



4066539

COMPLETE MICROBIOME MAPPING

General Macroscopic Description

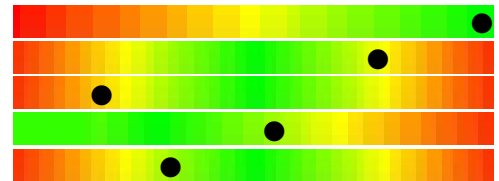
	Result	Markers
Stool Colour	Brown	Colour - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	Semi-formed	Form -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	Not Detected	Mucous - Mucous production may indicate the presence of an infection and/or inflammation.
Occult Blood	Negative	Blood (Macro) - The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection.

Short Chain Fatty Acids

Result Range Units

Methodology: GC/MS

Short Chain Fatty Acids, Beneficial	59.1	> 13.6	umol/g
Butyrate	32.4	10.8 - 33.5	%
Acetate	45.4	44.5 - 72.4	%
Propionate	20.4	0.0 - 32.0	%
Valerate	1.8	0.5 - 7.0	%

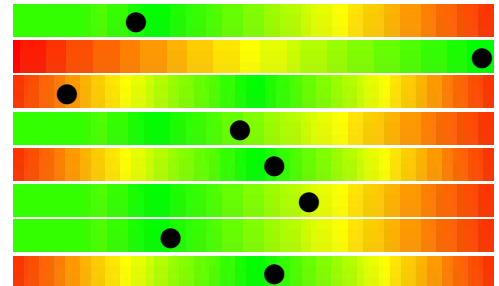


GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	<5.0	0.0 - 50.0	ug/g
Pancreatic Elastase	734.0	> 200.0	ug/g
Secretory (slgA)	187.0 *L	510.0 - 2040.0	ng/mL
Zonulin	57.4	0.0 - 107.0	ng/mL
Beta glucuronidase	4382.9	368.0 - 6266.0	U/g
Steatocrit	7.0	0.0 - 10.0	%
a-Transglutaminase IgA	29.0	0.0 - 100.0	units/L
pH	7.2	6.3 - 7.7	



Microbiome Mapping Summary

Parasites & Worms

Bacteria & Viruses

Methanobrevibacter smithii

Mycology

Candida albicans.

Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.35 < 1.00

RATIO



Relative Commensal Abundance of the 6 Phyla groups can be found on page 6 of this report





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Parasites and Worms.

Parasitic Organisms

Result	Range	Units	
Cryptosporidium species	<dl < 1.0	x10 ⁵ org/g	
Entamoeba histolytica.	<dl < 1.0	x10 ⁵ org/g	
Giardia intestinalis	<dl < 1.0	x10 ⁵ org/g	
Blastocystis hominis.	<dl < 1.0	x10 ⁵ org/g	
Dientamoeba fragilis.	<dl < 1.0	x10 ⁵ org/g	
Endolimax nana	<dl < 1.0	x10 ⁵ org/g	
Entamoeba coli.	<dl < 5.0	x10 ⁵ org/g	
Pentatrichomonas hominis	<dl < 1.0	x10 ⁵ org/g	

Worms

Ancylostoma duodenale, Roundworm	Not Detected		
Ascaris lumbricoides, Roundworm	Not Detected	Necator americanus, Hookworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected	Enterobius vermicularis, Pinworm	Not Detected
Enterocytozoon spp	Not Detected	Hymenolepis spp, Tapeworm	Not Detected
Strongyloides spp, Roundworm	Not Detected	Taenia species, Tapeworm	Not Detected

Comment: Not Detected results indicate the absence of detectable DNA in the sample for the worms reported.

