



GUT MICROBIOTA REPORT

uBioma Clinical Metagenomic Analysis

GUT MICROBIOTA REPORT

Patient

ID:

Age:

Gender: "Female"

Previous disease: N/A

Sample

Prescriber:

Health Center:

Physician:

Report history

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Analysis: 11-Jul.-2021

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Summary

COMPOSITION OF THE GUT MICROBIOTA

Parameter	Value	Reference	Assessment
HUMAN DNA	1.192	0 - 5	Normal
HUMAN DNA SEQUENCES	3 372		
BACTERIAL CONTENT	61.829	40 - 70	Normal
BACTERIAL SEQUENCES	174 962		
SAMPLE TOTAL SEQUENCES	282 976		
NUMBER OF BACTERIAL SPECIES	510	400 - 2000	Normal
NUMBER OF BACTERIAL SUBSPECIES	141		

Dominant bacterial phyla

BACTEROIDETES	52.345	20 - 40	High
PROTEOBACTERIA	2.422	0 - 5	Normal
FIRMICUTES	41.220	50 - 65	Low
ACTINOBACTERIA	1.570	2 - 5	Low
VERRUCOMICROBIA	0.829	2 - 5	Low

Bacterial phyla	Families	Genera	Species	Subspecies
21	184	357	510	141

ARCHAEA KINGDOM	0.052	0 - 1	Normal
FUNGI KINGDOM	0.460	0.1 - 1	Normal
VIRUSES	2.876	0.1 - 1	High
PARASITES	0.004	0 - 1	Normal

BIODIVERSITY INDEXES

Ratios	Value [%]	Reference [%]	Assessment
Firmicutes / Bacteroidetes	0.787	1 - 3	Low
Firmicutes + Bacteroidetes	93.564	85 - 90	High
Bacteroides / Prevotella	461.025	2 - 3	High

BACTERIAL OVERGROWTH

Species / subspecies	Value [%]	Reference [%]
Phocaeicola dorei	17.160	0.5 - 5

BACTERIA POSITIVELY RELATED TO INTESTINAL HOMEOSTASIS

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Anaerostipes hadrus</i>	Firmicutes	5.384	2 - 6	Normal
<i>Anaerobutyricum hallii</i>	Firmicutes	2.574	1 - 3	Normal
<i>[Eubacterium rectale</i>	Firmicutes	2.050	1 - 6	Normal
<i>Faecalibacterium prausnitzii</i>	Firmicutes	1.822	5 - 15	Low
<i>Roseburia intestinalis</i>	Firmicutes	0.967	1 - 3	Low
<i>Akkermansia muciniphila</i>	Verrucomicrobia	0.821	2 - 5	Low
<i>Roseburia hominis</i>	Firmicutes	0.211	1 - 3	Low

Microbiota functional structure	Total [%]	Assessment
Muconutritive microbiota. Butyrate producer	19.576	Normal
Regulatory microbiota of intestinal mucus	5.145	Normal
Intestinal mucus-consuming Microbiota	17.798	High
Protective and containment microbiota	9.578	Low
Immunomodulating microbiota	12.855	Normal
Metabolic / energy microbiota	44.745	High
Microbiota with proteolytic function	15.698	High
Bile salt metabolizing microbiota	18.769	High
GABA metabolism GABA-producing microbiota	37.329	High
GABA metabolism GABA-consuming microbiota	0.664	Low
Metabolism of isoflavones (S-EQUOL). M. producers	2.067	Low
Metabolism of isoflavones (S-EQUOL). M. consumers	4.774	Normal
Stroboloma-forming microbiota	12.260	Normal
Microbiota producing biogenic amines (Histamine)	0.709	Normal
Metabolic microbiota of Trimethylamine	0.257	Normal
Succinate-producing microbiota	12.399	Normal
Succinate-consuming microbiota	4.460	Normal
Indol producing microbiota	17.261	High
Tryptamine producing microbiota	2.512	Normal
Indol propionic acid (IPA) producing microbiota	0.634	Normal
Indol acetic acid producing microbiota (IAA)	0.147	Normal
Kynurenine producing microbiota	0.511	Normal
Kynurenate producing microbiota	2.820	Normal
Microbiota domain archaea Methane producer	0.018	Normal
Hydrogen sulfide producing microbiota	5.447	High
Ethanol producing microbiota	1.354	Normal

STRUCTURE OF THE BACTERIAL MICROBIOTA IN FECAL SAMPLE

The content of Human DNA in the sample is 1,19%

The Bacterial DNA content in the sample is 61,83%

Bacterial phyla	Families	Genera	Species	Subspecies
21	184	357	510	141

* *Bacteria potentially detectable:* 20.709

Description

The number of species that have been found to be associated with the human intestine globally (in all the different human populations) ranges from 250 to 3,000 species. This does not mean that everyone has them all. This number is increasing as new species are identified that until now were not cultivable (in fact, it is already being said that more than 4,000 bacterial species typical of our Gut Microbiota could be reached as a species). Although there is no consensus on what is the ideal number of species in a healthy individual; currently it is considered that a Healthy Microbiota should be between a minimum of 400 and a higher value of about 2,000 species. It is considered that levels above or below these limits are considered as pathological.

DOMINANT BACTERIAL PHYLA

Phylum	Value [%]	Reference [%]	Assessment
<i>BACTEROIDETES</i>	52.345	20 - 40	High
<i>PROTEOBACTERIA</i>	2.422	0 - 5	Normal
<i>FIRMICUTES</i>	41.220	50 - 65	Low
<i>ACTINOBACTERIA</i>	1.570	2 - 5	Low
<i>VERRUCOMICROBIA</i>	0.829	2 - 5	Low

Description

Firmicutes, Actinobacteria and Verrucomicrobia are important for muconutritional function, protection and immunoregulation. In a normal Microbiota, this set of Phyla should be in a range between 55% -72%

The Phylum Bacteroidetes is involved in the fermentation of various sources of polysaccharides, proteins and the production of vitamins and other essential molecules for our nutrition. The normal values would move in a range between 20 and 40%

Proteobacteria are one of the main phylum of bacteria. They include a wide variety of pathogens, free-living bacteria, and even bacteria responsible for nitrogen fixation. There is a great diversity of forms between them. All Proteobacteria are Gram negative, with a cell wall made up mainly of lipopolysaccharides. Regarding the type of metabolism, the vast majority are anaerobic. The normal values in the intestinal microbiota would move in a range below 5%.

BIODIVERSITY

Ratios	Value [%]	Reference [%]	Assessment
<i>Firmicutes / Bacteroidetes</i>	0.787	1 - 3	Low
<i>Firmicutes + Bacteroidetes</i>	93.564	85 - 90	High
<i>Bacteroides / Prevotella</i>	461.025	2 - 3	High

Description

Firmicutes and Bacteroidetes are the most abundant Phyla of the healthy Gut Microbiota. The sum of both has to be around 85-90% of the healthy Intestinal Microbiota. The ratio between them has to be between 1 and 3. Values below or above this range are indicative of Dysbiosis.

The Bacteroides / Prevotella index is related to the habits and type of feeding of the patient. High values of this index are indicative of a Western diet rich in proteins, carbohydrates and fats of animal origin compared to the consumption of other sources of protein and vegetable carbohydrates.

BACTERIAL OVERGROWTH

Species / subspecies	Value [%]	Reference [%]
<i>Phocaeicola dorei</i>	17.160	0.5 - 5

Se ha sugerido que, a niveles elevados, podrían desempeñar algún papel en algunas patologías clínicas, como la diabetes tipo 1. Por otro lado, también se ha descrito que *P. dorei* junto con *P. vulgatus* reducen la producción de los lipopolisacáridos microbianos intestinales e inhibición de la aterosclerosis. Fue más común en pacientes con enfermedad celíaca activa que en aquellos con enfermedad celíaca controlada. Algunos estudios de celiaquía han encontrado que, su presencia era más común en pacientes con enfermedad celíaca activa que en aquellos con enfermedad celíaca controlada.

BACTERIA POSITIVELY RELATED TO INTESTINAL HOMEOSTASIS

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Anaerostipes hadrus</i>	Firmicutes	5.384	2 - 6	Normal
<i>Anaerobutyricum hallii</i>	Firmicutes	2.574	1 - 3	Normal
<i>[Eubacterium rectale</i>	Firmicutes	2.050	1 - 6	Normal
<i>Faecalibacterium prausnitzii</i>	Firmicutes	1.822	5 - 15	Low
<i>Roseburia intestinalis</i>	Firmicutes	0.967	1 - 3	Low
<i>Akkermansia muciniphila</i>	Verrucomicrobia	0.821	2 - 5	Low
<i>Roseburia hominis</i>	Firmicutes	0.211	1 - 3	Low

Description

Bacteria important in muconutritional function are generally at normal or moderately low levels. Despite this, we believe that the whole of the Microbiota could be sufficient to satisfy the levels of butyrate necessary to nourish intestinal colonocytes. However, your nutritionist will assess whether you need an external supply of butyrate.

Akkermansia muciniphila when altered can negatively affect the stability of the intestinal mucosa. This bacterium is essential for the maintenance of mucus and maintaining the intestinal barrier function. Improves host metabolic markers, such as insulin sensitivity and endotoxemia. Producer of short chain fatty acids that are beneficial to the host and other members of the Microbiota. It is the key species in intestinal maintenance.

Estructura funcional de la microbiota

MUCONUTRITIVE MICROBIOTA. BUTYRATE PRODUCER

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>[Ruminococcus torques</i>	Firmicutes	3.401	0.9 - 1.3	High
<i>Anaerostipes caccae</i>	Firmicutes	0.125	0.01 - 0.1	Moderate
<i>Anaerostipes hadrus</i>	Firmicutes	5.384	2 - 6	Normal
<i>Anaerobutyricum hallii</i>	Firmicutes	2.574	1 - 3	Normal
<i>[Eubacterium rectale</i>	Firmicutes	2.050	1 - 6	Normal
<i>Lachnospiraceae bacterium Choco86</i>	Firmicutes	0.642	0.5 - 5	Normal
<i>Coprococcus catus</i>	Firmicutes	0.534	0.1 - 0.7	Normal
<i>Flavonifractor plautii</i>	Firmicutes	0.247	0.2 - 1	Normal
<i>Dysosmobacter welbionis</i>	Firmicutes	0.107	0 - 0.5	Normal
<i>Coprococcus sp. ART55/1</i>	Firmicutes	0.102	0 - 0.7	Normal
<i>Butyrivibrio fibrisolvens</i>	Firmicutes	0.056	0.01 - 0.1	Normal
<i>Butyrivibrio proteoclasticus B316</i>	Firmicutes	0.027	0.01 - 0.1	Normal
<i>Butyrivibrio hungatei</i>	Firmicutes	0.026	0 - 0.1	Normal
<i>Clostridium butyricum</i>	Firmicutes	0.019	0.01 - 0.1	Normal
<i>Clostridium pasteurianum</i>	Firmicutes	0.011	0.01 - 0.1	Normal
<i>Faecalibacterium prausnitzii</i>	Firmicutes	1.822	5 - 15	Low
<i>Roseburia intestinalis</i>	Firmicutes	0.967	1 - 3	Low
<i>Faecalibacterium prausnitzii L2-6</i>	Firmicutes	0.745	5 - 15	Low
<i>Lachnospiraceae bacterium GAM79</i>	Firmicutes	0.462	0.5 - 5	Low
<i>Faecalibacterium prausnitzii SL3/3</i>	Firmicutes	0.283	5 - 15	Low
<i>Roseburia hominis</i>	Firmicutes	0.211	1 - 3	Low
<i>[Eubacterium siraeum</i>	Firmicutes	0.201	1 - 6	Low
<i>butyrate-producing bacterium SS3/4</i>	Firmicutes	0.199	0.2 - 1	Low
<i>Lachnospira eligens</i>	Firmicutes	0.112	0.5 - 9	Low
<i>Oscillibacter sp. PEA192</i>	Firmicutes	0.092	0.1 - 0.5	Low
<i>Anaerostipes rhamnosivorans</i>	Firmicutes	0.057	1 - 6	Low
<i>Eubacterium limosum</i>	Firmicutes	0.055	1 - 6	Low
<i>Oscillibacter valericigenes Sjm18-20</i>	Firmicutes	0.030	0.1 - 0.5	Low
<i>Butyricimonas faecalis</i>	Bacteroidetes	0.026	0.25 - 1	Low
<i>Intestinimonas butyriciproducens</i>	Firmicutes	0.010	0.1 - 0.5	Low
<i>Eubacterium maltosivorans</i>	Firmicutes	0.006	1 - 6	Low
<i>Porphyromonas asaccharolytica</i>	Bacteroidetes	0.006	0.01 - 0.1	Low
<i>Clostridium tyrobutyricum</i>	Firmicutes	0.003	0.01 - 0.1	Low
<i>Megasphaera stantonii</i>	Firmicutes	0.003	0.01 - 0.1	Low
<i>Clostridium acetobutylicum</i>	Firmicutes	0.002	0.01 - 0.1	Low
<i>Clostridium drakei</i>	Firmicutes	0.002	0.01 - 0.1	Low
<i>Olsenella sp. GAM18</i>	Actinobacteria	0.002	0.01 - 0.1	Low

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Acidaminococcus intestini</i>	Firmicutes	0.001	0.1 - 1	Low
<i>Olsenella uli DSM 7084</i>	Actinobacteria	0.001	0.01 - 0.1	Low
<i>Faecalibacterium prausnitzii A2-165</i>	Firmicutes	0.001	5 - 15	Low
<i>Roseburia faecis</i>	Firmicutes	0.000	1 - 3	Not Present
<i>Eisenbergiella massiliensis</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Roseburia cecicola</i>	Firmicutes	0.000	1 - 3	Not Present
<i>Coprococcus eutactus</i>	Firmicutes	0.000	0.1 - 0.7	Not Present
<i>Butyricoccus pullicaecorum</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Agathobaculum desmolans</i>	Firmicutes	0.000	0.01 - 0.1	Not Present
<i>Roseburia inulinivorans</i>	Firmicutes	0.000	1 - 3	Not Present
<i>Eubacterium ramulus</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Holdemanella bififormis</i>	Firmicutes	0.000	0.01 - 0.1	Not Present
<i>Eisenbergiella tayi</i>	Firmicutes	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 19.576

Relative sum among genera, species and subspecies.

Description

Approximately 40-50% of the energy available from carbohydrates in the diet is converted to SCFAs such as acetate, propionate, and butyrate by the colonic microbiota. Butyrate, a short-chain fatty acid, and butyrate-producing bacteria both play an important role in maintaining intestinal homeostasis and intestinal epithelial integrity. Butyrate is a very important nutrient for colonocytes. It also has anti-cancer, antioxidant, and anti-inflammatory effects.

The butyrate-producing microbiota, below 15% might not be sufficient to satisfy the levels of butyrate to nourish intestinal colonocytes. However, your doctor will assess whether you need an external supply of butyrate.

Faecalibacterium prausnitzii is a fundamental member for intestinal homeostasis. It is one of the most abundant bacteria in the healthy human microbiota, its reference values are approximately between 5-15%. They are producers of butyrate (SCFA). It also has immunomodulatory properties, inducing anti-inflammatory effects by stimulating the secretion of the anti-inflammatory cytokine IL-10.

[*Eubacterium*] *rectale* and [*Eubacterium*] *siraeum* belong to the group of butyrate-producing bacteria of the Lachnospiraceae family.

[*Eubacterium*] *siraeum* has been described in the medical literature as it is elevated in some inflammatory diseases such as ankylosing spondylitis.

Roseburia intestinalis and *Roseburia hominis* are butyrate-producing intestinal bacteria. They protect the colonic mucosa against the development of inflammation and inflammatory bowel diseases (IBD). The genus *Roseburia*, between 1 and 3% is considered normal.

Anaerobutyricum halli, is a prominent member of the butyrate-producing microbiota in the gut.

Anaerostipes hadrus and *Anaerostipes rhamnosivorans* are butyrate-producing bacteria of our intestinal microbiome. They have been found to be more abundant in healthy individuals than in people with inflammatory bowel diseases.

REGULATORY MICROBIOTA OF INTESTINAL MUCUS

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
<i>Akkermansia muciniphila</i>	Verrucomicrobia	0.821	2 - 5	Low
<i>Bifidobacterium dentium</i>	Actinobacteria	0.000	0.02 - 0.2	Not Present
Relative Percentage of Bacterial Microbiota:		5.145		

Relative sum among genera, species and subspecies.

Description

Akkermansia muciniphila colonizes the outer mucus layer of the human intestine where it triggers metabolic and immune responses of the host. This bacterium is particularly effective in thickening mucus and increasing the intestinal barrier function. As a result, the host's metabolic markers improve. The host regulatory mechanism is believed to involve the composition of the outer membrane, including *A. muciniphila* type IV pili, which are direct signals from host immune receptors. At the same time, its metabolic activity leads to the production of short chain fatty acids, which are beneficial to the host and members of the microbiota. This contributes to the host microbiota and microbe syntrophy. Mucolytic activity and metabolite production make *Akkermansia muciniphila* a key species in the mucus layer, stimulating beneficial mucosal microbial networks.

