NutriPATH
INTEGRATIVE PATHOLOGY SERVICES

P: 1300 688 522
E: info@nutripath.com.au

-.VERA DAHLSTROM
RESTORING VITALITY NATUROPATHIC CLINIC
2 TOROKINA STREET

PETA WEAVER
06-Feb-1957 Female

PO BOX 63
HERBERTON QLD 4887

LAB ID :	**3896316**
UR NO. :	**6190724**
Collection Date :	**05-Jun-2023**
Received Date:	**07-Jun-2023**

3896316

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	**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

Short Chain Fatty Acids	Result	Range	Units
Short Chain Fatty Acids, Beneficial	**33.3**	> 13.6	umol/g
Butyrate	**11.0**	10.8 - 33.5	%
Acetate	**70.9**	44.5 - 72.4	%
Propionate	**14.5**	0.0 - 32.0	%
Valerate	**3.6**	0.5 - 7.0	%

GIT Functional Markers

GIT Functional Markers	Result	Range	Units
Calprotectin.	**<5.0**	0.0 - 50.0	ug/g
Pancreatic Elastase	***164.2* *L**	> 200.0	ug/g
Secretory (sIgA)	**665.0**	510.0 - 2010.0	ug/g
Zonulin	**62.0**	0.0 - 107.0	ng/g
Beta glucuronidase	**1250.1**	337.0 - 4433.0	U/g
Steatocrit	**13.0**	0.0 - 15.0	%
a-Transglutaminase IgA	**<20**	0.0 - 100.0	units/L

Microbiome Mapping Summary

Parasites & Worms	Bacteria & Viruses	Fungi and Yeasts
	Methanobrevibacter smithii	

Key Phyla Microbiota

	Result	Range	Units
Firmicutes:Bacteroidetes Ratio	**0.67**	< 1.00	RATIO

Relative Commensal Abundance of the 6 Phyla groups can be found on page 4 of this report

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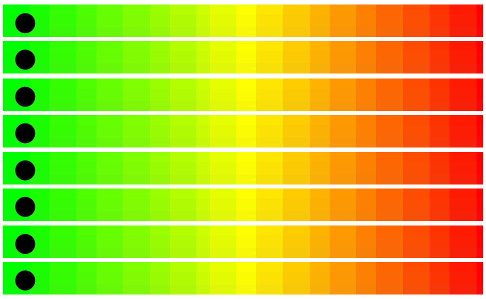
Parasites and Worms.	Result	Range	Units
Parasitic Organisms			
Cryptosporidium species	<dl	< 1.0	x10^6 org/g
Entamoeba histolytica.	<dl	< 1.0	x10^4 org/g
Giardia intestinalis	<dl	< 1.0	x10^3 org/g
Blastocystis hominis.	<dl	< 1.0	x10^3 org/g
Dientamoeba fragilis.	<dl	< 1.0	x10^5 org/g
Endolimax nana	<dl	< 1.0	x10^4 org/g
Entamoeba coli.	1.0	< 5.0	x10^6 org/g
Pentatrichomonas hominis	<dl	< 1.0	x10^2 org/g

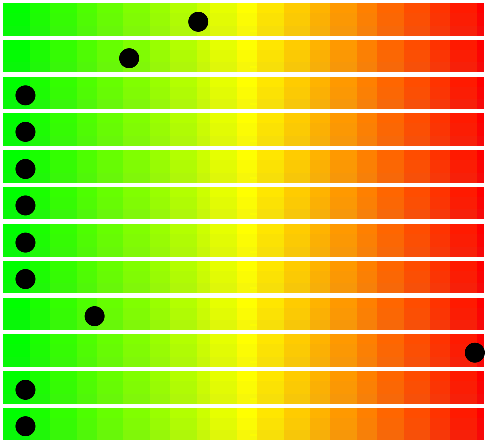


Worms

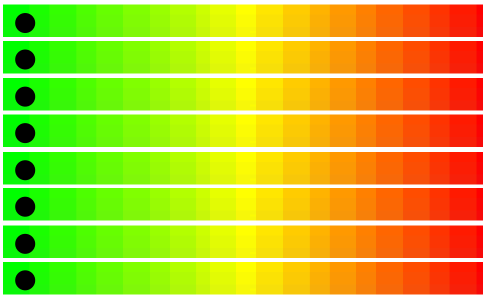
Ascaris lumbricoides, Roundworm	Not Detected	Necator americanus, Hookworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected	Enterobius vermicularis,Pinworm	Not Detected
Enterocytozoon spp	Not Detected	Hymenolepis spp, Tapeworm	Not Detected
Strongyloides spp, Roundworm	Not Detected	Taenia species,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

