GI360™; stool

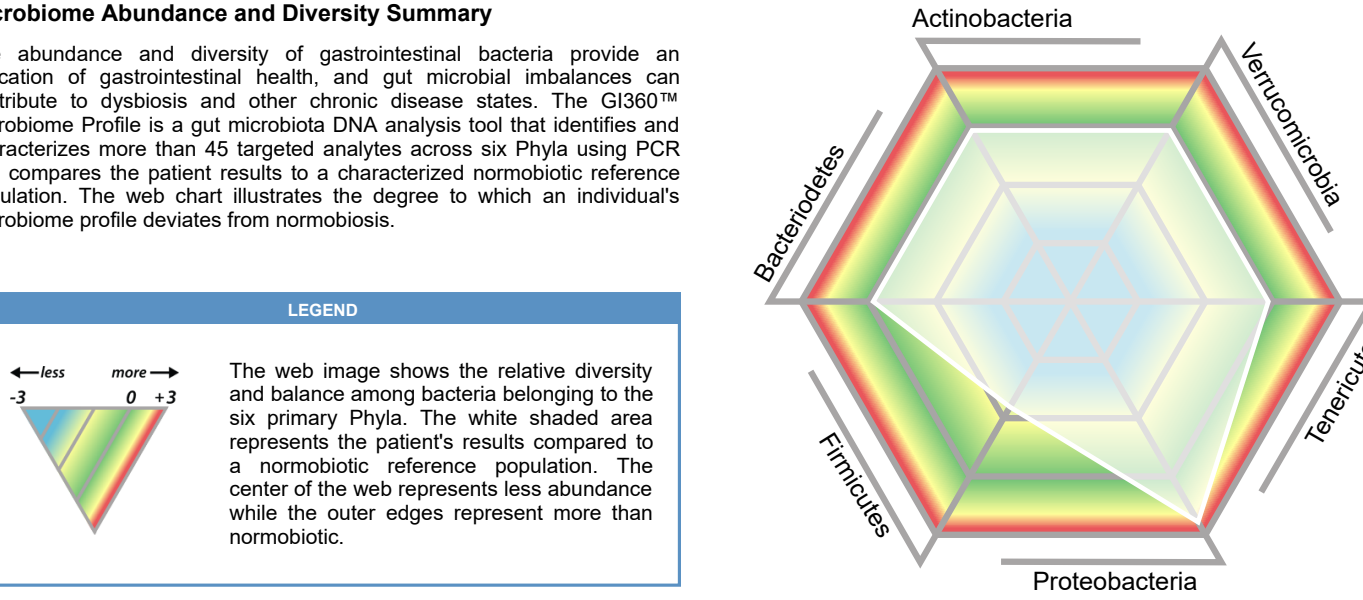
Order: SAMPLE REPORT
Client #: 12345
Doctor: Sample Doctor
Doctor's Data, Inc.
3755 Illinois Ave.
St. Charles, IL 60174

Patient: Sample Patient
Age: 35
Sex: Female

Sample Collection	Date/Time
Date Collected	08/12/2021
Date Received	08/13/2021
Date Reported	08/14/2021
Specimens Collected	3

Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



LEGEND

The web image shows the relative diversity and balance among bacteria belonging to the six primary Phyla. The white shaded area represents the patient's results compared to a normobiotic reference population. The center of the web represents less abundance while the outer edges represent more than normobiotic.

Dysbiosis Index

The Dysbiosis Index the (DI) is calculated strictly from the results of the Microbiome Profile, with scores from 1 to 5. A DI score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the DI above 2, the more the sample deviates from the normobiotic profile. The dysbiosis test and DI does not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

DI Score

5

Key Findings

Proteobacteria, Very High	↑	*Blastocystis* spp., Observed	
Escherichia spp., Very High	↑	*Dientamoeba fragilis*, Observed	
Clostridia Class, Very Low	↓	*Enterobacter cloacae* complex, Cultured	
Eubacterium hallii, Very Low	↓		
Faecalibacterium prausnitzii, Very Low	↓		
Lachnospiraceae, Very Low	↓		

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Microbiome Bacterial Abundance;Multiplex PCR

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LEGEND

-3	-2	-1	0	+1	+2	+3
Very Low		Low	Within Reference Interval	High	Very High	

Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.