NOTE: Reflex testing is performed on clinically indicated samples

Opportunistic Bacteria/Overgrowth

Result	Range	Units	
Bacillus species.	<dl < 1.00	x10 ⁴ CFU/g	
Enterococcus faecalis	<dl < 1.00	x10 ⁵ CFU/g	
Enterococcus faecium	<dl < 1.00	x10 ⁵ CFU/g	
Morganella species	<dl < 1.00	x10 ⁵ CFU/g	
Pseudomonas species	<dl < 1.00	x10 ⁴ CFU/g	
Pseudomonas aeruginosa.	<dl < 3.00	x10 ⁴ CFU/g	
Staphylococcus species	<dl < 1.00	x10 ³ CFU/g	
Staphylococcus aureus	<dl < 5.00	x10 ³ CFU/g	
Streptococcus agalactiae.	<dl < 3.00	x10 ⁴ CFU/g	
Streptococcus anginosus.	<dl < 1.00	x10 ⁶ CFU/g	
Streptococcus mutans.	<dl < 1.00	x10 ⁴ CFU/g	
Streptococcus oralis.	0.17 < 1.00	x10 ⁶ CFU/g	
Streptococcus salivarius.	0.16 < 5.00	x10 ⁶ CFU/g	
Methanobrevibacter smithii	4.60 *H < 1.00	x10 ⁵ CFU/g	
Desulfovibrio piger	5.32 < 18.00	x10 ⁶ CFU/g	
Enterobacter cloacae complex.	2.08 < 5.00	x10 ⁵ CFU/g	

Potential Autoimmune Triggers

Citrobacter species.	<dl < 5.00	x10 ⁴ CFU/g	
Citrobacter freundii complex.	<dl < 5.00	x10 ⁴ CFU/g	
Klebsiella species	<dl < 5.00	x10 ³ CFU/g	
Klebsiella pneumoniae complex.	<dl < 5.00	x10 ⁵ CFU/g	
Prevotella copri	<dl < 1.00	x10 ⁹ CFU/g	
Proteus species	<dl < 5.00	x10 ⁵ CFU/g	
Proteus mirabilis.	<dl < 1.00	x10 ⁴ CFU/g	
Fusobacterium species	4.50 < 20.00	x10 ⁴ CFU/g	



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Mycology	Result	Range	Units	
Candida dubliniensis.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida glabrata.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida intermedia.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida krusei.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida lambica.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida lusitanae.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida parapsilosis.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida tropicalis.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida albicans.	1.40 *H	< 1.00	x10 ⁵ CFU/g	
Candida famata.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida keyfr.	<dl	< 1.00	x10 ⁵ CFU/g	
Candida lipolytica.	<dl	< 1.00	x10 ⁵ CFU/g	
Geotrichum species.	<dl	< 1.00	x10 ⁵ CFU/g	
Rhodotorula species.	<dl	< 1.00	x10 ⁵ CFU/g	
Saccharomyces cerevisiae:	<dl	< 1.00	x10 ⁵ CFU/g	



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Bacterial Pathogens:	Result	Range	Units	
Aeromonas hydrophila.	<dl	< 1.00	x10 ³ CFU/g	●
Campylobacter species.	<dl	< 1.00	x10 ⁵ CFU/g	●
C. difficile, Toxin A	<dl	< 1.00	x10 ⁴ CFU/g	●
C. difficile, Toxin B	<dl	< 1.00	x10 ⁴ CFU/g	●
Enteraggregative E. coli	<dl	< 1.00	x10 ³ CFU/g	●
Enteropathogenic E. coli	<dl	< 1.00	x10 ³ CFU/g	●
E. coli O157	<dl	< 1.00	x10 ² CFU/g	●
Hypervirulent Clostridium difficile	<dl	< 1.00	x10 ³ CFU/g	●
Enteroinvasive E. coli/Shigella	<dl	< 1.00	x10 ³ CFU/g	●
Enterotoxigenic E. coli LT/ST	<dl	< 1.00	x10 ⁵ CFU/g	●
Salmonella species.	<dl	< 1.00	x10 ⁵ CFU/g	●
Shiga toxigenic E.coli	<dl	< 1.00	x10 ³ CFU/g	●
Vibrio species.	<dl	< 1.00	x10 ⁴ CFU/g	●
Yersinia species.	<dl	< 1.00	x10 ⁵ CFU/g	●
Helicobacter pylori	<dl	< 1.0	x10 ³ CFU/g	●