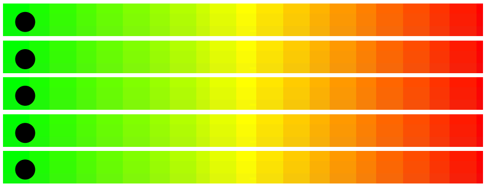
Opportunistic Bacteria/Overgrowth	Result	Range	Units
Bacillus species.	0.80	< 1.00	x10^5 CFU/g
Enterococcus faecalis	0.66	< 1.00	x10^4 CFU/g
Enterococcus faecium	0.41	< 1.00	x10^4 CFU/g
Morganella species	<dl	< 1.00	x10^3 CFU/g
Pseudomonas species	<dl	< 1.00	x10^4 CFU/g
Pseudomonas aeruginosa.	<dl	< 3.00	x10^2 CFU/g
Staphylococcus species	<dl	< 1.00	x10^4 CFU/g
Staphylococcus aureus	<dl	< 5.00	x10^2 CFU/g
Streptococcus species	1.73	< 3.00	x10^3 CFU/g
Methanobrevibacter smithii	*20.86* *H	< 3.50	x10^9 CFU/g
Desulfovibrio piger	<dl	< 18.00	x10^7 CFU/g
Enterobacter complex.	<dl	< 5.00	x10^6 CFU/g



Potential Autoimmune Triggers			
Citrobacter species.	<dl	< 5.00	x10^5 CFU/g
Citrobacter freundii.	<dl	< 5.00	x10^5 CFU/g
Klebsiella species	<dl	< 5.00	x10^3 CFU/g
Klebsiella pneumoniae.	<dl	< 5.00	x10^4 CFU/g
Prevotella copri	<dl	< 1.00	x10^7 CFU/g
Proteus species	<dl	< 5.00	x10^4 CFU/g
Proteus mirabilis.	<dl	< 1.00	x10^3 CFU/g
Fusobacterium species	0.66	< 10.00	x10^7 CFU/g



Fungi & Yeast	Result	Range	Units
Candida species.	<dl	< 5.00	x10^3 CFU/g
Candida albicans.	<dl	< 5.00	x10^2 CFU/g
Geotrichum species.	<dl	< 3.00	x10^2 CFU/g
Saccharomyces cerevisiae.	<dl	< 3.00	x10^3 CFU/g
Rhodotorula species.	<dl	< 1.00	x10^3 CFU/g



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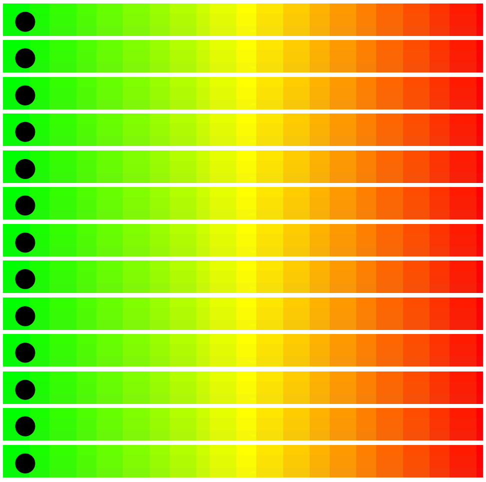
Bacterial Pathogens	Result	Range	Units
Aeromonas hydrophila.	<dl	< 1.00	x10^3 CFU/g
Campylobacter species.	<dl	< 1.00	x10^3 CFU/g
C. difficile, Toxin A	<dl	< 1.00	x10^3 CFU/g
C. difficile, Toxin B	<dl	< 1.00	x10^3 CFU/g
Enterohemorrhagic E. coli	<dl	< 1.00	x10^3 CFU/g
Enteroinvasive E. coli/Shigella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

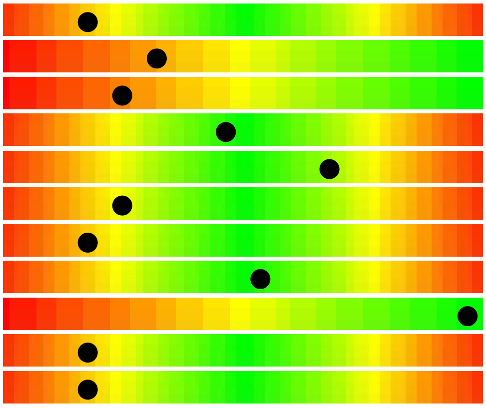


Comment: Helico Pylori virulence factors will be listed below if detected POSITIVE

H.pylori Virulence Factor, babA	Not Detected	H.pylori Virulence Factor, cagA	Not Detected
H.pylori Virulence Factor, dupA	Not Detected	H.pylori Virulence Factor, iceA	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		

Normal Bacterial GUT Flora	Result	Range	Units
Bacteroides fragilis	1.3 *L	1.6 - 250.0	x10^9 CFU/g
Bifidobacterium species	4.0 *L	> 6.7	x10^7 CFU/g
Bifidobacterium longum	2.2 *L	> 5.2	x10^6 CFU/g
Enterococcus species	960.0	1.9 - 2000.0	x10^5 CFU/g
Escherichia species	3228.0	3.7 - 3800.0	x10^6 CFU/g
Lactobacillus species	1102.6	8.6 - 6200.0	x10^5 CFU/g
Lactobacillus Rhamnosus	15.0	8.3 - 885.0	x10^4 CFU/g
Clostridium species	31.3	5.0 - 50.0	x10^6 CFU/g
Oxalobacter formigenes	94.87	> 15.00	x10^7 CFU/g
Akkermansia muciniphila	<dl *L	1.00 - 50.00	x10^3 CFU/g
Faecalibacterium prausnitzii	389.0	200.0 - 3500.0	x10^3 CFU/g



Methodology:
GIT Functional markers performed by GCMS,EIA,FEIA.
Bacteriology,Virology,Fungi,Parasites & Worms performed by PCR,qPCR.
<dl = result below detectable limit. *H = Result greater than the reference range. *L = Result less than the reference range

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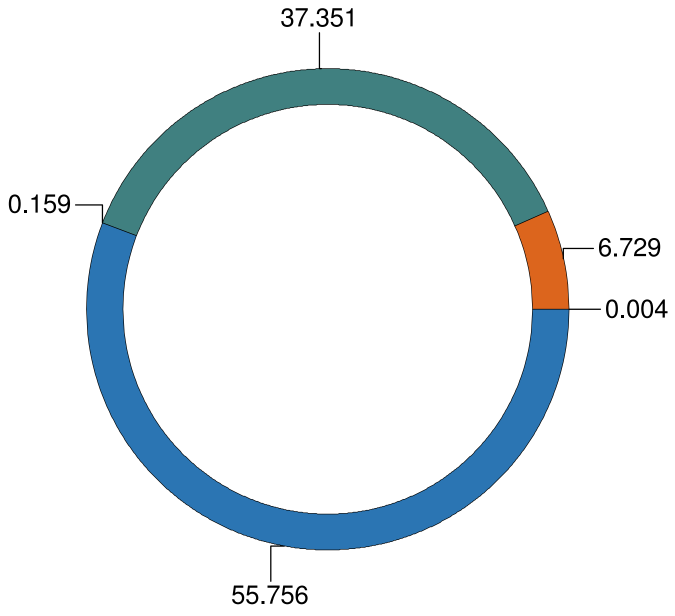
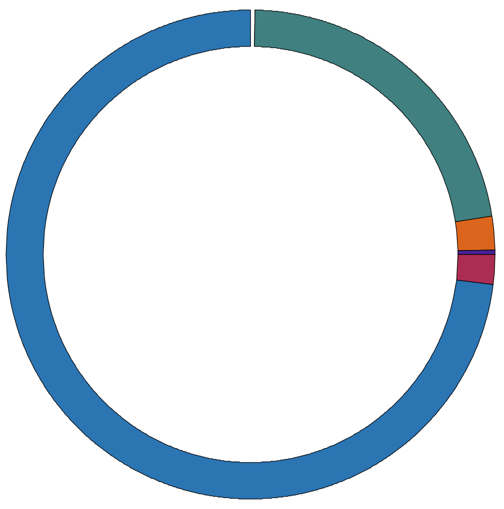
Introduction:
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, 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	55.756	50.000 - 95.000	%
🟩	Firmicutes Phylum	37.351	3.500 - 40.000	%
🟧	Proteobacteria Phylum	6.729	0.500 - 12.500	%
⬜	Euryarchaeota Phylum	0.159*H	0.000 - 0.017	%
🟥	Actinobacteria Phylum	0.004	0.001 - 4.818	%
🟪	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.

Pathogen Summary:

Macroscopy Comment

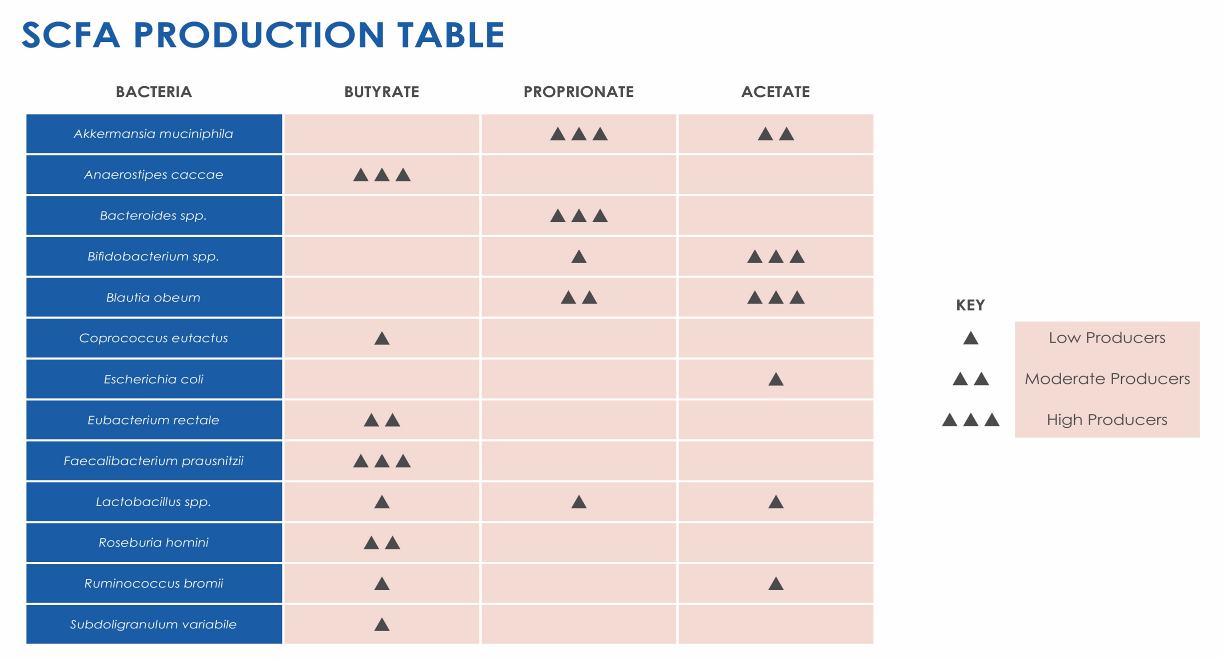
BROWN coloured stool is considered normal in appearance.

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 mucinphila, 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.



SCFA PRODUCTION TABLE

BACTERIA	BUTYRATE	PROPRIONATE	ACETATE
Akkermansia muciniphila		▲▲▲	▲▲
Anaerostipes caccae	▲▲▲		
Bacteroides spp.		▲▲▲	
Bifidobacterium spp.		▲	▲▲▲
Blautia obeum		▲▲	▲▲▲
Coprococcus eutactus	▲		
Escherichia coli			▲
Eubacterium rectale	▲▲		
Faecalibacterium prausnitzii	▲▲▲		
Lactobacillus spp.	▲	▲	▲
Roseburia homini	▲▲		
Ruminococcus bromii	▲		▲
Subdoligranulum variabile	▲		

KEY	
▲	Low Producers
▲▲	Moderate Producers
▲▲▲	High Producers

GIT Markers Comment

PANCREATIC ELASTASE: MILD TO MODERATE INSUFFICIENCY.
Pancreatic insufficiency reflects trypsin, chymotrypsin, amylase and lipase activity.
PE1 is also useful in monitoring exocrine pancreatic function caused by: Chronic pancreatitis, Autoimmunopathies & connective tissue diseases, Chronic inflammatory bowel disease, Intestinal malabsorption with mucosal atrophy.
Treatment:

- Digestive enzyme supplementation
- A low-fat diet to control steatorrhea (excess fat in stools)
- Vitamin and mineral supplementation
- Investigate underlying causes for reduced pancreatic function (for eg. Coeliac disease, duodenal enteropathy, pancreatitis).

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 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-GLUCORONIDASE NORMAL:
B-Glucuronidase is considered normal and is within reference range.

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.

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 SPECIES LOW:

PHYLUM: Actinobacteria

DESCRIPTION:
Bifidobacterium is a genus of gram-positive, nonmotile anaerobic bacteria that are ubiquitous inhabitants of the gastrointestinal tract and considered a probiotic. Bifidobacterium species prevent diarrhea and intestinal infections, alleviate constipation, and stimulate the immune system. Low levels may be associated with irritable bowel syndrome, asthma, autism, depressive disorder and with pathogenic bacterial infection.

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

BIFIDOBACTERIUM LONGUM LOW:

PHYLUM: Actinobacteria

DESCRIPTION:
Bifidobacterium longum is a Gram-positive, catalase-negative, rod-shaped bacterium present in the human gastrointestinal tract and one of the Bifidobacterium species. It can induce and regulate immune responses, reduce the expression of inflammatory cytokines, and maintain the normal intestinal barrier function.

Bifidobacterium longum is a clinically effective, well-established, multifunctional probiotic that has a long history of human use in alleviating gastrointestinal, immunological, and infectious diseases such as constipation, antibiotic associated diarrhoea, irritable bowel syndrome and ulcerative colitis. Low levels may be associated with irritable bowel syndrome, asthma, autism, depressive disorder and with pathogenic bacteria infection.

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

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 sup lactise, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius ssp 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