Actinobacteria	Result	Reference Interval
Actinobacteria	0	0
Actinomycetales	0	0
Bifidobacterium spp.	0	0

Bacteriodetes	Result	Reference Interval
Alistipes spp.	+1	0
Alistipes onderdonkii	0	0
Bacteroides fragilis	0	0
Bacteroides spp. & *Prevotella* spp.	0	0
Bacteroides spp.	-1	0
Bacteroides pectinophilus	-1	0
Bacteroides stercoris	+1	0
Bacteroides zoogleoformans	0	0
Parabacteroides johnsonii	0	0
Parabacteroides spp.	0	0

Firmicutes	Result	Reference Interval
Firmicutes	0	0
Bacilli Class	0	0
Catenibacterium mitsuokai	0	0

Notes:
The gray-shaded area of the bar graph represents reference values outside the reporting limits for this test.
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Methodology: Multiplex PCR

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Firmicutes	Result	Reference Interval
Clostridia Class	-3	0
Clostridium methylpentosum	-1	0
Clostridium L2-50	0	0
Coprobacillus cateniformis	0	0
Dialister invisus	0	0
Dialister invisus & Megasphaera micronuciformis	0	0
Dorea spp.	-1	0
Eubacterium biforme	0	0
Eubacterium hallii	-2	0
Eubacterium rectale	0	0
Eubacterium siraeum	0	0
Faecalibacterium prausnitzii	-2	0
Lachnospiraceae	-2	0
Lactobacillus ruminis & Pediococcus acidilactici	0	0
Lactobacillus spp.	0	0
Phascolarctobacterium spp.	0	0
Ruminococcus albus & R. bromii	0	0
Ruminococcus gnavus	0	0
Streptococcus agalactiae & Eubacterium rectale	-1	0
Streptococcus salivarius ssp. *thermophilus & S. sanguinis*	0	0

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Firmicutes	Result	Reference Interval
Streptococcus salivarius ssp. *thermophilus*	-1	0
Streptococcus spp.	0	0
Veillonella spp.	-1	0

Proteobacteria	Result	Reference Interval
Proteobacteria	+3	0
Enterobacteriaceae	0	0
Escherichia spp.	+3	0
Acinetobacter junii	0	0

Tenericutes	Result	Reference Interval
Mycoplasma hominis	0	0

Verrucomicrobia	Result	Reference Interval
Akkermansia muciniphila	0	0

Microbiome Abundance Information:

- The GI360™ Microbiome Profile is a focused gut microbiota DNA analysis tool that identifies more than 45 targeted analytes across six phyla using a CE-marked multiplex PCR system. Patient results are compared to a highly defined normobiotic reference population (n > 1,100). The white shadowed web plot within the hexagonal diagram illustrates the degree to which an individual's microbiome profile deviates from normobiosis. The center of the diagram represents less bacterial abundance while the outer edges represent greater than normobiosis. Deviation from a hexagon-shaped plot indicates variant diversity of the microbial community. Key findings for patient's microbiome profile are summarized in the table below the diagram, and detailed results for all of the analytes are presented on the next 3 pages of the report. Detailed results for the specific bacteria are reported as -3 to +3 standard deviations, as compared to the normobiotic reference population.

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Methodology: Multiplex PCR

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GI Pathogens;Multiplex PCR

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Viruses	Result
Adenovirus F40/41	Negative
Norovirus GI/GII	Negative
Rotavirus A	Negative

Pathogenic Bacteria	Result
Campylobacter (*C. jejuni*, *C. coli* and *C. lari*)	Negative
Clostridioides difficile (Toxin A/B)	Negative
Escherichia coli O157	Negative
Enterotoxigenic *Escherichia coli* (ETEC) lt/st	Negative
Salmonella spp.	Negative
Shiga-like toxin-producing *Escherichia coli* (STEC) stx1/stx2	Negative
Shigella (*S. boydii*, *S. sonnei*, *S. flexneri* & *S. dysenteriae*)	Negative
Vibrio cholerae	Negative

Parasites	Result
Cryptosporidium (*C. parvum* and *C. hominis*)	Negative
Entamoeba histolytica	Negative
Giardia duodenalis (AKA *intestinalis & lamblia*)	Negative

Notes:
Methodology: Multiplex PCR

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Parasitology; Microscopy

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Protozoa	Result
Balantidium coli	Not Detected
Blastocystis spp.	Few
Chilomastix mesnili	Not Detected
Dientamoeba fragilis	Rare
Endolimax nana	Not Detected
Entamoeba coli	Not Detected
Entamoeba hartmanni	Not Detected
Entamoeba histolytica/Entamoeba dispar	Not Detected
Entamoeba polecki	Not Detected
Enteromonas hominis	Not Detected
Giardia duodenalis	Not Detected
Iodamoeba bütschlii	Not Detected
Isospora belli	Not Detected
Pentatrichomonas hominis	Not Detected
Retortamonas intestinalis	Not Detected

