

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	91.1	> 13.6	umol/g	
Butyrate	10.3 *L	10.8 - 33.5	%	
Acetate	68.8	44.5 - 72.4	%	
Propionate	19.3	0.0 - 32.0	%	
Valerate	1.6	0.5 - 7.0	%	

GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	11.4	0.0 - 50.0	ug/g	
Pancreatic Elastase	>800.0	> 200.0	ug/g	
Secretory (slgA)	1036.5	510.0 - 2040.0	ng/mL	
Zonulin	100.1	0.0 - 107.0	ng/mL	
Beta glucuronidase	3674.8	368.0 - 6266.0	U/g	
Steatocrit	<1.0	0.0 - 10.0	%	
a-Transglutaminase IgA	<20	0.0 - 100.0	units/L	
pH	7.1	6.3 - 7.7		

Microbiome Mapping Summary

Parasites & Worms

Bacteria & Viruses

Citrobacter species.

Mycology

Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.95 < 1.00

RATIO



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



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-.RACHEAL LEE (NPINS)
THRIVE HEALTH
SHOP 6/115 SHINGLEY DRIVE
AIRLIE BEACH QLD 4802

JENNY HOWARTH
12-Jun-1989 **Female**

15 GRACE AVEUNE
CANNONVALE QLD 4802

LAB ID : 4039526
UR NO. : 6319510
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4039526

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> .	2.21	< 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> .	0.29	< 1.00	x10 ⁴ CFU/g	
<i>Streptococcus oralis</i> .	0.32	< 1.00	x10 ⁶ CFU/g	
<i>Streptococcus salivarius</i> .	1.05	< 5.00	x10 ⁶ CFU/g	
<i>Methanobrevibacter smithii</i>	0.90	< 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.	31.20 *H	< 5.00	x10 ⁴ CFU/g	
<i>Citrobacter freundii</i> complex.	<dl	< 5.00	x10 ⁴ CFU/g	
<i>Klebsiella</i> species	<dl	< 5.00	x10 ³ CFU/g	
<i>Klebsiella pneumoniae</i> complex.	<dl	< 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	0.16	< 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 lusitaniae.	<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.	<dl	< 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	
Enteroaggregative 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	
<i>Bacteroides fragilis</i>	2.0	1.6 - 250.0	x10 ⁵ CFU/g	
TOTAL BIFIDOBACTERIA	178.8	5.0 - 2000.0	x10 ⁶ CFU/g	
<i>Bifidobacterium adolescentis</i>	31.6	4.6 - 1000.0	x10 ⁶ CFU/g	
<i>Bifidobacterium bifidum</i> .	<dl	4.6 - 1000.0	x10 ⁶ CFU/g	
<i>Bifidobacterium breve</i> .	<dl	4.6 - 1000.0	x10 ⁶ CFU/g	
<i>Bifidobacterium longum</i>	147.1	4.6 - 1000.0	x10 ⁶ CFU/g	
<i>Enterococcus species</i>	<dl	1.9 - 2000.0	x10 ³ CFU/g	
<i>Escherichia species</i>	402.9	3.7 - 3800.0	x10 ⁴ CFU/g	
TOTAL LACTOBACILLI	4.0	1.7 - 3000.0	x10 ³ CFU/g	
<i>Lactobacillus acidophilus</i> .	<dl	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus casei</i> .	<dl	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus delbrueckii</i>	<dl	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus plantarum</i> .	<dl	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus rhamnosus</i>	2.0	1.7 - 500.0	x10 ³ CFU/g	
<i>Lactobacillus salivarius</i>	2.0	1.7 - 500.0	x10 ³ CFU/g	
<i>Clostridium species</i>	82.3*H	5.0 - 50.0	x10 ⁷ CFU/g	
<i>Oxalobacter formigenes</i>	<dl*L	> 5.00	x10 ⁶ CFU/g	
<i>Akkermansia muciniphila</i>	<dl*L	1.00 - 50.00	x10 ⁷ CFU/g	
<i>Faecalibacterium prausnitzii</i>	577.4	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

	<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. salivarius</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>B. animalis</i> subsp. <i>lactis</i> BS01	<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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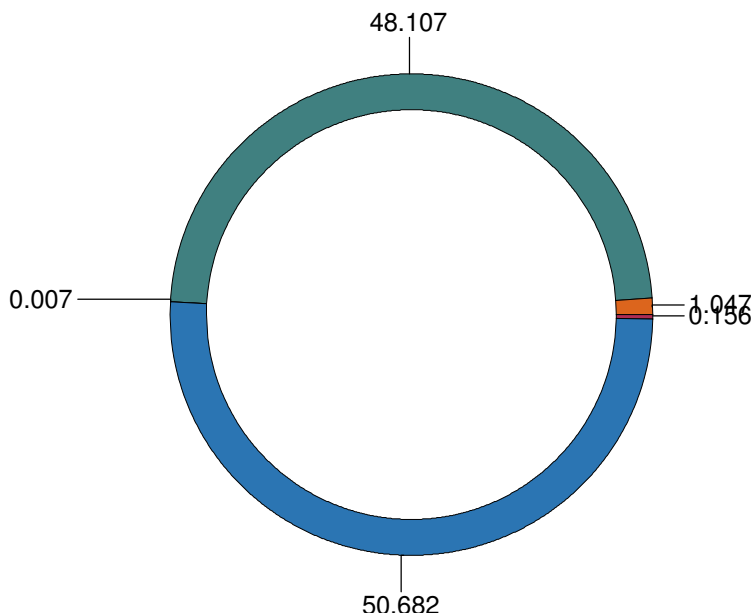
4039526