Bifidobacterium species colonize the intestinal mucus layer and can modulate mucus production by goblet cells. However, they can also degrade the protective glycans of mucin proteins.

Bifidobacterium dentium, a species of human origin, increases the synthesis and expulsion of intestinal mucus, without extensive degradation of mucin glycans. *B. dentium* lacks the enzymes necessary to extensively degrade mucin glycans. *B. dentium* is able to improve intestinal mucus layer and goblet cell function by upregulating gene expression and autophagy signaling pathways, with a net increase in mucin production.

Bifidobacterium dentium Fortifies the Intestinal Mucus Layer via Autophagy and Calcium Signaling Pathways. Melinda A. Engevik, Berkley Luk, Alexandra L. Chang- Graham, Anne Hall, Beatrice Herrmann, Wenly Ruan, Bradley T. Endres, Zhongcheng Shi, Kevin W. Garey, Joseph M. Hyser and James Versalovica

INTESTINAL MUCUS-CONSUMING MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0.5 - 1	High
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
[<i>Ruminococcus torques</i>	Firmicutes	3.401	0.15 - 2.7	Moderate
[<i>Ruminococcus gnavus</i>	Firmicutes	0.929	0.4 - 0.8	Moderate
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Phocaeicola vulgatus</i>	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Muribaculaceae bacterium DSM 108610</i>	Bacteroidetes	0.004	0 - 0.5	Normal
<i>Hafnia alvei</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Bacteroides cellulosilyticus</i>	Bacteroidetes	0.053	0.5 - 4	Low
<i>Bacteroides caccae</i>	Bacteroidetes	0.034	0.25 - 2.8	Low
<i>Mucispirillum schaedleri</i>	Deferribacteres	0.000	0 - 0.1	Not Present
<i>Bacteroides acidifaciens</i>	Bacteroidetes	0.000	0.5 - 1	Not Present

Relative Percentage of Bacterial Microbiota: 17.798

Relative sum among genera, species and subspecies.

Description

The intestinal mucosa is composed of a monolayer of polarized columnar epithelial cells, as well as the subepithelial region that contains the lamina propria, the enteric nervous system, the connective tissue, and the muscle layers. Enterocytes, Goblet cells, which synthesize and release mucin, Paneth cells, which synthesize antimicrobial peptides, enterochromaffin cells, which produce hormones and other substances, and intestinal stem cells are present in the epithelium.

Above the epithelial barrier is the mucus layer, which is composed of the non-agitated mucus layer, which contains glyocalyx, and then the agitated mucus layer, which contains the microbiota, secretory IgA, mucins, and antimicrobial peptides.

The mucosal surface of the gastrointestinal tract establishes an effective barrier between the internal environment and the external environment, preventing the passage of potentially harmful substances. The intestinal mucosa is a semi-permeable barrier that allows the selective passage of certain substances and prevents the access of others. It ensures adequate containment of luminal contents within the intestine while preserving the ability to absorb nutrients. The separation that this provides between the body and the intestine prevents the uncontrolled translocation of luminal contents to the body itself.

The intestinal barrier plays a role in protecting the tissues of the intestinal mucosa and the circulatory system against exposure to pro-inflammatory molecules, such as microorganisms, toxins, antigens and is vital for the maintenance of health and well-being.

Dysfunction of the intestinal barrier has been implicated in numerous pathologies such as: food allergies, microbial infections, irritable bowel syndrome, inflammatory bowel disease, celiac disease, metabolic syndrome, nonalcoholic fatty liver disease, diabetes, and septic shock.

The decrease in both types of bacteria is very negative for maintaining the integrity of the intestinal wall (intestinal homeostasis), which favors an increase in intestinal permeability due to a deterioration of tight junctions, which allows the passage of intestinal content to the stream blood, with its serious consequences such as: Increased liver toxic load and increased antigenic load among others.

PROTECTIVE AND CONTAINMENT MICROBIOTA

Global assessment: LOW

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	High
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
<i>Streptococcus</i>	Firmicutes	0.633	0.01 - 0.5	Moderate
<i>Blautia obeum</i>	Firmicutes	2.910	1 - 6	Normal
<i>Bifidobacterium</i>	Actinobacteria	0.582	0.5 - 1	Normal
<i>Bifidobacterium longum</i>	Actinobacteria	0.325	0.1 - 0.5	Normal
<i>Collinsella aerofaciens</i>	Actinobacteria	0.291	0.08 - 2.45	Normal
<i>Streptococcus salivarius</i>	Firmicutes	0.245	0.01 - 0.5	Normal
<i>Enterococcus</i>	Firmicutes	0.146	0.1 - 0.5	Normal
<i>Enterococcus faecium</i>	Firmicutes	0.056	0.01 - 0.1	Normal
<i>Enterococcus faecalis</i>	Firmicutes	0.040	0.01 - 0.1	Normal
<i>Bacillus</i>	Firmicutes	0.145	0.5 - 1	Low
<i>Streptomyces</i>	Actinobacteria	0.058	0.5 - 1	Low
<i>Eubacterium limosum</i>	Firmicutes	0.055	1 - 6	Low

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Leuconostoc</i>	Firmicutes	0.044	0.1 - 1	Low
<i>Lactococcus</i>	Firmicutes	0.042	0.1 - 1	Low
<i>[Eubacterium cellulosolvans 6</i>	Firmicutes	0.033	1 - 6	Low
<i>Lactobacillus</i>	Firmicutes	0.028	0.5 - 1	Low
<i>Weissella</i>	Firmicutes	0.016	0.1 - 1	Low
<i>Bifidobacterium breve</i>	Actinobacteria	0.011	0.1 - 0.5	Low
<i>Bifidobacterium adolescentis</i>	Actinobacteria	0.008	0.1 - 0.5	Low
<i>Lactobacillus salivarius</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Veillonella parvula</i>	Firmicutes	0.002	0.01 - 0.05	Low
<i>Lactobacillus reuteri</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus allii</i>	Firmicutes	0.000	0.06 - 0.1	Not Present
<i>Enterococcus durans</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Lactobacillus kefiri</i>	Firmicutes	0.000	0.06 - 0.1	Not Present
<i>Pediococcus inopinatus</i>	Firmicutes	0.000	0 - 0.1	Not Present

Relative Percentage of Bacterial Microbiota: 9.578

Relative sum among genera, species and subspecies.

Description

The protective bacterial microbiota provides the microenvironment that prevents the overgrowth of proteolytic bacteria and pathogens. The balance between the resident bacterial species confers stability to the entire microbial population. The barrier effect is due to the ability of certain bacteria to secrete antimicrobial substances (Bacteriocins), which inhibit the proliferation of other bacteria and also to the competition between bacteria for system resources, either nutrients or ecological spaces.

Bifidobacterium adolescentis when abundant, is usually due to the use of probiotics of the mentioned bacterial species. Probiotics should always be used under the supervision of a physician. Some experiments have described that metabolites proteins of *Bifidobacterium adolescentis* could generate hepatotoxicity in THLE-2 cells of human origin. Therefore, it would be advisable to carry out a control using liver markers.

B. thetaiotaomicron degrades plant polysaccharides essential for the human intestine, stimulates angiogenesis in the intestine. It also mediates the formation of the intestinal mucosa barrier, which protects the host from invasion by pathogens through the regulation of the expression of species-specific antibiotic proteins.

The genera *Bifidobacterium*, *Enterococcus* and *Lactobacillus* are part of the microbiota associated with the mucosa and play an important role in the protective function and containment of pathogens. Low levels of these genera can compromise their function.

Bifidobacteria reduce intestinal lipopolysaccharide (LPS) levels, decrease pro-inflammatory cytokine levels, improve intestinal motility, and can reduce inflammatory status. When its abundance is diminished it complicates this feature.

The genus *Enterococcus* are lactic acid bacteria (LAB), members of the commensal flora of the human colon. *Enterococcus* can produce Bacteriocins and antimicrobial compounds, which limit the proliferation of pathogens, although they can act as pathogens in certain pathologies.

Collinsella aerofaciens at physiological levels is capable of deconjugating bile acids and this ability to modify bile acids allows to modulate the virulence and pathogenicity of enteric pathogens. Bile acids in pathophysiological conditions are related to inflammatory processes and carcinogenesis of the digestive system.

Bacteria of the genus *Streptomyces* (Actinobacteria phylum) can be found both in the soil and in the intestine. Although there are pathogenic species, it is also a fact that they produce antiproliferative, anti-inflammatory, immunosuppressive and antibiotic compounds. These substances are good allies against allergy and autoimmunity, as well as against inflammatory bowel diseases.

IMMUNOMODULATING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0 - 0.5	High
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	High
<i>Blautia obeum</i>	Firmicutes	2.910	1 - 6	Normal
<i>Parabacteroides distasonis</i>	Bacteroidetes	1.658	0.5 - 2.3	Normal
<i>Blautia sp. SC05B48</i>	Firmicutes	1.278	1 - 6	Normal
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Bifidobacterium longum</i>	Actinobacteria	0.325	0.1 - 0.5	Normal
<i>Collinsella aerofaciens</i>	Actinobacteria	0.291	0.08 - 2.45	Normal
<i>Streptococcus salivarius</i>	Firmicutes	0.245	0.01 - 0.5	Normal
<i>Enterococcus</i>	Firmicutes	0.146	0.1 - 0.5	Normal
<i>Enterococcus faecium</i>	Firmicutes	0.056	0.01 - 0.1	Normal
<i>Enterococcus faecalis</i>	Firmicutes	0.040	0.01 - 0.1	Normal
<i>Enterococcus hirae</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Enterococcus cecorum</i>	Firmicutes	0.002	0 - 0.01	Normal
<i>Roseburia intestinalis</i>	Firmicutes	0.967	1 - 3	Low
<i>Blautia producta</i>	Firmicutes	0.414	1 - 6	Low
<i>Blautia sp. N6H1-15</i>	Firmicutes	0.345	1 - 6	Low
<i>Roseburia hominis</i>	Firmicutes	0.211	1 - 3	Low
<i>Bifidobacterium breve</i>	Actinobacteria	0.011	0.1 - 0.5	Low
<i>Lactobacillus ruminis</i>	Firmicutes	0.008	0.06 - 0.1	Low
<i>Bifidobacterium adolescentis</i>	Actinobacteria	0.008	0.1 - 0.5	Low
<i>Bifidobacterium choerinum</i>	Actinobacteria	0.001	0.1 - 0.5	Low
<i>Bifidobacterium bifidum</i>	Actinobacteria	0.001	0.1 - 1	Low
<i>Lactobacillus saerimneri</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Blautia sp. YL58</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Bifidobacterium dentium</i>	Actinobacteria	0.000	0.1 - 0.5	Not Present
<i>Blautia hansenii DSM 20583</i>	Firmicutes	0.000	1 - 6	Not Present

Relative Percentage of Bacterial Microbiota: 12.855

Relative sum among genera, species and subspecies.

Description

The immune system, in the gastrointestinal tract, acts by controlling the entry and eliminating microorganisms that are pathogens. The immunomodulatory microbiota acts by training our system to be able to differentiate the commensal microbiota from the pathogens and modulates the responses of the immune system reducing inflammatory processes. The loss of the intestinal mucosa and the lack of this immunomodulatory microbiota, allows inflammatory processes to be continuously taking place in the intestinal tract over time, and situations of intestinal permeability may occur.

Bacteroides fragilis at physiological levels this bacterium modulates the induction of host Treg cells and the production of anti-inflammatory cytokines IL-10. *Bacteroides fragilis* is a pathobiont that has the ability, under conditions of an altered ecosystem (Dysbiosis), to cause certain pathologies. When the levels are high in the sample, they are possibly producing a remarkably complex series of pro-inflammatory neurotoxins including surface lipopolysaccharides (BF- LPS) and toxic proteolytic peptides and pro-inflammatory cytokines.

Escherichia coli is a member of the Enterobacteriaceae family and is part of the microbiota of the human gastrointestinal tract. It is a gram-negative, non-demanding, oxidase-negative, catalase-positive, facultative anaerobic bacillus, whose preferential growth temperature is at 37 ° C (mesophilic), mobile by peritrichous flagella. It is the most abundant commensal facultative anaerobic bacterium in the microbiota of the gastrointestinal tract, where, together with other microorganisms, it is essential for the correct functioning of the digestive process: it participates in the production of vitamins B and K; it also exerts an immunomodulatory function when it is at its reference levels: 0.5 - 1%. At high levels, its proteolytic capacity predominates, and this function may be altered.

Parabacteroides distasonis, at physiological levels, appears to exert a metabolic benefit in reducing weight gain, hyperglycemia and hepatic steatosis in animal models (mice) fed a high-fat diet. Treatment with *P. distasonis* in vivo dramatically alters the bile acid profile. Elevates lithocholic acid and ursodeoxycholic acid; and increases the level of succinate in the intestine. In vitro *P. distasonis* demonstrated its ability to transform bile acids and to produce succinate. It appears that it can decrease hyperglycemia, in animal models, through the activation of intestinal gluconeogenesis. *Parabacteroides distasonis* at physiological levels modulate the induction of host Treg cells and the production of anti-inflammatory cytokines IL-10 through the release of PSA associated with the outer membrane vesicles.

Roseburia intestinalis is one of the dominant bacteria in the healthy intestine. It helps protect the lining of the colon against the development of inflammatory disease through the regulation of Treg cells and the inhibition of IL-17 production.

Roseburia hominis promotes intestinal barrier function, innate immunity in the healthy intestine by stimulating Treg cells, promoting tight junctions and adherent junctions of the subepithelial layer of the intestine.

The genus *Roseburia* formed by butyrate-producing and immunomodulating bacteria are healthy for our intestines.

The genus *Roseburia* formed by butyrate-producing and immunomodulating bacteria are healthy for our intestines. Bacteria within the Bacteroidetes and Proteobacteria phyla, at high levels, act negatively on the intestinal epithelium and stimulate inflammatory processes when in contact with the epithelium in the absence of intestinal mucus. Sulphatase-producing species within these groups degrade mucus polysaccharide, which also alters the intestinal mucosa. They promote the mucosal immune response by Th17 and the recruitment of neutrophils. It stimulates the production of IL-8, IL-6 and CCL 20 by epithelial cells. It activates the Toll 2 receptor, which stimulates the production of cytokines IL23, IL1 by Th17.

Bacteria within the Bacteroidetes and Proteobacteria phyla, at high levels, act negatively on the intestinal epithelium and stimulate inflammatory processes when in contact with the epithelium in the absence of intestinal mucus. Sulphatase-producing species within these groups degrade mucus polysaccharide, which also disrupts the intestinal mucosa. They promote the mucosal immune response by Th17 and the recruitment of neutrophils. It stimulates the production of IL-8, IL-6 and MIP3P (CCL20) by epithelial cells. It activates the Toll 2 receptor, which stimulates the production of IL23, IL1 cytokines by Th17.

Mucosal inflammation leads to the systemic spread of inflammatory mediators, bacteria, and bacterial products, which in turn can aggravate the outcomes of systemic disease.

METABOLIC / ENERGY MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Phocaeicola dorei</i>	Bacteroidetes	17.160	0.5 - 5	High
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0 - 0.5	High
<i>Alistipes onderdonkii subsp. vulgaris</i>	Bacteroidetes	2.258	0.175 - 0.8	High
<i>Alistipes onderdonkii</i>	Bacteroidetes	2.258	0.175 - 0.8	High
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
<i>Bacteroides caecimuris</i>	Bacteroidetes	0.125	0 - 0.1	Moderate
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Bacteroides xylanisolvens</i>	Bacteroidetes	3.444	0.5 - 5	Normal
<i>Blautia obeum</i>	Firmicutes	2.910	1 - 6	Normal
<i>Blautia sp. SC05B48</i>	Firmicutes	1.278	1 - 6	Normal
<i>Phocaeicola vulgatus</i>	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Bacteroides sp. A1C1</i>	Bacteroidetes	0.532	0.1 - 1	Normal
<i>Alistipes finegoldii</i>	Bacteroidetes	0.490	0.08 - 0.5	Normal
<i>Alistipes communis</i>	Bacteroidetes	0.473	0.25 - 2	Normal
<i>Ruthenibacterium lactatiformans</i>	Firmicutes	0.269	0.1 - 1	Normal
<i>Alistipes dispar</i>	Bacteroidetes	0.118	0.05 - 0.5	Normal
<i>Alistipes megaguti</i>	Bacteroidetes	0.109	0.02 - 0.2	Normal
<i>Alistipes sp. dk3624</i>	Bacteroidetes	0.037	0.02 - 0.2	Normal
<i>Phocaeicola salanitronis</i>	Bacteroidetes	0.034	0 - 0.1	Normal
<i>Ruminococcus champanellensis</i>	Firmicutes	0.015	0 - 0.04	Normal
<i>Ruminococcus albus</i>	Firmicutes	0.005	0 - 0.05	Normal
<i>Blautia producta</i>	Firmicutes	0.414	1 - 6	Low
<i>Blautia sp. N6H1-15</i>	Firmicutes	0.345	1 - 6	Low
<i>Alistipes shahii WAL 8301</i>	Bacteroidetes	0.102	0.175 - 0.8	Low
<i>Prevotella</i>	Bacteroidetes	0.091	0.5 - 5	Low
<i>Bacteroides intestinalis</i>	Bacteroidetes	0.057	0.2 - 1	Low
<i>Bacteroides cellulosilyticus</i>	Bacteroidetes	0.053	0.5 - 4	Low
<i>Paraprevotella xylaniphila</i>	Bacteroidetes	0.037	0.5 - 5	Low
<i>Bacteroides caccae</i>	Bacteroidetes	0.034	0.25 - 2.8	Low
<i>Ruminococcus bicirculans</i>	Firmicutes	0.017	0.5 - 2.5	Low
<i>Veillonella parvula</i>	Firmicutes	0.002	0.01 - 0.05	Low
<i>Acidaminococcus intestini</i>	Firmicutes	0.001	0.1 - 1	Low
<i>Blautia hansenii</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Blautia faecis</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Chlorobaculum sp. MV4-01-44b_2</i>	Chlorobi	0.000	0.175 - 0.8	Not Present

Relative Percentage of Bacterial Microbiota: **44.745**

Relative sum among genera, species and subspecies.