Cestodes - Tapeworms	Result
Diphyllobothrium latum	Not Detected
Dipylidium caninum	Not Detected
Hymenolepis diminuta	Not Detected
Hymenolepis nana	Not Detected
Taenia	Not Detected

Trematodes - Flukes	Result
Clonorchis sinensis	Not Detected
Fasciola hepatica/Fasciolopsis buski	Not Detected
Heterophyes heterophyes	Not Detected
Paragonimus westermani	Not Detected

Nematodes - Roundworms	Result
Ascaris lumbricoides	Not Detected

Notes:
Methodology: Microscopy

Parasitology; Microscopy

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Nematodes - Roundworms	Result
Capillaria hepatica	Not Detected
Capillaria philippinensis	Not Detected
Enterobius vermicularis	Not Detected
Hookworm	Not Detected
Strongyloides stercoralis	Not Detected
Trichuris trichiura	Not Detected

Other Markers	Result	Reference Interval
Yeast	Not Detected	Not Detected – Rare
RBC	Not Detected	Not Detected – Rare
WBC	Not Detected	Not Detected – Rare
Muscle fibers	Not Detected	Not Detected – Rare
Vegetable fibers	Not Detected	Not Detected – Few
Charcot-Leyden Crystals	Not Detected	Not Detected
Pollen	Not Detected	Not Detected

Macroscopic Appearance	Result	Reference Interval
Color	Brown	Brown
Consistency	Soft	Soft
Mucus	Negative	Negative

Parasitology Information:

- This test is not designed to detect *Cyclospora cayetanensis* or *Microsproridia* spp.
- Intestinal parasites are abnormal inhabitants of the gastrointestinal tract that have the potential to cause damage to their host. The presence of any parasite within the intestine generally confirms that the patient has acquired the organism through fecal-oral contamination. Damage to the host includes parasitic burden, migration, blockage and pressure. Immunologic inflammation, hypersensitivity reactions and cytotoxicity also play a large role in the morbidity of these diseases. The infective dose often relates to severity of the disease and repeat encounters can be additive.
- There are two main classes of intestinal parasites, they include protozoa and helminths. The protozoa typically have two stages; the trophozoite stage that is the metabolically active, invasive stage and the cyst stage, which is the vegetative inactive form resistant to unfavorable environmental conditions outside the human host. Helminths are large, multicellular organisms. Like protozoa, helminths can be either free-living or parasitic in nature. In their adult form, helminths cannot multiply in humans.

Notes:
Methodology: Microscopy, Macroscopic Observation

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Parasitology; Microscopy

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Parasitology Information:

- In general, acute manifestations of parasitic infection may involve diarrhea with or without mucus and or blood, fever, nausea, or abdominal pain. However these symptoms do not always occur. Consequently, parasitic infections may not be diagnosed or eradicated. If left untreated, chronic parasitic infections can cause damage to the intestinal lining and can be an unsuspected cause of illness and fatigue. Chronic parasitic infections can also be associated with increased intestinal permeability, irritable bowel syndrome, irregular bowel movements, malabsorption, gastritis or indigestion, skin disorders, joint pain, allergic reactions, and decreased immune function.
- In some instances, parasites may enter the circulation and travel to various organs causing severe organ diseases such as liver abscesses and cysticercosis. In addition, some larval migration can cause pneumonia and in rare cases hyper infection syndrome with large numbers of larvae being produced and found in every tissue of the body.
- **Red Blood Cells** (RBC) in the stool may be associated with a parasitic or bacterial infection, or an inflammatory bowel condition such as ulcerative colitis. Colorectal cancer, anal fistulas, and hemorrhoids should also be ruled out.
- **White Blood Cells** (WBC) and **Mucus** in the stool can occur with bacterial and parasitic infections, with mucosal irritation, and inflammatory bowel diseases such as Crohn's disease or ulcerative colitis
- **Muscle fibers** in the stool are an indicator of incomplete digestion. Bloating, flatulence, feelings of "fullness" may be associated with increase in muscle fibers.
- **Vegetable fibers** in the stool may be indicative of inadequate chewing, or eating "on the run".

