



3886830

COMPLETE MICROBIOME MAPPING

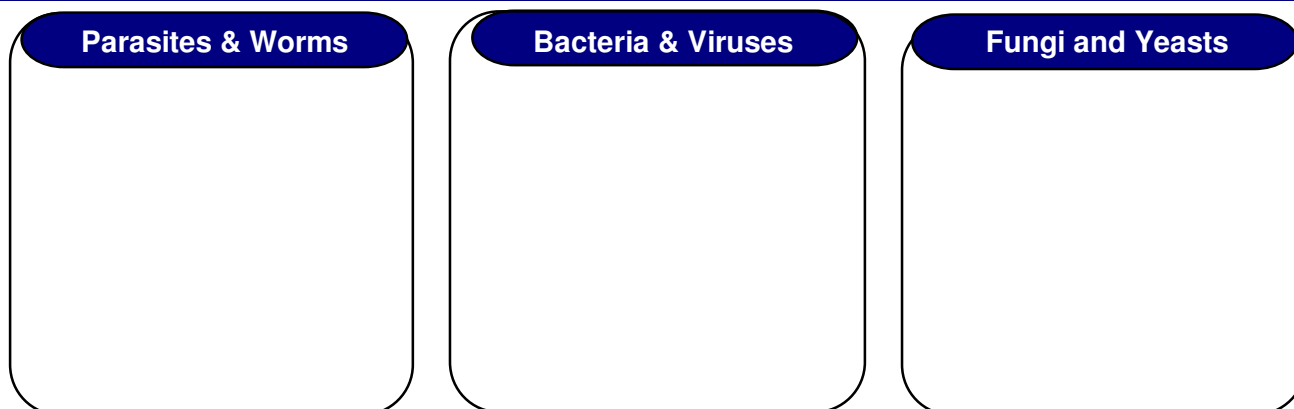
General Macroscopic Description

	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	Result	Range	Units	
Short Chain Fatty Acids, Beneficial	39.8	> 13.6	umol/g	
Butyrate	16.9	10.8 - 33.5	%	
Acetate	61.3	44.5 - 72.4	%	
Propionate	18.1	0.0 - 32.0	%	
Valerate	3.7	0.5 - 7.0	%	

GIT Functional Markers	Result	Range	Units	
Calprotectin.	<5.0	0.0 - 50.0	ug/g	
Pancreatic Elastase	292.3	> 200.0	ug/g	
Faecal Secretory IgA	705.0	510.0 - 2010.0	ug/g	
Faecal Zonulin	98.4	0.0 - 107.0	ng/g	
Faecal B-Glucuronidase	3287.2	337.0 - 4433.0	U/g	
Steatocrit	<1.0	0.0 - 15.0	%	
anti-Gliadin IgA	<20	0.0 - 100.0	units/L	

Microbiome Mapping Summary



Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.28 < 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.

Parasitic Organisms

Result	Range	Units	
<dl	< 1.0	x10 ⁶ org/g	●
<dl	< 1.0	x10 ⁴ org/g	●
<dl	< 1.0	x10 ³ org/g	●
<dl	< 1.0	x10 ³ org/g	●
<dl	< 1.0	x10 ⁵ org/g	●
<dl	< 1.0	x10 ⁴ org/g	●
<dl	< 5.0	x10 ⁶ org/g	●
<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	
<dl	< 1.00	x10 ⁵ CFU/g	●
<dl	< 1.00	x10 ⁴ CFU/g	●
<dl	< 1.00	x10 ⁴ CFU/g	●
<dl	< 1.00	x10 ³ CFU/g	●
<dl	< 1.00	x10 ⁴ CFU/g	●
<dl	< 3.00	x10 ² CFU/g	●
<dl	< 1.00	x10 ⁴ CFU/g	●
<dl	< 5.00	x10 ² CFU/g	●
1.11	< 3.00	x10 ³ CFU/g	●
0.66	< 5.00	x10 ⁹ CFU/g	●
<dl	< 18.00	x10 ⁷ CFU/g	●
26.36	> 15.00	x10 ⁷ CFU/g	●

Potential Autoimmune Triggers

<dl	< 5.00	x10 ⁵ CFU/g	●
<dl	< 5.00	x10 ⁵ CFU/g	●
<dl	< 5.00	x10 ³ CFU/g	●
<dl	< 5.00	x10 ⁴ CFU/g	●
<dl	< 1.00	x10 ⁷ CFU/g	●
<dl	< 5.00	x10 ⁴ CFU/g	●
<dl	< 1.00	x10 ³ CFU/g	●
0.30	< 10.00	x10 ⁷ CFU/g	●

