

P: 1300 688 522 E: info@nutripath.com.au A: PO Box 442 Ashburton VIC 3142 Date of Birth: 03-Jul-1977

Sex: F

Collected: 23/Feb/2021 Received: 25-Feb-2021 301/32 ENFIELD STREET MARRICKVILLE NSW 2204

Lab id: 3723512 UR#: 6066686

THE BALANCED WAY 19 MYRTLE STREET STANMORE NSW 2048

COMPLETE MICROBIOME MAPPING

General Macroscopic Description

	Result	Range	Markers	
Stool Colour	Brown		Colour - Brown is the colour of normal stool. Other colours may indicate abnormal GIT conditions.	
Stool Form	Formed		Form -A formed stool is considered normal. Variations to this may indicate abnormal GIT conditions.	
Mucous	NEG	<+	Mucous - Mucous production may indcate the presence of an infection, inflammation or malignancy.	
Occult Blood	NEG	<+	Blood (Macro) - The presence of blood in the stool may indicate possible GIT ulcer, and must always be investigated immediately.	

GIT Functional Markers	Result	Range	Units	
Calprotectin.	47.0	0.0 - 50.0	ug/g	
Pancreatic Elastase	102.0 *L	> 200.0	ug/g	•
Faecal Secretory IgA	<i>63.5</i> *L	510.0 - 2010.0	ug/g	•
Faecal Zonulin	71.0	0.0 - 107.0	ng/g	•
Faecal B-Glucuronidase	<i>6574.5</i> *H	337.0 - 4433.0	U/g	
Steatocrit	4.0	0.0 - 15.0	%	
anti-Gliadin IgA	<20	0.0 - 157.0	units/L	

Microbiome Mapping Summary

Parasites & Worms

Dientamoeba fragilis.

Bacteria & Viruses

Fungi and Yeasts

Key Phyla Microbiota

Bacteroidetes Firmicutes Firmicutes:Bacteroidetes Ratio

x10^11 org/g 4.70 *L 8.61 - 33.10 5.70 - 30.40 x10^10 org/g 8.30 **RATIO** 0.18 < 1.00