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Microbiology

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Pathogenic Bacteria	Result	Reference Interval
Aeromonas	NG	No Growth
Edwardsiella tarda	NG	No Growth
Plesiomonas shigelloides	NG	No Growth
Salmonella	NG	No Growth
Shigella spp.	NG	No Growth
Vibrio cholerae	NG	No Growth
Vibrio	NG	No Growth
Yersinia	NG	No Growth

Imbalance Bacteria	Result	Reference Interval
Klebsiella pneumoniae	2+	No Growth

Dysbiotic Bacteria	Result	Reference Interval
Enterobacter cloacae complex	3+	No Growth

Yeast	Result	Reference Interval
No yeast isolated	NG	

Microbiology Information:

- **Pathogenic bacteria** consist of known pathogenic bacteria that can cause disease in the GI tract. They are present due to the consumption of contaminated food or water, exposure to animals, fish, or amphibians known to harbor the organism. These organisms can be detected by either Multiplex PCR or microbiology culture.
- **Imbalanced bacteria** are usually neither pathogenic nor beneficial to the host GI tract. Imbalances can occur when there are insufficient levels of beneficial bacteria and increased levels of commensal bacteria. Certain commensal bacteria are reported as dysbiotic at higher levels.
- **Dysbiotic bacteria** consist of those bacteria that have the potential to cause disease in the GI tract. They can be present due to a number of factors including: exposure to chemicals that are toxic to beneficial bacteria; the use of antibiotics, oral contraceptives or other medications; poor fiber intake and high stress levels.
- **Yeast** may normally be present in small quantities on the skin, in the mouth and intestine. While small quantities of yeast may be normal, yeast observed in higher quantities is considered abnormal.

Notes:
NG = No Growth
Methodology: Culture and identification by MALDI-TOF and conventional biochemicals

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Bacterial Susceptibilities

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Enterobacter cloacae complex

Natural Agents	Low Sensitivity	High Sensitivity
Berberine*		
Black Walnut*		
Caprylic Acid*		
Uva Ursi*		
Oregano*		
Grapefruit Seed Extract*		
Silver*		

Prescriptive Agents	Resistant	Intermediate	Susceptible
Amoxicillin-Clavulanic Acid	●		
Ampicillin	●		
Cefazolin	●		
Ceftazidime			●
Ciprofloxacin			●
Sulfamethoxazole / Trimethoprim			●

Susceptibility Information:

- **Natural antibacterial** agents may be useful for treatment of patients when organisms display in-vitro sensitivity to these agents. The test is performed by using standardized techniques and filter paper disks impregnated with the listed agent. Relative sensitivity is reported for each natural agent based upon the diameter of the zone of inhibition surrounding the disk. Data based on over 5000 individual observations were used to relate the zone size to the activity level of the agent. A scale of relative sensitivity is defined for the natural agents tested.
- **Susceptible** results imply that an infection due to the bacteria may be appropriately treated when the recommended dosage of the tested antimicrobial agent is used. **Intermediate** results imply that response rates may be lower than for susceptible bacteria when the tested antimicrobial agent is used. **Resistant** results imply that the bacteria will not be inhibited by normal dosage levels of the tested antimicrobial agent.

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Introduction

This analysis of the stool specimen provides fundamental information about the overall gastrointestinal health of the patient. When abnormal microflora or significant aberrations in intestinal health markers are detected, specific commentaries are presented. If no significant abnormalities are found, commentaries are not presented.

Microbiome Abundance Information

Actinobacteria (phylum)

Actinobacteria is one of the largest bacterial phyla, comprised of Gram-positive bacteria. This phylum includes a wide range of species, with different morphological and physiological characteristics. Significant groups in the human colon include Actinomycetales and Bifidobacteriales. Actinomycetales were inversely associated with clinically significant depression in IBS patients, suggesting these bacteria may be depleted in depressed IBS patients. A strict vegetarian diet may increase the total count of *Actinomyces* spp. compared to following a Western diet.

Bacteriodetes (phylum)

Bacteriodetes make up approximately 28% of the gut microbiota in healthy human adults. They are early colonizers of the infant gut and are amongst the most stable, at a species and strain level, in the host. A low preponderance of Bacteriodetes in relation to Firmicutes has been associated with obesity, though this can increase with weight loss and restricted calorie intake.