Comment: Helico Pylori virulence factors will be listed below if detected **POSITIVE**

Gene: A2142C	Not Detected		
Gene: A2142G	Not Detected		
Gene: A2143G	Not Detected		
H.pylori Virulence Factor, babA	Not Detected	H.pylori Virulence Factor, cagA	Not Detected
H.pylori Virulence Factor, oipA	Not Detected	H.pylori Virulence Factor, vacA	Not Detected
H.pylori Virulence Factor, virB	Not Detected	H.pylori Virulence Factor, virD	Not Detected

Viral Pathogens	Result	Range	Units
Adenovirus 40/41	Not Detected		
Norovirus GI/II	Not Detected		
Rotavirus A	Not Detected		
Sapovirus (I,II,IV,V)	Not Detected		
Astrovirus (hAstro)	Not Detected		



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Normal Bacterial GUT Flora.	Result	Range	Units	
Bacteroides fragilis	1.9	1.6 - 250.0	x10 ⁵ CFU/g	
TOTAL BIFIDOBACTERIA	174.8	5.0 - 2000.0	x10 ⁶ CFU/g	
Bifidobacterium adolescentis	<dl	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium bifidum.	133.0	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium breve.	<dl	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium longum	41.7	4.6 - 1000.0	x10 ⁶ CFU/g	
Enterococcus species	<dl	1.9 - 2000.0	x10 ³ CFU/g	
Escherichia species	400.5	3.7 - 3800.0	x10 ⁴ CFU/g	
TOTAL LACTOBACILLI	2.3	1.7 - 3000.0	x10 ³ CFU/g	
Lactobacillus acidophilus.	1.7	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus casei.	0.6 *L	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus delbrueckii	<dl	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus plantarum.	<dl	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus rhamnosus	<dl	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus salivarius	<dl	1.7 - 500.0	x10 ³ CFU/g	
Clostridium species	18.4	5.0 - 50.0	x10 ⁷ CFU/g	
Oxalobacter formigenes	17.38	> 5.00	x10 ⁶ CFU/g	
Akkermansia muciniphila	<dl *L	1.00 - 50.00	x10 ⁷ CFU/g	
Faecalibacterium prausnitzii	172.5	100.0 - 3500.0	x10 ⁶ CFU/g	

A total count of Lactobacillus and Bifidobacterium has been included to offer a broad overview of the species present in the microbiome, which may assist in guiding clinical treatment decisions. However, identifying individual strains of Lactobacillus and Bifidobacterium can yield more detailed and clinically specific information, as different strains exhibit distinct physiological effects, as outlined in the probiotics action chart below.

Actions

	L. plantarum HEAL19	L. paracasei 8700:2	L. plantarum 6595	L. plantarum 299V	L. rhamnosus GG	L. acidophilus LA02	B. animalis subsp. lactis BS01	L. casei LC03	B. breve BR03	L. fermentum LF08	L. crispatus strains	B. animalis subsp. lactis BA05	L. plantarum LP01	L. rhamnosus LR06	B. longum 04	L. fermentum LF16	L. salivarius LS01	B. breve B632	L. fermentum LF10	L. salivarius LS03	L. helveticus Rosell-52	L. rhamnosus Rosell-11	B. longum Rosell-75	S. boulardii CNCM I-1079	S. thermophilus FP4
Intestinal epithelial barrier health																									
Mucous membrane health																									
Normalisation of bowel movements																									
Normalisation of bloating																									
Normalisation of peristalsis																									
Autoimmune immunomodulation																									
Inhibition of pathogenic overgrowth																									
Inactivate microbial toxins																									
Increase infection resistance																									
Th1/Th2 immune cell modulation																									
Staphylococci inhibition																									
Gut-brain axis support																									
GABA production																									
Bone resorption inhibition																									
E. coli inhibition																									
Oxalate degradation																									