Description

The species associated with this function perform metabolic conversions that are essential for the host, often related to the degradation of structurally diverse complex proteins or polysaccharides, both of animal and vegetable origin. This metabolic activity is what provides us with sources of energy and nutrients that our body cannot obtain with its own resources. Within the whole of the bacterial microbiota, the Bacteroides present represent the community with the highest fermentation capacity from both animal and vegetable sources.

MICROBIOTA WITH PROTEOLYTIC FUNCTION

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Enterocloster bolteae</i> *** [p]	Firmicutes	0.413	0 - 0.07	High
<i>Clostridioides difficile</i> *** [p]	Firmicutes	0.406	0 - 0.01	High
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	High
[<i>Clostridium innocuum</i> *** [f] [p]	Firmicutes	0.157	0 - 0.01	High
<i>Lacrimispora saccharolytica</i> *** [F] [p]	Firmicutes	0.145	0 - 0.01	High
<i>Enterocloster clostridioformis</i> *** [ff] [p]	Firmicutes	0.110	0 - 0.01	High
<i>Campylobacter</i>	Proteobacteria	0.099	0 - 0.01	High
<i>Alistipes onderdonkii subsp. vulgaris</i>	Bacteroidetes	2.258	0.25 - 2	Moderate
<i>Alistipes onderdonkii</i>	Bacteroidetes	2.258	0.25 - 2	Moderate
<i>Streptococcus</i>	Firmicutes	0.633	0.01 - 0.5	Moderate
<i>Staphylococcus</i>	Firmicutes	0.108	0.01 - 0.1	Moderate
<i>Lacrimispora sphenoides</i> *** [ff] [p]	Firmicutes	0.047	0 - 0.01	Moderate
<i>Salmonella enterica</i>	Proteobacteria	0.013	0 - 0.01	Moderate
<i>Anaerostipes hadrus</i> *** [f] [p]	Firmicutes	5.384	2 - 6	Normal
<i>Phocaeicola vulgatus</i> *** [ff] [p]	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Bacteroides ovatus</i> *** [ff] [p]	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Escherichia coli</i> *** [p]	Proteobacteria	0.593	0.5 - 1	Normal
<i>Alistipes finegoldii</i>	Bacteroidetes	0.490	0.25 - 2	Normal
<i>Alistipes communis</i>	Bacteroidetes	0.473	0.25 - 2	Normal
<i>Clostridium</i>	Firmicutes	0.405	0.2 - 1	Normal
[<i>Clostridium scindens</i> *** [p]	Firmicutes	0.381	0 - 0.5	Normal
<i>Pseudomonas</i>	Proteobacteria	0.298	0 - 0.5	Normal
<i>Enterococcus</i>	Firmicutes	0.146	0.1 - 0.5	Normal
<i>Parabacteroides sp. CT06</i>	Bacteroidetes	0.117	0.1 - 1	Normal
<i>Enterococcus faecium</i>	Firmicutes	0.056	0.01 - 0.1	Normal
<i>Enterococcus faecalis</i>	Firmicutes	0.040	0.01 - 0.1	Normal
<i>Klebsiella pneumoniae</i> *** [F]	Proteobacteria	0.006	0 - 0.01	Normal
<i>Helicobacter</i>	Proteobacteria	0.005	0 - 0.01	Normal
<i>Fusobacterium nucleatum</i>	Fusobacteria	0.004	0 - 0.01	Normal
<i>Clostridium cochlearium</i> *** [F] [p]	Firmicutes	0.004	0 - 0.01	Normal
<i>Fusobacterium varium</i> *** [F] [p]	Fusobacteria	0.004	0 - 0.01	Normal
<i>Citrobacter freundii</i> *** [F] [p]	Proteobacteria	0.003	0 - 0.02	Normal

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Acidaminococcus fermentans</i>	Firmicutes	0.003	0 - 0.04	Normal
<i>Selenomonas ruminantium</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Morganella morganii</i> *** [F]	Proteobacteria	0.002	0 - 0.01	Normal
<i>Lancefieldella</i>	Actinobacteria	0.002	0 - 0.01	Normal
<i>Enterobacter cloacae</i> *** [F]	Proteobacteria	0.002	0 - 0.01	Normal
<i>Proteus vulgaris</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Olsenella uli</i> *** [F] [p]	Actinobacteria	0.001	0 - 0.01	Normal
<i>Citrobacter koseri</i> *** [F]	Proteobacteria	0.001	0 - 0.02	Normal
<i>Propionibacterium</i>	Actinobacteria	0.001	0 - 0.01	Normal
<i>Klebsiella aerogenes</i> *** [F]	Proteobacteria	0.001	0 - 0.01	Normal
<i>Bacillus</i>	Firmicutes	0.145	0.5 - 1	Low
<i>Alistipes dispar</i>	Bacteroidetes	0.118	0.25 - 2	Low
<i>Alistipes megaguti</i>	Bacteroidetes	0.109	0.25 - 2	Low
<i>Alistipes shahii</i> WAL 8301	Bacteroidetes	0.102	0.25 - 2	Low
<i>Streptomyces</i>	Actinobacteria	0.058	0.5 - 1	Low
<i>Alistipes sp. dk3624</i>	Bacteroidetes	0.037	0.25 - 2	Low
<i>Bacteroides caccae</i> *** [f] [p]	Bacteroidetes	0.034	0.25 - 2.8	Low
<i>Bifidobacterium longum subsp. infantis</i> *** [p]	Actinobacteria	0.025	0.1 - 0.5	Low
<i>Enterobacter</i>	Proteobacteria	0.013	0.1 - 0.5	Low
<i>Megasphaera stantonii</i>	Firmicutes	0.003	0.01 - 0.1	Low
<i>Veillonella parvula</i> *** [f] [p]	Firmicutes	0.002	0.01 - 0.05	Low
<i>Clostridium paraputrificum</i> *** [p]	Firmicutes	0.000	0.01 - 0.5	Not Present
<i>Clostridium tetanomorphum</i> *** [F]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Clostridium malenominatum</i> *** [F]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Lacrimispora indolis</i> *** [f] [p]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Lacrimispora celerecrescens</i> *** [f] [p]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Blautia hydrogenotrophica</i> *** [p]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Klebsiella oxytoca</i> *** [F]	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Romboutsia lituseburensis</i> *** [p]	Firmicutes	0.000	0 - 0.01	Not Present
<i>Klebsiella michiganensis</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Cronobacter sakazakii</i> *** [F]	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Fusobacterium necrogenes</i> *** [p]	Fusobacteria	0.000	0 - 0.01	Not Present
<i>Enterococcus durans</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Fusobacterium russii</i> *** [F]	Fusobacteria	0.000	0 - 0.01	Not Present
<i>Fusobacterium necrophorum subsp. necrophorum</i> *** [F]	Fusobacteria	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 15.698

Relative sum among genera, species and subspecies.

Description

Bacteria in the table can be marked with [p] when they are producers of p-cresol, with [f] when they are producers of phenol [F] when they are large producers of phenol or marked with [p] + [f] or [p] + [F] when they are producers of both substances.

The human colonic microbiota is a dense and complex community of commensal microbes, mainly bacteria, which obtain energy and feed in strict anaerobiosis from various types of sources. non-digestible dietary substrates such as carbohydrates (oligosaccharides and polysaccharides) and secretions derived from the host. And the other important source of carbon and energy for colon bacteria is dietary protein.

Proteins ingested in the diet and not absorbed in the small intestine reach the colon and are fermented by the colonic microbiota, producing a variety of harmful metabolites. The results of these metabolic processes are a variety of organic acids, ammonium, H₂S, N-nitroso compounds, indole, skatole, thiol, phenol, and p-cresol resulting from the breakdown and fermentation of proteins. These products are harmful to health and have a variety of harmful effects, including systemic toxicity, nephrotoxicity, and carcinogenesis.

P-cresol is a neurotoxic and nephrotoxic carcinogenic aromatic substance produced by the intestinal microbiota from the amino acid tyrosine. It is found in millimolar concentrations in human feces. 0.8 mM p-cresol inhibits cell proliferation, accumulation of cells in S phase and causes increased cell shedding.

P-cresol is capable of inhibiting the respiration of intestinal cells by proton leakage through the inner mitochondrial membrane, reducing mitochondrial bioenergetic activity and causing a decrease in intracellular ATP content. At concentrations of 1.6 to 3.2 mM p-cresol can have a genotoxic role.

Ultimately p-cresol can uncouple cellular respiration and ATP synthesis, increase DNA damage, and ultimately decrease cellular ATP content. Therefore, p-cresol could act as a metabolic disruptor and as a genotoxic agent for colonocytes.

P-cresol is a potent uremic toxin that accumulates in patients with renal dysfunction. It is clinically relevant in these patients and may have toxicological importance in the treatment of these patients.

P-cresol exerts a selective action on certain commensal bacteria, affecting their reproduction mechanism. And ultimately promoting intestinal dysbiosis.

BILE SALT METABOLIZING MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0.1 - 0.5	High
<i>[Ruminococcus gnavus</i>	Firmicutes	0.929	0 - 0.1	High
<i>Romboutsia ilealis</i>	Firmicutes	0.504	0 - 0.01	High
<i>Enterocloster bolteae</i>	Firmicutes	0.413	0 - 0.01	High
<i>Clostridioides difficile</i>	Firmicutes	0.406	0 - 0.01	High
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	High
<i>Enterocloster clostridioformis</i>	Firmicutes	0.110	0 - 0.01	High
<i>[Ruminococcus torques</i>	Firmicutes	3.401	0.2 - 2.75	Moderate
<i>Blautia obeum</i>	Firmicutes	2.910	0.3 - 2	Moderate
<i>Blautia sp. SC05B48</i>	Firmicutes	1.278	0.7 - 1	Moderate
<i>Anaerocolumna sp. CBA3638</i>	Firmicutes	0.039	0 - 0.01	Moderate
<i>Clostridium perfringens</i>	Firmicutes	0.037	0 - 0.01	Moderate
<i>Coprococcus comes</i>	Firmicutes	1.148	0.2 - 1.3	Normal
<i>Phocaeicola vulgatus</i>	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Roseburia intestinalis</i>	Firmicutes	0.967	0.7 - 2.7	Normal
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Blautia producta</i>	Firmicutes	0.414	0.07 - 1	Normal

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Blautia sp. N6H1-15</i>	Firmicutes	0.345	0.07 - 1	Normal
<i>Roseburia hominis</i>	Firmicutes	0.211	0.2 - 1	Normal
<i>Eubacterium limosum</i>	Firmicutes	0.055	0.01 - 0.1	Normal
<i>Hungatella hathewayi</i>	Firmicutes	0.050	0.02 - 1	Normal
<i>Romboutsia hominis</i>	Firmicutes	0.009	0 - 0.01	Normal
<i>Filifactor alocis</i>	Firmicutes	0.002	0 - 0.01	Normal
<i>Paraclostridium bifermentans</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Paeniclostridium sordellii</i>	Firmicutes	0.019	0.05 - 1.5	Low
<i>Lactobacillus plantarum</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus salivarius</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus fermentum</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Lactobacillus casei</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Lactobacillus buchneri</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Lactobacillus acidophilus</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Tyzzarella nexilis</i>	Firmicutes	0.000	0.22 - 2.73	Not Present
<i>Eubacterium barkeri</i>	Firmicutes	0.000	0.01 - 0.06	Not Present
[<i>Clostridium symbiosum</i>	Firmicutes	0.000	0 - 0.5	Not Present
<i>Eubacterium oxidoreducens</i>	Firmicutes	0.000	0.01 - 0.1	Not Present
<i>Enterocloster lavalensis</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Enterocloster citroniae</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Anaerocolumna aminovalerica</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Lactobacillus leichmannii</i>	Firmicutes	0.000	0.06 - 0.1	Not Present
<i>Enterocloster asparagiformis</i>	Firmicutes	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 18.769

Relative sum among genera, species and subspecies.

Description

After a meal, bile acids are secreted into the small intestine, through the bile duct, where they play a very important role in digestion as they act as detergents (emulsifiers) to help digest fats (turn them into droplets smaller to facilitate the work of digestive enzymes). The vast majority of bile acids are reabsorbed in the ileum and returned to the liver. The rest, approximately 3%, reach the large intestine and here they will be modified by bile salt deconjugant bacteria and will be transformed into secondary bile acids. In addition, glycine and taurine (which were part of the bile salts) will be released, apart from the secondary bile acids deoxycholic acid and lithocholic acid. These excess secondary bile acids can cause steatorrhea (fat malabsorption) as they do not digest fat as well as primary bile acids. For this reason, if this panel is elevated, it could cause diarrhea due to malabsorption of fats. On the other hand, the production by these bacteria of deoxycholic acid has been shown to have a positive effect by limiting the growth of the pathogenic bacterium *Clostridioides difficile*.

In general, the effects of high bile acid deconjugant bacteria are negative since they could increase the risk of developing colon cancer among other pathologies.

GABA METABOLISM GABA-PRODUCING MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Phocaeicola dorei</i>	Bacteroidetes	17.160	0.5 - 5	High
<i>Alistipes</i>	Bacteroidetes	3.780	0.25 - 2	High
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0 - 0.5	High
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Parabacteroides distasonis</i>	Bacteroidetes	1.658	0.5 - 2.3	Normal
<i>Phocaeicola vulgatus</i>	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Alistipes finegoldii</i>	Bacteroidetes	0.490	0.08 - 0.5	Normal
<i>Bifidobacterium longum</i>	Actinobacteria	0.325	0.1 - 0.5	Normal
<i>Streptococcus thermophilus</i>	Firmicutes	0.012	0.01 - 0.5	Normal
<i>Alistipes indistinctus</i>	Bacteroidetes	0.036	0.05 - 0.5	Low
<i>Bacteroides caccae</i>	Bacteroidetes	0.034	0.25 - 2.8	Low
<i>Bifidobacterium adolescentis</i>	Actinobacteria	0.008	0.1 - 0.5	Low
<i>Lactobacillus delbrueckii</i>	Firmicutes	0.005	0.06 - 0.1	Low
<i>Lactobacillus hilgardii</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus plantarum</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactococcus lactis subsp. lactis</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus reuteri</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus brevis</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Bifidobacterium angulatum</i>	Actinobacteria	0.001	0.1 - 0.5	Low
<i>Bifidobacterium dentium</i>	Actinobacteria	0.000	0.1 - 0.5	Not Present
<i>Parabacteroides merdae</i>	Bacteroidetes	0.000	0 - 0.1	Not Present
<i>Alistipes putredinis</i>	Bacteroidetes	0.000	0.25 - 2	Not Present
<i>Lactobacillus paracasei</i>	Firmicutes	0.000	0.06 - 0.1	Not Present
<i>Ruminococcus bromii</i>	Firmicutes	0.000	0.1 - 1	Not Present
<i>Dorea longicatena</i>	Firmicutes	0.000	0 - 0.1	Not Present

Relative Percentage of Bacterial Microbiota: 37.329

Relative sum among genera, species and subspecies.

GABA METABOLISM GABA-CONSUMING MICROBIOTA

Global assessment: LOW

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Staphylococcus</i>	Firmicutes	0.108	0.01 - 0.1	Moderate
<i>Pseudomonas</i>	Proteobacteria	0.298	0 - 0.5	Normal
<i>Acinetobacter</i>	Proteobacteria	0.032	0 - 0.1	Normal
<i>Corynebacterium</i>	Actinobacteria	0.019	0 - 0.1	Normal
<i>Brevibacterium</i>	Actinobacteria	0.002	0 - 0.1	Normal
<i>Kocuria</i>	Actinobacteria	0.001	0 - 0.1	Normal
<i>Bacillus</i>	Firmicutes	0.145	0.5 - 1	Low
<i>Streptomyces</i>	Actinobacteria	0.058	0.5 - 1	Low
<i>Evtapia gabavorous</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Chlorobaculum sp. MV4-01-44b_2</i>	Chlorobi	0.000	0.175 - 0.8	Not Present

Relative Percentage of Bacterial Microbiota: 0.664

Relative sum among genera, species and subspecies.