***Alistipes* (genus)**

Alistipes does not contribute significantly to short chain fatty acid production. A diet rich in animal protein and fat increases the abundance of *Alistipes.* High abundance of *Alistipes* was identified as a possible predictor of successful weight loss. Increased abundance of *Alistipes* has been correlated with a greater frequency of pain in pediatric irritable bowel syndrome patients. In contrast, *Alistipes onderdonkii* was shown to be decreased in patients diagnosed with ulcerative colitis. Lower abundance of the *Alistipe*s genus has been observed in patients with psoriatic arthritis and pediatric Crohn's disease. *Alistipes* may positively correlate with depression.

***Bacteroides pectinophilus* (species)**

Bacteroides pectinophilus contributes to breakdown of dietary pectins which are prebiotics. Pectins are complex, plant-derived carbohydrates that are indigestible by human enzymes, but can be easily degraded by certain commensal bacteria in the gut. Subsequent microbial fermentation of constituent sugar moieties yields important short chain fatty acids and other metabolites. The pectin-derived microbial fermentation products have important functions including reduction of ammonia, delay of gastric emptying and postprandial glucose regulation, induction of gut immunity, and maintenance of the mucosal barrier. Adequate intake and microbial metabolism of pectins appears to stimulate growth of various beneficial bacteria, including *Lachnospiraceae*, *Dorea* species, *Bifidobacterium*, *Lactobacillus* species, *Faecalibacterium prausnitzii*, and *Eubacterium rectale*. The abundance of *B. pectinophilus* has been positively correlated with a healthy fasting serum lipid profile, and negatively correlated with biomarkers of for insulin resistance and dyslipidemia. *B. pectinophilus* was less abundant for IBS patients compared to healthy controls. High consumption of kimchi (fermented cabbage) may be associated with lower than normal levels of *B. pectinophilus.*

***Bacteroides* (species)**

Species in the genus *Bacteroides* carry out broad metabolic functions, including degradation of complex plant polysaccharides, proteolytic activities, de-conjugation of bile acids, mucosal barrier integrity, short chain fatty acid production, fatty acid storage and glucose metabolism. *Bacteroides* spp. are maintained at a higher abundance in breastfed individuals into adulthood. *Bacteroides fragilis* plays an important role in the prevention of intestinal inflammation. An energy-restricted diet has been shown to increase *B. fragilis* in overweight adolescents. An increase in *B. stercoris* has been associated with higher risk of colon cancer. Decreased levels of *Bacteroides* spp. have been reported in association with multiple sclerosis, rheumatoid arthritis and Parkinson's disease.

Firmicutes (phylum)

The phylum Firmicutes constitutes the most diverse and abundant group of gastrointestinal microbiota which are grouped into four classes, Bacilli, Clostridia, Erysipelotrichia, and Negativicutes. They constitute about 39% of gut bacteria in healthy adults, but may increase to as high as 80% in an imbalanced microbial community.

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Microbiome Abundance Information continued...

***Clostridium* (genus)**

Clostridium spp. represents an extremely heterogeneous class of organisms that are still actively undergoing taxonomic revision. *Clostridium* spp. are strict anaerobic, spore-forming bacteria. Decreased abundance of the genus *Clostridium* was found to be associated with prediabetes. Some *Clostridium* spp. are transferred to infants from breast milk within the first months of life. Increased levels of some *Clostridium* spp. were observed in irritable bowel syndrome patients. Many species, some of them related to diarrhea, were decreased after consumption of inulin combined with maltodextrin.

***Clostridium methylpentosum* (species)**

Appropriate digestion and metabolism of complex dietary carbohydrates from plants drives healthy diversity in the gut microbiota. *Clostridium methylpentosum* ferments the naturally occurring sugar L-rhamnose that is released by microbial breakdown of plant-derived pectin. Rhamnose is fermented to propionate and acetate which are short chain fatty acids that have pivotal regulatory roles in the maintenance of mucosal barrier integrity, gut microbiota balance, post-prandial appetite suppression and normoglycemia. Lower levels of *C. methylpentosum* were reported for children with autism and pervasive developmental disorder compared to neurotypicals controls. Consumption of probiotic yogurt LKM512 containing *Bifidobacterium animalis* (subspecies lactis LKM512) increased the levels of *C. methylpentosum*.

***Dorea* (genus)**

Dorea is a genus within the *Lachnospiraceae* family that is in the Firmicutes phylum. *Dorea* species are known to produce hydrogen and carbon dioxide as end-products of glucose fermentation and may be associated with bloating. Decreased levels of *Dorea* spp. were observed in patients with Parkinson's disease. Recent studies have identified increased levels of *Dorea* spp. in patients diagnosed with IBS, nonalcoholic fatty liver disease and non-alcoholic steatohepatitis, multiple sclerosis and colorectal cancer.