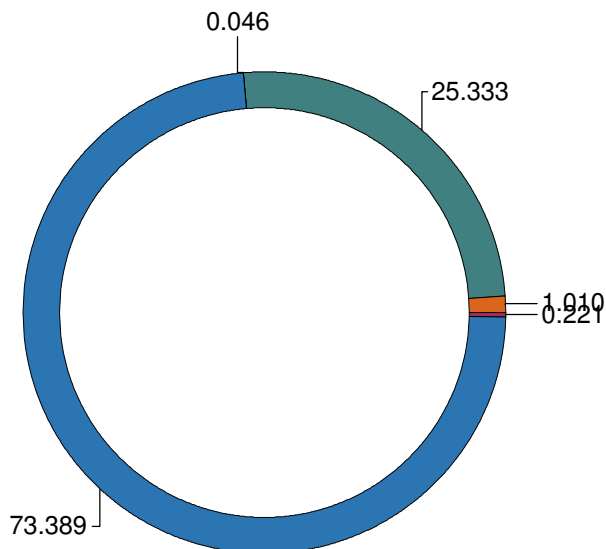
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Introduction:

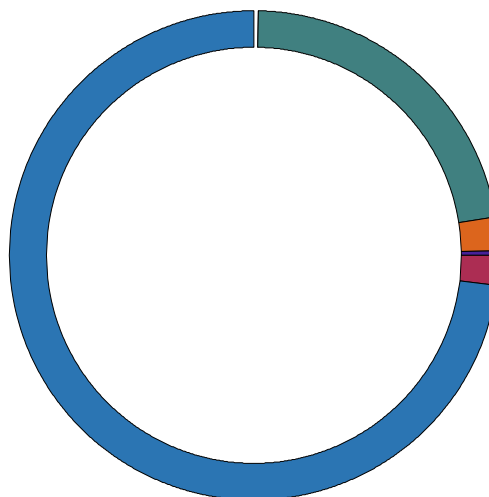
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider only cell counts, we are only about half human. In terms of gene counts, the microbiome contains about 200 times more genes than the human genome, making bacterial genes responsible for over 99% of our body's gene content! Of all the microbial communities in the human body, the gut microbiome is by far the most dense, diverse, and physiologically important ecosystem to our overall health.

Relative Commensal Abundance	Result	Range	Units
 Bacteroidetes Phylum	73.389	50.000 - 95.000	%
 Firmicutes Phylum	25.333	3.500 - 40.000	%
 Proteobacteria Phylum	1.010	0.050 - 12.500	%
 Actinobacteria Phylum	0.221	0.001 - 4.818	%
 Euryarchaeota Phylum	0.046*H	0.000 - 0.010	%
 Verrucomicrobia Phylum	0.000	0.000 - 2.400	%

Your Phyla:



Healthy Phyla:



References:

NOTE: Relative abundance reference ranges have been based on a healthy population study.

King CH, et., al. (2019) Baseline human gut microbiota profile in healthy people and standard reporting template. PLoS One. 2019 Sep 11;14(9):e0206484.



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Pathogen Summary:

Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

Faecal Occult Blood Negative:

Faecal occult blood has not been detected in this specimen. If the test result is negative and clinical symptoms persist, additional follow-up testing using other clinical methods is recommended.

Metabolism Comment

In a healthy gut Short Chain Fatty Acids (SCFAs) exhibited in the following proportions; Butyrate, Acetate, Propionate (16%:60%:24%).

The primary SCFAs butyrate, propionate and acetate are produced by predominant commensal bacteria via fermentation of soluble dietary fibre and intestinal mucus glycans.

Key producers of SCFAs include *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Bacteroides fragilis*, *Bifidobacterium*, *Clostridium* and *Lactobacillus* Spp.

The SCFAs provide energy for intestinal cells and regulate the actions of specialised mucosal cells that produce anti-inflammatory and antimicrobial factors, mucins that constitute the mucus barriers, and gut active peptides that facilitate appetite regulation and euglycemia. Abnormal SCFAs may be associated with dysbiosis, intestinal barrier dysfunction and inflammatory conditions.