Description

Gamma-aminobutyric acid (GABA) is a widely distributed neurotransmitter in neurons of the cerebral cortex. It is used by the neurons of the nervous system to communicate with each other in the so-called synaptic spaces by which they connect with each other. Its function is to be an inhibitory neurotransmitter, since it sends chemical messages through the brain and nervous system. In other words, it participates in the communication between neurons. The role of GABA is to inhibit or reduce neuronal activity. It is important in behavior, cognition, and the body's response to stress. Helps control fear and anxiety when neurons are over-excited. Low GABA levels are associated with anxiety disorders, sleep problems, depression, and schizophrenia.

Bacteria of the genus *Alistipes* can express glutamate decarboxylase, an enzyme that metabolizes glutamate to aminobutyric acid (GABA). When *Alistipes* levels are high, you could be increasing your intestinal GABA levels.

Your doctor or nutritionist will assess how possible alterations may affect you.

METABOLISM OF ISOFLAVONES (S-EQUOL). M. PRODUCERS

Global assessment: LOW

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	High
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Bifidobacterium longum</i>	Actinobacteria	0.325	0.1 - 0.5	Normal
<i>Enterococcus faecium</i>	Firmicutes	0.056	0.01 - 0.1	Normal
<i>Fingoldia magna</i>	Firmicutes	0.022	0 - 0.1	Normal
<i>Blautia producta</i>	Firmicutes	0.414	1 - 6	Low
<i>Eggerthella sp. YY7918</i>	Actinobacteria	0.005	0.01 - 0.1	Low
<i>Adlercreutzia sp. 8CFGBH1</i>	Actinobacteria	0.005	0.01 - 0.1	Low
<i>Bifidobacterium pseudolongum</i>	Actinobacteria	0.002	0.1 - 0.5	Low
<i>Bifidobacterium animalis</i>	Actinobacteria	0.002	0.1 - 0.5	Low

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Adlercreutzia equolifaciens</i>	Actinobacteria	0.002	0.01 - 0.3	Low
<i>Lactococcus garvieae</i>	Firmicutes	0.001	0.01 - 0.1	Low
<i>Asaccharobacter celatus</i>	Actinobacteria	0.001	0.01 - 0.1	Low
<i>Lactobacillus mucosae</i>	Firmicutes	0.001	0.01 - 0.1	Low
<i>Streptococcus intermedius</i>	Firmicutes	0.001	0.01 - 0.5	Low
<i>Enterorhabdus mucosicola</i>	Actinobacteria	0.000	0.01 - 0.1	Not Present
<i>Paraeggerthella sp. SNR40-432</i>	Actinobacteria	0.000	0.01 - 0.1	Not Present
<i>Slackia equolifaciens</i>	Actinobacteria	0.000	0.01 - 0.1	Not Present
<i>Slackia isoflavoniconvertens</i>	Actinobacteria	0.000	0.01 - 0.1	Not Present
<i>Eggerthella sinensis</i>	Actinobacteria	0.000	0.01 - 0.1	Not Present

Relative Percentage of Bacterial Microbiota: 2.067

Relative sum among genera, species and subspecies.

METABOLISM OF ISOFLAVONES (S-EQUOL). M. CONSUMERS

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Tannerella forsythia</i>	Bacteroidetes	0.001	0 - 0.01	Normal
<i>Bacteroides acidifaciens</i>	Bacteroidetes	0.000	0.5 - 1	Not Present

Relative Percentage of Bacterial Microbiota: 4.774

Relative sum among genera, species and subspecies.

Description

People with diets rich in isoflavones have a significantly lower incidence of cardiovascular disease, osteoporosis, and some types of cancer. The clinical effectiveness of soy isoflavones may be a function of their biotransformation by the Intestinal Microbiota of each person. Bacteria involved in isoflavone metabolism are usually decompensated.

S-equol, estrogen isoflavandiol, is the product of the metabolism of daidzein, a type of isoflavone found in soybeans and other vegetable sources, by the bacterial flora in the intestine. Therefore, the bioconversion of isoflavones into S-equol is only possible if there is a presence of viable S-equol-producing bacterial taxa.

STROBOLOMA-FORMING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Shigella</i>	Proteobacteria	0.033	0 - 0.01	Moderate
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Bacteroides xylanisolvens</i>	Bacteroidetes	3.444	0.5 - 5	Normal
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Clostridium</i>	Firmicutes	0.405	0.2 - 1	Normal
<i>Salmonella</i>	Proteobacteria	0.014	0 - 0.1	Normal
<i>Roseburia intestinalis</i>	Firmicutes	0.967	1 - 3	Low
<i>Faecalibacterium prausnitzii L2-6</i>	Firmicutes	0.745	5 - 15	Low
<i>Roseburia hominis</i>	Firmicutes	0.211	1 - 3	Low
<i>Lachnospira eligens</i>	Firmicutes	0.112	0.5 - 9	Low
<i>Faecalibacterium prausnitzii A2-165</i>	Firmicutes	0.001	5 - 15	Low
<i>Faecalibacterium prausnitzii M21/2</i>	Firmicutes	0.000	5 - 15	Not Present
Relative Percentage of Bacterial Microbiota:		12.260		

Relative sum among genera, species and subspecies.

Description

We call stroboloma the set of bacteria that have genes capable of producing the so-called beta-glucuronidase enzyme, which will modulate the enterohepatic circulation of estrogens and thus determine the circulating amounts of these hormones and their excretion.

During phase II of liver detoxification, estrogens bind to glucuronic acid in order to be subsequently eliminated via the intestine. They reach the intestine through the bile, and are subsequently eliminated with the feces. But a part of these estrogens are deconjugated by the beta-glucuronidase enzyme at the intestinal level, and when they are released in an active form, they are reabsorbed into the bloodstream. In healthy patients there is a balance that serves to maintain proper estrogen hemostasis.

In patients with intestinal dysbiosis, this enzyme may be elevated or decreased, and this will deconjugate a greater or lesser amount of estrogens at the intestinal level. Which will produce an increase or decrease in circulating active estrogens, thus being able to bind to hormone receptors and, therefore, affect all the processes that depend on it.

Estrogen regulates fat deposits and adipocyte differentiation, the reproductive cycle, cardiovascular wellness, bone turnover, and cell replication. Intestinal dysbiosis, therefore, can disrupt the stroboloma, which in turn adversely affects estrogen homeostasis and sugar and lipid metabolism.

Among the bacteria that produce this enzyme, we have 94% of all species and strains of *E. coli*. Also some strains of *Shigella* and *Salmonella*. But we also have, *Roseburia intestinalis*, *Roseburia hominis*, *Faecalibacterium prausnitzii M21 / 2*, *Faecalibacterium prausnitzii L2-6*, *Faecalibacterium prausnitzii A2-165* (DMS 17677), *Bacteroidetes ovatus* and bacteria of the genus *Clostridium*.

When in a microbiota we find elevated *Bacteroides ovatus* and bacteria of the genus *Clostridium*, there may be an increase in circulating active estrogens, to be confirmed or ruled out with an analysis.

When estrogens increase they can lead to:

- Premenstrual syndrome with fluid retention, breast pain, mood alteration among others.
- Alterations in menstruation with irregular or very abundant periods.
- Endometrial hyperplasia, a condition that causes an increase in the amount of menstruation and is a known risk factor for endometrial cancer. Precise treatment and periodic control.
- Breast pain (mastalgia and mastodynia).
- Risk factor for breast cancer, endometrial cancer.
- Promotes estrogen-dependent gynecological diseases such as fibroids and endometriosis.
- When they decrease they can have a negative effect on polycystic ovaries and premenopause.

MICROBIOTA PRODUCING BIOGENIC AMINES (HISTAMINE)

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Clostridium perfringens</i>	Firmicutes	0.037	0 - 0.01	Moderate
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Lactococcus lactis</i>	Firmicutes	0.029	0.01 - 0.05	Normal
<i>Yarrowia lipolytica</i>	Ascomycota	0.007	0 - 0.01	Normal
<i>Klebsiella pneumoniae</i>	Proteobacteria	0.006	0 - 0.01	Normal
<i>Debaryomyces hansenii</i>	Ascomycota	0.002	0 - 0.01	Normal
<i>Tetragenococcus halophilus</i>	Firmicutes	0.002	0 - 0.1	Normal
<i>Cyberlindnera jadinii</i>	Ascomycota	0.002	0 - 0.01	Normal
<i>Proteus vulgaris</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Morganella morganii</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Klebsiella aerogenes</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Raoultella planticola</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Hafnia alvei</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Enterobacter</i>	Proteobacteria	0.013	0.1 - 0.5	Low
<i>Lactobacillus reuteri</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus hilgardii</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Oenococcus oeni</i>	Firmicutes	0.002	0.01 - 0.05	Low
<i>Lactobacillus casei</i>	Firmicutes	0.001	0.01 - 0.05	Low
<i>Lactobacillus vaginalis</i>	Firmicutes	0.001	0.01 - 0.05	Low
<i>Lactobacillus parabuchneri</i>	Firmicutes	0.001	0.01 - 0.05	Low
<i>Lactobacillus buchneri</i>	Firmicutes	0.001	0.01 - 0.05	Low
<i>Lactobacillus saerimneri</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Lactobacillus sakei</i>	Firmicutes	0.001	0.01 - 0.05	Low
<i>Pediococcus parvulus</i>	Firmicutes	0.000	0.01 - 0.05	Not Present
<i>Streptomyces thermovulgaris</i>	Actinobacteria	0.000	0 - 0.01	Not Present
<i>Geotrichum candidum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Tetragenococcus muriaticus</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Photobacterium phosphoreum</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 0.709

Relative sum among genera, species and subspecies.

Description

Histamine is a biogenic amine that can accumulate in food due to the enzymatic decarboxylation of histidine carried out by certain microorganisms of the Gut Microbiota. The consumption of foods with high concentrations of histamine can cause a series of toxicological effects of a neurological, gastrointestinal or respiratory nature. In fact, histamine is one of the most toxic biogenic amines and is most frequently found in foods, mainly fish and fermented foods. Among fermented foods, it is in cheese where the highest quantities are found, having reported concentrations higher than 1,800 mg of histamine per kg of cheese. Histamine intolerance is usually associated with alterations in the serum expression of the enzyme Diamine Oxidase. Alterations in the AOC1 gene, some pathological genetic variants, can generate a DAO deficit.

METABOLIC MICROBIOTA OF TRIMETHYLAMINE

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Lacrimispora sphenoides</i>	Firmicutes	0.047	0 - 0.01	Moderate
<i>Clostridium sporogenes</i>	Firmicutes	0.036	0 - 0.01	Moderate
<i>Clostridium botulinum</i>	Firmicutes	0.033	0 - 0.01	Moderate
<i>Klebsiella</i>	Proteobacteria	0.009	0 - 0.1	Normal
<i>Clostridium baratii</i>	Firmicutes	0.007	0 - 0.01	Normal
<i>Desulfovibrio desulfuricans</i>	Proteobacteria	0.005	0 - 0.01	Normal
<i>Pseudomonas putida</i>	Proteobacteria	0.005	0 - 0.01	Normal
<i>Clostridium scatologenes</i>	Firmicutes	0.004	0 - 0.01	Normal
<i>Tissierella</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Clostridium formicaceticum</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Hathewayia histolytica</i>	Firmicutes	0.002	0 - 0.01	Normal
<i>Proteus vulgaris</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Hathewayia</i>	Firmicutes	0.002	0 - 1	Normal
<i>Gottschalkia</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Shewanella putrefaciens</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Serratia marcescens</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Prevotella</i>	Bacteroidetes	0.091	0.5 - 5	Low
<i>Streptococcus sanguinis</i>	Firmicutes	0.009	0.01 - 0.5	Low
<i>Clostridium putrefaciens</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Clostridium oceanicum</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Mobiluncus curtisii</i>	Actinobacteria	0.000	0 - 0.01	Not Present
<i>Mobiluncus mulieris</i>	Actinobacteria	0.000	0 - 0.01	Not Present
<i>Clostridium carnis</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Aminobacter aminovorans</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Clostridium sardiniense</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Clostridium sordelli</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Sinorhizobium meliloti</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Hathewayia limosa</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Acinetobacter calcoaceticus</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 0.257

Relative sum among genera, species and subspecies.

Description

Trimethylamine is an organic compound that is a product of the decomposition of animals and plants. It is the main substance responsible for the unpleasant odor associated with spoiled fish, some infections, and bad breath. It is found associated with taking large doses of choline and carnitine.

Trimethylamine is made by some intestinal bacteria mainly from choline and carnitine from food. Afterwards, it is absorbed through the intestine, and reaches the liver where it is oxidized to trimethylamine N-oxide (TMAO), which is associated with the development of disease cardiovascular and renal. If there is an overgrowth of trimethylamine-producing bacteria, so as not to increase the risk of atherosclerosis, it is recommended to have a diet low in choline and carnitine (reduce foods of animal origin, especially red meat).

Trimethylaminuria is an autosomal recessive genetic disorder that involves a deficiency of trimethylamine oxidase. It is characterized because the affected organism is unable to metabolize trimethylamine acquired with food. Patients develop a characteristic 'fishy smell'; in sweat, urine and breath after having eaten foods rich in choline.

SUCCINATE-PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0 - 0.5	High
<i>Alistipes onderdonkii subsp. vulgaris</i>	Bacteroidetes	2.258	0.175 - 0.8	High
<i>Alistipes finegoldii DSM 17242</i>	Bacteroidetes	0.490	0.07 - 0.3	Moderate
<i>Parabacteroides distasonis</i>	Bacteroidetes	1.658	0.5 - 2.3	Normal
<i>Phocaeicola vulgatus</i>	Bacteroidetes	1.109	0.5 - 4	Normal
<i>Alistipes communis</i>	Bacteroidetes	0.473	0.25 - 2	Normal
<i>Alistipes dispar</i>	Bacteroidetes	0.118	0.05 - 0.5	Normal
<i>Alistipes megaguti</i>	Bacteroidetes	0.109	0.02 - 0.2	Normal
<i>Alistipes sp. dk3624</i>	Bacteroidetes	0.037	0.02 - 0.2	Normal
<i>Ruminococcus albus</i>	Firmicutes	0.005	0 - 0.05	Normal
<i>Citrobacter freundii</i>	Proteobacteria	0.003	0 - 0.02	Normal
<i>Acidipropionibacterium acidipropionici</i>	Actinobacteria	0.001	0 - 0.01	Normal
<i>Faecalibacterium prausnitzii</i>	Firmicutes	1.822	5 - 15	Low
<i>Akkermansia muciniphila</i>	Verrucomicrobia	0.821	2 - 5	Low
<i>Alistipes shahii WAL 8301</i>	Bacteroidetes	0.102	0.175 - 0.8	Low
<i>Erysipelatoclostridium ramosum</i>	Firmicutes	0.097	0.1 - 1	Low
<i>Bacteroides cellulosilyticus</i>	Bacteroidetes	0.053	0.5 - 4	Low
<i>Paraprevotella xylaniphila</i>	Bacteroidetes	0.037	0.5 - 5	Low
<i>Alistipes indistinctus</i>	Bacteroidetes	0.036	0.05 - 0.5	Low
<i>Barnesiella intestinihominis</i>	Bacteroidetes	0.000	0.01 - 1.5	Not Present
<i>Paraprevotella clara</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Blautia wexlerae</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Propionibacterium freudenreichii subsp. shermanii</i>	Actinobacteria	0.000	0 - 0.01	Not Present
<i>Alloprevotella tanneriae</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Succinivibrio dextrinosolvens</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>uncultured Alistipes sp.</i>	Bacteroidetes	0.000	0.25 - 2	Not Present

Relative Percentage of Bacterial Microbiota: 12.399

Relative sum among genera, species and subspecies.

SUCCINATE-CONSUMING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides thetaiotaomicron</i>	Bacteroidetes	4.323	0.5 - 4	Moderate
<i>Barnesiella viscericola</i>	Bacteroidetes	0.127	0.01 - 1.5	Normal
<i>Phascolarctobacterium faecium</i>	Firmicutes	0.007	0 - 1.5	Normal
<i>Veillonella parvula</i>	Firmicutes	0.002	0.01 - 0.05	Low
<i>Dialister propionificaciens</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Dialister succinatiphilus</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Phascolarctobacterium succinatutens</i>	Firmicutes	0.000	0 - 1.5	Not Present
<i>Ruminococcus bromii</i>	Firmicutes	0.000	0.1 - 1	Not Present

Relative Percentage of Bacterial Microbiota: 4.460

Relative sum among genera, species and subspecies.

Description

The fermentation of plant and dietary fibers, by some bacteria of the intestinal microbiota, produce a large amount of succinate. They can also produce it from the fermentation of amino acids. Succinate is a substrate for the formation of glucose in the intestine. This succinate is believed to help improve glucose and insulin tolerance in the blood, which improves glycemic control. In a healthy intestine, succinate is rarely found because it is quickly consumed by other bacteria to produce propionate (*Bacteroides* among other bacteria). In a situation of dysbiosis due to a series of different causes (having consumed antibiotics, intestinal motility problems, existence of inflammatory bowel disease, etc.), an accumulation of succinate can occur in the intestinal lumen. The causes are believed to be: a reduction in succinate-consuming bacteria, or an increase in succinate-producing bacteria such as *Bacteroides*, *Alistipes*, etc.