***Eubacterium hallii* (species)**

Eubacterium hallii and *Eubacterium rectale* are both part of the *Lachnospiraceae* family that is in the Firmicutes phylum. *E. hallii* and *E. rectale* produce butyrate that is a key regulator of mucosal barrier integrity and function. Decreased levels of *Eubacterium* spp. have been associated with very high protein diets. *Eubacterium hallii* is capable of metabolizing glucose into products with antimicrobial properties.

***Faecalibacterium prausnitzii* (species)**

Faecalibacterium prausnitzii is one of the most abundant butyrate producing bacteria in a healthy gastrointestinal tract. As such, *F. prausnitzii* is a protective factor for the intestinal mucosa and supports very important intestinal barrier functions. *F. prausnitzii* exerts anti-inflammatory effects via metabolites such as short-chain fatty acids. *F. prausnitzii* is reduced in inflammatory bowel disease, irritable bowel syndrome, celiac disease and gastrointestinal inflammation in general. It is reduced in patients diagnosed with Parkinson's disease, bipolar disorder, colorectal cancer, diabetes and chronic idiopathic diarrhea. Diminished levels of *F. prausnitzii* were found in patients with major depressive disorder. The abundance of *F. prausnitzii* together with *E. coli* has been proposed as a discrimination tool between ulcerative colitis and Crohn's disease. *F. prausnitzii* has been correlated with pediatric obesity in instances of high consumption of foods that are rich in unabsorbed carbohydrate (banana, maize, rice). The prebiotic inulin has been shown to increase the proportion of *F. prausnitzii* in the human intestinal microbiota. Low FODMAP diets are associated with diminished *F. prausnitzii* and butyrate production.

***Lachnospiraceae* (family)**

The *Lachnospiraceae* family is a diverse group of butyric acid producers, which have been associated with beneficial microbial and epithelial cell growth. Consumption of a Mediterranean diet decreased levels of species belonging to *Lachnospiraceae*. *Lachnospiraceae* are known to increase with intake of cruciferous vegetables and wheat bran, and decrease with a resistant starch diet.

***Streptococcus* (genus)**

Higher abundance of *S. salivarius* and *S. thermophilus* (Firmicutes phylum) have been associated with a moderate to severe disease course in newly diagnosed ulcerative colitis (UC) patients. These findings are in accordance with a study that showed that UC patients have significantly increased *Streptococcus* spp. and depletion of *Bifidobacterium* spp. Higher levels of *Streptococcus* spp. were also observed in patients with colorectal cancer compared to healthy controls. Administration of *S. salivarius* together with *Bifidobacterium bifidum* was shown to reduce the incidence of acute diarrhea and rotavirus shedding in infants. *S. salivarius* and S. *thermophilus* are also widely used in dairy products like yogurt and cheese.

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Order: SAMPLE REPORT
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Doctor: Sample Doctor
Doctor's Data, Inc.
3755 Illinois Ave.
St. Charles, IL 60174

Patient: Sample Patient
Age: 35
Sex: Female

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Date Reported	08/14/2021
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Microbiome Abundance Information continued...

***Veillonella* (genus)**

Veillonella (Firmicutes phylum) are known for their ability to ferment lactate, producing the short chain fatty acids propionate and acetate. *Veillonella* spp. were shown to be significantly increased in patients with Crohn's disease, type 1 diabetes, and patients diagnosed with liver cirrhosis. Increased amounts of *Veillonella* have been found in patients with constipation dominant irritable bowel syndrome (IBS-C). It is hypothesized that the relationship between *Veillonella* strains and IBS stems from its robust production of organic acids (propionate and acetate) which contribute to bloating, anxiety and abdominal pain. Higher levels of *Veillonella* were found in formula-fed infants compared to breast-fed infants.

Proteobacteria (phylum)

Proteobacteria include a wide variety of pathogens, including species within the *Escherichia*, *Shigella Salmonella*, *Vibrio*, and *Helicobacter* genera. The phylum includes a number of species that are permanent residents of the microbiota and capable of inducing nonspecific inflammation and diarrhea when their presence is increased. Proteobacteria make up approximately 2% of the gut microbiota in healthy adults.

Proteobacteria

A high-fat diet is positively associated with an abundance of Proteobacteria. Slightly increased abundance of Proteobacteria may be associated with low-grade inflammation. Proteobacteria are increased in inflammatory bowel disease and irritable bowel syndrome. Higher abundance of Proteobacteria has been associated with a moderate to severe disease course in newly discovered ulcerative colitis patients. They are associated with diarrhea in IBS.