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Parasites and Worms.	Result	Range	Units	
Parasitic Organisms				
Cryptosporidium.	<dl< th=""><th>< 1.0</th><th>x10^6 org/g</th><th></th></dl<>	< 1.0	x10^6 org/g	
Entamoeba histolytica.	<dl< th=""><th>< 1.0</th><th>x10^4 org/g</th><th></th></dl<>	< 1.0	x10^4 org/g	
Giardia lamblia.	<dl< th=""><th>< 5.0</th><th>x10^3 org/g</th><th></th></dl<>	< 5.0	x10^3 org/g	
Blastocystis hominis.	<dl< th=""><th>< 2.0</th><th>x10^3 org/g</th><th></th></dl<>	< 2.0	x10^3 org/g	
Dientamoeba fragilis.	1.0 *H	< 1.0	x10^5 org/g	
Endolimax nana	<dl< th=""><th>< 1.0</th><th>x10^4 org/g</th><th></th></dl<>	< 1.0	x10^4 org/g	
Entamoeba coli.	<dl< th=""><th>< 5.0</th><th>x10^6 org/g</th><th></th></dl<>	< 5.0	x10^6 org/g	
Pentatrichomonas hominis	<dl< th=""><th>< 1.0</th><th>x10^2 org/g</th><th></th></dl<>	< 1.0	x10^2 org/g	
Worms				
Ancylostoma duodenale, Roundworm	Not Do	etected		Comment: Not Detected results indicate
Ascaris lumbricoides, Roundworm	Not Do	etected		the absence of detectable DNA in this
Necator americanus, Hookworm	Not Do	etected		sample for the worms reported.
Trichuris trichiura, Whipworm		etected		
Taenia species, Tapeworm		etected		
Enterobius vermicularis, Pinworm	Not Do	etected		
Opportunistic Bacteria/Overgr	Result	Range	Units	
Bacillus species.	0.6	< 1.5	x10^5 org/g	•
Enterococcus faecalis	<dl< th=""><th>< 1.0</th><th>x10^4 org/g</th><th></th></dl<>	< 1.0	x10^4 org/g	
Enterococcus faecium	0.3	< 1.0	x10^4 org/g	
Morganella species	<dl< th=""><th>< 1.0</th><th>x10^3 org/g</th><th></th></dl<>	< 1.0	x10^3 org/g	
Pseudomonas species	<dl< th=""><th>< 1.0</th><th>x10^4 org/g</th><th></th></dl<>	< 1.0	x10^4 org/g	
Pseudomonas aeruginosa.	1.8	< 5.0	x10^2 org/g	
Staphylococcus species	<dl< th=""><th>< 1.0</th><th>x10^4 org/g</th><th></th></dl<>	< 1.0	x10^4 org/g	
Staphylococcus aureus	<dl< th=""><th>< 5.0</th><th>x10^2 org/g</th><th></th></dl<>	< 5.0	x10^2 org/g	
Streptococcus species	<dl< th=""><th>< 1.0</th><th>x10^3 org/g</th><th></th></dl<>	< 1.0	x10^3 org/g	
Methanobacteriaceae	0.40	< 5.00	x10^9 org/g	
Potential Autoimmune Triggers				
Citrobacter species.	<dl< th=""><th>< 5.0</th><th>x10^5 org/g</th><th></th></dl<>	< 5.0	x10^5 org/g	
Citrobacter freundii.	<dl< th=""><th>< 5.0</th><th>x10^5 org/g</th><th>•</th></dl<>	< 5.0	x10^5 org/g	•
Klebsiella species	<dl< th=""><th>< 5.0</th><th>x10^3 org/g</th><th></th></dl<>	< 5.0	x10^3 org/g	
Klebsiella pneumoniae.	2.6	< 5.0	x10^4 org/g	•
Prevotella copri	<dl< th=""><th>< 1.0</th><th>x10^7 org/g</th><th></th></dl<>	< 1.0	x10^7 org/g	
Proteus species	<dl< th=""><th>< 5.0</th><th>x10^4 org/g</th><th></th></dl<>	< 5.0	x10^4 org/g	
Proteus mirabilis.	<dl< th=""><th>< 1.0</th><th>x10^3 org/g</th><th></th></dl<>	< 1.0	x10^3 org/g	
Fusobacterium species	0.10	< 10.00	x10^7 org/g	
Fungi & Yeast	Result	Range	Units	
Candida species.	3.0	< 5.0	x10^3 org/g	•
Candida albicans.	<dl< th=""><th>< 5.0</th><th>x10^2 org/g</th><th></th></dl<>	< 5.0	x10^2 org/g	
Geotrichum species.	<dl< th=""><th>< 3.0</th><th>x10^2 org/g</th><th></th></dl<>	< 3.0	x10^2 org/g	
Microsporidium species	<dl< th=""><th>< 5.0</th><th>x10^3 org/g</th><th></th></dl<>	< 5.0	x10^3 org/g	
Rhodotorula species.	<dl< th=""><th>< 1.0</th><th>x10^3 org/g</th><th></th></dl<>	< 1.0	x10^3 org/g	



