What Can Clinicians and Patients Expect from Healthpath Gut Health Testing?

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The Healthpath Gut Test shows you what's going on in your gut. By looking at imbalances in bacteria, yeasts, parasites and other intestinal health biomarkers, you find out what's contributing to your symptoms. You also receive targeted diet, supplement and lifestyle recommendations to help you take back control.

The biomarkers provide clinical information on three key areas:

150,1





1 | Digestion/Absorption

- pH
- Pancreatic elastase
- Zonulin



2 | Immune activity/Inflammation

- Calprotectin
- Haemoglobin
- Secretory IgA
- H. Pylori
- Archaea/methanogens
- E. Coli, Lactobacillus species, Enterococcus species
- Akkermansia muciniphila, Faecalibacterium prausnitzii



3 | Gut Microbiome/Mycobiome

- Microbiome diversity
- Enterotype
- Dysbiosis index
- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria
- Fusobacteria
- Verrucomicrobia
- Hydrogen-sulphide production
- Oxalate-degrading bacteria
- Yeasts/moulds
- Parasites
- Helminths



Gut Advanced
Gut Gut
Health
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Stool properties		
Colour	/	✓
Consistency	/	✓
рН	/	✓

Diversity:

Your diversity is key, which is why our microbiome analysis covers hundreds of parameters. High bacterial diversity is known to protect against intestinal infections. But low bacterial diversity is common, especially in disease states or after a course of antibiotics. When diversity is low, opportunistic bacteria like pathogens, fungi and viruses can proliferate.

Rather than focusing on individual species, it's more important to investigate how the different bacteria interact. Together, they're responsible for a host of intestinal functions.

Biodiversity

Diversity	✓	✓
Dysbiosis index	/	✓

There are four large phyla (groups) of bacteria: Bacteroidetes, Firmicutes, Actinobacteria and Proteobacteria. We also report on two smaller, clinically relevant phyla: Verrucomicrobia and Fusobacteria.

Bacterial distribution

Actinobacteria	/	/
Bacteroidetes	/	✓
Firmicutes	/	✓
Fusobacteria	✓	✓
Proteobacteria	/	✓
Verrucomicrobia	/	✓
Other	/	✓
Firmicutes/ Bacteroidetes Ratio	/	✓

Enterotype:

Recent research suggests there are three different types of gut microbiomes, known as 'enterotypes'. Not only do the different enterotypes influence the absorption of minerals, but they also have different metabolic properties.

Enterotype 1 has high levels of Bacteroides species, which use fat and protein effectively. Enterotype 2 has a strong Prevotella population, which is better at metabolising carbohydrates. Enterotype 3 is the rarest enterotype. It has high levels of Ruminococcus flora, though we don't yet know which macronutrients it prefers.

Enterotypes aren't affected by a person's age or gender and they remain stable for years. They can be influenced, however, by a long-term change of diet and by taking prebiotics.

Enterotype

1, 2 or 3	✓	✓
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Actinobacteria				
Bit	fidobacteria	/	✓	
Equol-producing bacteria		/	✓	
	Adlercreutzia species		/	
	Eggerthella lenta		✓	
	Slackia species		/	

Bacteroidetes				
Bacteroides				
Prevotella	✓	✓		
Prevotella copri	✓	/		

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Firmicutes:

Butyrate is a short-chain fatty acid that's produced by bacteria in the colon. It's quickly absorbed by the intestinal mucosa, which means the only reliable way to measure it is to look at the number of butyrate-producing bacteria.

Firmicutes bacteria are key butyrate producers. One of these, Faecalibacterium prausnitzii, typically makes up 5–15% of human intestinal bacteria. This important butyrate-producing species has anti-inflammatory properties—so much so that an absence of Faecalibacterium prausnitzii typically correlates with higher levels of inflammation.

