**Supplementary table**: Frequency of occurrence of phyla, genera, and species of microorganisms before and after treatment and their role in metabolism.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Before** | **After** | **Role in metabolism** | **Ref.** |
|  | N(%) | N(%) |  |  |
| **Phylum Firmicutes** | | | | |
| *Blautia hydrogenotrophica* | 10 (22) | 36(80) | Involved in regulating the coexistence of anaerobic respiratory pathways. | 1 |
| *Blautia obeum* | 3(6) | 34(75) | It can inhibit the growth of *C. perfringens* and vancomycin-resistant enterococci, demonstrating its potential as a probiotic with beneficial probiotic effects. | 1 |
| *Butyrivibrio fibrisolvens* | 4(8) | 28(62) | Lack of information in the literature. | - |
| *Catenibacterium faecis* | 4(8) | 19(42) | Individuals at a heightened risk of cardiovascular disease exhibit decreased levels of *Catenibacterium* species in their microbiota. | 2 |
| *Clostridium celerecrescens* | 2(4) | 11(24) | Lack of information in the literature. | - |
| *Clostridium coccoides* | 2(4) | 12(26) | There is a positive association between the prevalence of *Clostridium coccoides* and a substantial consumption of monounsaturated fatty acids and polyunsaturated fatty acids. | 3 |
| *Enterocloster clostridioformis* | 1(2) | 14(31) | Lack of information in the literature. | - |
| *Clostridium fusiformis* | 1(2) | 15(33) | Lack of information in the literature. | - |
| *Clostridium indolis* | 0 | 16(35) | Lack of information in the literature. | - |
| *Clostridium perfringens* | 2(4) | 5(11) | *Clostridium perfringens* constitutes a significant factor behind histotoxic and intestinal infections in both humans and other animals. | 4 |
| *Clostridium phoceensis* | 2(4) | 11(24) | This Family in the gut microbiome is reduced in athletes' metabolism and increased in sedentary people. | 5 |
| *Coprococcus catus* | 2(4) | 23(51) | Contributes to the production of essential short-chain fatty acids, including butyrate and propionate, which collectively support the well-being of the digestive system and metabolic functions. | 6 |
| *Dorea longicatena* | 20(44) | 0 | Biomarkers of inflammation show a positive connection with *Dorea longicatena*, indicating its potential role in influencing inflammatory processes. | 7 |
| *Enterococcus faecalis* | 4(8) | 4(8) | This Family might cause infections and is resistant to oxidative stress. | 8 |
| *Eubacterium contortum* | 1(2) | 10(22) | *Eubacterium contortum* can produce p-cresol, an organic compound associated with health implications. | 9 |
| *Eubacterium coprostanoligenes* | 9(20) | 0 | Found in obese people's microbiome, might decrease cholesterol levels. | 10 |
| *Eubacterium eligens* | 2(4) | 17(37) | Promising potential of probiotic as a prospective therapeutic focus for addressing atherosclerosis. | 11 |
| *Dorea formicigenerans* | 1(2) | 24(53) | It has been found to exhibit an inverse correlation with insulin resistance. | 7 |
| *Eubacterium halii* | 1(2) | 23(51) | It is being assessed in preclinical and clinical trials as potential next-gen probiotic for advancing innovative dietary supplement formulations. | 12 |
| *Eubacterium ramulus* | 3(6) | 25(55) | Exhibits proficiency in breaking down diverse dietary flavonoids (which provides health benefits). | 13 |
| *Eubacterium ventriosum* | 2(4) | 22(48) | Demonstrates higher prevalence among individuals with elevated body mass index and serves as a producer of butyrate (molecule that contributes to a healthy gut). | 14 |
| *Faecalibacterium prausnitzii* | 13(28) | 44(97) | This anti-inflammatory family holds the position of being the most prevalent bacterium in the intestinal microbiota of healthy adults. | 15 |
| *Limosilactobacillus reuteri* | 0 | 36(80) | Describes multiple metabolic pathways that boost the creation of anti-inflammatory cytokines and regulate the gut microbiota through the generation of molecules with antimicrobial properties. | 16 |
| *Limosilactobacillus fermentum* | 31(68) | 30(66) | Positively influences the host's antioxidant and anti-inflammatory systems, leading to improved glucose regulation in diabetes. | 17 |