There is a strong association between the gut microbiota and circulating succinate in humans, and it is believed that it is more increased in plasma, the higher the intestinal permeability. For example, in patients with Crohn's disease, it has been observed that there is not only an increase in succinate in the intestinal lumen but also in the plasma.

In the event that the microbiota associated with succinate metabolism are decompensated, your doctor will assess how these levels may affect you.

METABOLISM OF TRYPTOPHAN BY THE MICROBIOTA AND THE INTESTINE-BRAIN AXIS

The gut microbial community can modulate the functions of the gut-brain axis through various microbial metabolites, called neuroactive metabolites. These are produced among others through the metabolism of tryptophan. Tryptophan is an essential amino acid in our diet, and it enters this through a series of foods that are particularly rich in this amino acid. Among the foods, especially rich in tryptophan, which consequently increase serotonin levels, are turkey, chicken, milk, cheese, fish, eggs, tofu, soy; sesame, sunflower and pumpkin seeds; walnuts, almonds, hazelnuts; banana, avocado; rice, oatmeal. Legumes such as lentils, beans, and chickpeas.

Tryptophan is metabolized in the intestine through various metabolic pathways in the various intestinal bacterial phyla. The study of the Microbiota in healthy individuals and patients with neurological diseases suggests that there is an association between these metabolic pathways of tryptophan with the etiology of different diseases. Recent studies have speculated on the link between the dysbiotic Gut Microbiota and diseases or disorders of the nervous system such as autism, multiple sclerosis, Parkinson's disease, etc.

Also gut bacteria can limit the availability of tryptophan by metabolizing it to produce indole, tryptamine, indole acetic acid (IAA) and indole propionic acid (IPA), limiting the availability of tryptophan to the host itself. The reduction of circulating tryptophan levels by the Intestinal Microbiota thus affects serotonergic neurotransmission, which influences the functioning of the central and enteric nervous systems. Low serotonin levels are linked to depression, fatigue, and impaired cognitive functions. The production of tryptamine by intestinal bacteria through the action of tryptophan decarboxylase, influences the inhibitory response of cells to serotonin and its release by enterochromaffin cells.

Other metabolites derived from tryptophan by intestinal bacteria are: kinurenine, quinolinate, indole, and indole derivatives. Quinurenine, quinolinate, for example, disrupt brain functions and cause symptoms similar to depression. The sequestration of tryptophan from the host to produce kynurenine and quinolinate reduces the concentration of tryptophan in the blood, which limits the production of serotonin in the brain.

Indole and indole derivatives, including indole acetic acid (IAA) and indole propionic acid (IPA) have been shown to alter CNS metabolism in human and animal studies. Overall, gut microbiome mediated tryptophan catabolism appears to be one of the crucial regulatory factors that is important to the gut-brain axis.

INDOL PRODUCING MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Bacteroides fragilis</i>	Bacteroidetes	3.172	0 - 0.5	High
<i>Alistipes onderdonkii</i>	Bacteroidetes	2.258	0.175 - 0.8	High
<i>Alistipes onderdonkii subsp. vulgaris</i>	Bacteroidetes	2.258	0.175 - 0.8	High
<i>Alistipes finegoldii DSM 17242</i>	Bacteroidetes	0.490	0.07 - 0.3	Moderate
<i>Bacteroides uniformis</i>	Bacteroidetes	4.773	0.5 - 5	Normal
<i>Bacteroides xyloxylophilus</i>	Bacteroidetes	3.444	0.5 - 5	Normal
<i>Bacteroides ovatus</i>	Bacteroidetes	0.961	0.5 - 1	Normal
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Alistipes communis</i>	Bacteroidetes	0.473	0.25 - 2	Normal
<i>Lachnospiraceae bacterium</i>	Firmicutes	0.360	0.1 - 0.5	Normal
<i>Alistipes dispar</i>	Bacteroidetes	0.118	0.05 - 0.5	Normal
<i>Alistipes megaguti</i>	Bacteroidetes	0.109	0.02 - 0.2	Normal
<i>Alistipes sp. dk3624</i>	Bacteroidetes	0.037	0.02 - 0.2	Normal
<i>Prevotella intermedia</i>	Bacteroidetes	0.020	0 - 0.07	Normal
<i>Citrobacter</i>	Proteobacteria	0.015	0 - 0.1	Normal
<i>Clostridiales bacterium</i>	Firmicutes	0.009	0 - 0.01	Normal
<i>Fusobacterium varium</i>	Fusobacteria	0.004	0 - 0.01	Normal
<i>Citrobacter freundii</i>	Proteobacteria	0.003	0 - 0.02	Normal
<i>Fusobacterium ulcerans</i>	Fusobacteria	0.003	0 - 0.01	Normal
<i>Desulfotobacterium hafniense</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Fusobacterium necrophorum</i>	Fusobacteria	0.002	0 - 0.01	Normal
<i>Fusobacterium gonidiaformans</i>	Fusobacteria	0.001	0 - 0.01	Normal
<i>Oxalobacter formigenes</i>	Proteobacteria	0.001	0 - 0.1	Normal
<i>Fusobacterium periodonticum</i>	Fusobacteria	0.001	0 - 0.01	Normal
<i>Fusobacterium nucleatum subsp. animalis</i>	Fusobacteria	0.001	0 - 0.01	Normal
<i>Fusobacterium necrophorum subsp. funduliforme</i>	Fusobacteria	0.001	0 - 0.01	Normal
<i>Propionibacterium</i>	Actinobacteria	0.001	0 - 0.01	Normal
<i>Bacteroides eggerthii</i>	Bacteroidetes	0.162	1 - 5	Low
<i>Alistipes shahii WAL 8301</i>	Bacteroidetes	0.102	0.175 - 0.8	Low
<i>Bacteroides intestinalis</i>	Bacteroidetes	0.057	0.2 - 1	Low
<i>Bacteroides cellulosilyticus</i>	Bacteroidetes	0.053	0.5 - 4	Low
<i>Alistipes indistinctus</i>	Bacteroidetes	0.036	0.05 - 0.5	Low

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Tannerella</i>	Bacteroidetes	0.004	0.1 - 0.6	Low
<i>Acidaminococcus intestini</i>	Firmicutes	0.001	0.1 - 1	Low
<i>Citrobacter youngae</i>	Proteobacteria	0.000	0 - 0.02	Not Present
<i>Dysgonomonas gadei</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Dysgonomonas mossii</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Edwardsiella tarda</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Bacteroides sp. D20</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Escherichia coli D9</i>	Proteobacteria	0.000	0.5 - 1	Not Present
<i>Escherichia coli MS 107-1</i>	Proteobacteria	0.000	0.5 - 1	Not Present
<i>Escherichia coli SE11</i>	Proteobacteria	0.000	0.5 - 1	Not Present
<i>Escherichia coli SE15</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Bacteroides stercoris</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Bacteroides sp. HPS0048</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Bacteroides sp. D22</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Bacteroides sp. D2</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Bacteroides sp.</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Fusobacterium periodonticum 2_1_31</i>	Fusobacteria	0.000	0 - 0.01	Not Present
<i>Bacteroides salyersiae</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Fusobacterium ulcerans ATCC 49185</i>	Fusobacteria	0.000	0 - 0.01	Not Present
<i>Bacteroides oleiciplenus</i>	Bacteroidetes	0.000	0 - 0.1	Not Present
<i>Bacteroides fluxus</i>	Bacteroidetes	0.000	0 - 0.1	Not Present
<i>Odoribacter laneus</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Bacteroides clarus</i>	Bacteroidetes	0.000	0 - 0.1	Not Present
<i>Anaerotruncus colihominis</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Anaerococcus hydrogenalis</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Alistipes putredinis</i>	Bacteroidetes	0.000	0.25 - 2	Not Present
<i>Providencia alcalifaciens</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia rettgeri DSM 1131</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia rustigianii DSM 4541</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia stuartii</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Oxalobacter formigenes OXCC13</i>	Proteobacteria	0.000	0 - 0.1	Not Present

Relative Percentage of Bacterial Microbiota: 17.261

Relative sum among genera, species and subspecies.

Description

Indole, like other metabolites produced by bacteria from tryptophan, is a substance that has the ability to cross the intestinal wall and pass into the blood. Upon reaching the liver, it can be transformed into indoxyl sulfate, which at high concentrations has cytotoxic effects. This can produce an increase in the detoxifying activity of the liver which, if maintained over time, can cause alterations in this organ.

The overgrowth of indole-producing bacteria as a result of the consumption of tryptophan can induce the release of GLP-1 (gluc-like peptide) from the hormone-producing enteroendocrine L-cells of the intestine. GLP-1 has the ability to suppress appetite, insulin release, and can also delay gastric emptying. Low levels of tryptophan decrease intestinal motility.

Indole can cross the blood-brain barrier (BBB) producing chronic inflammatory processes in the brain, which can cause serious cognitive impairment. Increasing indole causes a decrease in tryptophan levels, which decreases levels of serotonin, a neurotransmitter related to mood, depression, and sleep disturbances.

Bacteria of the genus *Alistipes* are also indole positive organisms, which can be produced by hydrolysis of tryptophan in the diet. The sequestration of tryptophan, which is a precursor of serotonin, by these bacteria can negatively affect the gut-brain axis by reducing the bioavailability of serotonin. Therefore, *Alistipes* can have a significant effect on diseases such as depression, anxiety, chronic fatigue syndrome, autism, cirrhosis, and aging.

TRYPTAMINE PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Coprococcus</i>	Firmicutes	1.807	0.2 - 0.7	High
<i>[Ruminococcus gnavus ATCC 29149</i>	Firmicutes	0.273	0 - 0.1	Moderate
<i>Clostridium sporogenes</i>	Firmicutes	0.036	0 - 0.01	Moderate
<i>Lachnospiraceae bacterium</i>	Firmicutes	0.360	0.1 - 0.5	Normal
<i>Desulfitobacterium dehalogenans</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Xenorhabdus nematophila</i>	Proteobacteria	0.001	0 - 0.1	Normal
<i>Bifidobacterium catenulatum</i>	Actinobacteria	0.034	0.1 - 0.5	Low
<i>Lactobacillus delbrueckii subsp. bulgaricus</i>	Firmicutes	0.001	0.06 - 0.1	Low
<i>Holdemania filiformis DSM 12042</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Collinsella tanakaei YIT 12063</i>	Actinobacteria	0.000	0 - 0.1	Not Present
<i>Bifidobacterium catenulatum DSM 16992 = JCM 1194 = LMG 11043</i>	Actinobacteria	0.000	0.1 - 0.5	Not Present
<i>Coprococcus sp. HPP0048</i>	Firmicutes	0.000	0.1 - 0.68	Not Present
<i>Coprococcus sp. HPP0074</i>	Firmicutes	0.000	0.1 - 0.68	Not Present
<i>Collinsella tanakaei</i>	Actinobacteria	0.000	0 - 0.1	Not Present
<i>Enterocloster asparagiformis</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Holdemania filiformis</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Clostridium sporogenes ATCC 15579</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Bacillus atrophaeus</i>	Firmicutes	0.000	0.5 - 1	Not Present
<i>Lachnospiraceae bacterium 2_1_46FAA</i>	Firmicutes	0.000	0.1 - 0.5	Not Present
<i>Lachnospiraceae bacterium 2_1_58FAA</i>	Firmicutes	0.000	0.1 - 0.5	Not Present
<i>Lachnospiraceae bacterium 6_1_37FAA</i>	Firmicutes	0.000	0.1 - 0.5	Not Present
<i>Lachnospiraceae bacterium 6_1_63FAA</i>	Firmicutes	0.000	0.1 - 0.5	Not Present
<i>Lachnospiraceae bacterium 9_1_43BFAA</i>	Firmicutes	0.000	0.1 - 0.5	Not Present
<i>Blautia hansenii</i>	Firmicutes	0.000	1 - 6	Not Present
<i>Tyzzereella nexilis</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Tyzzereella nexilis DSM 1787</i>	Firmicutes	0.000	0 - 0.1	Not Present
<i>Blautia hansenii DSM 20583</i>	Firmicutes	0.000	1 - 6	Not Present

Relative Percentage of Bacterial Microbiota: 2.512

Relative sum among genera, species and subspecies.

Description

Tryptamine is a neurotransmitter with a wide variety of biological activities. Tryptamine-mediated signaling could affect the transit of food particles and bacterial cells through the intestinal lumen. As a trace amine found in small amounts in the brain, it is a ligand for the TAAR receptors that enhances the inhibitory response of cells to serotonin, as well as a ligand for the sigma-2 receptor. Tryptamine in stool induces the release of serotonin by enterochromaffin cells.

Fluctuations in intestinal serotonin levels are believed to modulate gastrointestinal motility and may play a role in the pathology of inflammatory bowel diseases. Serotonin plays a critical role as a signaling molecule in the enteric nervous system, where modulation of serotonin receptors has been proposed as a treatment for irritable bowel syndrome.

Tryptophan decarboxylases in the Gut Microbiota increase the possibility that microbes can sequester tryptophan from the diet, convert it to tryptamine, and thus alter the spectrum and distribution of the resulting tryptophan metabolites in the host. Reducing the level of tryptophan in plasma would decrease the production of serotonin in the brain and could represent a mechanism by which the Microbiota influences behavior.

INDOL PROPIONIC ACID (IPA) PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Clostridium sporogenes</i>	Firmicutes	0.036	0 - 0.01	Moderate
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Lactobacillus plantarum</i>	Firmicutes	0.002	0.06 - 0.1	Low
<i>Lactobacillus hilgardii</i>	Firmicutes	0.002	0.06 - 0.1	Low

Relative Percentage of Bacterial Microbiota: 0.634

Relative sum among genera, species and subspecies.

INDOL ACETIC ACID PRODUCING MICROBIOTA (IAA)

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Staphylococcus</i>	Firmicutes	0.108	0.01 - 0.1	Moderate
<i>Citrobacter</i>	Proteobacteria	0.015	0 - 0.1	Normal
<i>Klebsiella</i>	Proteobacteria	0.009	0 - 0.1	Normal
<i>Streptococcus equinus</i>	Firmicutes	0.007	0 - 0.01	Normal
<i>Citrobacter freundii</i>	Proteobacteria	0.003	0 - 0.02	Normal
<i>Providencia rettgeri</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Proteus mirabilis</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Enterobacter cancerogenus</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Enterobacter cloacae subsp. cloacae</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Proteus penneri</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Hafnia alvei</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Corynebacterium ammoniagenes</i>	Actinobacteria	0.001	0 - 0.01	Normal
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Listeria grayi</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Acinetobacter radioresistens</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Enterobacteriaceae bacterium</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia alcalifaciens</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Edwardsiella tarda</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia rustigianii</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Providencia stuartii</i> ATCC 25827	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Citrobacter youngae</i>	Proteobacteria	0.000	0 - 0.02	Not Present
<i>Cedecea davisae</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Yokenella regensburgei</i>	Proteobacteria	0.000	0 - 0.01	Not Present
Relative Percentage of Bacterial Microbiota:		0.147		

Relative sum among genera, species and subspecies.

Description

Indoleacetic acid originates from the degradation of tryptophan, like indoles, by intestinal bacteria and is subsequently sulfated in the liver to indoxyl sulfate. Indoles and phenols are protein-bound uremic toxins.

KYNURENINE PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Pseudomonas</i>	Proteobacteria	0.298	0 - 0.5	Normal
<i>Streptococcus equinus</i>	Firmicutes	0.007	0 - 0.01	Normal
<i>Paenisporsarcina</i>	Firmicutes	0.002	0 - 0.1	Normal
<i>Proteus penneri</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Bacillus</i>	Firmicutes	0.145	0.5 - 1	Low
<i>Streptomyces</i>	Actinobacteria	0.058	0.5 - 1	Low
<i>Lactobacillus brevis</i> subsp. <i>gravesensis</i>	Firmicutes	0.000	0.06 - 0.1	Not Present
<i>Providencia rustigianii</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Bacteroides clarus</i>	Bacteroidetes	0.000	0 - 0.1	Not Present
<i>Pseudomonas oleovorans</i>	Proteobacteria	0.000	0 - 0.1	Not Present
<i>Ralstonia</i> sp. 5_2_56FAA	Proteobacteria	0.000	0 - 0.1	Not Present
<i>Paenisporsarcina</i> sp.	Firmicutes	0.000	0 - 0.1	Not Present
Relative Percentage of Bacterial Microbiota:		0.511		

Relative sum among genera, species and subspecies.