Firmicutes

Bu	tyrate-producing bacteria	/	\checkmark
	Faecalibacterium prausnitzii	/	/
	Eubacterium rectale	/	/
	Eubacterium hallii	/	/
	Roseburia species	\checkmark	\checkmark
	Ruminococcus species	/	\checkmark
	Coprococcus	/	/
	Butyrivibrio species		/
	Cl. butyricum		✓
Total bacterial count		/	/
Clo	ostridia	/	/
	Clostridia total bacterial count	/	/
	Clostridia cluster 1	/	✓
	Clostridia histolytium		/
	Clostridium perfringens		/
Clostridium sporenges			✓
Other			/
	Christensenellaceae		/
	Dialister invisus		/

Verrucomicrobia		
Akkermansia muciniphila	/	/

Proteobacteria

✓	✓			
/	/			
✓	/			
\checkmark	/			
\checkmark	\checkmark			
	\checkmark			
\checkmark	\checkmark			
	\checkmark			
\checkmark	\checkmark			
	\checkmark			
	\checkmark			
	/			
✓	/			
✓	✓			

Hydrogen-sulphide production:

Bacterial metabolism isn't always a good thing. Some bacteria reduce sulphate to create hydrogen sulphide—a toxic metabolic by-product that can damage the gut lining. The species Bilophila wadsworthii, Desulfomonas pigra and Desulfovibrio piger are thought to be potent hydrogen-sulphide developers.

	Sulphate-reducing bacteria	/	\checkmark
	Desulfovibrio piger		✓
	Desulfomonas pigra		✓
	Bilophila wadsworthii		/
0	xalate-degrading bacteria		✓
	Oxalobacter formigenes		✓

Archaea:

Archaea have been overlooked in microbiome studies until recently. New research suggests that 1) archaea are part of the microbiome in plants, animals and humans, 2) they form biofilms and 3) they interact with the human immune system. Some archaea are also methanogens, which may play a role in chronic constipation.

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Methanobrevibacter	/	\checkmark

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Immunogenically effective bacteria		
Escherichia coli	/	✓
Enterococcus species	/	✓

Mucin production/mucosal barrier:

Lactobacillus species

A healthy colon has a protective mucous layer. If this layer is damaged—or only small amounts of mucous are produced—pathogens, pollutants and allergens can come into direct contact with the mucosa. This leads to inflammation.

The bacterium Akkermansia muciniphila is important because it encourages goblet cells to produce this protective mucous. Parts of this mucous also provide a special type of carbohydrate called oligosaccharides, which feed the bacteria that make gut-healing butyrate. With the right bacteria, it becomes a virtuous circle!

Mucin production/ mucosal barrier Akkermansia muciniphila Faecalibacterium prausnitzii

Yeasts/moulds					
Candida albicans	/	✓			
Candida species	/	✓			
Geotrichum candidum	✓	✓			
Moulds	/	✓			

Functional markers					
Calprotectin	/	✓			
Haemoglobin in faeces immunologically	/	✓			
Secretory IgA	/	✓			
Pancreatic elastase	/	✓			
Zonulin		✓			

Parasites:

The Multiplex Real-time PCR (Multiplex quantitative real-time PCR) is a faster and more effective method for detecting parasites. This new test:

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Test

- provides reliable analysis, even with minimal attack
- gives no false positives with non-pathogens
- can be sent out with regular mail
- gives reliable results in symptom-free patients and also after treatment

Parasites						
Pá	athobionts	✓	✓			
	Blastocystis hominis	/	✓			
	Dientamoeba fragilis	✓	✓			
	Helicobacter AG	✓	✓			
Pa	athogenic intestinal protozoa	✓	✓			
	Giardia lamblia	/	/			
	Entamoeba histolytica	✓	✓			
	Cryptosporidium species	✓	/			
	Cyclospora cayetanensis	✓	✓			
Не	elminths COMING SOON		✓			
	Taenia species		V			
	Taenia solium		/			
	Taenia saginata		/			
	Ascaris species		/			
	Enterobius vermicularis		/			
	Ancylostoma species		/			
	Ancylostoma duodenale		/			
	Hymenolepsis species		/			
	Hymenolepsis nana		/			
	Hymenolepsis diminuta		/			
	Trichuris trichiura		/			
	Necator americanus		V			
	Strongyloides species		/			
	Strongyloides stercoralis		/			
	Microsporidia		\(\square \) \(\square \) \(\square \) \(\square \) \(\square \)			
	Enterocytozoon species		/			