Introduction:

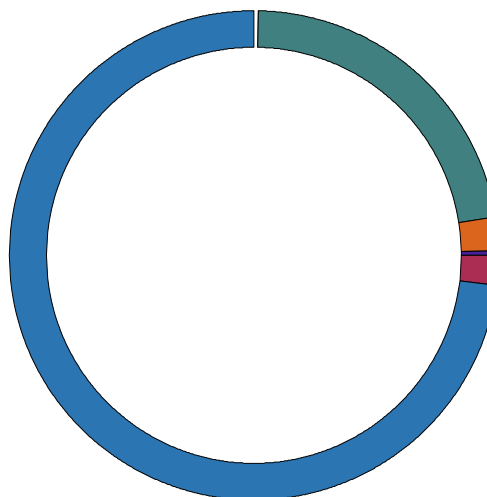
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider 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	50.682	50.000 - 95.000	%
 Firmicutes Phylum	48.107 *H	3.500 - 40.000	%
 Proteobacteria Phylum	1.047	0.050 - 12.500	%
 Actinobacteria Phylum	0.156	0.001 - 4.818	%
 Euryarchaeota Phylum	0.007	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.

LOW BUTYRATE LEVEL:

Butyrate is a short chain fatty acid that is extremely important for gut health. It is the main fuel source for gut cells, which helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Low levels of butyrate production have been observed in individuals with inflammatory bowel diseases, insufficient fibre intake, slow transit time, recent antibiotic therapy. Low butyrate may also be associated with an increased risk of colon cancer & constipation.

Consuming foods high in resistant starch has been shown to increase butyrate levels.



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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).

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 HIGH NORMAL:

Zonulin is a protein that modulates intestinal barrier function and can also be considered as a potential inflammatory marker. Although this result is within range, the result should be interpreted with patient clinical symptoms as well as reviewing the presence of other proteobacteria that may be the result of increased Zonulin.

BETA-GLUCURONIDASE NORMAL:

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

Potential Autoimmune Comments

CITROBACTER SPECIES ELEVATED:

PHYLUM: Proteobacteria

DESCRIPTION:

Citrobacter species are straight, facultative anaerobic, Gram-negative bacilli, generally regarded as being a commensal bacteria found in a healthy human gut. However, elevated Citrobacter species may associated with an increased risk of Irritable bowel disease and has potential as an autoimmune trigger via the induction of inflammatory cytokines.

TREATMENT SUGGESTIONS:

A practitioner may take into consideration a range of patient factors and symptoms to determine if treatment is necessary. Treatments may include herbal antimicrobials and/or pre-pro-biotics.



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Phyla Microbiota Comment

FIRMICUTES (PHYLUM) ELEVATED:

DESCRIPTION:

Firmicutes are a phylum of diverse bacteria which are primarily grouped into classes, Bacilli, Clostridia, Erysipelotrichia and Negativicutes. They are found in various environments, including the intestinal tract, and the group includes some notable pathogens. Firmicutes are involved in energy resorption in the gut microbiome and levels may be affected by diet. Elevated levels and disturbance of gastrointestinal microbiome balance, particularly Firmicutes/Bacteroidetes ratio, have been associated with inflammation, obesity, diabetes and with a high sugar/ fat diet.

TREATMENT SUGGESTIONS: Consider using Bifidobacterium or Saccharomyces containing probiotics. It may also be suggested to optimise the patient diet. A lower fat diet may help to normalize Firmicutes levels.



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Normal Bacterial Flora Comment

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.

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 ACIDOPHILUS LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Lactobacillus acidophilus is a Gram-positive, rod-shaped, non-spore-forming bacterium commonly found in the human gut and fermented foods. It plays a key role in oxalate degradation, bowel normalisation and may assist patients with bloating.

TREATMENT SUGGESTIONS:

Consider probiotic supplementation containing L. acidophilus.

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



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CANNONVALE QLD 4802

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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.

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*.

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, arabinosyl, guar gum and starch).

OXOLOBACTER FORMIGENES LOW:

PHYLUM: Proteobacterium

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 oxalate 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.

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