0076] Summary - The enrichment of microorganisms from six representative microbiomes was studied, from a representative set of donors selected according to the donor stratification in enterotype (Arumugam M, et al. (2011) Enterotypes of the human gut microbiome. Nature 474(7353):666-666; Costea PI, et al. (2018) Enterotypes in the landscape of gut microbial

community composition. Nat Microbiol 3(1):8-16.), on minimal media supplemented with Lynside® Wall Basic. Diluted fecal slurries were selectively enriched on medium supplemented with Lynside® Wall Basic using strict anaerobic culture techniques. Cultivation was performed for 48h in order to allow growth on the complex substrate. Metabolite production and changes in microbiome composition after 48h of enrichment were analyzed and compared to non-selective enrichments and a non-supplemented minimal medium in order to identify functional groups predictive for response to the tested fiber substrate.

Prebiotic agent - Lynside® Wall Basic

[0077] Preparation of the inoculum - Fresh fecal samples from six donors representative of the three described enterotypes (i.e. *Ruminococcus*, *Prevotella* and *Bacteroides*) were used as inoculum for substrate utilization experiments. Two aliquots of 200 g were collected for each fresh fecal sample, 978 µL of 50 mM EDTA solution was added to each aliquot for stabilization and the aliquots were stored at -20°C for subsequent extraction and microbiota profiling. Two aliquots of 1 mL of the 1:10 diluted fecal slurry used for inoculation were collected and centrifuged at 16000 g for 5', the supernatant was removed, 978 µL of 50 mM EDTA solution were added to the pellet for protection and the pellet was stored at -20°C.

[0078] Substrate enrichment - Experiments starting from fecal sample dilutions of the six donors were performed in triplicates in M2-based minimal medium with and without Lynside® Wall Basic supplementation and in broth M2GSC medium (Miyazaki K, Martin J., Marinsek-Logar R, Flint H. (1997) Degradation and Utilization of Xylans by the Rumen Anaerobe *Prevotella bryantii* (formerly *P. ruminicola* subsp. *brevis*) B14. Anaerobe 3(6):373-381), resulting in 54 enrichments. Enrichments were performed for 48 h at 37°C. From each enrichment, 1 mL of culture was centrifuged at 16000 g for 5', the supernatant was removed, 978 µL of 50mM EDTA solution was added to the pellet for stabilization and the pellet was stored at -20°C.

[0079] SCFA analysis - The SCFA analysis is an assessment of the microbial carbohydrate metabolism i.e. the relative metabolite concentration after 48 h of incubation of acetate, propionate and butyrate.

[0080] Metabolic profiles of the six fecal samples and supernatants with and without Lynside® Wall Basic supplementation were determined by high performance liquid chromatography (HPLC). HPLC analysis was performed with a Hitachi LaChrome device (Merck, Switzerland) using a SecurityGuart™ Carbo-H+ cartridge (4 × 32 mm) connected to a Resex™ ROA-Organic Acid H+ (8 %) column (300 × 7.8 mm). Analysis was carried out with an injection volume of 40 µL, at a temperature of 80 °C and with a flow rate of 0.6 mL/min. H₂SO₄ (10 mM) containing sodium azide (0.005%) was used as eluent. Metabolite concentrations were quantified by refractive index (RI) detection. The detection limits (mM) for the three analytes were as follows:

2.06 mM for acetate, 1.61 mM for propionate and 1.55 mM for butyrate. The quantification limits (mM) for the three analytes were as follows: 6.23 mM for acetate, 4.89 mM for propionate and 4.69 mM for butyrate.