| *Lactobacillus acidophilus* | 27(60) | 32(71) | It can degrade oxalate (a substance that can cause problems) effectively, even when there are other types of carbon sources available that it prefers. | 18 |
| *Lactobacillus crispatus* | 5(11) | 32(71) | It shows promise as a probiotic option for managing dysbiosis, especially in women, with potential applications for both prevention and treatment. | 19 |
| *Lactobacillus gasseri* | 1(2) | 32(71) | It can degrade oxalate (substance that can cause problems) effectively, even when there are other types of carbon sources available that it prefers. | 18 |
| *Lactobacillus ingluviei* | 35(77) | 25(55) | It is related to weight increase. | 20 |
| *Lactobacillus johnsonii* | 0 | 30(66) | It has been extensively researched for its probiotic actions, which involve inhibiting pathogens, attaching to epithelial cells, and modulating the immune system. | 21 |
| *Lactobacillus rogosae* | 1(2) | 35(77) | It has anti-inflammatory properties and improves insulin sensitivity. | 22 |
| *Lactobacillus ruminis* | 5(11) | 29(64) | Probiotic resides as a commensal species in the digestive tract and offers potential for application in the functional food field. | 23 |
| *Lactobacillus sakei* | 4(8) | 32(71) | Exhibits probiotic potential based on in vitro assessment and has the ability to potentially lower inflammation by regulating intestinal metabolism. | 24 |
| *Lachnospira pectinoschiza* | 28(62) | 17(37) | It's recognized as a type of *Lachnospiraceae* bacteria in the human gut that can make use of pectin, a dietary fiber. | 6 |
| *Lachnospira multipara* | 1(2) | 28(62) | It is a 2 butyrate producer, a short-chain fatty acid which improves the gut health. | 25 |
| *Lachnospira straminea* | 1(2) | 24(53) | Lack of information in the literature. | - |
| *Bacillus nealsonii* | 1(2) | 27(60) | Lack of information in the literature. | - |
| *Odoribacter splanchnicus* | 0 | 29(64) | Produces short-chain fatty acids. Reduced levels of *Odoribacter* have been linked to microbiota-related diseases, including non-alcoholic fatty liver disease, cystic fibrosis, and inflammatory bowel disease (IBD). | 26 |
| *Oribacterium sinus* | 39(86) | 15(33) | Lack of information in the literature. | - |
| *Oscillibacter valericigenes* | 2(4) | 32(71) | Is a valerate producer, a type of short-chain fatty acid, generally considered beneficial for gut health. | 27 |
| *Phascolarctobacterium faecium* | 2(4) | 31(68) | It has the capability to generate beneficial short-chain fatty acids like acetate and propionate, which can promote the well-being of the gut. | 28 |
| *Pediococcus pentosaceus* | 1(2) | 31(68) | Certain varieties have been documented to alleviate inflammation, encephalopathy, obesity, and fatty liver in animal studies. | 29 |
| *Roseburia hominis* | 3(6) | 38(84) | Enhances the host's intestinal microbial balance and positively impacts the absorption of nutrients. | 30 |
| *Roseburia intestinalis* | 7(15) | 38(84) | Demonstrates higher prevalence among individuals with elevated body mass index and serves as a producer of butyrate (molecule that contributes to a healthy gut). | 14 |
| *Roseburia inulinivorans* | 3(6) | 32(71) | Contributes to the synthesis of butyrate. | 31 |
| *Roseburia faecis* | 3(6) | 32(71) | Generates short-chain fatty acids, with a particular emphasis on butyrate. | 32 |
| *Roseburia cecicola* | 1(2) | 34(75) | Also generates short-chain fatty acids, with a particular emphasis on butyrate. | 32 |
| *Ruminococcus gnavus* | 34(75) | 7(15) | Among adults, *R. gnavus* exhibited the most pronounced responsiveness to disturbances in circadian rhythms. | 33 |
| *Ruminococcus bromii* | 3(6) | 33(73) | A crucial species responsible for breaking down resistant starch (a substantial energy source) in the human colon. | 34 |
| *Ruminococcus torques* | 4(8) | 22(48) | Generates an essential enzyme that plays a vital role in the effective production of ursodeoxycholic acid (UDCA), a potent medication used to treat primary biliary cirrhosis and human cholesterol gallstones. | 35 |
| **Phylum Bacteroidetes** | | | | |
| *Alistipes finegoldii* | 17(37) | 35(77) | Examination showed a direct link between the prevalence of this group and the acetylation of glycoproteins in overweight women. These glycoproteins have significant roles in biological functions. | 36 |