Encephalitozoon species

Example report

External ID Date of Birth 26.07.1977 Order ID 11399854 Name First Name Sex Female Order Date 09.01.2018 Sampling Date Validation Date Findings Status **Final Report** 09.01.2018 11:59 Sample Material Validation on 09.01.2018 Findings Date 17.01.2018 **Previous Result** Test Result Unit Standard Range **Stool Diagnostics** Moleculargenetic Microbiomeanalysis MAXI **Stool Properties** Colour lightbrown FE NA) VISU mushy Consistency FE NA) TESTS 5,8 - 6,5 6,0 pН **Biodiversity** FE NA) MGSEO > 5,0 Diversity 5,63 The bacterial diversity in the intestinal tract may vary considerably from person to person. Antibiotic therapies, infections, increasing age, Grad unbalanced diets or smoking are causes of declining diversity. Bacteria Phyla (Distribution) 1,0 - 5 % Actinobacteria 1,6 30 - 60 **Bacteroidetes** 31,3 % 30 - 60 % **Firmicutes** 60,2 0,0 - 1,0 Fusobacteria 0,0 % FE NA) MGSEQ 1,5 - 5,0 Proteobacteria 3,5 % 1,5 - 5 FE NA) MGSEQ Verrucomicrobia 1,0 % Other 2,4 NA) MGSEQ Ratio Firmicutes/Bacteroidetes Quotient < 1,5 FE NA) RECHN 1,93 Enterotype NA) MGSEQ **Bacteroides** Human intestinal microbiomes can be differentiated into three Enterotypes Enterotypes are defined by dominant bacterial clusters with distinct metabolic Enterotyp properties. Dysbiosis index The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered. Index

Name		- Date of	Birth	26.07.1977	Order ID	11399854
First Name		- Sex		Female	Order Date	09.01.2018
Test		Result	Unit	Standard Range		Previous Result
Bacteria Phyla - most impo	ortant genera a	nd species				
Actinobacteria						
Bifidobacteria		1,5 x 10^10 CFU/	g faeces	> 5,0 x 10^9		F NA) MGSE
Bifidobacterium ac	lolescentis	53	%			F NA) MGSE
Bifidobacterium	longum	27	%			F NA) MGSE
Equol producing bacteria		8,1 x 10^8 CFU/	g faeces	> 5,0 x 10^9		F NA) MGSE
Adlercreutzia spp.						F NA) MGSE
Eggerthella lenta						, NA) MGSE
Slackia. spp.						F NA) MGSE
Bacteroidetes						,
Bacteroides		1,8 x 10^11 CFU/	g faeces	> 1,5 x 10^11		F NA) MGSE
Bacteroides	uniformis	31	%			F NA) MGSE
Bacteroides	ovatus	8	%			F NA) MGSE
Prevotella		6,0 x 10^7 CFU/	g faeces	> 1,0 x 10^10		F NA) MGSE
Firmicutes						INA) MOSE
Butyrate producing bacteri	a					
Faecalibacterium prausnit	zii	9,2 x 10^10 CFU/	g faeces	> 5,0 x 10^10		F NA) MGSE
Eubacterium rectale		1,8 x 10^10 CFU/	g faeces	> 1,0 x 10^10		F NA) MGSE
Eubacterium hallii		1,3 x 10^9 CFU/	g faeces	> 5,0 x 10^9		NA) MGSE
Roseburia spp.		2,9 x 10^9 CFU/	g faeces	> 2,0 x 10^10		NA) MGSE
Ruminococcus spp.		6,2 x 10^10 CFU/	g faeces	> 3,0 x 10^10		F NA) MGSE
Coprococcus		8,4 x 10^9 CFU/	g faeces	> 2,0 x 10^10		F NA) MGSE
Butyrivibrio spp.		5,0 x 10^8 CFU/	g faeces	> 5,0 x 10^9		F NA) MGSE
CI. butyricum		1,0 x 10^9 CFU/	g faeces	> 1,0 x 10^10		F NA) MGSE
Total bacterial count		1,8 x 10^11 CFU/	g faeces	> 1,3 x 10^11		F
Clostridia						NA) MGSE
Clostridia total bacterial co	unt	3,2 x 10^9 CFU/	g faeces	< 4,0 x 10^9		F NA) MGSE
Clostridia cluster I		< 1,0 x 10^6 CFU/9	g faeces	< 2,0 x 10^9		F NA) MGSE
Clostridium histolyticum		< 1,0 x 10^6 CFU/9	g faeces	< 2,0 x 10^9		F
Clostridium perfringens		< 1,0 x 10^6 CFU/9	g faeces	< 1,0 x 10^8		NA) MGSE
Clostridium sporogenes		< 1,0 x 10^6 CFU/9	g faeces	< 1,0 x 10^8		NA) MGSE
Other						NA) MGSE
Christensenellaceae		1,7 x 10^8 CFU/	g faeces	> 1,0 x 10^9		F NA) MGSE
Dialister invisus		< 1,0 x 10^6 CFU/9	g faeces	< 4,0 x 10^10		
Fusobacteria						NA) MGSE
Fusobacterium spp.		< 1,0 x 10^6 CFU/9	g faeces	< 1,0 x 10^7		F NA) MGSE
Verrucomicrobia						INA) MGSE