[0081] Results of the SCFA analysis - The SCFA concentrations obtained are shown in table 1 below:

Table 1

Spl	Tr	L	ΔA	ΔP	ΔB	Spl	Tr	L	ΔA	ΔP	ΔB
D1	#1	w/	14,16	6,83	5,08	D1	#1	w/o	8,05	1,86	2,70
D1	#2	w/	14,24	6,36	4,83	D1	#2	w/o	7,17	0,96	4,75
D1	#3	w/	15,36	6,95	6,27	D1	#3	w/o	8,52	1,83	4,54
D2	#1	w/	11,73	1,64	2,77	D2	#1	w/o	8,13	1,45	2,56
D2	#2	w/	8,45	2,32	2,31	D2	#2	w/o	5,82	2,00	4,69
D2	#3	w/	9,93	3,33	2,42	D2	#3	w/o	6,89	1,47	2,89
D3	#1	w/	14,52	5,67	5,41	D3	#1	w/o	8,34	0,66	3,23
D3	#2	w/	14,34	3,54	6,44	D3	#2	w/o	8,91	1,58	3,32
D3	#3	w/	15,67	1,93	5,22	D3	#3	w/o	9,37	1,43	2,76
D4	#1	w/	11,18	2,61	4,95	D4	#1	w/o	6,64	0,63	1,85
D4	#2	w/	10,61	1,96	7,21	D4	#2	w/o	6,50	0,76	3,75
D4	#3	w/	9,83	5,42	6,78	D4	#3	w/o	5,41	1,09	4,38
D5	#1	w/	9,07	5,79	9,64	D5	#1	w/o	7,14	1,48	1,74
D5	#2	w/	9,22	8,82	7,86	D5	#2	w/o	6,72	0,75	1,11
D5	#3	w/	11,92	8,03	6,45	D5	#3	w/o	7,47	0,94	1,62
D6	#1	w/	8,84	0,93	2,44	D6	#1	w/o	6,30	3,48	3,41
D6	#2	w/	11,72	0,97	5,11	D6	#2	w/o	6,01	0,95	3,88
D6	#3	w/	9,36	1,64	5,44	D6	#3	w/o	6,38	3,82	3,25

Note - "Spl" for donor sample (amongst 6); "Tr" for the number of the test for each donor (made in triplicate); "w/L" or "w/o L" for tests carried out with and without Lynside® Wall Basic supplementation; " ΔA " for the acetate concentration (mM); " ΔP " for the propionate concentration (mM); and " ΔB " for the butyrate concentration (mM).

[0082] DNA microbial extraction - Extraction of microbial DNA was performed for one frozen aliquot from fresh fecal samples of each donor, one pellet of the 1:10 dilution of the fecal matter, and for all pellets collected from the enrichment experiments. Microbial DNA was extracted using the FastDNATM SPIN Kit for Soil (MP Biomedicals, USA) as indicated by the producers. Quality of DNA extracts was confirmed on a TAE- 1.5% agarose gel, and the concentration of total DNA of the extracted samples was determined by dsDNA Qubit assay

using a Tecan Spark M10 multimode plate reader.

[0083] 16S rRNA gene amplicon sequencing - Microbial composition was determined by 16S rRNA gene amplicon sequencing of the V3V4 region. Sequencing was performed on the MiSeq (Illumina, USA) platform using the MiSeq v3 paired-end reagent kit obtaining ca. 7 Mio. good quality stitched reads (average 17k reads per sample, and average 51k per treatment) of about 450 bp length.

[0084] Bioinformatic processing - The raw reads were trimmed, merged and quality filtered. Operational taxonomic units (OTU) picking was performed using the denoising algorithm `unoise3` (cf. Edgar RC (2016) UNOISE2: improved error-correction for Illumina 16S and ITS amplicon sequencing. *bioRxiv*:81257). A first taxonomic classification of the obtained OTUs was performed using the Human intestinal tract database (HITdb - Ritari J, Salojärvi J, Lahti L, de Vos WM (2015) Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. BMC Genomics 16(1):1056) with a final manual refinement using a phylogenetic tree with the HITdb and the obtained 881 OTUs (with no singletons).

[0085] Results - Next generation sequencing of the 16S rRNA gene amplicon of the V3V4 variable regions was performed on the total bacterial DNA of the fecal samples.

