



COMPLETE MICROBIOME MAPPING

General Macroscopic Description

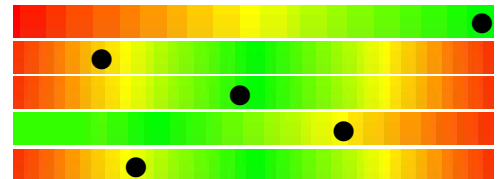
	Result	Markers
Stool Colour	Brown	Colour - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	Liquid	Form -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	Not Detected	Mucous - 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	154	> 13.6	umol/g
Butyrate	12.1	10.8 - 33.5	%
Acetate	57.0	44.5 - 72.4	%
Propionate	29.4	0.0 - 32.0	%
Valerate	1.4	0.5 - 7.0	%

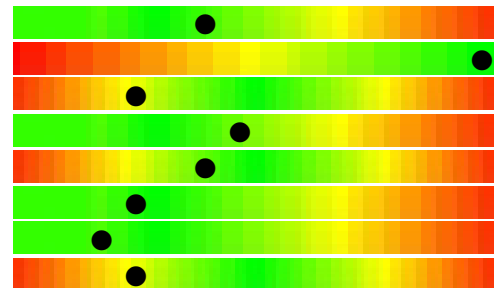


GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	16.0	0.0 - 50.0	ug/g
Pancreatic Elastase	397.0	> 200.0	ug/g
Secretory (slgA)	730.1	510.0 - 2040.0	ng/mL
Zonulin	49.9	0.0 - 107.0	ng/mL
Beta glucuronidase	2386.7	368.0 - 6266.0	U/g
Steatocrit	<1.0	0.0 - 10.0	%
a-Transglutaminase IgA	<20	0.0 - 100.0	units/L
pH	6.5	6.3 - 7.7	



Microbiome Mapping Summary

Parasites & Worms

Bacteria & Viruses

Streptococcus oralis.
Methanobrevibacter smithii
Fusobacterium species

Fungi and Yeasts

Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.35 < 1.00

RATIO



Relative Commensal Abundance of the 6 Phyla groups can be found on page 5 of this report



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THRIVE HEALTH
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AIRLIE BEACH QLD 4802

REBECCA WAGHORN
07-Mar-1992 **Female**

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Parasites and Worms.

Parasitic Organisms

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

Worms

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

Opportunistic Bacteria/Overgrowth	Result	Range	Units	
<i>Bacillus</i> species.	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Enterococcus faecalis</i>	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Enterococcus faecium</i>	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Morganella</i> species	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Pseudomonas</i> species	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Pseudomonas aeruginosa</i> .	<dl	< 3.00	x10 ⁴ CFU/g	●
<i>Staphylococcus</i> species	<dl	< 1.00	x10 ³ CFU/g	●
<i>Staphylococcus aureus</i>	<dl	< 5.00	x10 ³ CFU/g	●
<i>Streptococcus agalactiae</i> .	<dl	< 3.00	x10 ⁴ CFU/g	●
<i>Streptococcus anginosus</i> .	<dl	< 1.00	x10 ⁶ CFU/g	●
<i>Streptococcus mutans</i> .	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Streptococcus oralis</i> .	2.01 *H	< 1.00	x10 ⁶ CFU/g	●
<i>Streptococcus salivarius</i> .	1.09	< 5.00	x10 ⁶ CFU/g	●
<i>Methanobrevibacter smithii</i>	6.03 *H	< 1.00	x10 ⁵ CFU/g	●
<i>Desulfovibrio piger</i>	<dl	< 18.00	x10 ⁶ CFU/g	●
<i>Enterobacter cloacae</i> complex.	<dl	< 5.00	x10 ⁵ CFU/g	●

Potential Autoimmune Triggers

<i>Citrobacter</i> species.	<dl	< 5.00	x10 ⁴ CFU/g	●
<i>Citrobacter freundii</i> .	<dl	< 5.00	x10 ⁴ CFU/g	●
<i>Klebsiella</i> species	<dl	< 5.00	x10 ³ CFU/g	●
<i>Klebsiella pneumoniae</i> .	0.60	< 5.00	x10 ⁵ CFU/g	●
<i>Prevotella copri</i>	<dl	< 1.00	x10 ⁹ CFU/g	●
<i>Proteus</i> species	<dl	< 5.00	x10 ⁵ CFU/g	●
<i>Proteus mirabilis</i> .	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Fusobacterium</i> species	12.90 *H	< 10.00	x10 ⁴ CFU/g	●