***Escherichia* (genus)**

Clinically, *Escherichia* has been reported to contribute to irritable bowel syndrome. *Escherichia* spp. are commonly recovered from inflamed tissues of both Crohn's disease and ulcerative colitis patients. Untreated inflammatory bowel disease patients were shown to have higher abundance of *Escherichia* and lower abundance of *Faecalibacterium prausnitzii*. Increased levels of *Escherichia* were observed in colorectal cancer patients. Patients diagnosed with nonalcoholic steatohepatitis have higher abundance of *Escherichia*. Consumption of a Western diet is positively associated with *Escherichia* levels. Increased levels of *E. coli* were observed in people on a gluten-free diet. A non-pathogenic strain of *Escherichia*, *Escherichia nissle*, is a widely used probiotic for treating gut related diseases such as chronic constipation.

Tenericutes (phylum)

Tenericutes are cell wall-less bacteria that do not synthesize precursors of peptidoglycan. Tenericutes consist of four main clades designated as the *Acholeplasma, Spiroplasma, Pneumoniae* and *Hominis* clusters.Tenericutes are typically parasites or commensals of eukaryotic hosts.

Verrucomicrobia (phylum)

Verrucomicrobia is a less common phylum in the human gut microbiota, but one with increasing recognition with regards to health. Verrucomicrobia includes *Akkermansia muciniphila*. The obligate anaerobe *A. muciniphila* constitutes 3-5% of total bacteria in a healthy microbiome, and has a protective or anti-inflammatory role in the intestinal mucosa.

GI Pathogens

Introduction

The GI Pathogen profile is performed using an FDA-cleared multiplex PCR system. It should be noted that PCR testing is much more sensitive than traditional techniques and allows for the detection of extremely low numbers of pathogens. PCR testing does not differentiate between viable and non-viable pathogens and should not be repeated until 21 days after completion of treatment or resolution to prevent false positives due to lingering traces of DNA. PCR testing can detect multiple pathogens in the patient's stool but does not differentiate the causative pathogen. All decisions regarding the need for treatment should take the patient's complete clinical history and presentation into account.

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Parasitology

Parasites

Parasites were detected by microscopic examination in this stool specimen. Intestinal parasites are abnormal inhabitants of the GI tract that live off and have the potential to cause damage to their host. Factors such as contaminated food and water supplies, day care centers, increased international travel, pets, carriers such as mosquitoes and fleas, and sexual transmission have contributed to an increased prevalence of intestinal parasites.

In general, acute manifestations of parasitic infection may involve diarrhea with or without mucus and/or blood, fever, nausea, or abdominal pain. However, these symptoms do not always occur. Consequently, parasitic infections may not be diagnosed and eradicated. If left untreated, chronic parasitic infections can cause damage to the intestinal lining and can be an unsuspected cause of illness and fatigue. Chronic parasitic infections can also be associated with increased intestinal permeability, irritable bowel syndrome, irregular bowel movements, malabsorption, gastritis or indigestion, skin disorders, joint pain, allergic reactions, decreased immune function, and fatigue.

Blastocystis spp

Blastocystis spp was identified in this specimen. *Blastocystis* is a common protozoan found throughout the world. *Blastocystis* is transmitted via the fecal-oral route or from contaminated food or water. Whether *Blastocystis* infection can cause symptoms is still considered controversial. Symptoms may be compounded by concomitant infection with other parasitic organisms, bacteria, or viruses. Often, *Blastocystis* is found along with other such organisms. Nausea, diarrhea, abdominal pain, anal itching, weight loss, and excess gas have been reported in some persons with *Blastocystis* infection.

Metronidazole has been the traditionally considered the most effective drug (recommended adult dosage varies from 250 mg bid for 5-7 days to 750 mg tid x 10 days). Iodoquinol is also an effective medication (650 mg tid x 20 days). Recommended therapy can also eliminate *G. lamblia, E. histolytica* and *D. fragilis*. Various herbs may be effective, including oil of oregano. Limit refined carbohydrates in diet.

Dientamoeba fragilis

Dientamoeba fragilis, an ameboflagellate, was detected in this specimen. *D. fragilis* infects the large intestine. This parasite does not have a cyst stage, and cannot survive long outside the body alone. It may be spread in pinworm (*Enterobius vermicularis*) eggs. Infection is common worldwide, including in the United States. *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 include diarrhea, stomach pain, and stomach cramping. Loss of appetite and weight, nausea, and fatigue are also common.