[0086] The key objective was to identify the phylogenetic taxa selectively promoted by the studied substrate Lynside® Wall Basic. Therefore, all sequenced samples were categorized into three experimental groups: (1) Donor samples, including fecal samples from the six donors and a 1:10 dilution, respectively; (2) Lynside samples, composed of all samples from enrichments in minimal medium supplemented with the test substrate Lynside® Wall Basic; and (3) Negative control enrichments in minimal medium without substrate supplementation.

[0087] In a cross-comparison including all samples, a linear discriminant analysis (LDA - Segata N, et al. (2011) Metagenomic biomarker discovery and explanation. Genome Biol 12(6):R60) was performed to identify the phylogenetic taxa significantly ($LDA \geq 2$) enriched in either one of the three experimental groups as compared to all other groups. LDA scores revealed that enrichments in medium supplemented with the studied substrate Lynside® Wall Basic showed a significant increase of phylogenetic taxa belonging to the phylum *Bacteroidetes* by up to four orders of magnitude. The promotion of representatives within the phylum of *Bacteroidetes* upon Lynside® Wall Basic supplementation was observed in all donors, independently of their enterotype or initial *Bacteroidetes* abundance.

[0088] The LDA scores obtained are shown in table 2 below:

Table 2

Sample	Phylogenetic taxa	LDA score	p-value
With Lynside®	<i>Bacteria</i> > <i>Bacteroidetes</i>	4,9	3,60 ⁻¹⁰
With Lynside®	<i>Bacteria</i> >> <i>Bacteroidia</i>	4,9	3,60 ⁻¹⁰

Sample	Phylogenetic taxa	LDA score	p-value
With Lynside®	<i>Bacteria >>> Bacteroidales</i>	4,9	3,60 ⁻¹⁰
With Lynside®	<i>Bacteria >>>> Bacteroidaceae</i>	4,8	2,51 ⁻¹⁰
With Lynside®	<i>Bacteria >>>>> Bacteroides</i>	4,8	2,51 ⁻¹⁰
With Lynside®	<i>Bacteria >>>>>> Bacteroides_uniformis</i>	4,1	7,91 ⁻¹⁰
With Lynside®	<i>Bacteria >>>>>> Bacteroides_faecis</i>	4,1	1,23 ⁻¹⁰
With Lynside®	<i>Bacteria >>>>>> Bacteroides_xylanisolvens</i>	3,8	5,39 ⁻¹⁰
With Lynside®	<i>Bacteria >>>>>> Bacteroides_ovatus</i>	3,6	9,74 ⁻¹⁰
Negative control	<i>Bacteria >>>>>> Bacteroides_Species</i>	3,9	4,02 ⁻¹⁰
Negative control	<i>Bacteria >>>>>> Bacteroides_vulgatus</i>	3,6	4,35 ⁻¹⁰
Negative control	<i>Bacteria >>>>>> Bacteroides_salyersiae</i>	2,8	4,02 ⁻¹⁰
Donor	<i>Bacteria >>>>>> Bacteroides_cellulosilyticus</i>	2,8	1,60 ⁻¹⁰
Donor	<i>Bacteria >>>>>> Bacteroides_caccae</i>	2,4	9,11 ⁻¹⁰
Note - The phylogenetic taxa are as follows <i>Bacteria > Bacteroidetes > Bacteroidia > Bacteroidales > Bacteroidaceae > Bacteroides > Bacteroides species</i>			

[0089] A significant and selective enrichment of substrate degraders present in the stool samples of all six studied donors in medium supplemented with the test substrate Lynside® Wall Basic was shown. Minor variations in metabolite composition were observed between donors, whereas no enterotype dependent pattern was observed. The results of next generation sequencing revealed a clear pattern with the enrichment of a clearly defined phylogenetic taxon, *Bacteroidetes*, in media supplemented with the test substrate Lynside® Wall Basic. Moreover, *Bacteroidetes* presented the best performance independently from the initial microbial composition of the donor, indicating the need for a complex set of enzymes for degradation of the substrate. These results demonstrate that Lynside® Wall Basic, which is a yeast cell wall product, stimulates the growth of bacteria of the *Bacteroidetes* phylum, such as bacteria of the *Bacteroides* genus, in the human gut microbiota.