Description

Quinurenine is produced from tryptophan, by the enzyme tryptophan dioxygenase, which is produced primarily, but not exclusively, in the liver, and indoleamine 2,3-dioxygenase, which is produced in many tissues in response to immune activation. Quinurenine and its metabolites have a number of biological functions, such as the dilation of blood vessels during inflammation and the regulation of the immune response. When kynurenine is increased, it can disrupt brain (cognitive) functions and cause depression-like symptoms. It is also associated with the tics that ASD patients present. We find it increased in some tumors, where it favors their growth, and in Alzheimer's disease.

KYNURENATE PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Coprococcus</i>	Firmicutes	1.807	0.2 - 0.7	High
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>Lachnospiraceae bacterium</i>	Firmicutes	0.360	0.1 - 0.5	Normal
<i>Corynebacterium ammoniagenes</i>	Actinobacteria	0.001	0 - 0.01	Normal
<i>Enterobacter cancerogenus</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Streptomyces</i>	Actinobacteria	0.058	0.5 - 1	Low
<i>Coprobacillus</i>	Firmicutes	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 2.820

Relative sum among genera, species and subspecies.

Description

Kynurenic acid is a tryptophan metabolite of the kinurenine pathway. Quinolinic acid has a powerful neurotoxic effect that is involved in neurodegenerative processes in the brain, such as in the AIDS dementia complex, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, multiple sclerosis, and Parkinson's disease. Within the brain, quinolinic acid is only produced by activated microglia and macrophages.

MICROBIOTA DOMAIN ARCHAEA METHANE PRODUCER

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Methanobrevibacter smithii</i>	Euryarchaeota	0.003	0 - 0.07	Normal
<i>Methanosphaera stadtmanae</i>	Euryarchaeota	0.002	0 - 0.07	Normal
<i>Methanobacterium paludis</i>	Euryarchaeota	0.002	0 - 0.07	Normal
<i>Methanobrevibacter olleyae</i>	Euryarchaeota	0.002	0 - 0.07	Normal
<i>Methanococcus maripaludis</i>	Euryarchaeota	0.002	0 - 0.07	Normal
<i>Methanosphaera sp. BMS</i>	Euryarchaeota	0.002	0 - 0.07	Normal
<i>Methanobrevibacter ruminantium M1</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Methanobrevibacter sp. AbM4</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Methanosarcina barkeri</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Methanohalobium evestigatum</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Methanohalophilus portucalensis</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Methanosarcina sp. MTP4</i>	Euryarchaeota	0.001	0 - 0.07	Normal
<i>Candidatus Methanomassiliicoccus intestinalis</i>	Euryarchaeota	0.000	0 - 0.07	Not Present
<i>Methanosarcina acetivorans C2A</i>	Euryarchaeota	0.000	0 - 0.07	Not Present
<i>Methanosarcina acetivorans</i>	Euryarchaeota	0.000	0 - 0.07	Not Present
<i>Methanomassiliicoccus luminyensis</i>	Euryarchaeota	0.000	0 - 0.07	Not Present
<i>Methanocorpusculum labreanum Z</i>	Euryarchaeota	0.000	0 - 0.07	Not Present
<i>Methanocaldococcus jannaschii</i>	Euryarchaeota	0.000	0 - 0.07	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Methanospirillum hungatei</i>	Euryarchaeota	0.000	0 - 0.07	Not Present

Relative Percentage of Bacterial Microbiota: 0.018

Relative sum among genera, species and subspecies.

Description

Archaeas, mainly methanogenic ones, can be relatively abundant components of the gastrointestinal microbiota.

Methanobrevibacter smithii is recognized as the most abundant and often exclusive methanogen in the human gastrointestinal microbiota. Other Archaeas that may be present in the human intestine are: Methanaphaera stadmaniae, Methanobacterium paludis, Methanosarcina barkeri, Methanospirillum hungatei, Methanomassiliococcus luminyensis, Methanosarcina barkeri, etc.

The methanogenic Archaeas have been widely studied, since the process of synthesis of methane from carbon dioxide and hydrogen produces an important elimination of gases in the gastrointestinal tract. The role of methanogenic Archaeas could be particularly relevant for bloating, which is one of the symptoms in some irritable bowel syndromes.

Methane is irritating to the epithelial cells of the intestinal mucosa. It alters intestinal motility since it varies the form of contraction of the smooth muscle of the intestine, this can cause constipation, causing food to stay longer in the intestine. Also, the increase in archaea can cause a deconjugation of bile acids.

HYDROGEN SULFIDE PRODUCING MICROBIOTA

Global assessment: HIGH

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Alistipes</i>	Bacteroidetes	3.780	0.25 - 2	High
<i>Campylobacter</i>	Proteobacteria	0.099	0 - 0.01	High
<i>Odoribacter splanchnicus</i>	Bacteroidetes	1.139	0.01 - 1	Moderate
<i>Fusobacterium</i>	Fusobacteria	0.033	0 - 0.01	Moderate
<i>Treponema</i>	Spirochaetes	0.024	0 - 0.01	Moderate
<i>Salmonella enterica</i>	Proteobacteria	0.013	0 - 0.01	Moderate
<i>Candidatus Desulfovibrio trichonymphae</i>	Proteobacteria	0.002	0 - 0.001	Moderate
<i>Collinsella aerofaciens</i>	Actinobacteria	0.291	0.08 - 2.45	Normal
<i>Shewanella</i>	Proteobacteria	0.010	0 - 0.01	Normal
<i>Desulfovibrio vulgaris</i>	Proteobacteria	0.009	0 - 0.01	Normal
<i>Desulfovibrio piger</i>	Proteobacteria	0.007	0 - 0.01	Normal
<i>Klebsiella pneumoniae</i>	Proteobacteria	0.006	0 - 0.01	Normal
<i>Desulfovibrio desulfuricans</i>	Proteobacteria	0.005	0 - 0.01	Normal
<i>Desulfotobacterium hafniense</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Citrobacter freundii</i>	Proteobacteria	0.003	0 - 0.02	Normal
<i>Desulfotomaculum ruminis</i>	Firmicutes	0.003	0 - 0.01	Normal
<i>Enterobacter cloacae</i>	Proteobacteria	0.002	0 - 0.1	Normal
<i>Desulfobulbus oralis</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Desulfovibrio gigas</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Desulfovibrio fairfieldensis</i>	Proteobacteria	0.002	0 - 0.01	Normal
<i>Desulfotalea psychrophila</i>	Proteobacteria	0.002	0 - 0.01	Normal

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Fusobacterium necrophorum</i>	Fusobacteria	0.002	0 - 0.01	Normal
<i>Desulfobacter postgatei</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfotomaculum reducens</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Desulfomicrobium baculatum</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfovibrio alaskensis</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Thermococcus barophilus</i>	Euryarchaeota	0.001	0 - 0.01	Normal
<i>Desulfococcus oleovorans</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfococcus multivorans</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfitobacterium dehalogenans</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Desulfuromonas sp. DDH964</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfobacula toluolica</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfurella acetivorans</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfomicrobium orale</i>	Proteobacteria	0.001	0 - 0.01	Normal
<i>Desulfosporosinus meridiei</i>	Firmicutes	0.001	0 - 0.01	Normal
<i>Salmonella sp.</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Desulfurivibrio alkaliphilus</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Desulfuromonas soudanensis</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Desulfovibrio hydrothermalis</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Desulfocapsa sulfexigens</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Desulfatibacillum aliphaticivorans</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Thermococcus barophilus MP</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Citrobacter portucalensis</i>	Proteobacteria	0.000	0 - 0.02	Not Present
<i>Caldivirga maquilingensis</i>	Crenarchaeota	0.000	0 - 0.001	Not Present
<i>Desulfovibrio salexigens</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Bilophila wadsworthia</i>	Proteobacteria	0.000	0 - 0.001	Not Present
<i>Desulfovibrio carbinoliphilus</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Archaeoglobus fulgidus</i>	Euryarchaeota	0.000	0 - 0.001	Not Present
<i>Thermococcus paralvinellae</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Thermococcus piezophilus</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Thermococcus profundus</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Thermococcus radiotolerans</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Thermococcus sp. 4557</i>	Euryarchaeota	0.000	0 - 0.01	Not Present
<i>Desulfovibrio sp. G11</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 5.447

Relative sum among genera, species and subspecies.

Description

Sulfate-reducing bacteria produce hydrogen sulfide (gas that smells like rotten eggs). This gas, at high levels, is toxic to the intestinal mucosa, it can cause diarrhea and constipation in the large intestine. It can also contribute to the appearance of gastrointestinal diseases such as irritable bowel syndrome (IBS), inflammatory bowel disease, etc.

Elevated levels of the hydrogen sulfide-producing microbiota may be indicative of a hydrogen sulfide LIBO. When levels are

low, discard LIBO. In case of suspicion of LIBO you would have to consult with your doctor for a possible treatment.

ETHANOL PRODUCING MICROBIOTA

Global assessment: NORMAL

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Saccharomyces cerevisiae</i>	Ascomycota	0.027	0 - 0.01	Moderate
<i>Candida albicans</i>	Ascomycota	0.011	0 - 0.01	Moderate
<i>Escherichia coli</i>	Proteobacteria	0.593	0.5 - 1	Normal
<i>[Clostridium] scindens</i>	Firmicutes	0.381	0 - 0.5	Normal
<i>Collinsella aerofaciens</i>	Actinobacteria	0.291	0.08 - 2.45	Normal
<i>Clostridium butyricum</i>	Firmicutes	0.019	0.01 - 0.1	Normal
<i>Clostridium pasteurianum</i>	Firmicutes	0.011	0.01 - 0.1	Normal
<i>Klebsiella pneumoniae</i>	Proteobacteria	0.006	0 - 0.01	Normal
<i>Clostridium saccharobutylicum</i>	Firmicutes	0.005	0 - 0.02	Normal
<i>Citrobacter freundii</i>	Proteobacteria	0.003	0 - 0.02	Normal
<i>Schizosaccharomyces pombe</i>	Ascomycota	0.003	0 - 0.01	Normal
<i>Pichia kudriavzevii</i>	Ascomycota	0.002	0 - 0.01	Normal
<i>Clostridium acetobutylicum</i>	Firmicutes	0.002	0.01 - 0.1	Low
<i>Klebsiella oxytoca</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Metschnikowia pulcherrima</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Hanseniaspora uvarum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomyces bayanus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomyces boulardii (nom. inval.)</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Candida parapsilosis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Scheffersomyces stipitis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Anaerocolumna aminovalerica</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Thermoanaerobacterium thermosaccharolyticum</i>	Firmicutes	0.000	0 - 0.01	Not Present
<i>Zygosaccharomyces bailii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Zymomonas mobilis</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Relative Percentage of Bacterial Microbiota: 1.354

Relative sum among genera, species and subspecies.

Description

The overgrowth of ethanol-producing bacteria and yeasts, from the sugars in ingested food, can cause the well-known 'Internal Brewery Syndrome' that generates high blood alcohol.

Oral Bacterias

ORAL BACTERIA PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>[Eubacterium sulci</i>	Firmicutes	0.018	0 - 0.01	Presence
<i>Prevotella copri</i>	Bacteroidetes	0.014	0 - 0.01	Presence
<i>Prevotella intermedia</i>	Bacteroidetes	0.020	0 - 0.07	Not Significant
<i>Prevotella fusca JCM 17724</i>	Bacteroidetes	0.019	0 - 0.04	Not Significant
<i>Prevotella melaninogenica</i>	Bacteroidetes	0.015	0 - 0.24	Not Significant
<i>Prevotella scopos</i>	Bacteroidetes	0.006	0 - 0.01	Not Significant
<i>Porphyromonas gingivalis</i>	Bacteroidetes	0.006	0 - 0.01	Not Significant
<i>Prevotella enoeca</i>	Bacteroidetes	0.005	0 - 0.01	Not Significant
<i>Prevotella denticola</i>	Bacteroidetes	0.002	0 - 0.04	Not Significant
<i>Prevotella oris</i>	Bacteroidetes	0.002	0 - 1.08	Not Significant
<i>Aggregatibacter actinomycetemcomitans</i>	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Prevotella dentalis</i>	Bacteroidetes	0.001	0 - 0.08	Not Significant
<i>Prevotella sp. oral taxon 299</i>	Bacteroidetes	0.001	0 - 0.6	Not Significant
<i>Tannerella forsythia</i>	Bacteroidetes	0.001	0 - 0.01	Not Significant
<i>Prevotella nigrescens</i>	Bacteroidetes	0.000	0 - 0.01	Not Present
<i>Prevotella ruminicola</i>	Bacteroidetes	0.000	0 - 0.06	Not Present

Description

Bacteria typical of the oral mucosa have been detected in the fecal sample. The microbiota plays a central role in human health and disease by shaping immune development, immune responses, metabolism, and protecting from invading pathogens. Some strains of *Prevotella* may be clinically important pathobionts that may be involved in human disease by promoting chronic inflammation. The increase of *Prevotella* in the mucosa (including the oral one) has been associated with localized and systemic diseases, including periodontitis, bacterial vaginosis, rheumatoid arthritis, metabolic disorders and low-grade systemic inflammation.

Increased *Prevotella* is associated with mucosal inflammation through the systemic spread of inflammatory mediators, bacteria, and bacterial products, which in turn can affect the outcomes of systemic disease. Colonization experiments carried out in mouse studies support the causal role of *Prevotella*, since they promote the clinical and inflammatory characteristics of human diseases. When compared to strict commensal bacteria, *Prevotella* exhibits increased inflammatory properties, as evidenced by the increased release of inflammatory mediators from immune cells and various stromal cells.

Prevotella copri is a Gram Negative intestinal bacteria. The cells are anaerobic and do not form spores. Cells grow best at 37 degrees Celsius and are rod-shaped. Its anaerobic qualities allow it to grow successfully in the intestines of humans. *Prevotella copri* may cause a reduction in other beneficial commensal microbes. Recent studies have shown a correlation between *Prevotella copri* and the development of rheumatoid arthritis. It has been shown to be more prevalent in patients with rheumatoid arthritis than in healthy individuals. Although a definitive link with the increase in *Prevotella copri* and rheumatoid arthritis cannot be established, studies are still being carried out to determine what effect it has on this autoimmune disease.

Pathogens

PATHOGENIC BACTERIA PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Clostridioides difficile</i>	Firmicutes	0.406	0 - 0.01	High
[<i>Clostridium innocuum</i>	Firmicutes	0.157	0 - 0.01	High
<i>Pseudomonas aeruginosa</i>	Proteobacteria	0.147	0 - 0.01	High
<i>Enterocloster bolteae</i>	Firmicutes	0.413	0 - 0.07	Presence
<i>Eggerthella lenta</i>	Actinobacteria	0.269	0.01 - 0.04	Presence
<i>Campylobacter jejuni</i>	Proteobacteria	0.038	0 - 0.01	Presence
<i>Clostridium perfringens</i>	Firmicutes	0.037	0 - 0.01	Presence
<i>Clostridium botulinum</i>	Firmicutes	0.033	0 - 0.01	Presence
<i>Shigella flexneri</i>	Proteobacteria	0.021	0 - 0.01	Presence
<i>Salmonella</i>	Proteobacteria	0.014	0 - 0.01	Presence
<i>Salmonella enterica</i>	Proteobacteria	0.013	0 - 0.01	Presence
<i>Klebsiella pneumoniae</i>	Proteobacteria	0.006	0 - 0.01	Not Significant
<i>Fusobacterium nucleatum</i>	Fusobacteria	0.004	0 - 0.01	Not Significant
<i>Fusobacterium varium</i>	Fusobacteria	0.004	0 - 0.01	Not Significant
<i>Fusobacterium mortiferum</i>	Fusobacteria	0.003	0 - 0.01	Not Significant
<i>Fusobacterium ulcerans</i>	Fusobacteria	0.003	0 - 0.01	Not Significant
<i>Fusobacterium necrophorum</i>	Fusobacteria	0.002	0 - 0.01	Not Significant
<i>Morganella morganii</i>	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Providencia rettgeri</i>	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Haemophilus parainfluenzae</i>	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Helicobacter pylori</i>	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Dialister pneumosintes</i>	Firmicutes	0.001	0 - 0.01	Not Significant
<i>Fusobacterium nucleatum subsp. animalis</i>	Fusobacteria	0.001	0 - 0.01	Not Significant
<i>Borrelia garinii</i>	Spirochaetes	0.001	0 - 0.01	Not Significant
<i>Klebsiella michiganensis</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Atlantibacter hermannii</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Mycoplasma pneumoniae</i>	Tenericutes	0.000	0 - 0.01	Not Present
<i>Borrelia coriaceae</i> ATCC 43381	Spirochaetes	0.000	0 - 0.01	Not Present
<i>Borrelia afzelii</i>	Spirochaetes	0.000	0 - 0.01	Not Present
<i>Klebsiella oxytoca</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Description

Shigella flexneri is a bacillus-shaped bacterium belonging to the Enterobacteriaceae family, they are Gram negative, immobile, non-spore-forming and incapable of fermenting lactose, which can cause diarrhea in living beings. They are facultative anaero-bias fecal coliforms with acid-mixed fermentation.

Enterococcus avium, a species of the genus *Enterococcus*, is most commonly found in birds. In rare cases, it is also a cause of infection in humans, and in such cases, it can be resistant to vancomycin and is known as VREA.