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Mycology	Result	Range	Units	
<i>Candida dubliniensis</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida glabrata</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida intermedia</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida krusei</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida lambica</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida lusitanae</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida parapsilosis</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida albicans</i> .	0.40	< 1.00	x10 ⁵ CFU/g	●
<i>Candida famata</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida keyfr</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Candida lipolytica</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Geotrichum species</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Rhodotorula species</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Saccharomyces cerevisiae</i> :	<dl	< 1.00	x10 ⁵ CFU/g	●

Bacterial Pathogens	Result	Range	Units	
<i>Aeromonas hydrophila</i> .	<dl	< 1.00	x10 ³ CFU/g	●
<i>Campylobacter species</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>C. difficile</i> , Toxin A	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>C. difficile</i> , Toxin B	<dl	< 1.00	x10 ⁴ CFU/g	●
Enterohemorrhagic <i>E. coli</i>	<dl	< 1.00	x10 ⁵ CFU/g	●
Enteroinvasive <i>E. coli</i> /Shigella	<dl	< 1.00	x10 ³ CFU/g	●
Enterotoxigenic <i>E. coli</i> LT/ST	<dl	< 1.00	x10 ⁵ CFU/g	●
Shiga-like Toxin <i>E. coli</i> stx1	<dl	< 1.00	x10 ⁴ CFU/g	●
Shiga-like Toxin <i>E. coli</i> stx2	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Salmonella species</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Vibrio species</i> .	<dl	< 1.00	x10 ⁴ CFU/g	●
<i>Yersinia species</i> .	<dl	< 1.00	x10 ⁵ CFU/g	●
<i>Helicobacter pylori</i>	<dl	< 1.0	x10 ³ CFU/g	●

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

<i>H.pylori</i> Virulence Factor, babA	Not Detected	<i>H.pylori</i> Virulence Factor, cagA	Not Detected
<i>H.pylori</i> Virulence Factor, dupA	Not Detected	<i>H.pylori</i> Virulence Factor, iceA	Not Detected
<i>H.pylori</i> Virulence Factor, oipA	Not Detected	<i>H.pylori</i> Virulence Factor, vacA	Not Detected
<i>H.pylori</i> Virulence Factor, virB	Not Detected	<i>H.pylori</i> 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	
<i>Bacteroides fragilis</i>	274.0 *H	1.6 - 250.0	x10 ⁵ CFU/g	
<i>Bifidobacterium adolescentis</i>	<dl *L	4.6 - 1000.0	x10 ⁵ CFU/g	
<i>Bifidobacterium bifidum</i>	<dl *L	4.6 - 1000.0	x10 ⁶ CFU/g	
<i>Bifidobacterium breve</i>	<dl *L	4.6 - 1000.0	x10 ³ CFU/g	
<i>Bifidobacterium longum</i>	6.9	4.6 - 1000.0	x10 ⁴ CFU/g	
<i>Enterococcus species</i>	30.5	1.9 - 2000.0	x10 ³ CFU/g	
<i>Escherichia species</i>	400.1	3.7 - 3800.0	x10 ⁴ CFU/g	
<i>Lactobacillus acidophilus</i>	2.0	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus casei</i>	<dl *L	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus delbrueckii</i>	2.9	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus plantarum</i>	<dl *L	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus rhamnosus</i>	<dl *L	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus salivarius</i>	<dl *L	1.7 - 500.0	x10 ³ CFU/g	
<i>Clostridium species</i>	63.0 *H	5.0 - 50.0	x10 ⁷ CFU/g	
<i>Oxalobacter formigenes</i>	1.87 *L	> 5.00	x10 ⁶ CFU/g	
<i>Akkermansia muciniphila</i>	16.00	1.00 - 50.00	x10 ⁷ CFU/g	
<i>Faecalibacterium prausnitzii</i>	577.4	200.0 - 3500.0	x10 ⁶ CFU/g	