Example 2

[0090] Prebiotic agent- Two materials were tested i.e. AGENT #1; and AGENT #2. Both

materials are protein-rich insoluble sub-fractions obtained after disruption treatment and then treatment with ribonucleases and glucanases, according to the method disclosed in the unpublished French application 1853748 filed on 27th April 2018. Both materials comprise 34.0 wt% total glucans (including 31.0 wt% β -glucans), and 31.0 wt% mannans. They have different particle sizes.

[0091] Nutritional medium - The nutritional medium is a sugar-depleted nutritional medium containing basal nutrients present in the colon (e.g. host-derived glycans such as mucin).

[0092] Dose - The prebiotic agents were tested at an optimal dose of 5 g/L, and against a blank (negative control).

[0093] Inoculum - As a source of the colonic microbiota, a freshly prepared human fecal inoculum was added.

[0094] Incubations - Incubations were performed for 48 h at 37°C, under shaking (90 rpm) and anaerobic conditions. This procedure allowed to assess the specific effect of test ingredients on the metabolic and community composition profile of the colonic microbiota.

[0095] Parameters measured - Different aspects were monitored, i.e. overall microbial fermentation (pH and gas production), changes in microbial activity to compare the kinetics in the production of bacterial metabolites (short-chain fatty acids or SCFAs, and lactate analysis), and changes in the microbial community composition (targeted qPCR and 16S-based illumina sequencing).

[0096] pH - The degree of acidification during the experiment is a measure for the intensity of bacterial metabolism of the potential prebiotic (fermentation). The pH of the incubations was determined at 0, 3, 6, 24 and 48 h after starting the incubation, thus giving a rough indication of the speed of fermentation of the different fiber blends.

[0097] Gas production - The colon incubations were performed in closed incubation systems. This allowed to evaluate the accumulation of gas in the headspace, which can be measured with a pressure meter. Gas production is a measure of microbial activity, and thus of the speed of fermentation of the potentially prebiotic substrates. H₂ and CO₂ are the first gasses to be produced upon microbial fermentation; they can subsequently be utilized as substrates for CH₄ production, reducing the gas volume. H₂ can also be utilized to reduce sulfate to H₂S, resulting from proteolytic fermentation. As a result, N₂, O₂, CO₂, H₂ and CH₄ constitute for 99% the volume of intestinal gas. The remaining 1% consists of NH₃, H₂S, volatile amino acids and short chain fatty acids. Gas production during the incubations was determined at 0, 3, 6, 24 and 48 h after starting the incubation.

[0098] SCFA analysis - The SCFA analysis is an assessment of the microbial carbohydrate metabolism (acetate, propionate and butyrate) and can be compared to typical fermentation

patterns for normal GI microbiota. Samples for SCFA analysis were analyzed after 0, 3, 6, 24 and 48 h of incubation.

[0099] Lactate analysis - The human intestine harbors both lactate-producing and lactate-utilizing bacteria. Lactate is produced by lactic acid bacteria and decreases the pH of the environment, thereby also acting as an antimicrobial agent. Protonated lactic acid can penetrate the microbial cell after which it dissociates and releases protons within the cell, resulting in acidification and microbial cell death. It can also be rapidly converted into especially butyrate by other microorganisms. Samples for lactate analysis were analyzed after 0, 3, 6, 24 and 48 h of incubation.

[0100] Targeted qPCR - Quantitative PCR (qPCR) is a molecular technique that is based on the quantification of specific bacterial sequences (16S rRNA genes) through amplification. For the current project, a quantification of bifidobacteria and lactobacilli was performed at the start of the incubation, after 24 h and after 48 h.

[0101] 16S-based Illumina sequencing - Because the Illumina sequencing method is PCR-based, microbial sequences are amplified till a saturation level is reached. Therefore, the results that are expressed at different phylogenetic levels (microbial phylum, family and genus or OTU level) are presented as proportional values versus the total amount of sequences within each sample, thus providing semi-quantitative results. The methodology applied involves primers that span 2 hypervariable regions (V3-V4) of the 16S rDNA. Using a pair-end sequencing approach, sequencing of 2 × 250 bp results in 424 bp amplicons. Such fragments are taxonomically more useful as compared to smaller fragments that are taxonomically less informative. Samples were taken at the beginning and at the end of the 48h of incubation.