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GIT Markers Comment

PANCREATIC ELASTASE: Normal exocrine pancreatic function.

Pancreatic Elastase reflects trypsin, chymotrypsin, amylase and lipase activity.

This test is not affected by supplements of pancreatic enzymes.

Healthy individuals should be producing >500 ug/g of PE-1 under normal/healthy conditions.

PE-1 levels between 200 - 500 ug/g may indicate suboptimal production.

PE-1 levels <200 ug/g indicate clear inadequate production.

The clinician should therefore consider digestive enzyme supplementation if one or more of the following conditions is present:

Loose watery stools, Undigested food in the stools, Post-prandial abdominal pain, Nausea or colicky abdominal pain, Gastroesophageal reflux symptoms, Bloating or food intolerance.

Testing performed by chemiluminescence immunoassay (CLIA).

CALPROTECTIN Normal:

Faecal calprotectin values <50 ug/g are not indicative of inflammation in the gastrointestinal tract. Subjects with low faecal calprotectin levels normally do not need to be further investigated by invasive procedures. In patients with strong clinical indications of intestinal inflammation, repeat testing may be useful.

Test performed by Diasorin Liaison XL chemiluminescent immunoassay (CLIA).

LOW SECRETORY IGA:

Secretory IgA represents the first line of defence of the gastrointestinal mucosa and is central to the normal function of the gastrointestinal tract as an immune barrier.

Secretory IgA binds to invading microorganisms and toxins and entrap them in the mucus layer or within the epithelial cells, so inhibiting microbial motility, agglutinating the organisms, and neutralising their exotoxins and then assist in their harmless elimination from the body in the faecal flow. sIgA also 'tags' food as acceptable, so low sIgA leads to increased sensitivity to foods. Several studies link stress and emotionality with levels of sIgA. Production is adversely affected by stress, which is mediated by cortisol levels.

Often low levels of Secretory IgA correlates with low beneficial flora levels and an increase in pathogenic and parasitic organism being present.

Treatment: Investigate the root cause and rule out parasitic organisms or pathogenic bacteria. Consider the use of probiotics (saccharomyces boulardii), choline, essential fatty acids, glutathione, glycine, glutamine, phosphatidylcholine, Vitamin C and Zinc which are all required for efficient production of Secretory IgA.

PLEASE NOTE: A low Secretory IgA should be reviewed in conjunction with the stool formation. An artefactually low level may be due to fluid dilution effects in a watery or unformed/loose stool sample.

ZONULIN NORMAL:

Zonulin is a protein that modulates intestinal barrier function. This results is considered normal.

Beta-GLUCORONIDASE NORMAL:

B-Glucuronidase is considered normal and is within reference range.



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Opportunistic Bacteria Comment

METHANOBREVIBACTER SMITHII ELEVATED:

PHYLUM: Euryarchaeota

DESCRIPTION:

Methanobrevibacter smithii is a methane-producing microbe that plays an important role in the gut ecosystem by facilitating carbohydrate fermentation and production of short-chain fatty acids by commensal bacteria. Elevated levels may be associated with abdominal bloating, constipation, flatulence, inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), colorectal cancer, diverticulosis or obesity and often correlate with a positive SIBO test.

Methanobrevibacter smithii has also been closely correlated with the presence of Blastocystis hominis.

TREATMENT SUGGESTIONS:

Elimination of methanogenic flora using antibiotic treatment may contribute to therapeutic benefits and include neomycin or rifaximin. Antimicrobial herbs may also be beneficial in treatment (including garlic and oregano). Rule out allergy to above medication before prescribing/taking.