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Aeromonas species						
Campylobacler.	Bacterial Pathogens	Result	Range	Units		
C. difficile, Toxin A C. difficile, Toxin B C. difficile, Toxin GFUg C.	Aeromonas species.	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
C. difficile, Toxin B Enterohemorrhagic E. coll E. coli O157 C. difficile, Toxin B Enterohemorrhagic E. coll E. coli O157 C. difficile, Toxin B Enterohemorrhagic E. coll E. coli O157 C. difficile, Toxin E E. coli O157 C. difficile, Toxin E Enterohemorrhagic E. coli CT/ST Coli O157 C. difficile, Toxin E Coli O157 C. difficile C. coli CT/ST Coli O157 C. difficile C. coli CT/ST	Campylobacter.	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Enterohemorrhagic E. coli	C. difficile, Toxin A	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
E. coli O157 Enteroinvasive E. coli/Shigella	C. difficile, Toxin B	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Enteroinvasive E. coll/Shigella Enterotoxigenic E. coli LT/ST Shiga-like Toxin E. coli stx1 Shiga-like Toxin E. coli stx2 Salmonella. vibrio cholerae versinia enterocolitica. Helicobacter pylori Comment: Helico Pylori virulence factors will be listed H.pylori Virulence Factor, dupA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, olipA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence H.pylori Virulence H.pylo	Enterohemorrhagic E. coli	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Enterotoxigenic E. coli LT/ST	E. coli O157	<dl< th=""><th>< 1.0</th><th>x10^2 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^2 CFU/g		
Shiga-like Toxin E. coli stx1	Enteroinvasive E. coli/Shigella	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Shiga-like Toxin E. coli stx2	Enterotoxigenic E. coli LT/ST	<dl< th=""><th>< 1.0</th><th></th><th></th><th></th></dl<>	< 1.0			
Salmonella.	Shiga-like Toxin E. coli stx1	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Vibrio cholerae Versinia enterocolitica. Helicobacter pylori Comment: Helico Pylori virulence factors will be listed below if detected POSITIVE H.pylori Virulence Factor, babA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, virB Not Detected H.pylori	Shiga-like Toxin E. coli stx2	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
Yersinia enterocolitica. Add < 1.0	Salmonella.	<dl< th=""><th>< 1.0</th><th>x10^4 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^4 CFU/g		
Helicobacter pylori cdl <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, oipA Not Detected H.pylori Virulence Factor, oipA Not Detected H.pylori Virulence Factor, vacA Not Detected H.pylori Virulence Factor, virD Not Detected H.pylori Virulence Factor, virD Not Detected Viral Pathogens Result Range Units Adenovirus 40/41 <dl <1.0="" bocavirus<="" cfu="" g="" th="" x10^40=""><th>Vibrio cholerae</th><th><dl< th=""><th>< 1.0</th><th></th><th></th><th></th></dl<></th></dl>	Vibrio cholerae	<dl< th=""><th>< 1.0</th><th></th><th></th><th></th></dl<>	< 1.0			
Comment: Helico Pylori virulence factors will be listed below if detected POSITIVE H.pylori Virulence Factor, babA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, vacA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virD Not Detected H.pylori Virulence Factor, vacA Not Detected H.pylori Virulence Factor, virD Not Detected H.pylori Virulence Factor No	Yersinia enterocolitica.	<dl< th=""><th>< 1.0</th><th>x10^5 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^5 CFU/g		
H.pylori Virulence Factor, babA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, vacA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, vacA H.pylori Virulence Factor, virD Not Detected H.pylori Virulence Factor, virD Not Detected Not Detecte	Helicobacter pylori	<dl< th=""><th>< 1.0</th><th>x10^3 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^3 CFU/g		
H.pylori Virulence Factor, babA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, dupA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, vacA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, vacA H.pylori Virulence Factor, virD Not Detected H.pylori Virulence Factor, virD Not Detected Not Detecte	Comment: Helico Pylori virulence	factors v	vill be listed	d below if det	ected POSITIVE	