Klebsiella is a genus of immobile, Gram negative, facultative anaerobic bacteria belonging to the Phylum Proteobacteria.

Bacteria of this genus are frequently human pathogens, they can generate a wide range of infectious states: respiratory tract infections, urinary tract infections, septicemia, soft tissue infections, atrophic rhinitis, digestive tract infections and colitis, acute pharyngitis, etc.

Klebsiella pneumoniae: urinary tract infections, septicemia, and soft tissue infections.

Klebsiella oxytoca is a Gram negative, indole positive bacterial species, capable of growing on melectoses, and not on 3-hydroxybutyrate. It is a pathogenic bacteria that can cause infection and disease in humans. *Klebsiella oxytoca* is rarely isolated in cases of bacteremia. Most of the *Klebsiella oxytoca* infections are urinary or bile duct infections, in many cases they are polymicrobial infections, or acquired in the hospital, especially in diabetic patients, previously treated with antibiotics or who have a previous serious illness. It has also been isolated in cases of infections in the digestive tract, colitis and acute pharyngitis.

Klebsiella michiganensis are nitrogen fixers and are ubiquitous in nature.

Campylobacter jejuni is a species in the genus *Campylobacter*. It is a Gram negative bacillus, it is mobile by one or two polar flagella. It is microaerophilic and does not use carbohydrates. It causes intestinal infections with clinical symptoms of diarrhea, vomiting, abdominal pain, headache and general malaise. *Campylobacter* invades cells in the small intestine, injuring them, and impairing fluid absorption.

There are studies that would indicate that *Campylobacter* is the leading cause of diarrhea in developed countries, ahead of other pathogens such as *Salmonella*, *Shigella* and *Escherichia coli*.

Clostridium perfringens is a Gram-positive, capsulated, sporulated and immobile anaerobic bacterium that is widely distributed in the environment, of great ecological plasticity. It is found in the intestines of humans and various homeothermic animals, in soil, in water, in food (especially in meats that are not well cooked), etc. *C. perfringens* is common in the normal intestinal microbiota and is the most frequently isolated clostridium in clinical samples responsible for clinical conditions such as food poisoning, necrotizing enteritis, gas gangrene, cellulitis, and nonspecific infections. *C. perfringens* is common in the normal intestinal microbiota and is the most frequently isolated clostridium in clinical specimens.

Clostridioides difficile is a commensal bacterium of the human intestine. In small numbers, they do not tend to cause harm of clinical significance. Antibiotics, especially broad-spectrum ones, cause an imbalance of the intestinal flora, leading to overpopulation by *C. difficile*. This leads to pseudomembranous colitis. Also in recent studies it has been shown that this bacterium is a producer of p-cresol. This substance exerts a selective action on certain commensal bacteria, affecting their reproduction mechanism. And ultimately promoting intestinal dysbiosis.

Clostridium botulinum is a Gram-positive, rod-shaped spore-forming bacterium. It is an obligate anaerobic but tolerates traces of oxygen due to the enzyme superoxide dismutase. *C. botulinum* is capable of producing the neurotoxin only during sporulation, which can only occur in an anaerobic environment. *C. botulinum* is divided into four distinct phenotypic groups (I-IV) and is also classified into seven serotypes (A-G) based on the antigenicity of the botulinum toxin produced.

[*Clostridium*] *innocuum* is an anaerobic, nonmotile, Gram-positive bacterium that reproduces by sporulation. Although it is not normally considered an aggressive human pathogen, it has been isolated in some disease processes. [*Clostridium*] *innocuum* and other *Clostridium*s line the oropharynx and gastrointestinal tract and are considered normal intestinal flora. Although they are usually present and harmless in healthy people, they have been isolated in various infections and predominantly in immunosuppressed patients and with previous pathologies such as opportunistic bacteria.

Helicobacter pylori is a spiral-shaped bacterium that grows in the mucous layer that lines the inside of the human stomach. In this hostile, acidic environment of the stomach, *H. pylori* bacteria secrete an enzyme called urease, which converts the chemical urea into ammonia. The production of ammonia neutralizes the acidity of the stomach around *Helicobacter pylori*, to make it more welcoming to the bacteria. The spiral shape of *H. pylori* allows it to penetrate the mucous layer, which is less acidic than the inner space, or lumen, of the stomach. *H. pylori* can also adhere to cells that line the inner surface of the stomach.

H. pylori has created means of interfering with local immune reactions, rendering them ineffective in eliminating this bacteria.

Although *H. pylori* infection does not cause disease in most infected people, it is a major risk factor for peptic ulcer disease and is responsible for most ulcers of the stomach and upper small intestine.

In 1994, the International Office for Cancer Research classified the *H. pylori* bacteria as a carcinogen, or cancer-causing, in humans. Since then, colonization of the stomach with *H. pylori* has been increasingly accepted as an important cause of stomach cancer and gastric mucosa-associated lymphoid tissue lymphoma. *H. pylori* infection is also associated with a lower risk of esophageal adenocarcinoma.

Salmonella is a bacterial genus belonging to the Enterobacteriaceae family consisting of gram-negative bacilli, facultative anaerobes with peritrichous flagella. It constitutes an important group of pathogens for humans and animals. They are present in the intestines of healthy people and animals. Faeces are the main source of contamination in food and water; when the pathogen reaches fresh food it has the ability to multiply rapidly and therefore contaminated food can cause a gastrointestinal infection, "Salmonellosis".

It is mainly composed of two species: *S. enterica* and *S. bongori*. Of both, the most pathogenic species is *S. enterica*.

Salmonella enterica is divided into six subspecies that include over 2500 serotypes. They do not develop capsules (except for the Typhi serotype) or spores. They are mobile bacteria. They produce hydrogen sulfide (H₂S). They use glucose, but not lactose, and they do not produce urease or have a fermentative metabolism. It is a responsible agent of zoonoses of worldwide distribution. It is transmitted by direct contact or cross contamination during food handling. The natural habitat of these species is normally the intestines of any type of homeothermic animal (including humans).

Enterocloster bolteae is an anaerobic mesophilic human pathogenic bacterium that was isolated from fecal samples from children with ASD. They are bacteria that produce p-cresol and dejugate bile salts. P-cresol is a carcinogenic, neurotoxic and nephrotoxic aromatic substance produced by the intestinal microbiota from the amino acid tyrosine. It is capable of inhibiting intestinal cell respiration, decreasing mitochondrial bioenergetic activity and causing a decrease in intracellular ATP content. It also exerts a selective action on certain commensal bacteria, affecting their reproduction mechanism and promoting intestinal dysbiosis.

Several studies have pointed out the possibility that this type of bacteria affect behavior through the production of these neurotoxic metabolites that alter the gut-brain axis.

Eggerthella lenta is a bacterium that can cause bacteremia by translocation of the bacterium from the gastrointestinal tract to the blood. It is frequently found in bacteremia in patients with intestinal neoplasms, genitourinary pathologies, or postsurgical infections.

Eggerthella lenta is capable of deconjugating primary to secondary bile acids through 7 α -dehydroxylation activity. These secondary bile acids are potentially cytotoxic to the host and have been associated with colon cancer and the formation of cholesterol gallstones.

Fusobacterium ulcerans. Anaerobic, Gram-negative, spindle-shaped rod-shaped bacteria of Phylum Fusobacteria. This species does not form spores, it is negative indole, catalase, urease, lipase, esculin and oxidase, it does not produce hydrogen sulfide, but it reduces nitrate, produces large amounts of butyrate and converts threonine into propionic acid. *Fusobacterium ulcerans*, as its name suggests, causes ulcers in humans in tropical countries. It has an adhesin called FadA, a virulence factor, which is expressed on its surface. This factor provides the ability to some pathogenic bacteria, not only to evade the immune system, but also to infiltrate deeper tissues. The presence of this FadA homologue in these bacteria poses a risk in the development of CRC and other intestinal diseases.

Fusobacterium varium located in the colonic mucosa of patients with ulcerative colitis stimulates species-specific antibodies.

Fusobacterium nucleatum are part of the normal microbiota or flora of the oropharynx, gastrointestinal and genital tracts. *Fusobacterium nucleatum* is a common resident of the oropharyngeal microbiota in humans, and is an acute pathogen in periodontal diseases. Of the oral anaerobes, it is also the most likely to cause extraoral infections. Its metastatic infections can involve the brain, liver, joints, and heart valves. Septic thrombophlebitis has also been documented in extrapharyngeal areas. The role of *F. nucleatum* in intrauterine infections and preterm birth has recently been studied.

Fusobacterium nucleatum subsp. *animalis* is a strictly anaerobic, Gram negative bacterial species that has been associated with dental infections, premature delivery, appendicitis, inflammatory bowel disease, and, more recently, colorectal cancer. In fact, it is the most prevalent subspecies of *F. nucleatum* in human colorectal cancers. Studies of inflammatory cytokines in colorectal cancer samples found that the expression of the cytokines IL17A and TNF α was markedly increased and IL21 decreased in colorectal tumors. In in vitro coculture assays, *F. nucleatum* ssp. *animalis* induced the expression of the CCL20 protein in colorectal cancer cells and monocytes. It also stimulated monocyte / macrophage activation and migration.

These observations suggest that infection by *F. nucleatum* ssp. *Animalis* in colorectal tissue could induce an inflammatory response and promote the development of colorectal cancer.

Dialister pneumosintes is an anaerobic bacterium from the Phylum Firmicute that plays an important role in the pathogenesis of human periodontitis. *D. pneumosintes* has been found in 83% of patients with severe periodontitis and in 19% of patients with mild periodontitis.

Haemophilus parainfluenzae is a species of bacteria, Phylum Proteobacteria, found mainly in the human oral cavity, and may be present in the normal vaginal microbiota. They also live in the dental plaque that forms on the surface of the teeth. They are Gram negative, pleomorphic forms usually filamentous.

It is an increasingly recognized pathogen in invasive infections, particularly in immunocompromised people and where there is an alteration of the skin or mucosa barriers. In addition to endocarditis, it has been isolated from cases of bacteremic epiglottitis, bronchitis, sinusitis, otitis media, COPD, pneumonia, genital infections, abscesses, among others. It has also been isolated on rare occasions as a cause of urinary tract infection in adults, as well as rare hepatobiliary infections.

Morganella morganii is a bacterial species of the Morganellaceae family, gram negative bacilli. They commonly inhabit the environment and intestinal tract of humans, mammals and reptiles as saprophytic flora and occasionally cause urinary infections and other nosocomial infections.

Citrobacter koseri, opportunistic pathogen of immunosuppressed human patients that has been identified as causing urinary tract infections and is found in wounds, respiratory tract, meningitis, sepsis, myocarditis. *C. koseri* has caused frequent nosocomial outbreaks of neonatal meningitis. In several cases, outbreaks have been accompanied by high rates of intestinal colonization by the body in infants and by the transport of the bacteria on the hands of health workers.

PATHOGENIC STRAINS OF ESCHERICHIA COLI PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Escherichia coli</i> O157:H7	Proteobacteria	0.011	0 - 0.01	Presence
<i>Escherichia coli</i> ED1a	Proteobacteria	0.003	0 - 0.01	Not Significant
<i>Escherichia coli</i> UM146	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Escherichia coli</i> O157	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Escherichia coli</i> O18:H1	Proteobacteria	0.002	0 - 0.01	Not Significant
<i>Escherichia coli</i> O27:H7	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O55:H7	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O45:H2	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O55:H7 str. RM12579	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O22:H8	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O6:H16	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O16:H48	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> RS218	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> 536	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O145	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O104:H4	Proteobacteria	0.001	0 - 0.01	Not Significant
<i>Escherichia coli</i> O42	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> B7A	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> BL21	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> BL21(DE3)	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> 'BL21-Gold(DE3)pLysS AG'	Proteobacteria	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Escherichia coli</i> BW25113	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> C	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> CFT073	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> DH1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> DSM 30083 = JCM 1649 = ATCC 11775	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> E110019	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> EC302/04	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ECC-1470	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> B171	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ETEC H10407	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> FAP1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> HB101	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> HS	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> IAI1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> IAI39	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> IHE3034	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> JJ1886	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> LF82	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> LW1655F+	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> M12	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> M8	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> N37139PS	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> N40607	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> NCCP15648	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> NU14	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O1:H42	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O10:H32	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O103	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O103 str. RM8385	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O103:H2	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O103:H2 str. 12009	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> B str. REL606	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O104:H4 str. 2009EL-2050	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O104:H4 str. 2009EL-2071	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O104:H4 str. 2011C-3493	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O104:H4 str. C227-11	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O111	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O111 str. RM9322	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O111:H-	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O111:H- str. 11128	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O111:NM	Proteobacteria	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Escherichia coli</i> O113:H21	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O114:H49	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O119	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O119:H6	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O121	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O121 str. RM8352	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O121:H19	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O127:H6	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O127:H6 str. E2348/69	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O128:H27	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O139:H28	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O139:H28 str. E24377A	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> B	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O145 str. RM9872	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O145:H28	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O145:H28 str. RM12761	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O145:NM	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O15:H11	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ATCC 8739	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H16	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H16 str. 98-3133	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H39	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H43	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H45	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ATCC 25922	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. EC10	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. EC4115	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. EDL933	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. F8092B	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. Sakai	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. SS17	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. SS52	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O157:H7 str. TW14359	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> APEC O78	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O169:H41	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O178:H19	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> APEC O2-211	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O182:H21	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O2:H6	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> APEC O18	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O25:H16	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O25:NM	Proteobacteria	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Escherichia coli</i> O25b:H4	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O25b:H4-ST131	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26 str. RM10386	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26 str. RM8426	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26:H-	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26:H11	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O26:H11 str. 11368	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> APEC O1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O32:H37	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O32:H37 str. P4	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O39:NM	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O39:NM str. F8704-2	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O43	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O43 str. RM10042	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O44:H18	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> APEC IMT5155	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O55:H6	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ACN001	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O55:H7 str. CB9615	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> ABU 83972	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> 55989	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O7:K1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O7:K1 str. CE10	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O8:H8	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O80:H26	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O83:H1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O83:H1 str. NRG 857C	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O91	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O91 str. RM7190	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> O91:H21	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> P12b	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> PCN033	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> PCN061	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> PMV-1	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> 53638	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> S88	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> SE15	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> SMS-3-5	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> str. 'clone D i14'	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> str. K-12 substr. MDS42	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli</i> str. K-12 substr. MG1655	Proteobacteria	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Escherichia coli str. K-12 substr. W3110</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli str. Sanji</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli 1303</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli UMN026</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli UMNK88</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli Vir68</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli VR50</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli W</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>Escherichia coli Xuzhou21</i>	Proteobacteria	0.000	0 - 0.01	Not Present
<i>synthetic Escherichia coli C321.deltaA</i>	Proteobacteria	0.000	0 - 0.01	Not Present

Fungi

FUNGI PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Verticillium dahliae</i>	Ascomycota	0.038	0 - 0.01	Presence
<i>Pyricularia oryzae</i>	Ascomycota	0.028	0 - 0.01	Presence
<i>Saccharomyces cerevisiae</i>	Ascomycota	0.027	0 - 0.01	Presence
<i>Trichoderma reesei</i>	Ascomycota	0.018	0 - 0.01	Presence
<i>Aspergillus flavus</i>	Ascomycota	0.018	0 - 0.01	Presence
<i>Fusarium oxysporum</i>	Ascomycota	0.017	0 - 0.01	Presence
<i>Bipolaris sorokiniana</i>	Ascomycota	0.013	0 - 0.01	Presence
<i>Thermothelomyces thermophilus</i>	Ascomycota	0.013	0 - 0.01	Presence
<i>Pyricularia pennisetigena</i>	Ascomycota	0.011	0 - 0.01	Presence
<i>Candida albicans</i>	Ascomycota	0.011	0 - 0.01	Presence
<i>Neurospora crassa</i>	Ascomycota	0.010	0 - 0.01	Presence
<i>Exserohilum turcicum</i>	Ascomycota	0.010	0 - 0.01	Not Significant
<i>Botrytis cinerea</i>	Ascomycota	0.010	0 - 0.01	Not Significant
<i>Apiotrichum mycotoxinovorans</i>	Basidiomycota	0.007	0 - 0.01	Not Significant
<i>Pyricularia grisea</i>	Ascomycota	0.007	0 - 0.01	Not Significant
<i>Fusarium fujikuroi</i>	Ascomycota	0.007	0 - 0.01	Not Significant
<i>Yarrowia lipolytica</i>	Ascomycota	0.007	0 - 0.01	Not Significant
<i>Epichloe festucae</i>	Ascomycota	0.006	0 - 0.01	Not Significant
[<i>Candida auris</i>	Ascomycota	0.006	0 - 0.01	Not Significant
<i>Byssoscllamys spectabilis</i>	Ascomycota	0.006	0 - 0.01	Not Significant
<i>Beauveria bassiana</i>	Ascomycota	0.006	0 - 0.01	Not Significant
<i>Podospora comata</i>	Ascomycota	0.006	0 - 0.01	Not Significant
<i>Pochonia chlamydosporia</i>	Ascomycota	0.006	0 - 0.01	Not Significant
<i>Talaromyces rugulosus</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Fusarium venenatum</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Saccharomycopsis malanga</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Saccharomycopsis fibuligera</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Kluyveromyces marxianus</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Zymoseptoria tritici</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Agaricus bisporus</i>	Basidiomycota	0.005	0 - 0.01	Not Significant
<i>Hyphopichia pseudoburtonii</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Penicillium digitatum</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Lichtheimia ramosa</i>	Mucoromycota	0.005	0 - 0.01	Not Significant
<i>Sporisorium reilianum</i>	Basidiomycota	0.005	0 - 0.01	Not Significant
<i>Thermothielavioides terrestris</i>	Ascomycota	0.005	0 - 0.01	Not Significant
<i>Talaromyces marneffeii</i>	Ascomycota	0.004	0 - 0.01	Not Significant
<i>Cordyceps militaris</i>	Ascomycota	0.004	0 - 0.01	Not Significant
<i>Cryptococcus neoformans</i>	Basidiomycota	0.004	0 - 0.01	Not Significant