| *Alistipes indistinctus* | 3(6) | 23(51) | It exhibits a direct relationship with mast cells and substances that stimulate the immune system. | 37 |
| *Alistipes inops* | 7(15) | 24(53) | Lack of information in the literature. | - |
| *Alistipes putredinis* | 1(2) | 32(71) | It is a probiotic microorganism that provides advantages to the host organism. | 38 |
| *Alistipes senegalensis* | 39(6) | 12(26) | Is a common family related to people without obesity. | 39 |
| *Alistipes obesi* | 31(68) | 37(82) | In lean individuals, it was notably more abundant, and its numbers increased as they pursued their dieting regimen. | 40 |
| *Alistipes shahii* | 6(13) | 17(37) | Is also a common family related to people without obesity. | 39 |
| *Bacteroides caccae* | 4(8) | 16(35) | Lack of information in the literature. | - |
| *Bacteroides dorei* | 39(86) | 29(64) | Might decrease the production of lipopolysaccharides by gut microbes and prevent the development of atherosclerosis. | 41 |
| *Bacteroides eggerthii* | 3(6) | 10(22) | Lack of information in the literature. | - |
| *Bacteroides fragilis* | 4(8) | 10(22) | It serves a significant nutritional function compared to other microorganisms and encourages immune cells to exhibit anti-inflammatory responses. | 42 |
| *Bacteroides massiliensis* | 2(4) | 11(24) | It has been correlated with distinct probabilities of prostate cancer onset or the degree of prostate cancer progression. | 43 |
| *Bacteroides ovatus* | 3(6) | 12(26) | The existence of this bacterium appears to elevate immune cell levels, potentially associating it with an increased risk of Type 2 diabetes in obese individuals. | 44 |
| *Bacteroides stercoris* | 1(2) | 9(20) | Is noticeably more abundant in stool samples from individuals with Diabetic Neuropathy. | 45 |
| *Bacteroides thetaiotaomicron* | 3(6) | 13(28) | It influences the expression of numerous genes involved in various aspects of the host's physiology, aiding the organism in crucial functions. | 46 |
| *Bacteroides uniformis* | 6(13) | 14(31) | Lack of information in the literature. | - |
| *Bacteroides vulgatus* | 5(11) | 14(31) | Has the ability to produce GABA. | 47 |
| *Bacteroides xylanisolvens* | 0 | 17(37) | Has the ability to degrade Xylan, a polysaccharide that can serve as a prebiotic. | 48 |
| *Parabacteroides distasonis* | 4(8) | 7(15) | Aerotolerant anaerobic microbe, exhibiting increasing resistance to antimicrobials, and playing dual roles in human health as both a pathogen and a probiotic. | 49 |
| *Parabacteroides merdae* | 1(2) | 9(20) | This group is increased in individuals with hypertension. | 50 |
| *Prevotella bivia* | 5(11) | 15(33) | Lack of information in the literature. | - |
| *Prevotella buccalis* | 3(6) | 21(46) | The changes in the level of IL-1β and TNF-α (immune-related molecules) is associated with this family. | 51 |
| *Prevotella copri* | 15(33) | 32(71) | It plays a crucial role in the digestive system of many people, making it one of the key components. | 52 |
| *Prevotella oris* | 2(4) | 15(33) | A strong positive link exists between the occurrence of *P. oris* in the oral microbiota and both a person's age and their level of insulin resistance. | 53 |
| *Prevotella stercorea* | 4(8) | 13(28) | These bacteria may collaborate with *P. copri* to aid in the digestion of dietary fiber present in our food. | 54 |
| *Barnesiella intestinihominis* | 2(4) | 19(42) | Is responsible in the gut for amino acid, carbohydrate and fatty acid degradation. | 55 |
| **Phylum Actinobacteria** | | | | |
| *Atopobiom vaginae* | 14(31) | 8(17) | It has been demonstrated to have a significant impact on the development and progression of bacterial vaginosis. | 56 |
| *Bifidobacterium adolescentis* | 18(40) | 27(60) | It is a crucial component of the human gut microbial community, influencing the production of GABA and regulating the communication between the gut and the brain through the gut-brain axis. | 57 |
| *Bifidobacterium bifidum* | 21(46) | 32(71) | It is more common in infants and is associated with lower occurrence of diarrhea caused by the use of antibiotics. | 58 |