H.pylori Virulence Factor, dupA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, oipA H.pylori Virulence Factor, virB Result Range Viral Pathogens Result Range Adenovirus 40/41 Norovirus Gl/II Bocavirus Normal Bacterial GUT Flora Result Range Wiff CFU/g Biffdobacterium species Escherichia species Lactobacillus species Lactobacillus species Enterobacter spec	•					Not Detected
H.pylori Virulence Factor, oipA H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virD Not Detected Not Detected H.pylori Virulence Factor, virD Not Detected Not Detected H.pylori Virulence Factor, virD Not Detected Not Detected Not Detected Not Detected H.pylori Virulence Factor, virD Not Detected Not Purple Not Not Detected Not Purple Not Not Detected Not Not Detected Not Not Detected Not Not Purple Not	• •					
H.pylori Virulence Factor, virB Not Detected H.pylori Virulence Factor, virD Not Detected					•	
Viral Pathogens Result Range Units Adenovirus 40/41 <dl>< 1.0 ×10⁴10 CFU/g Norovirus GI/II <dl>< 1.0 ×10⁴10 CFU/g Bocavirus <dl>< 1.0 ×10⁴10 CFU/g Normal Bacterial GUT Flora Result Range Units Bacteroides fragilis 1.2 *L 1.6 - 250.0 ×10⁴9 CFU/g Bifidobacterium species 12.4 > 6.7 ×10⁴7 CFU/g Enterococcus species 1.8 *L 1.9 - 2000.0 ×10⁴5 CFU/g Escherichia species 122.9 3.7 - 3800.0 ×10⁴6 CFU/g Lactobacillus species 4.5 *L 8.6 - 6200.0 ×10⁴6 CFU/g Clostridium species 10.1 5.0 - 50.0 ×10⁴6 CFU/g Enterobacter species 115.3 *H 1.0 - 50.0 ×10⁴6 CFU/g Akkermansia muciniphila 0.62 0.01 - 50.00 ×10⁴6 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 ×10⁴3 CFU/g Short Chain Fatty Acids Result Range Units</dl></dl></dl>						
Adenovirus 40/41	Viral Pathogens	Result	Range	Units		
Norovirus GI/II						
Result Range Units	Adenovirus 40/41	<dl< th=""><th>< 1.0</th><th>x10^10 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^10 CFU/g		
Bacteroides fragilis 1.2 *L 1.6 - 250.0 ×10^9 CFU/g Bifidobacterium species 12.4 > 6.7 ×10^7 CFU/g Enterococcus species 1.8 *L 1.9 - 2000.0 ×10^5 CFU/g Escherichia species 122.9 3.7 - 3800.0 ×10^6 CFU/g Lactobacillus species 4.5 *L 8.6 - 6200.0 ×10^5 CFU/g Clostridium species 10.1 5.0 - 50.0 ×10^6 CFU/g Enterobacter species 115.3 *H 1.0 - 50.0 ×10^6 CFU/g Akkermansia muciniphila 0.62 0.01 - 50.00 ×10^6 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 ×10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %				_		
Bacteroides fragilis 1.2 *L 1.6 - 250.0 x10^9 CFU/g Bifidobacterium species 12.4 > 6.7 x10^7 CFU/g Enterococcus species 1.8 *L 1.9 - 2000.0 x10^5 CFU/g Escherichia species 122.9 3.7 - 3800.0 x10^6 CFU/g Lactobacillus species 4.5 *L 8.6 - 6200.0 x10^6 CFU/g Clostridium species 10.1 5.0 - 50.0 x10^6 CFU/g Enterobacter species 115.3 *H 1.0 - 50.0 x10^6 CFU/g Akkermansia muciniphila 0.62 0.01 - 50.00 x10^3 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 x10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II	<dl< th=""><th>< 1.0</th><th>x10^7 CFU/g</th><th></th><th></th></dl<>	< 1.0	x10^7 CFU/g		
Bifidobacterium species	Norovirus GI/II Bocavirus	<dl< th=""><th>< 1.0 < 1.0</th><th>x10^7 CFU/g x10^10 CFU/g</th><th></th><th></th></dl<>	< 1.0 < 1.0	x10^7 CFU/g x10^10 CFU/g		
Enterococcus species	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora	<dl <dl Result</dl </dl 	< 1.0 < 1.0 Range	x10^7 CFU/g x10^10 CFU/g Units	•	
Lactobacillus species	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis	<dl><dl <dl Result 1.2 *L</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0	x10^7 CFU/g x10^10 CFU/g Units x10^9 CFU/g	•	
Lactobacillus species 4.5 *L 8.6 - 6200.0 x10^5 CFU/g Clostridium species 10.1 5.0 - 50.0 x10^6 CFU/g Enterobacter species 115.3 *H 1.0 - 50.0 x10^6 CFU/g Akkermansia muciniphila 0.62 0.01 - 50.00 x10^3 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 x10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species	<dl <="" <dl="" li=""> Result 1.2 *L 12.4 </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7	x10^7 CFU/g x10^10 CFU/g Units x10^9 CFU/g x10^7 CFU/g		