Phyla Microbiota Comment

EURYARCHAEOTA (PHYLUM) ELEVATED:

DESCRIPTION:

Euryarchaeota are a phylum of a diverse range of bacteria, including methanogens, halophiles and sulfate-reducers. Three distinct species within the group of Euryarchaeota have been regularly detected within the human body. Among these is the primary colonizer of the human gut system Methanobrevibacter smithii and the less frequently found species Methanosphaera stadtmanae, while in the oral cavity M. oralis is the predominating methanogenic species. Methanogens support the growth of fermenting bacteria, which themselves could be either true pathogens or at least opportunistic pathogens but also members of the commensal flora.

They may also transform heavy metals or metalloids into volatile methylated derivatives which are known to be more toxic than the original compounds. Elevated Euryarchaeota may be associated with inflammatory bowel disease, Crohn's, irritable bowel syndrome, colorectal cancer, diverticulosis, and obesity. It may also affect short chain fatty acid production and absorption.

TREATMENT SUGGESTIONS: If treatment is warranted, Statins may be used to inhibit methanogenic archaea growth without affecting bacterial numbers. Symptoms may also be treated with dietary modification (low FODMAP) and probiotics.

A lactulose SIBO test may be considered to assess Methanogen levels.



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Normal Bacterial Flora Comment

BIFIDOBACTERIUM ADOLESCENTIS LOW:

PHYLUM: Actinobacteria

DESCRIPTION:

Bifidobacterium adolescentis is an anaerobic species of bacteria found in the gastrointestinal tracts of humans. It is one of the most abundant and prevalent Bifidobacterium species commonly found in adults. It contributes to the production of GABA, a neurotransmitter that plays a role in reducing stress and anxiety. Some strains can synthesise B vitamins, such as folic acid. B. adolescentis enhances the growth of all bifidobacteria.

TREATMENT SUGGESTIONS:

Consider a probiotic supplement containing B. adolescentis and consuming prebiotic-rich foods like garlic, onions, and whole grains. Increase dietary fibre from fruits, vegetables, and legumes, and incorporate fermented foods such as yogurt and kefir.

BIFIDOBACTERIUM BREVE LOW:

PHYLUM: Actinobacteria

DESCRIPTION:

Bifidobacterium breve is a Gram-positive, anaerobic bacterium that is commonly found in the human gastrointestinal tract, particularly in the intestines of infants. B. breve is known for its ability to metabolise various carbohydrates, including human milk oligosaccharides, which is essential for the development of a healthy gut flora in newborns. Studies demonstrate that B. breve exhibits several beneficial properties, including the production of short-chain fatty acids (SCFAs) such as acetate, which contribute to gut health by lowering pH and inhibiting the growth of pathogenic bacteria. Additionally, B. breve may alleviate symptoms of irritable bowel syndrome (IBS) and improve symptoms of atopic dermatitis.

ENTEROCOCCUS SPECIES LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Enterococci are Gram-positive facultative anaerobic cocci commonly found in the environment, water, food, human skin, oral cavity and intestine. Strains belonging to the genus Enterococcus produce a wide variety of bacteriocins which are active against Gram-positive foodborne pathogens. Certain Enterococcus species have also been found to produce butyrate, a metabolic product that induces significant anti-inflammatory effects and contributes to intestine epithelial integrity. Low levels of enterococcus species may be associated with increased inflammation and susceptibility to foodborne pathogens. Review this with other beneficial flora.

TREATMENT SUGGESTIONS: Commensal probiotic cocktails are suggested to elevate colonization.

LACTOBACILLUS CASEI LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus casei is a Gram-positive, rod-shaped, non-spore-forming, anaerobic probiotic bacterium involved in the fermentation of foods like cheese and yogurt. It produces antimicrobial substances, enhances gut barrier function, reduces pathogenic bacteria, and modulates the immune system. This bacterium is used to prevent and may assist various forms of diarrhea, including infectious diarrhea, traveller's diarrhea, and antibiotic-associated diarrhea.

TREATMENT SUGGESTIONS:

Consider probiotic supplementation containing L. casei and consuming fermented foods such as cheese and yogurt.