Fungi & Yeast

Result	Range	Units	
<dl	< 5.00	x10 ³ CFU/g	●
<dl	< 5.00	x10 ² CFU/g	●
<dl	< 3.00	x10 ² CFU/g	●
<dl	< 3.00	x10 ³ CFU/g	●
<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	41.4	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	162.4	1.9 - 2000.0	x10 ⁵ CFU/g	
Escherichia species	1233.0	3.7 - 3800.0	x10 ⁶ CFU/g	
Lactobacillus species	1247.8	8.6 - 6200.0	x10 ⁵ CFU/g	
Lactobacillus Rhamnosus	880.0	8.3 - 885.0	x10 ⁴ CFU/g	
Clostridium species	10.2	5.0 - 50.0	x10 ⁶ CFU/g	
Enterobacter species	2.0	1.0 - 50.0	x10 ⁶ CFU/g	
Akkermansia muciniphila	4.00	1.00 - 50.00	x10 ³ CFU/g	
Faecalibacterium prausnitzii	157.0 *L	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



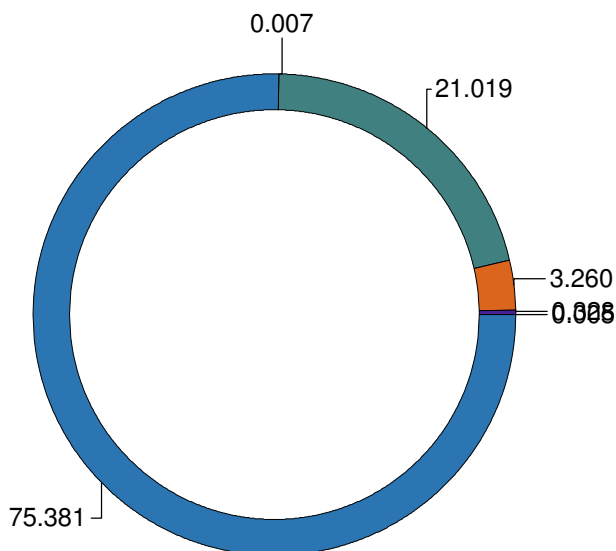
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Introduction:

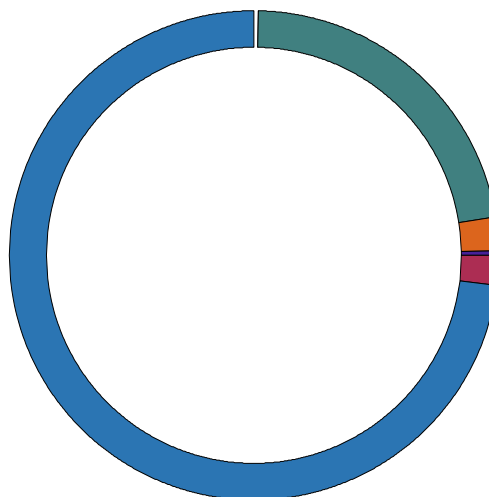
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider 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	75.381	50.000 - 95.000	%
 Firmicutes Phylum	21.019	3.500 - 40.000	%
 Proteobacteria Phylum	3.260	0.500 - 12.500	%
 Verrucomicrobia Phylum	0.328	0.000 - 2.400	%
 Euryarchaeota Phylum	0.007	0.000 - 0.177	%
 Actinobacteria Phylum	0.005	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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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.

SCFA PRODUCTION TABLE

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

KEY

▲ Low Producers

▲▲ Moderate Producers

▲▲▲ High Producers

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 produce on average 500 ug/g of PE-1. Thus, levels below 500 ug/g and above 200 ug/g suggest a deviation from optimal pancreatic function.

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.

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.



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

-RACHAEL IDDON
THE MATERNAL NUTRITIONIST
86 ANSTRUTHER ROAD
MANDURAH WA 6210

ASHLEIGH EVANS
07-May-1992 **Female**

64 ARIZONA PARADE
GOLDEN BAY WA 6174

LAB ID : 3886830
UR NO. : 6189696
Collection Date : 26-Apr-2023
Received Date: 01-May-2023



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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.



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Normal Bacterial Flora Comment

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.

FAECALIBACTERIUM PRAUSNITZII LOW:

PHYLUM: Firmicutes

DESCRIPTION:

Faecalibacterium prausnitzii is gram-positive, rod-shaped, anaerobic and is one of the most abundant and important commensal bacteria of the human gut microbiota. It is a key producer of Short Chain Fatty acids, has anti-inflammatory properties and may improve the imbalance in intestinal bacteria that leads to dysbiosis. Decreased colonisation of F. prausnitzii in the intestines have been associated with Crohn's disease, obesity, asthma, and major depressive disorders.

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

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 subsp. salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccharomyces 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	Saccharomyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccharomyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management