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Parastagonospora nodorum</i>	Ascomycota	0.004	0 - 0.01	Not Significant
<i>Tetrapisispora blattae</i>	Ascomycota	0.004	0 - 0.01	Not Significant
<i>Blumeria graminis</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Schizosaccharomyces pombe</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Talaromyces pinophilus</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Aspergillus sojae</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Talaromyces funiculosus</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Torulasporea delbrueckii</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Kluyveromyces lactis</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Candida dubliniensis</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Candida tropicalis</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Saccharomyces paradoxus</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Fusarium verticillioides</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Pyrenophora tritici-repentis</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Cercospora sojina</i>	Ascomycota	0.003	0 - 0.01	Not Significant
<i>Alternaria solani</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Debaryomyces hansenii</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Zygosaccharomyces parvii</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Hyphopichia burtonii</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Kazachstania africana</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Pichia kudriavzevii</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Exophiala lecanii-corni</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Eremothecium cymbalariae</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>[Candida] hispaniensis</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Metschnikowia aff. pulcherrima</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Fusarium graminearum</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Sclerotinia sclerotiorum</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Venturia effusa</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Sporisorium scitamineum</i>	Basidiomycota	0.002	0 - 0.01	Not Significant
<i>Saccharomyces jurei</i>	Ascomycota	0.002	0 - 0.01	Not Significant
<i>Cercospora beticola</i>	Ascomycota	0.001	0 - 0.01	Not Significant
<i>Sporisorium graminicola</i>	Basidiomycota	0.001	0 - 0.01	Not Significant
<i>Metarhizium brunneum</i>	Ascomycota	0.001	0 - 0.01	Not Significant
<i>Fusarium culmorum</i>	Ascomycota	0.001	0 - 0.01	Not Significant
<i>Millerozyma farinosa</i>	Ascomycota	0.001	0 - 0.01	Not Significant
<i>Aspergillus pseudotamarii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Ceraceosorus guamensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Capronia epimyces</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Capronia coronata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Chaetomium globosum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Chaetomium thermophilum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cladonia uncialis</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Cladophialophora bantiana</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cladophialophora carrionii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cladophialophora immunda</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cladophialophora psammophila</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Clavispora lusitaniae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Coccidioides immitis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Colletotrichum fructicola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Colletotrichum orchidophilum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Colletotrichum scovillei</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Coniophora puteana</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Coprinopsis cinerea</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Cordyceps fumosorosea</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cantharellus cibarius</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Candida parapsilosis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cryptococcus wingfieldii</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Cutaneotrichosporon oleaginosum</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Cyberlindnera americana</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cyberlindnera fabianii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Cyphellophora europaea</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Dactylella tenuis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Daldinia childiae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Debaryomyces fabryi</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Blastomyces gilchristii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Dichomitus squalens</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Didymella exigua</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Diplodia corticola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Diutina rugosa</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Dothideomyces sp. TRN 80</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Dothidotthia symphoricarpi</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Encephalitozoon intestinalis</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Endocarpon pusillum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Epichloe coenophiala</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Bipolaris zeicola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Eremomyces bilateralis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Bipolaris oryzae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Eremothecium gossypii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Exophiala aquamarina</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Exophiala dermatitidis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Bipolaris maydis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Exophiala mesophila</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Exophiala oligosperma</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Exophiala spinifera</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Baudoinia panamericana</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fibroporia radiculosa</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Flammulina velutipes</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Fomitiporia mediterranea</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Fonsecaea monophora</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Batrachochytrium dendrobatidis</i>	Chytridiomycota	0.000	0 - 0.01	Not Present
<i>Fonsecaea pedrosoi</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fusarium coffeatum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Babjeviella inositovora</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aureobasidium subglaciale</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aureobasidium pullulans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fusarium odoratissimum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus welwitschiae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fusarium proliferatum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fusarium sp. NRRL 13405</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fusarium vanettenii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus vadensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus uvarum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Gaeumannomyces tritici</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Ganoderma boninense</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Glarea lozoyensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Gloeophyllum trabeum</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Glomus sp.</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Groenewaldozyma salmanticensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Grosmanina clavigera</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Hemileia vastatrix</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Heterobasidion irregulare</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Hirsutella rhossiliensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Histoplasma capsulatum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Hyaloscypha bicolor</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus tubingensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus terreus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Hypocrella siamensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Jaminaea rosea</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Janackia debaisieuxii</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Kalmanozyma brasiliensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus tanneri</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Kazachstania naganishii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus steynii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus sclerotioniger</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Kockovaella imperatae</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Kwoniella bestiolae</i>	Basidiomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Kwoniella dejecticola</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Kwoniella mangrovensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Kwoniella pini</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Laccaria bicolor</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Lachancea lanzarotensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Fonsecaea multimorphosa</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Lasiodiplodia theobromae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Lentinula edodes</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Leptosphaeria biglobosa</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Leptosphaeria maculans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Leucosporidium scottii</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus saccharolyticus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Lindgomyces ingoldianus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Lobosporangium transversale</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Lodderomyces elongisporus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Malassezia furfur</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Malassezia globosa</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Malassezia pachydermatis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Malassezia restricta</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Malassezia sympodialis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Marssonina brunnea</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Meira miltonrushii</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Melampsora larici-populina</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Melanopsichium pennsylvanicum</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Metarhizium acridum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus pseudonomius</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus piperis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Metschnikowia bicuspidata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Meyerozyma guilliermondii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Microsporium canis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus novofumigatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Moesziomyces antarcticus</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Monosiga brevicollis</i>	Salpingoecidae	0.000	0 - 0.01	Not Present
<i>Mytilinidion resinicola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Nakaseomyces bacillisporus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Nannizzia gypsea</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Naumovozyima castelli</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Neohortaea acidophila</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus nomiae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Neurospora tetrasperma</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Nosema ceranae</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Ogataea polymorpha</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Paraphaeosphaeria sporulosa</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus niger</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Peltaster fructicola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Penicillium zonata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Penicillium arizonense</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Lachancea thermotolerans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Penicillium rubens</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pestalotiopsis fici</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Phaeoacremonium minimum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Phaffia rhodozyma</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Phakopsora pachyrhizi</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Phanerochaete carnosa</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Phellinus lamaoensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Phialemoniopsis curvata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Phialocephala scopiformis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Phialophora attinorum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Phlebia radiata</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Phycomyces blakesleanus</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Aspergillus nidulans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pneumocystis carinii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pneumocystis jirovecii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pneumocystis murina</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus neoniger</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Podospora anserina</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus mulundensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Postia placenta</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Pseudocercospora fijiensis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pseudogymnoascus destructans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pseudogymnoascus verrucosus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pseudomicrostroma glucosiphilum</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Pseudovirgaria hyperparasitica</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Pseudozyma hubeiensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Puccinia graminis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Punctularia strigosozonata</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Purpureocillium lilacinum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus japonicus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus ibericus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus homomorphus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus heteromorphus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Ramularia collo-cygni</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Rasamsonia emersonii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Rhinocladiella mackenziei</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Rhizophagus irregularis</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Rhizophagus sp. DAOM 213198</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Rhizopus microsporus</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Rhodotorula graminis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Ricasolia amplissima</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus fumigatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomyces eubayanus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus fischeri</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomyces kudriavzevii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus eucalypticola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomyces pastorianus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Saccharomycetaceae sp. 'Ashbya aceri'</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus clavatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus candidus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Salpingoeca rosetta</i>	Salpingoecidae	0.000	0 - 0.01	Not Present
<i>Saprochaete ingens</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Scedosporium apiospermum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Scheffersomyces stipitis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Schizophyllum commune</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Schizosaccharomyces cryophilus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Schizosaccharomyces japonicus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus caelatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sclerococcum vrijmoediae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus brunneoviolaceus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sodiomyces alkalinus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sordaria macrospora</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sparassis crispa</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Sparassis latifolia</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Spathaspora passalidarum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sphaerulina musiva</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Spizellomyces punctatus</i>	Chytridiomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus bombycis</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus alliaceus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus aculeatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sporobolomyces johnsonii</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Sporothrix schenckii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Sugiyamaella lignohabitans</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Synchytrium microbalum</i>	Chytridiomycota	0.000	0 - 0.01	Not Present
<i>Talaromyces atroroseus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aspergillus aculeatinus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Ascoidea rubescens</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Arthroderma uncinatum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Arthrotrichum oligospora</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Talaromyces stipitatus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Armillaria ostoyae</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Aplosporella prunicola</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Apiotrichum porosum</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Tilletiaria anomala</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Anthracocestis flocculosa</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Amorphotheca resiniae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trametes hirsuta</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Trematosphaeria pertusa</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Tremella mesenterica</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma asperellum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma atroviride</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma citrinoviride</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma gamsii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma harzianum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Amanita inopinata</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Trichoderma virens</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichophyton benhamiae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichophyton rubrum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Trichosporon asahii</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Tuber melanosporum</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Uncinocarpus reesii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>uncultured fungus</i>	environmental samples	0.000	0 - 0.01	Not Present
<i>uncultured Neocallimastigales</i>	Chytridiomycota	0.000	0 - 0.01	Not Present
<i>uncultured Paraglomus</i>	Mucoromycota	0.000	0 - 0.01	Not Present
<i>Ustilago bromivora</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Ustilago maydis</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Alternaria alternata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Venustampulla echinocandica</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Verruconis gallopava</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Aaosphaeria arxii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Verticillium nonalfalfae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Vittaforma corneae</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Wallemia ichthyophaga</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Wallemia mellicola</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Westerdykella ornata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Wickerhamiella sorbophila</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Wickerhamomyces anomalus</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Wickerhamomyces ciferrii</i>	Ascomycota	0.000	0 - 0.01	Not Present

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Xylobolus sp. YZ-2018c</i>	Basidiomycota	0.000	0 - 0.01	Not Present
<i>Xylona heveae</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Yamadazyma tenuis</i>	Ascomycota	0.000	0 - 0.01	Not Present
[<i>Candida intermedia</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Zasmidium cellare</i>	Ascomycota	0.000	0 - 0.01	Not Present
[<i>Candida glabrata</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Zygosaccharomyces rouxii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Zygorhynchus mrakii</i>	Ascomycota	0.000	0 - 0.01	Not Present
<i>Tilletiopsis washingtonensis</i>	Basidiomycota	0.000	0 - 0.01	Not Present

Parasites

PARASITES PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>Toxoplasma gondii</i>	Apicomplexa	0.006	0 - 0.01	Not Significant
<i>Entamoeba histolytica</i>	Evosea	0.000	0 - 0.01	Not Significant
<i>Theileria parva</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Plasmodium yoelii</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Cryptosporidium hominis</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Cryptosporidium parvum</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Plasmodium malariae</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Plasmodium chabaudi</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Neospora caninum</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Plasmodium relictum</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Babesia microti</i>	Apicomplexa	0.000	0 - 0.01	Not Significant
<i>Entamoeba coli</i>	Evosea	0.000	0 - 0.01	Not Present
<i>Entamoeba dispar</i>	Evosea	0.000	0 - 0.01	Not Present
<i>Entamoeba hartmanni</i>	Evosea	0.000	0 - 0.01	Not Present
<i>Endolimax nana</i>	Evosea	0.000	0 - 0.01	Not Present
<i>Encephalitozoon intestinalis</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Enterocytozoon bienersi</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Giardia intestinalis</i>	Fornicata	0.000	0 - 0.01	Not Present
<i>Haemonchus contortus</i>	Nematoda	0.000	0 - 0.01	Not Present
<i>Hymenolepis microstoma</i>	Platyhelminthes	0.000	0 - 0.01	Not Present
<i>Hyobanche atropurpurea</i>	Streptophyta	0.000	0 - 0.01	Not Present
<i>Encephalitozoon hellem</i>	Microsporidia	0.000	0 - 0.01	Not Present
<i>Dientamoeba fragilis</i>	Parabasalia	0.000	0 - 0.01	Not Present
<i>Cyclospora cayetanensis</i>	Apicomplexa	0.000	0 - 0.01	Not Present
<i>Plasmodium reichenowi</i>	Apicomplexa	0.000	0 - 0.01	Not Present
<i>Blastocystis sp. subtype 4</i>	Blastocystidae	0.000	0 - 0.01	Not Present
<i>Blastocystis sp. subtype 3</i>	Blastocystidae	0.000	0 - 0.01	Not Present
<i>Strongyloides stercoralis</i>	Nematoda	0.000	0 - 0.01	Not Present
<i>Blastocystis hominis</i>	Blastocystidae	0.000	0 - 0.01	Not Present
<i>Entamoeba moshkovskii</i>	Evosea	0.000	0 - 0.01	Not Present

VIRUSES AND PHAGES

VIRUSES AND PHAGES PRESENT IN FECAL SAMPLE

Species / subspecies	Phylum	Value [%]	Reference [%]	Assessment
<i>uncultured human fecal virus</i>	environmental samples	0.956	0.001 - 0.01	High
<i>CrAssphage LMMB</i>	Uroviricota	0.402	0.001 - 0.01	High
<i>CrAssphage sp. O-152</i>	Uroviricota	0.364	0.001 - 0.01	High
<i>uncultured crAssphage</i>	Uroviricota	0.303	0.001 - 0.01	High
<i>CrAssphage ZA</i>	Uroviricota	0.105	0.001 - 0.01	High
<i>Microviridae sp.</i>	Phixviricota	0.010	0.001 - 0.01	Presence
<i>Bacteriophage sp.</i>	unclassified bacterial viruses	0.007	0.001 - 0.01	Not Significant
<i>Faecalibacterium virus Toutatis</i>	Uroviricota	0.002	0.001 - 0.01	Not Significant
<i>Faecalibacterium phage FP_Toutatis</i>	Uroviricota	0.002	0.001 - 0.01	Not Significant
<i>Pandoravirus quercus</i>	unclassified dsDNA viruses	0.002	0.001 - 0.01	Not Significant
<i>Faecalibacterium virus Oengus</i>	Uroviricota	0.002	0.001 - 0.01	Not Significant
<i>uncultured Caudovirales phage</i>	Uroviricota	0.002	0.001 - 0.01	Not Significant
<i>Poophage SC_4_H6H8_2017</i>	Phixviricota	0.002	0.001 - 0.01	Not Significant
<i>Faecalibacterium phage FP_oengus</i>	Uroviricota	0.002	0.001 - 0.01	Not Significant

Description

The human intestinal virome is the total collection of viruses and phages present in the human intestine. Viruses lack cellular organization and are not microbes. They do not have extracellular life. Viruses can infect both human cells and microbes in our Microbiome (bacteriophages). Some viruses can cause illness, while others can be asymptomatic. These entities can influence the balance between health and disease because we are continually exposed to numerous viruses that enter through the air, food, and contact with other people, animals, or plants.

Bacterial viruses or bacteriophages, which are specialized in attacking bacteria, represent the majority of the viral particles present in the human intestinal lumen. The potential contribution of bacteriophages to the maintenance of human health, through their ability to eliminate pathogenic bacterial communities, will influence our concepts of health and disease.

TECHNIQUE USED IN THIS ANALYSIS

Clinical metagenomic analysis of massive high-resolution in-silic data, from nucleic acid sequencing with next-generation nanotechnology on biological samples of the human Gut Microbiota, and intelligent classification of species and subspecies with Machine Learning and its own knowledge base, trained to the nucleotide Terabase scale.

DETECTABLE MICROORGANISMS WITH THIS TECHNIQUE

The tables in this report describe the microorganisms that have been detected in the patient sample and that are bibliographically referenced. These tables are continually updated based on advances in knowledge of medical evidence and the corresponding publications from the scientific community.

As of the date of this report, the laboratory has the potential capacity to detect 75,083 microorganisms:

Archea	728	Fungi:	49.015
Bacteria:	20.709	Viruses:	4.631

TECHNIQUE VALIDATION

The validation of our tests is already covered by an independent agency. In accordance with the UNE-EN ISO / IEC 17043: 2010 standard criteria for testing, ENAC grants accreditation to the technical entity SEIMC (Spanish Society of Infectious Diseases and Clinical Microbiology), which verifies the Xenogene Laboratory monthly.

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