Clostridium species	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species	<dl><dl <="" <dl="" li="">Result1.2 *L12.41.8 *L</dl></dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0	x10^7 CFU/g x10^10 CFU/g Units x10^9 CFU/g x10^7 CFU/g x10^5 CFU/g		•
Enterobacter species 115.3 *H 1.0 - 50.0 x10^6 CFU/g Akkermansia muciniphila 0.62 0.01 - 50.00 x10^3 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 x10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial Butyrate 29.4 > 13.6 umol/g Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species	<dl><dl><dl><dl>Result1.2 *L12.41.8 *L122.9</dl></dl></dl></dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0	x10^7 CFU/g x10^10 CFU/g Units x10^9 CFU/g x10^7 CFU/g x10^5 CFU/g x10^6 CFU/g		•
Akkermansia muciniphila 0.62 0.01 - 50.00 x10^3 CFU/g Faecalibacterium prausnitzii 679.7 1.0 - 500000 x10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial Butyrate 29.4 > 13.6 umol/g Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0	x10^7 CFU/g x10^10 CFU/g WID X10^9 CFU/g x10^7 CFU/g x10^5 CFU/g x10^6 CFU/g x10^5 CFU/g		•
Faecalibacterium prausnitzii 679.7 1.0 - 500000 x10^3 CFU/g Short Chain Fatty Acids Result Range Units Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0	x10^7 CFU/g x10^10 CFU/g X10^9 CFU/g X10^7 CFU/g X10^5 CFU/g X10^6 CFU/g X10^5 CFU/g X10^6 CFU/g		•
Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.0	x10^7 CFU/g x10^10 CFU/g Wnits x10^9 CFU/g x10^7 CFU/g x10^5 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g		•
Short Chain Fatty Acids, Beneficial 29.4 > 13.6 umol/g Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species Akkermansia muciniphila	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H 0.62</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.0 0.01 - 50.00	x10^7 CFU/g x10^10 CFU/g X10^9 CFU/g X10^7 CFU/g X10^5 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g		
Butyrate 11.6 10.8 - 33.5 % Acetate 70.0 44.5 - 72.4 % Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species Akkermansia muciniphila Faecalibacterium prausnitzii	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H 0.62 679.7</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.0 0.01 - 50.00 1.0 - 500000	x10^7 CFU/g x10^10 CFU/g X10^9 CFU/g x10^7 CFU/g x10^5 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^3 CFU/g x10^3 CFU/g		
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Propionate 15.1 0.0 - 32.0 %	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species Akkermansia muciniphila Faecalibacterium prausnitzii Short Chain Fatty Acids, Beneficial	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H 0.62 679.7 Result 29.4</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.0 0.01 - 50.00 1.0 - 500000 Range > 13.6	x10^7 CFU/g x10^10 CFU/g X10^10 CFU/g X10^9 CFU/g X10^7 CFU/g X10^5 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^3 CFU/g X10^3 CFU/g X10^3 CFU/g Units		
	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species Akkermansia muciniphila Faecalibacterium prausnitzii Short Chain Fatty Acids, Beneficial Butyrate	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H 0.62 679.7 Result 29.4 11.6</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.0 0.01 - 50.00 1.0 - 500000 Range > 13.6 10.8 - 33.5	x10^7 CFU/g x10^10 CFU/g X10^10 CFU/g X10^9 CFU/g X10^7 CFU/g X10^5 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^6 CFU/g X10^3 CFU/g X10^3 CFU/g X10^3 CFU/g X10^3 CFU/g		
TAIDIAGO /V	Norovirus GI/II Bocavirus Normal Bacterial GUT Flora Bacteroides fragilis Bifidobacterium species Enterococcus species Escherichia species Lactobacillus species Clostridium species Enterobacter species Akkermansia muciniphila Faecalibacterium prausnitzii Short Chain Fatty Acids Butyrate Acetate	<dl><dl <dl Result 1.2 *L 12.4 1.8 *L 122.9 4.5 *L 10.1 115.3 *H 0.62 679.7 Result 29.4 11.6 70.0</dl </dl </dl>	< 1.0 < 1.0 Range 1.6 - 250.0 > 6.7 1.9 - 2000.0 3.7 - 3800.0 8.6 - 6200.0 5.0 - 50.0 1.0 - 50.00 1.0 - 50.0000 Range > 13.6 10.8 - 33.5 44.5 - 72.4	x10^7 CFU/g x10^10 CFU/g x10^10 CFU/g x10^9 CFU/g x10^7 CFU/g x10^5 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^6 CFU/g x10^3 CFU/g		•

