

Sampling instructions

SPECIAL TEST KIT REQUIRED: PLEASE CONTACT US.

1. Collect your stool sample (the easiest is to collect some on toilet paper, or in a clean, dry plastic container). The stool should not have been in contact with water or urine in the toilet.

2. Open the tube. Be careful not to discard the stabilizing solution; avoid contact with the solution. Use the spoon attached to the cap of the collection tube to collect a small amount of stool: DO NOT TAKE MORE THAN A FULL SPOON.

3. Stir and smash the stool with the spoon to completely mix it in the stabilizing solution. Tightly screw the cap closed.

4. Place the closed tube in the safety bag, close the bag using the adhesive strip, place in the provided envelop and send to our laboratory, at the following address:

RED Laboratories

Z.1 Researchpark 100

1731 Zellik BELGIUM

5. Do not forget to include the request form, filled and signed.

6. Sample is stable for up to three days; you may have to use priority postal service (FedEx) if you live outside Belgium. Preferably send sample early in the week (Monday or Tuesday) to guarantee delivery before the week-end.

7. Please use the kit within one month.



R.E.D. Laboratories

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MSA assay

***Metagenomic Stool
Analysis:***

***A new procedure to
analyze bacterial
populations in a
stool sample***

www.redlabs.com

Report Example

MSA ASSAY - Metagenomic Stool Analysis

Alterations in the bowel flora are now believed to be contributing factors to many chronic diseases such as allergies, autoimmune and inflammatory disorders, or degenerative diseases.

Until recently research into microbiota composition relied almost exclusively on culture, while:

- 40 to 80% of gut bacteria cannot be cultured
- Identification of colonies can be difficult
- Bacteria must be alive: studies of anaerobes very difficult, major loss during collection and processing of samples
- Culture approach may address only a small fraction of all bacterial species (10%?)
- E.coli once thought to be a dominant species, is a minor member...

R.E.D. Labs scientists have developed and validated a new procedure to analyze bacterial populations in a stool sample

Methods

Bacterial DNA is extracted from stool samples, PCR amplification is performed on 16S rRNA gene regions, and PCR amplicons are sequenced.

New molecular technique involving sequencing of specific regions of bacterial DNA (metagenomics):

- ⇒ Can be performed on dead organisms (exposure to oxygen, freezing are not a problem)
- ⇒ Identification of each bacteria by comparing sequence with public databases: extremely precise, not subjective
- ⇒ High-throughput technology allows identification of tens or even hundreds of thousands organisms in a single sample