[0102] Results - The following results were obtained:

pH decrease - The pH was monitored. The pH measurements obtained are shown in table 3 below:

Table 3

Time of incubation	AGENT #1	AGENT #2	Blank
0 h	6.59	6.53	6.55
3 h	6.40	6.39	6.51
6 h	6.25	6.26	6.49
24 h	6.01	6.13	6.53
48 h	5.98	6.05	6.44

[0103] The initial pH decrease (after 3 h and 6 h) was comparable between both products and stronger than the blank incubation.

[0104] The pH decrease of the products mainly occurred between 0-24 h, and was much stronger than for the blank. After 24 h fermentation, there was a slightly stronger pH decrease

for AGENT #1 versus AGENT #2.

[0105] The pH remained relatively constant during the 24-48 h interval for the incubation with AGENT #1, while slightly further decreasing in the incubation with AGENT #2.

[0106] Stronger decreases in pH with prebiotic agents versus the blank consistently illustrated a high fermentability of both test products.

[0107] Gas production - The average gas production (kPa) in different time intervals upon fermentation of 5 g/L of the prebiotic agents tested and the negative control was monitored. The measurements obtained are shown in table 4 below:

Table 4

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	2.4	2.0	4.0
6-24 h	26.2	22.9	10.9
3-6 h	7.4	9.5	3.6
0-3 h	9.1	10.5	5.5

[0108] The initial gas production (from 0-3 h and from 3-6 h) was considerably higher for AGENT #1 and for AGENT #2 than for the blank.

[0109] Gas production was highest within the 6-24 h period. In comparison to the blank both products suggested a high fermentation rate.

[0110] Both products resulted in a similar but small additional increase in gas production during the 24-48 h time interval, being slightly lower than the blank.

[0111] Higher levels of gas production with both prebiotic agents versus the blank consistently illustrated a high fermentability of both test products

[0112] SCFA production - The average productions of acetate, propionate, butyrate and total SCFAs (mM) in different time intervals upon fermentation of 5g/L of the prebiotic agents tested and the negative control were monitored.

[0113] The measurements obtained for the total SCFAs production (mM) are shown in table 5 below:

Table 5

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	4.5	7.2	6.5
6-24 h	40.2	35.0	16.4
3-6 h	8.6	10.6	3.6

Time interval	AGENT #1	AGENT #2	Blank
0-3 h	13.8	14.5	7.5

[0114] Both prebiotic agents strongly and similarly increased total SCFA levels to almost 70 mM, thus doubling the SCFA production compared to the control.

[0115] The measurements obtained for the lactate production (mM) are shown in table 6 below:

Table 6

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	0.2	1.7	1.0
6-24 h	23.9	21.3	12.2
3-6 h	4.7	6.0	2.1
0-3 h	8.1	8.5	3.5

[0116] Both prebiotic agents doubled acetate levels compared to the negative control, with an increase of approximately almost 20 mM.

[0117] The measurements obtained for the propionate production (mM) are shown in table 7 below:

Table 7

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	1.5	2.6	2.3
6-24 h	15.8	13.0	3.6
3-6 h	3.9	4.5	1.4
0-3 h	3.4	3.7	1.8

[0118] Like acetate, propionate can be produced by a wide range of gut microbes, with the most abundant propionate producers being *Bacteroides spp.* (phylum = *Bacteroidetes*) and *Akkermansia muciniphila* (phylum = *Verrucomicrobia*). As the latter is a mucin-degrading microbe, the observed propionate productions can probably be attributed to *Bacteroides spp.* Again, both products more than doubled the final propionate levels versus the negative control.

[0119] The measurements obtained for the butyrate production (mM) are shown in table 8 below:

Table 8

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	1.08	1.30	1.03
6-24 h	4.20	4.11	2.54
3-6 h	0.25	0.30	0.12
0-3 h	0.46	0.50	0.17

[0120] Butyrate production was strongly increased upon administration of both products.

[0121] In conclusion, both prebiotic agents doubled total SCFA production compared to the control. This increase was related to the increased production of acetate, propionate and butyrate that were all three almost doubled versus the control. In agreement with the results of the pH and gas production, the increases were strongest during the first 24h, indicating a high fermentation rate induced by both products.

[0122] Lactate production - The average lactate production (mM) in different time intervals upon fermentation of 5g/L of the prebiotic agents tested and the negative control was monitored.

[0123] The measurements obtained for the lactate production (mg/L) are shown in table 9 below:

Table 9

Time interval	AGENT #1	AGENT #2	Blank
24-48 h	-0.43	-0.24	-0.12
6-24 h	-1.28	-1.61	0.01
3-6 h	-0.17	-0.19	-0.21
0-3 h	1.90	2.16	0.71

[0124] Both prebiotic agents resulted in high initial lactate production (0-3h) compared to the control. From 3 h of incubation onwards lactate was consumed, with mild consumption during the 3-6 h and 24-48 h periods and highest consumption during the 6-24 h timeframe. Lactate consumption within the 6-24 h timeframe corresponds well to high butyrate production that mainly occurred in this time frame, thus indicating that lactate might have served as precursor of butyrate.

[0125] Bifidobacteria level - The level of bifidobacterial (average absolute *Bifidobacterium* numbers expressed as 16S rRNA gene copies/mL) at different time points upon fermentation of 5g/L of the prebiotic agents tested and the negative control was monitored.

[0126] The average absolute *Bifidobacterium* numbers, expressed as 16S rRNA gene

copies/mL, are shown in table 10 below:

Table 10

Time of incubation	AGENT #1	AGENT #2	Blank
0 h	BDL	BDL	BDL
24 h	1.9×10^5	2.0×10^5	1.8×10^5
48 h	1.8×10^5	2.1×10^5	2.0×10^5
BDL: below detection limit			

[0127] At the start of the incubation, *Bifidobacterium* levels were below the limit of detection. During the incubation, Bifidobacteria were enriched in a similar way as the blank. As such, no stimulatory effect of the treatments on Bifidobacteria was observed.

[0128] Lactobacilli level - The level of *Lactobacillus* (average absolute *Lactobacillus* numbers expressed as 16S rRNA gene copies/mL) at different time points upon fermentation of 5 g/L of the prebiotic agents tested and the negative control was monitored.

[0129] The average absolute *Lactobacillus* numbers, expressed as 16S rRNA gene copies/mL, are shown in the table 11 below:

Table 11

Time of incubation	AGENT #1	AGENT #2	Blank
0 h	1.5×10^5	1.5×10^5	1.5×10^5
24 h	1.2×10^6	2.5×10^6	2.7×10^6
48 h	1.7×10^6	2.7×10^6	2.5×10^6

[0130] The prebiotic agents did not stimulate *Lactobacillus* levels versus the blank.

[0131] 16S-targeted Illumina sequencing (phylum level) - The relative abundance (%) of the different phyla in the original inoculum and in the colon incubations upon addition of the prebiotic agents versus the blank was determined.

[0132] The relative abundance of the different phyla is shown in table 12 below:

Table 12

Phylum	Inoculum	AGENT #1	AGENT #2	Blank
<i>Actinobacteria</i>	3.8%	0.6%	0.6%	1.3%
<i>Bacteroidetes</i>	45.2%	78.5%	69.7%	58.2%
<i>Firmicutes</i>	50.9%	13.1%	19.3%	20.5%
<i>Proteobacteria</i>	0.1%	7.9%	10.4%	20.1%

[0133] All major phyla that were originally present in the inoculum were also preserved during the in vitro incubations. Both prebiotic agents enriched the *Bacteroidetes* levels after 48h of incubation, when compared to both the original inoculum as well as when compared to the blank. The proportion of *Bacteroidetes*, containing many propionate-producing species, was higher in the incubations with AGENT #1 (78.5%) versus AGENT #2 (69.7%), which was in line with the slightly higher propionate concentrations that were associated with fermentation for this product. Due to the strong increase of *Bacteroidetes*, the relative abundance of *Firmicutes* significantly decreased during incubations with the test products.