Actions






	<i>S. thermophilus</i> FP4	<i>S. boulardii</i> CNCM I-1079	<i>B. longum</i> Rosell-75	<i>L. rhamnosus</i> Rosell-11	<i>L. helveticus</i> Rosell-52	<i>L. salivarius</i> LS03	<i>L. fermentum</i> LF10	<i>B. breve</i> B632	<i>L. scivarius</i> LS01	<i>L. fermentum</i> LF16	<i>B. longum</i> 04	<i>L. rhamnosus</i> LR06	<i>L. plantarum</i> LP01	<i>B. animalis</i> subsp. <i>lactis</i> BA05	<i>L. crispatus</i> strains	<i>L. fermentum</i> LF08	<i>B. breve</i> BR03	<i>L. casei</i> LC03	<i>L. acidophilus</i> LA02	<i>L. rhamnosus</i> GG	<i>L. plantarum</i> 299V	<i>L. plantarum</i> 6595	<i>L. plantarum</i> HEAL19	<i>L. paracasei</i> 8700:2	<i>L. plantarum</i> HEAL9
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																									



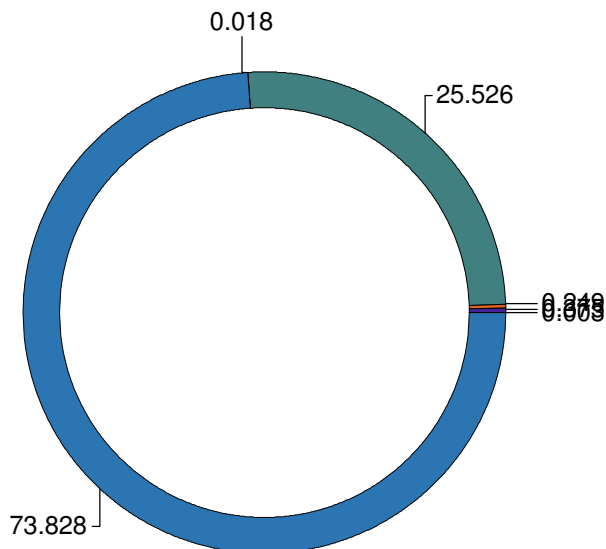
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Introduction:

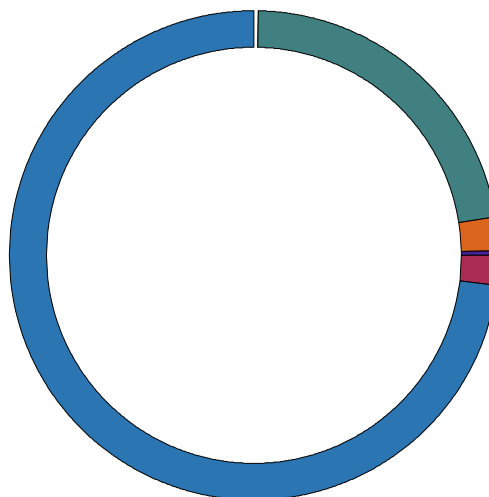
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider 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	73.828	50.000 - 95.000	%
 Firmicutes Phylum	25.526	3.500 - 40.000	%
 Verrucomicrobia Phylum	0.375	0.000 - 2.400	%
 Proteobacteria Phylum	0.249	0.050 - 12.500	%
 Euryarchaeota Phylum	0.018*H	0.000 - 0.010	%
 Actinobacteria Phylum	0.003	0.001 - 4.818	%

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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REBECCA WAGHORN
07-Mar-1992 **Female**

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Pathogen Summary:

Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

LIQUID stool may indicate an infection (bacteria or viral), amoeba or Giardia, Irritable Bowel Syndrome, laxative use or abuse, Coeliac Disease. Review other gut markers contained within this report.

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 Phadia ELiA Fluorescence enzyme immunoassay (FEIA).

SECRETORY IGA NORMAL:

Secretory IgA is within range.

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. Review this level with other pathogenic bacteria and normal commensal flora. Lower levels within reference range should be interpreted clinically.

ZONULIN NORMAL:

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

BETA-GLUCURONIDASE NORMAL:

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



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Opportunistic Bacteria Comment

STREPTOCOCCUS ORALIS ELEVATED:

PHYLUM: Firmicutes

DESCRIPTION:

Streptococcus oralis is a Gram-positive bacterium in the gut and oral microbiome, part of the Streptococcus mitis group. In the gut, S. oralis is part of the complex microbial community that supports digestive health. However, in immunocompromised individuals or those with disrupted microbiomes, S. oralis can become an opportunistic pathogen.

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.

