

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	Unformed	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	45.6	> 13.6	umol/g	
Butyrate	22.8	10.8 - 33.5	%	
Acetate	60.6	44.5 - 72.4	%	
Propionate	13.8	0.0 - 32.0	%	
Valerate	2.8	0.5 - 7.0	%	

GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	9.5	0.0 - 50.0	ug/g	
Pancreatic Elastase	>800.0	> 200.0	ug/g	
Secretory (slgA)	54.5 *L	510.0 - 2040.0	ng/mL	
Zonulin	19.9	0.0 - 107.0	ng/mL	
Beta glucuronidase	2768.0	368.0 - 6266.0	U/g	
Steatocrit	5.0	0.0 - 10.0	%	
a-Transglutaminase IgA	<20	0.0 - 100.0	units/L	
pH	6.3	6.3 - 7.7		

Microbiome Mapping Summary

Parasites & Worms

Dientamoeba fragilis.

Bacteria & Viruses

Enterococcus faecalis
Streptococcus salivarius.
Methanobrevibacter smithii

Mycology

Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.89 < 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

MELINDA BUTCHER
14-Jul-1975 **Female**

LOT 12 SIMPSON ROAD
STRATHDICKIE QLD 4800

LAB ID : 4029709
UR NO. :
Collection Date : 01-Oct-2024
Received Date: 03-Oct-2024



4029709

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.	21.1 *H < 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	3.09 *H < 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.	0.59 < 1.00	x10 ⁴ CFU/g	
Streptococcus oralis.	0.69 < 1.00	x10 ⁶ CFU/g	
Streptococcus salivarius.	7.27 *H < 5.00	x10 ⁶ CFU/g	
Methanobrevibacter smithii	6.10 *H < 1.00	x10 ⁵ CFU/g	
Desulfovibrio piger	<dl < 18.00	x10 ⁶ CFU/g	
Enterobacter cloacae complex.	<dl < 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	18.00 < 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.	0.60	< 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	●
Enterococcal species	<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 toxin-producing 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	1.0*L	1.6 - 250.0	x10 ⁵ CFU/g	
TOTAL BIFIDOBACTERIA	426.8	5.0 - 2000.0	x10 ⁶ CFU/g	
Bifidobacterium adolescentis	58.2	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium bifidum.	162.3	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium breve.	<dl	4.6 - 1000.0	x10 ⁶ CFU/g	
Bifidobacterium longum	206.3	4.6 - 1000.0	x10 ⁶ CFU/g	
Enterococcus species	184.4	1.9 - 2000.0	x10 ³ CFU/g	
Escherichia species	601.6	3.7 - 3800.0	x10 ⁴ CFU/g	
TOTAL LACTOBACILLI	460.4	1.7 - 3000.0	x10 ³ CFU/g	
Lactobacillus acidophilus.	4.0	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus casei.	452.0	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus delbrueckii	2.1	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus plantarum.	<dl	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus rhamnosus	2.3	1.7 - 500.0	x10 ³ CFU/g	
Lactobacillus salivarius	<dl	1.7 - 500.0	x10 ³ CFU/g	
Clostridium species	46.6	5.0 - 50.0	x10 ⁷ CFU/g	
Oxalobacter formigenes	<dl *L	> 5.00	x10 ⁶ CFU/g	
Akkermansia muciniphila	<dl *L	1.00 - 50.00	x10 ⁷ CFU/g	
Faecalibacterium prausnitzii	289.2	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 HEAL9	L. paracasei 8700:2	L. plantarum HEAL19	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 F08	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																										



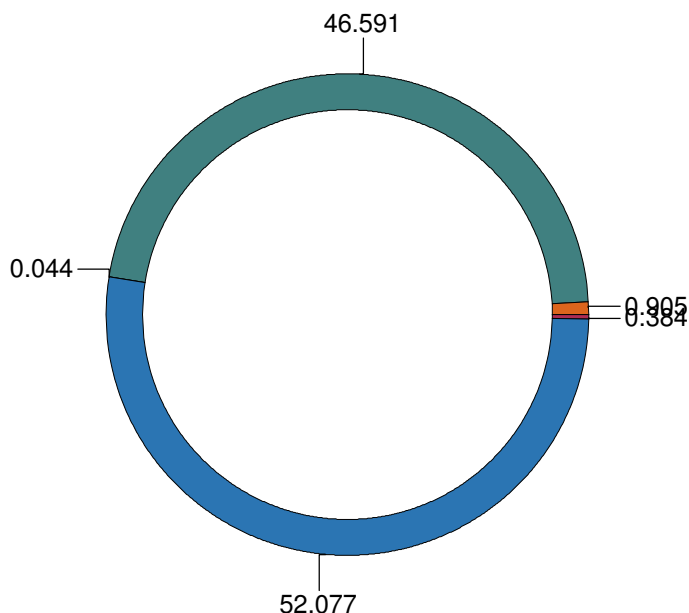
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Introduction:

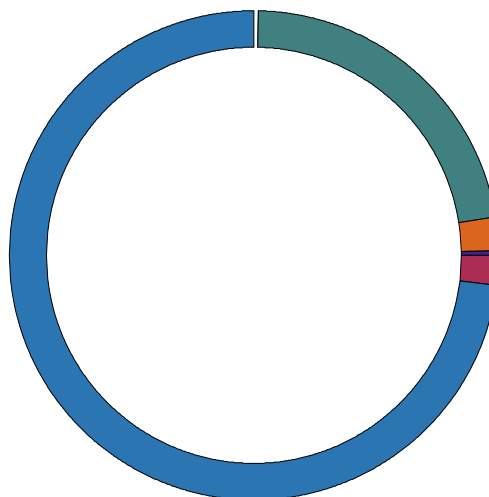
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider 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	52.077	50.000 - 95.000	%
 Firmicutes Phylum	46.591 *H	3.500 - 40.000	%
 Proteobacteria Phylum	0.905	0.050 - 12.500	%
 Actinobacteria Phylum	0.384	0.001 - 4.818	%
 Euryarchaeota Phylum	0.044 *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.

UNFORMED/LIQUID stools may indicate the presence of infection and/or inflammation.

Consider dysbiosis, food sensitivity, high dose vitamin C and magnesium, infection, intestinal permeability, laxative use, malabsorption, maldigestion, stress. Other causes: bacterial, fungal, viral and other parasitic infections.

Treatment:

- Investigate and treat possible underlying cause.
- Assess other gut markers (e.g pH, pancreatic elastase 1, etc).

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-GLUCURONIDASE NORMAL:

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

Parasites/Worms Comment

ELEVATED DIENTAMOEBIA FRAGILIS LEVEL:

Dientamoeba fragilis appears to be extremely common and may have a cosmopolitan distribution, although there are large variations in prevalence. Dientamoeba fragilis has been linked to intestinal symptoms, especially in children. The most common symptoms associated with this organism are abdominal pain, intermittent diarrhoea, bloating and anorexia.

TREATMENT SUGGESTIONS:

Mild symptoms are self-limiting.

If treatment is warranted, metronidazole for 10 days or a single 2g dose of Tinidazole may be used. Tetracycline has also proven effective in adults.

Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

Opportunistic Bacteria Comment

ENTEROCOCCUS FAECALIS ELEVATED:

PHYLUM: Firmicutes



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DESCRIPTION:

Enterococcus faecalis is a gram-positive bacterium commensal bacterium inhabiting the gastrointestinal tracts of humans. It can however, be implicated in a variety of infections of which urinary tract infections are the most common. Enterococci have recently emerged as a prevalent multidrug-resistant nosocomial pathogen. Resistant Enterococci densely colonize the gut particularly following antibiotic treatment, which can deplete the GI tract of protective commensals.

TREATMENT SUGGESTIONS:

Treatment of *Enterococcus* species in gut flora may not be necessary or recommended. However, if there is overgrowth of this genus with implicated infection, treatment may be warranted. Enterococci are challenging to treat due their drug-resistant mechanisms. Ampicillin is the preferred antibiotic used to treat enterococci infections if required. Rule out allergy to above medication before prescribing/taking.

STREPTOCOCCUS SALIVARIUS ELEVATED:

PHYLUM: Firmicutes

DESCRIPTION:

Streptococcus salivarius is a Gram-positive bacterium primarily found in the oral and upper respiratory microbiomes but also present in the gut microbiome. It plays a protective role by producing bacteriocins (BLIS), which inhibit pathogens such as *Streptococcus pyogenes*. In the gut, *S. salivarius* contributes to maintaining a balanced microbial environment, supporting overall gut health and enhancing the immune system. Its ability to produce antimicrobial substances helps to prevent the overgrowth of harmful bacteria, promoting a healthy gut microbiome.

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

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.

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,



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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 LOW:

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. Low Bacteroides fragilis levels have been associated with inflammatory bowel disease and Crohn's.

TREATMENT SUGGESTIONS: Treatment may involve the use of probiotics and dietary modification.

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 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 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.

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 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



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MELINDA BUTCHER
14-Jul-1975 **Female**

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STRATHDICKIE QLD 4800

LAB ID : 4029709
UR NO. :
Collection Date : 01-Oct-2024
Received Date: 03-Oct-2024



4029709

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