Akkermansia muciniphila

9,6 x 10^9 CFU/g faeces

name	- Date of Birth	26.07.1977	Order ID	11399854
First Name	- Sex	Female	Order Date	09.01.2018
Test	Result Unit	Standard Range		Previous Result
Proteobacteria				
Pathogenic or potentially pathogenic	; bacteria			
Haemophilus	2,3 x 10^8 CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Acinetobacter	< 1,0 x 10^6 CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Escherichia coli Biovare	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Proteus species	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Klebsiella species	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Enterobacter species	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Serratia species	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Hafnia species	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Morganella spp.	< 1,0 x 10^4 CFU/g faeces	< 1,0 x 10^4		FE NA) MIB
H2S production				10.1, 1112
Sulphate reducing bacteria	4,1 x 10^8 CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Desulfovibrio piger	< 1,0 x 10^6 CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Desulfomonas pigra	< 1,0 x 10^6 CFU/g faeces	< 1,0 x 10^9		FE
Bilophila wadsworthii	< 1,0 x 10^6 CFU/g faeces	< 2,0 x 10^9		NA) MGSEQ FE
Oxalate degrading bacteria				NA) MGSEQ
Oxalobacter formigenes	< 1,0 x 10^6 CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ
Immunogenicity / Mucus production				,
Immunogenically effective bacteria				
Escherichia coli	2,0 x 10^6 CFU/g faeces	10^6 - 10^7		FE A) KULTAZ
Enterococcus species	4,0 x 10^5 CFU/g faeces	10^6 - 10^7		FE A) KULTAZ
Lactobacillus species	6,0 x 10^5 CFU/g faeces	10^5 - 10^7		FE A) KULTAZ
Mucin production / Mucosa barrier				, .
Akkermansia muciniphila	9,6 x 10^9 CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Faecalibacterium prausnitzii	9,2 x 10^10 CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEC
Yeasts / Molds				IVA) INCOLO
Candida albicans	< 1,0 x 10^3 CFU/g faeces	< 1,0 x 10^3		FE A) KULTAZ
Candida species	< 1,0 x 10^3 CFU/g faeces	< 1,0 x 10^3		FE A) KULTAZ
Geotrichum candidum	< 1,0 x 10^3 CFU/g faeces	< 1,0 x 10^3		FE
Moulds	negative	negative		A) KULTAZ FE A) KULTAZ
Parasites				A) NOLTAZ
Giardia lamblia	negative	negative		FE
Entamoeba histolytica	negative	negative		NA) MOLEK
Cryptosporidium spp.	negative	negative		NA) MOLEK
Blastocystis hominis	negative	negative		NA) MOLEK
Dientamoeba fragilis	negative	negative		NA) MOLEK
Cyclospora cayetanensis	negative	negative		NA) MOLEK
Cyclospora cayetarierisis	педануе	nogauve		NA) MOLEK

26.07.1977

Date of Birth

Order ID

11399854

Name

11399854 - - 26.07.1977