Potential Autoimmune Comments

FUSOBACTERIUM SPECIES ELEVATED:

PHYLUM: Fusobacteriota

DESCRIPTION:

Fusobacterium species are gram-negative bacteria and are common members of the human oral and faecal microbiome. It has been demonstrated to promote the release of intestinal inflammatory factors and disrupt the intestinal barrier function. As such F. nucleatum elevation may contribute to the etiology of some gastrointestinal disorders, such as appendicitis, colon cancer, and inflammatory bowel disease (IBD). It may also induce an increase in secretory IgA and a decrease in beneficial bacteria levels such as Lactobacillus. Review this level with faecal calprotectin.

TREATMENT SUGGESTIONS: If treatment is warranted, effective antibiotics may include metronidazole or erythromycin. The use of herbal antimicrobials (Tea polyphenols- green and black tea extracts and peppermint) and probiotic treatment may also be effective. 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

BACTEROIDES FRAGILIS ELEVATED:

PHYLUM: Bacteroidetes

DESCRIPTION:

Bacteroides fragilis is an anaerobic, Gram-negative bacterium. It is part of the normal microbiota of the human colon and is generally commensal. *Bacteroides fragilis* plays an intricate role in the human colon and usually has a beneficial relationship with the host. However, elevated levels may be potentially pathogenic. Disruption of tissue barriers and the spread of *Bacteroides fragilis* into adjacent tissue can cause polymicrobial infection. Enterotoxigenic *Bacteroides fragilis* (ETBF) strains are strains of *B. fragilis* that secrete an enterotoxin termed the *B. fragilis* toxin (BFT) and may have a role in inflammatory diarrhea and flare-ups of inflammatory bowel disease.

TREATMENT SUGGESTIONS: If treatment is warranted, Piperacillin/tazobactam, meropenem, and metronidazole have high susceptibility rates.

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 BIFIDUM LOW:

PHYLUM: Actinobacteria

DESCRIPTION:

Bifidobacterium bifidum is a Gram-positive, anaerobic bacterium integral to the human gut microbiota, especially in infants. It ferments a variety of carbohydrates, including human milk oligosaccharides, aiding in digestion, and promoting a healthy gut flora. *B. bifidum* produces short-chain fatty acids that lower gut pH and inhibit pathogenic bacteria while supporting intestinal cells. It also modulates the immune system, enhancing immune responses and reducing inflammation, and strengthens the intestinal barrier. Clinically, *B. bifidum* has shown promise in alleviating gastrointestinal disorders.

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.

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:



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REBECCA WAGHORN
07-Mar-1992 **Female**

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CANNONVALE QLD 4802

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

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.

CLOSTRIDIUM SPECIES ELEVATED:

PHYLUM: Firmicutes

DESCRIPTION:

Clostridium is a genus of anaerobic, Gram-positive bacteria found in the environment and the intestinal tract. This genus includes several species and can utilize large amounts of nutrients that cannot be digested by host and produce short-chain fatty acids (SCFAs), which play a noticeable role in intestinal homeostasis. Colonisation of *Clostridium* species may be affected by diet (carbohydrate and protein in diet) and general health and may be protective against inflammation and infection. However, some species may act as potential pathogens. Elevated *Clostridium* species may indirectly damage the intestinal epithelial cells. Another symptom may include constipation.

TREATMENT SUGGESTIONS: Treatment may involve the use of probiotics, treatment of any intestinal infections and dietary modification (reduce consumption of different fibres, such as inulin, oligofructose, arabinoxylan, guar gum and starch).

OXOLOBACTER FORMIGENES LOW:

PHYLUM: Proteobacterium



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DESCRIPTION:

Oxalobacter formigenes is a Gram negative oxalate-degrading anaerobic bacterium. Oxalate is formed in the liver by amino acid catabolism as well as present in a wide range of foods including tea, coffee, chocolate and certain fruits and vegetables. High concentration of oxalate in the urine is related to the potential formation of calcium oxalate kidney stones. Oxalobacter Formigenes is the main known bacterial species involved in oxalate degradation in the gut and maintains oxalate homeostasis. Levels of O. Formigenes tends to decrease with age as well as with the use of antibiotics or other drugs. Low levels may be associated with calcium oxide stone formation, inflammatory bowel disease or Crohn's.

TREATMENT SUGGESTIONS:

Treatment options include probiotic treatment and low oxalate diet modification. Urinary oxalate levels may also need to be investigated.



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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