LACTOBACILLUS DELBRUECKII LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus delbrueckii is a beneficial Gram-positive bacterium commonly found in the gut microbiome and known for its role in maintaining gastrointestinal health. It produces lactic acid through the fermentation of carbohydrates, contributing to a lower gut pH, which inhibits the growth of pathogenic microorganisms such as Clostridium and Candida species. Additionally, L. delbrueckii can enhance the intestinal barrier function and modulate the host immune response by promoting the production of anti-inflammatory cytokines. Its presence in the gut is associated with improved digestion and nutrient absorption, making it an important component in supporting overall gut health and microbial balance.



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LACTOBACILLUS PLANTARUM LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus plantarum is a Gram-positive, non-spore-forming, rod-shaped bacterium. L. plantarum plays a crucial role in gut health by enhancing intestinal barrier function, modulating the immune system, and inhibiting pathogenic bacteria. Additionally, it is beneficial for conditions such as irritable bowel syndrome, ulcerative colitis, and high cholesterol.

TREATMENT SUGGESTIONS:

Consider probiotic supplementation containing L. plantarum.

LACTOBACILLUS RHAMNOSUS LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus Rhamnosus is a Gram-positive anaerobic bacterium and is one of the most widely used probiotic strains, of which various health effects are well documented including the prevention and treatment of gastro-intestinal infections and diarrhea and even preventing certain allergic symptoms.

Decreased Lactobacillus rhamnosus colonisation has been shown to decrease gastro-intestinal health, increasing the risk of gastro-intestinal infections and diarrhea as well as extra-intestinal infections including oral and respiratory health. Studies have also revealed that chronic psychological stress and alcohol use may be associated with a decrease in Lactobacillus species, as well as antibiotic / medication use.

TREATMENT SUGGESTIONS: Treatment may involve the use of Lactobacillus containing probiotics and treatment of any intestinal infections.

LACTOBACILLUS SALIVARIUS LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus salivarius is a Gram-positive, rod-shaped, non-spore-forming bacterium predominantly found in the human oral cavity, gastrointestinal tract, and vagina. It plays a significant role in maintaining oral and gut health by producing lactic acid and bacteriocins, which inhibit the growth of pathogenic bacteria. L. salivarius enhances gut barrier function, modulates the immune system, and helps in the digestion of proteins and complex carbohydrates. It has been studied for its potential benefits in managing conditions such as irritable bowel syndrome (IBS), periodontal disease, and atopic dermatitis, highlighting its importance in promoting overall health and preventing infections.

TREATMENT SUGGESTIONS:

Consider L. salivarius as a probiotic strain which may improve intestinal permeability and immune response.

AKKERMANSIA MUCINIPHILA LOW:

PHYLUM: Verrucomicrobia

DESCRIPTION:

Akkermansia muciniphila is a Gram-negative, strictly anaerobic, non-motile bacterium, often considered a human intestinal symbiont. There is growing evidence to suggest that the prevalence of this bacteria is associated with intestinal homeostasis, immunity, and a healthy gut. Decreased colonisation levels may be associated with obesity, type 2 diabetes, and inflammation.

TREATMENT SUGGESTIONS: Treatment may involve the use of probiotics, treatment of any intestinal infections and dietary modification.



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The Four “R” Treatment Protocol

REMOVE	Using a course of antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or medication that may be acting as antagonists. Consider testing IgG96 foods as a tool for removing offending foods.	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
		ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
		ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
		ANTIVIRAL	Cat's claw, berberine, echinacea, vitamin C, vitamin D3, zinc, reishi mushrooms
		BIOFILM	Oil of oregano, protease
REPLACE	In cases of maldigestion or malabsorption, it may be necessary to restore proper digestion by supplementing with digestive enzymes.	DIGESTIVE SUPPORT	Betaine hydrochloride, tilactase, amylase, lipase, protease, apple cider vinegar, herbal bitters
REINOCULATE	Recolonisation with healthy, beneficial bacteria. Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
		PROBIOTICS	Bifidobacterium animalis subsp. lactis, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
REPAIR & REBALANCE	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole body health and lifestyle factors so as to prevent future GI dysfunction.	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccaromyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management