KATIE BARGET

-.NICOLA PRICE



P: 1300 688 522 E: info@nutripath.com.au A: PO Box 442 Ashburton VIC 3142 Date of Birth: 03-Jul-1977

Sex: F

Collected: 23/Feb/2021 Received: 25-Feb-2021 301/32 ENFIELD STREET MARRICKVILLE NSW 2204

Lab id: 3723512 UR#: 6066686

THE BALANCED WAY 19 MYRTLE STREET STANMORE NSW 2048

Pathogen Summary:

Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

Metabolism Comment

In a healthy gut Short Chain Fatty Acids are exhibited in the following proportions; Butyrate, Acetate, Propionate (16%:60%:24%)

VALERATE:

Valerate is a short chain fatty acid that is important for gut health. Although Acetate, propionate, and butyrate make up the the most abundant SCFAs in gastrointestinal tract (95%), Valerate and other SCFA's make up the remaining and work optimally when within range.

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 eq. 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.

FAECAL SECRETORY IgA:

Production of sIgA is important to the normal function of the gastrointestinal mucosa as an immune barrier.

It represents the first line immune defense of the GIT.

Elevated levels are associated with an upregulated immune response.

LOW sIgA LEVEL:

The primary function of secretory IgA (sIgA) is an antibody protein secreted into the gastrointestinal tract as a first line of immune defence against pathogenic microorganisms. sIgA binds to invading micro organisms 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.

**Reduced sIgA levels may be associated with sub optimal adrenal output. Consider an Adrenocortex Stress profile.

Treatment: Investigate the root cause of inflammation. 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 sIqA.

beta GLUCURONIDASE ELEVATED:

Suspect increased activation and enterohepatic recirculation of toxins, hormones, and various drugs within the body. Increased burden on glucuronidation pathway is associated with increased risk of colorectal, prostate and breast cancers.

Treatment:

Consider Calcium-D-glucarate which may assist with lowering B-glucuronidase levels. It is also suggested to introduce a low-calorie/vegetarian diet for 4 weeks which may also be beneficial with lowering faecal B-glucuronidase levels.

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Parasites/Worms Comment

ELEVATED DIENTAMOEBA FRAGILIS LEVEL:

Significant copies per gene of Dientamoeba fragilis have been detected in this stool sample. Dientamoeba fragilis is closely related to Histomonas and Trichomonas species. D. fragilis is known to cause non-invasive diarrheal illness in humans. 90% of children are symptomatic, whereas only 15-20% of adults are. The most common symptoms associated with D. fragilis are intermittent diarrhoea, fatigue, abdominal pain, fatigue, nausea, anorexia, malaise and unexplained eosinophilia. Diarrhea is predominately seen during the first 1-2 weeks of infection and abdominal pain may persist for 1-2 months.

Treatment:

Iodoquinol, tetracycline or metronidazole have been used to treat D. fragilis. Another alternative is paromomycin. Using a combination of herbs that contain berberine (e.g. Golden seal, Coptis chinensis, Barberry, Oregon grape and Phellodendron) is desirable for the treatment of certain organisms. It is important to investigate the percentage of berberine contained in the dry weight extract of the berberine containing herb and then dose accordingly for the therapeutic dose of berberine.

Total therapeutic dose of berberine: 200mg four times daily.

Further Investigation:

PCR stool analysis should be considered in 4 weeks' time to ensure infection has cleared.

Opportunistic Bacteria Comment

METHANOBACTERIACEAE:

Family of bacteria-like microbes that produce methane. Facilitates carbohydrate fermentation and short-chain fatty acid production by beneficial bacteria.

LOW levels may indicate reduced production of short-chain fatty acids and may be associated with inflammation.

HIGH levels linked to chronic constipation, as well as some types of SIBO and IBS.

Potential Autoimmune Comments

FUSOBACTERIUM SPECIES:

Fusobacterium species is a gram-negative bacteria in the Fusobacteria phylum. The bacteria is a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut. In the mouth, high levels are strongly linked to oral hygiene. In the gut, high levels have been observed in individuals with colon cancer and appendicitis. Sources:

It primarily uses protein as its main source. However, research also shows that it can thrive from sugar.

Treatment:

Antimicrobial botanicals such as berberine, oregano, quercetin, curcumin, green and black tea extracts, blueberry extract, cinnamon and rosemary have shown to decrease levels.

Phyla Microbiota Comment

LOW BACTEROIDETES LEVEL:

Gram-negative Bacteroidetes are a bacterial phyla that make up a large proportion of the human digestive tract, including the mouth, nose, throat, and colon. A low result in bacteroidetes may suggest imbalanced normal microbes in the GI tract. A lower level of bacteroidetes is considered an unfavourable outcome which allows for the potential of elevated firmicutes leading to a possible imbalanced firmicutes:bacteroidetes ratio.

Treatment:

It is suggested to eat a diverse range of foods including polyphenols. It is further suggested to decrease foods rich in fat and sugar as they encourage firmicute levels to rise. Investigate other causes relating to a low bacteroidetes level.

Normal Bacterial Flora Comment

LOW BACTEROIDES FRAGILIS LEVEL:

Organism of the Bacteroidetes phylum. Immune-modulating normal gut species believed to be involved in microbial balance, barrier integrity, and neuroimmune health.

Low levels may contribute to reduced anti- inflammatory activity in the intestine.

LOW ENTEROCOCCUS SPECIES LEVEL:

Page 5 of 7 Complete Microbiome Map Lab ID: 3723512 Patient Name: KATIE BARGET Printed: 05/Mar/21 18:44

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Organism of the Firmicutes phylum.

Low levels may indicate insufficiency of beneficial bacteria.

LOW LACTOBACILLUS SPECIES LEVEL:

Lactate-producing bacteria in the Firmicutes phylum.

Low levels may be due to low carbohydrate intake or high salt intake, and may also indicate reduced mucosal health.

ELEVATED ENTEROBACTER SPECIES LEVEL:

Organism of the Proteobacteria phylum. Closely related to E. coli (in the same taxonomic family).

High levels may indicate increased intestinal inflammatory activity.

Page 6 of 7 Complete Microbiome Map Lab ID: 3723512 Patient Name: KATIE BARGET Printed: 05/Mar/21 18:44



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The Four "R" Treatment Protocol

	Using a course of	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
	antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or	ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
REMOVE		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
REM	medication that may be acting as antagonists.	ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
	Consider testing IgG96 foods as a tool for removing offending foods.	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
щ	Recolonisation with healthy, beneficial bacteria.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
REINOCULATE	Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	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
ALANCE	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
& REB	body health and lifestyle factors so as to prevent future Gl dysfunction.	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
REPAIR		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management