[0134] 16S-targeted Illumina sequencing (family and OTU) -The relative abundance (%) of bacteria of *Bacteroidetes* phylum / *Bacteroidaceae* family and *Firmicutes* phylum / *Erysipelotrichaceae* family in the original inoculum and in the colon incubations upon addition of the prebiotic agents versus the blank was determined.

[0135] The relative abundance of bacteria of *Bacteroidetes* phylum / *Bacteroidaceae* family and bacteria of *Firmicutes* phylum / *Erysipelotrichaceae* family is shown in table 13 below:

Table 13

Phylum Family	Inoculum	AGENT #1	AGENT #2	Blank
<i>Bacteroidetes Bacteroidaceae</i>	43.1%	78.0%	69.1%	57.2%
<i>Firmicutes Erysipelotrichaceae</i>	1.0%	4.1%	8.4%	0.1%

[0136] In the inoculum, the remaining proportion of bacteria of the *Bacteroidetes* phylum comprised essentially of bacteria of *Porphyromonadaceae* family (1.3%) and of bacteria of *Rikenellaceae* family (0.8%).

[0137] It is shown a stronger enrichment of *Bacteroidaceae* and *Erysipelotrichaceae* by the prebiotic agents, than in the blank.

[0138] Amongst the bacteria of *Bacteroidetes* phylum / *Bacteroidaceae* family, the relative abundance of the species *Bacteroides ovatus* was determined. Likewise, amongst the bacteria of *Firmicutes* phylum / *Erysipelotrichaceae* family, the relative abundance of the species *Clostridium XVIII* (OTU5) was determined. The data is shown in table 14 below:

Table 14

Species	AGENT #1	AGENT #2	Blank
<i>Bacteroides ovatus</i>	68.4%	57.0%	9.8%
<i>Erysipelotrichaceae Clostridium XVIII</i> OTU5	3.9%	8.1%	0.0%

[0139] Amongst the bacteria of the *Bacteroidaceae* family, the prebiotic agents induced a very strong enrichment in *Bacteroides ovatus* versus the blank. Amongst the bacteria of the

Erysipelotrichaceae family, the prebiotic agents induced a very strong enrichment of *Clostridium XVIII* versus the blank.

[0140] Conclusion - The potential of the prebiotic agents tested was assessed in short-term colonic incubations and was compared to a negative control *i.e.* incubation without fibers. Multiple endpoints demonstrated the large prebiotic potential of both agents, resulting in: (1) a pH decrease and increase in gas production; (2) an increase in production of the health-promoting SCFA acetate, propionate and butyrate; (3) the stimulation of the initial lactate production, followed by consumption, probably leading to increased butyrate concentrations. Further, no stimulatory effect of both prebiotic agents towards Bifidobacteria and Lactobacilli could be observed. In addition, a stimulatory effect of prebiotic agents on *Bacteroidetes*, particularly on *Bacteroides ovatus*, could be observed, thus explaining their stimulatory effect on acetate and propionate production.

REFERENCES CITED IN THE DESCRIPTION

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PATENTKRAV

1. Gærprodukt, eller en sammensætning omfattende det, til anvendelse som et præbiotisk middel til stimulering af bakterievæksten af *Bacteroidetes*-stammen i pattedyrs tarmmikrobiota;
5 hvor gærproduktet er en opløselig underfraktion af væggene af gærceller;
hvor den opløselige underfraktion opnås ved udsættelse af hele gærceller for en disruptionsbehandling, separering af en opløselig fraktion fra en uopløselig fraktion, derefter behandling af den uopløselige fraktion med ribonukleaser og glucanaser, før separering af en proteinrig, uopløselig underfraktion fra en opløselig underfraktion; eller ved udsættelse af hele
10 gærceller for en disruptionsbehandling, derefter behandling af blandingen opnået med ribonukleaser og glucanaser, før separering af en proteinrig, uopløselig underfraktion fra en opløselig underfraktion.
2. Gærprodukt, eller en sammensætning omfattende det, for anvendelse ifølge krav 1, hvor
15 gæren vælges fra gruppen bestående af slægterne *Saccharomyces*, *Pichia*, *Candida*, *Kluyveromyces*, *Yarrowia* og/eller *Wickehomomyces*; fortrinsvis hvor gæren vælges fra gruppen bestående af arterne *Saccharomyces cerevisiae*, *Pichia jadinii*, *Kluyveromyces marxianus*; mere fortrinsvis hvor gæren er *Saccharomyces cerevisiae*.
- 20 3. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, hvor bakterierne af *Bacteroidetes*-stammen er bakterier af *Bacteroidia*-klassen; fortrinsvis bakterier af *Bacteroidales*-ordenen; mere fortrinsvis bakterier af *Bacteroidaceae*-familien; endnu mere fortrinsvis bakterier af *Bacteroides*-slægten; mest fortrinsvis *Bacteroides ovatus* spp.
25
4. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, hvor gærproduktet øger forholdet mellem bakterier af *Bacteroidetes*-stammen og bakterier af *Firmicutes*-stammen i pattedyrs tarmmikrobiota.
- 30 5. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, hvor gærproduktet har et β -glucanindhold (udtrykt som ækvivalent masse af glucose) fra 15 til 50 masse-% på tørstofbasis; og/eller et mannanindhold (udtrykt som ækvivalent masse af mannose) fra 10 til 40 masse-% på tørstofbasis.

6. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, hvor gærproduktet ikke stimulerer bakterievæksten af *Bifidobacterium*-slægten og/eller bakterier af *Lactobacillus*-slægten.

5 7. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, hvor gærproduktet, eller sammensætningen omfattende det, administreres oralt; fortrinsvis hvor gærproduktet, eller sammensætningen omfattende det, administreres oralt ved en daglig dosis fra 500 mg til 15 g; fortrinsvis hvor gærproduktet, eller sammensætningen omfattende det, administreres oralt ved en daglig dosis fra 500 mg til 5 g i op til 10 indtagelser.

10 8. Sammensætning til anvendelse ifølge et hvilket som helst foregående krav, hvor sammensætningen formuleres som en gummi, en tablet, en kapsel, en pille, et pulver, granulater eller en suspension.

15 9. Gærprodukt, eller en sammensætning omfattende det, til anvendelse ifølge et hvilket som helst foregående krav, til anvendelse, der endvidere omfatter forebyggelse eller begrænsning af tarmpatologier såsom diarré og irritable tarm-syndrom, til stimulering af immunitet, til regulering af glykæmi og/eller lipidæmi, til behandling eller begrænsning af metaboliske forstyrrelser forbundet med fedme.

20 10. Ikke-terapeutisk anvendelse af et gærprodukt, eller en sammensætning omfattende det, som et præbiotisk middel til stimulering af bakterievæksten af *Bacteroidetes*-stammen i pattedyrs tarmmikrobiota hos et raskt individ; hvor gærproduktet er en opløselig underfraktion af væggene af gærceller, opnået ved udsættelse af hele gærceller for en disruptionsbehandling, 25 separering af en opløselig fraktion fra en uopløselig fraktion, derefter behandling af den uopløselige fraktion med ribonukleaser og glucanaser, før separering af en proteinrig, uopløselig underfraktion fra en opløselig underfraktion; eller ved udsættelse af hele gærceller for en disruptionsbehandling, derefter behandling af blandingen opnået med ribonukleaser og glucanaser, før separering af en proteinrig, uopløselig underfraktion fra en opløselig 30 underfraktion.

11. Ikke-terapeutisk anvendelse af en sammensætning ifølge krav 10, hvor sammensætningen er en fødevarer eller et kosttilskud; fortrinsvis et mejeriprodukt, et frugtbaseret produkt, en drikkevarer, en fast fødevarer eller et kosttilskud.