| *Bifidobacterium catenulatum* | 7(15) | 22(48) | It is a commensal gut bacteria in healthy adults. | 59 |
| *Bifidobacterium pseudocatenulatum* | 12(26) | 22(48) | Has also the ability to degrade Xylan, a polysaccharide that can serve as a prebiotic. | 60 |
| *Bifidobacterium angulatum* | 10(22) | 21(46) | This bacterial group's β-galactosidase enzymes break down lactose and foster the growth of beneficial gut bacteria, boosting overall gut health. | 61 |
| *Bifidobacterium animalis* | 5(11) | 14(31) | Using it as a probiotic supplement is highly promising for supporting obesity treatment. | 62 |
| *Bifidobacterium dentium* | 6(13) | 18(40) | It has the capacity to process diverse nutrient sources, including many of plant origin, indicating that *B. dentium* can utilize dietary compounds. | 63 |
| *Bifidobacterium breve* | 3(6) | 17(37) | Is connected to the maintenance of a stable gut microbiome in individuals who are in a healthy condition. | 64 |
| *Collinsella aerofaciens* | 0 | 10(22) | This bacterium's presence is linked to higher secondary bile acid levels, indicating a possible involvement in their production or metabolism in the gut | 65 |
| **Phylum Proteobacteria** | | | | |
| *Staphylococcus aureus* | 21(46) | 5(11) | Is a primary reason for biofilm infections on medical equipment, such as prosthetic joints, which impose a substantial healthcare challenge. | 66 |
| *Klebsiella pneumoniae* | 13(28) | 4(8) | It has the potential to act as a pathogen and a driving factor in the onset of hypertension. | 67 |
| *Acinetobacter baumannii* | 14(31) | 7(15) | Contributes significantly to the mortality of patients in the intensive care unit (ICU) by causing a variety of infections in this vulnerable ICU population. | 68 |
| *Escherichia coli* | 45(100) | 44(97) | They are frequently found in the human microbiota, and these isolates can play probiotic, commensal, or pathogenic roles within the host. | 69 |
| *Proteus mirabilis* | 9(20) | 3(6) | It's recognized for its ability to produce urease and the potential infections it can lead to. | 70 |
| *Desulfovibrio piger* | 9(20) | 1(2) | The most frequently encountered sulfate-reducing bacteria in the gut within a surveyed group of healthy adults from the United States. | 71 |
| *Bilophila wadsworthia* | 5(11) | 1(2) | Is able to convert taurine, a common gut substance, into the harmful compound hydrogen sulfide (H2S) by its metabolism. This conversion is linked to inflammatory bowel disease and colorectal cancer. | 72 |
| *Parasutterella excrementihominis* | 8(17) | 1(2) | The study found that higher levels of *Parasutterella* bacteria in the gut were associated with the activation of a pathway involved in making fatty acids, potentially leading to weight gain. This connection was reinforced when *Parasutterella excrementihominis* levels decreased in participants who followed a low-carb diet as part of a weight loss program. | 73 |
| *Citrobacter freundii* | 7(15) | 2(4) | *C. freundii,* as an opportunistic pathogen, can lead to a wide range of infections, including those affecting the urinary tract, respiratory tract, wounds, and bloodstream. | 74 |
| **Phylum Verrucomicrobia** | | | | |
| *Akkermansia muciniphila* | 11(24) | 45(100) | It is being assessed in preclinical and clinical trials as a potential next-gen probiotic for advancing innovative dietary supplement formulations. | 12 |
| **Phylum Euryarchaeota** | | | | |
| *Methanobrevibacter smithii* | 27(60) | 23(51) | Is considered a biomarker that can indicate a healthy colon. | 75 |
| **Phylum Tenericutes** | | | | |
| *Mycoplasma hominis* | 10(22) | 37(82) | One of the mycoplasma species that is widely acknowledged for its role in causing the most clinically relevant infections. | 76 |
| **Phylum Fusobacteria** | | | | |
| *Fusobacterium nucleatum* | 0 | 28(62) | It has been traditionally associated with opportunistic infections. Nevertheless, it is a frequent component of the oral microbiome and can establish a mutually beneficial relationship with its host. | 77 |
| *Fusobacterium varium* | 10(22) | 1(2) | *F. varium* has been associated with both advantageous and detrimental interactions between bacteria and their host. | 78 |

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