Recommended treatment is iodoquinol (650 mg tid x 20 days, adult dose). Alternatives include tetracycline (500 mg qid x 10 days, adult dose) and metronidazole (500-750 mg tid x 10 days, adult dose). Natural agents include berberine, wormwood, black walnut, grapefruit seed extract, and oil of oregano.

Microbiology

Pathogenic/Dysbiotic Flora

In a healthy balanced state of intestinal flora, the beneficial bacteria make up a significant proportion of the total microflora. However, in many individuals there is an imbalance or deficiency of beneficial flora (insufficiency dysbiosis) and an overgrowth of non-beneficial (imbalance) or even pathogenic microorganisms. This can be due to a number of factors including: consumption of contaminated water or food; daily exposure of chemicals that are toxic to beneficial bacteria; the use of antibiotics, oral contraceptives or other medications; poor fiber intake and high stress levels.

A number of toxic substances can be produced by the dysbiotic bacteria including amines, ammonia, hydrogen sulfide, phenols, and secondary bile acids which may cause inflammation or damage to the brush border of the intestinal lining. If left unchecked, long-term damage to the intestinal lining may result in leaky gut syndrome, allergies, autoimmune disease (e.g. rheumatoid arthritis), irritable bowel syndrome, fatigue, chronic headaches, and sensitivities to a variety of foods. In addition, pathogenic bacteria can cause acute symptoms such as abdominal pain, nausea, diarrhea, vomiting, and fever in cases of food poisoning.

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Microbiology continued...

Bacterial sensitivities to a variety of prescriptive and natural agents have been provided for the pathogenic bacteria that were cultured from this patient's specimen. This provides the practitioner with useful information to help plan an appropriate treatment regimen. Supplementation with probiotics or consumption of foods (yogurt, kefir, miso, tempeh, tamari sauce) containing strains of lactobacilli, bifidobacteria, and enterococci may help restore healthy flora levels. Soluble fiber and polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been found to increase the numbers of beneficial bacteria. Hypochlorhydria may also predispose an individual to bacterial overgrowth, particularly in the small intestine. Nutritional anti-inflammatories can aid in reversing irritation to the GI lining. These include quercetin, vitamin C, curcumin, gamma-linoleic acid, omega-3 fatty acids (EPA, DHA), and aloe vera. Other nutrients such as zinc, beta-carotene, pantothenic acid, and L-glutamine provide support for regeneration of the GI mucosa. A comprehensive program may be helpful in individuals in whom a dysbiotic condition has caused extensive GI damage.

Enterobacter cloacae complex

Enterobacter cloacae complex is part of the *Enterobacteriaceae* family. *E cloacae* complex is a group of six closely related species with similar resistance patterns: *E. cloacae, E. asburiae, E. hormaechei, E. kobei, E. ludwigii,* and *E. nimipressuralis*. This gram-negative bacterium is considered dysbiotic at levels of 3+ or greater. *E. cloacae* complex is considered an opportunistic pathogen associated with diarrhea in children. A Shiga-like toxin-producing *E. cloacae* was isolated from the feces of an infant with hemolytic-uremic syndrome. However, *E. cloacae* complex is most often involved in extraintestinal infections including the urinary tract, respiratory tract, and cutaneous wounds.

Widely distributed in the environment, *Enterobacter* spp. is commonly isolated from both human and animal feces. Environmental strains of *Enterobacter* spp. are capable of growth in foods at refrigeration temperature.

E. cloacae complex is known to possess inducible ß-lactamases. Isolates may become resistant to all cephalosporins after initiation of therapy. Avoid ß-lactam-inhibitor drugs such as amoxicillin/ clavulanate, ampicillin/sulbactam, and piperacillin/tazobactam.

Antibiotics may be indicated in systemic infections if symptoms are prolonged. Refer to the antimicrobial susceptibilities for treatment.

Imbalanced Flora

Imbalanced flora are those bacteria that reside in the host gastrointestinal tract and neither injure nor benefit the host. Certain dysbiotic bacteria may appear under the imbalanced category if found at low levels because they are not likely pathogenic at the levels detected. Imbalanced bacteria are commonly more abundant in association with insufficiency dysbiosis, and/or a fecal pH more towards the alkaline end of the reference range (5.8 - 7.0). Treatment with antimicrobial agents is unnecessary unless bacteria appear under the dysbiotic category.

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