Metagenomics Stool Analysis Report

Patient	
Birthdate	
Analysis	

PHYLUM	FAMILY	GENUS	% of total	Ref.		
Firmicutes (gram +)	Lachnospiraceae	Anaerostipes	0,03	<1		
		Coprococcus	2,49	<10		
		Dorea	3,75	<15		
		Moryella	0,03	<1		
		Roseburia	0,15	<5,0		
		Sporobacterium	0	<1		
		Syntrophococcus	0	<1		
		Ruminococcaceae	Acetanaerobacterium	0	<5	
			Acetivibrio	0	<1	
			Ethanoligens	0,01	<1	
	Faecalibacterium		28,92	<25		
	Pegibacter		0	<1		
	Ruminococcus		0	>2		
	Sporobacter		0	<1		
	Subdoligranulum		0	<25		
	Clostridiaceae		Butyricicoccus	1,52	<5	
			Clostridium Sensu Stric.	0	<5	
		Lactonifactor	0	0		
		Eubacteriaceae	Anaerofant	0	<0,5	
			Eubacterium	0,01	0	
		Blautia	Blautia	9,08	<5,0	
			Howardella	0	<1	
			Lactobacillaceae	Lactobacillus	0,29	<1
				Enterococcaceae	Enterococcus	0,03
			Streptococcaceae	Lactococcus	0,03	<1
	Streptococcus			6,53	<5	
	Leuconastaceae		Leuconastoc	0	<0,3	
			Frysipolarichaeaceae	Catanibacterium	0	<0,3
				Coprobacillus	0	<1
			Holdemania	0	<1	
Turicibacter		0	>0,5			
Veillonellaceae	Dialister	0,17	0-1			
	Megamonas	0	0			
Megasphaera	Megasphaera	0,01	0			
	Oscillospiraceae	Oscillibacter	0,01	<4		
Staphylococcus	Staphylococcus	0	<0,05			
Bacteroidetes (gram -)	Bacteroidaceae	Bacteroides	32,05	<10		
		Allistipes	0	<3		
	Porphyromonadaceae	Barnesiella	0	<2		
		Odoribacter	0,01	<0,5		
	Parabacteroides	0,82	<3			
	Prevotellaceae	Prevotella	0	<5		
Nymphaeaster		0	<1			
Actinobacteria (gram -)	Bifidobacteriaceae	Bifidobacterium	0,06	>5		
	Actinomycetaceae	Actinomycetes	1,77	<1		
	Micrococccaceae	Rothia	0,15	<0,2		
	Coriobacteriaceae	Asaccharobacter	0	>0,1		
		Collinsella	18,24	<25		
Olsenella	0	0				
Shackelia	0	<1				
Proteobacteria (gram -)	Enterobacteriaceae	Escherichia/Shigella	1,02	<0,5		
		Klebsiella	0	<0,5		
	Sutterellaceae	Sutterella	0,92	<1		
	Desulfobriaceae	Lawsonia	0	<0,5		

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Phone: +32 2 481 53 10

Average
Unusual

	Value	Ref.
Total Lachnospiraceae	8,45	>5
Total Ruminococcaceae	23,33	>5
Total Clostridiaceae	1,52	<5
Enterococcus	0,03	0
Streptococcus	5,53	<5
Ruminococcus	0	>2
Lactonifactor	0	0
Turicibacter	0	>0,5
Bacteroides	32,05	<10
Prevotella	0	<5
Bifidobacterium	0,06	>5
Asaccharobacter	0	>0,1

	%
Firmicutes	>0,06 %
Bacteroidetes	32,88 %
Actinobacteria	15,24 %
Proteobacteria	1,34 %
Other	0,48 %

Range of Firmicutes % in European population: 50-95%

Firmicutes/Bacteroidetes ratio	Value
High	
Average	1,52
Low	

Low ratio may be associated with gut inflammation

Gram / Gram ratio	Value
High	
Average	1,01
Low	

Diversity Index	Value
Low < 4, Average 4-6, High > 6	5,07

Diversity associated with low diversity

Electronically validated on:
Requesting physician:
Observations:

Others:

Clostridium IV	0,03
Clostridium XI	0
Clostridium XIX	0
Clostridium XIVa	0,14
Clostridium XIVb	0
Clostridium XVIII	0
Acidaminococcus	0
Anaerofilum	0
Anaerotruncus	0
Anaerovorax	0,01
Carnobacterium	0
Corynebacterium	0,01
Eggerthella	0,01
Flavobacterium	0
Gemella	0,14
Gordonibacter	0
Granulicatella	0,08
Lachnobacterium	0
Lutispora	0
Methanobrevibacter	0
Methylobacterium	0
Mitsuokella	0
Mogibacterium	0,04
Paraprevotella	0
Parasutterella	0
Pediococcus	0
Peptoniphilus	0
Peptostreptococcus	0,01
Phascolarctobacterium	0
Porphyromonas	0
Propionibacterium	0
Ralstonia	0
Robinsoniella	0
Sporacetigenium	0
Varibaculum	0
Victivallis	0
Weissella	0,03
Akkermansia	0
Hallella	0
Hydrogenoanaerobacterium	0
Neisseria	0

Electronically validated on:
Requesting physician:
Observations:

