



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

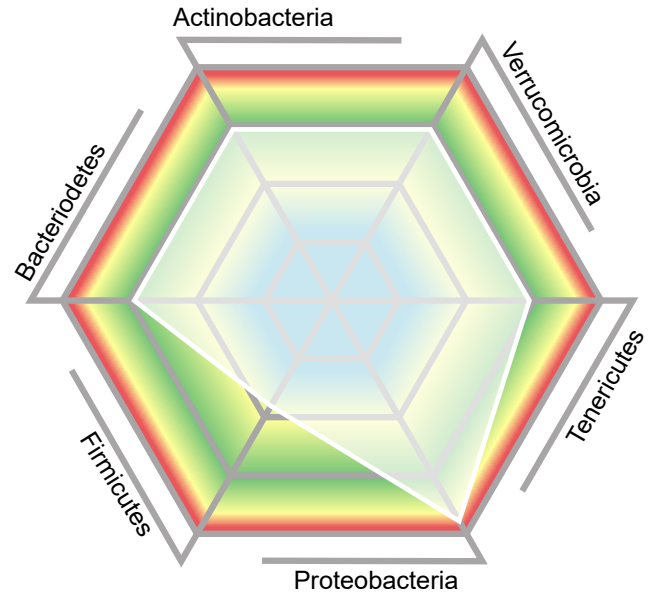
08/14/2021

Specimens Collected

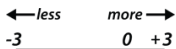
3

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	↑	<i>Blastocystis</i> spp., Observed
<i>Escherichia</i> spp., Very High	↑	<i>Dientamoeba fragilis</i> , Observed
Clostridia Class, Very Low	↓	<i>Enterobacter cloacae</i> complex, Cultured
<i>Eubacterium hallii</i> , Very Low	↓	Secretory IgA, Very High
<i>Faecalibacterium prausnitzii</i> , Very Low	↓	Butyrate, Low
Lachnospiraceae, Very Low	↓	

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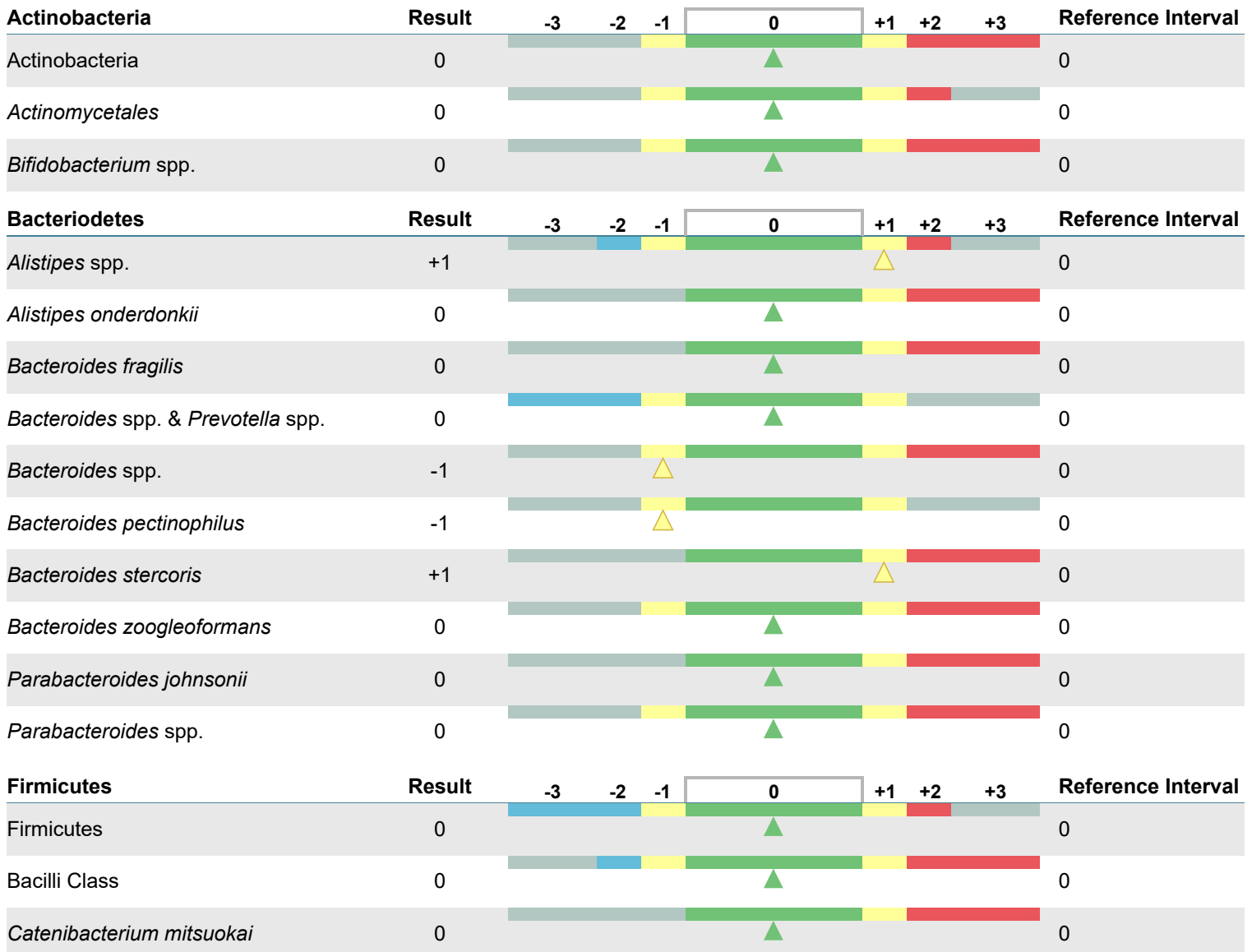
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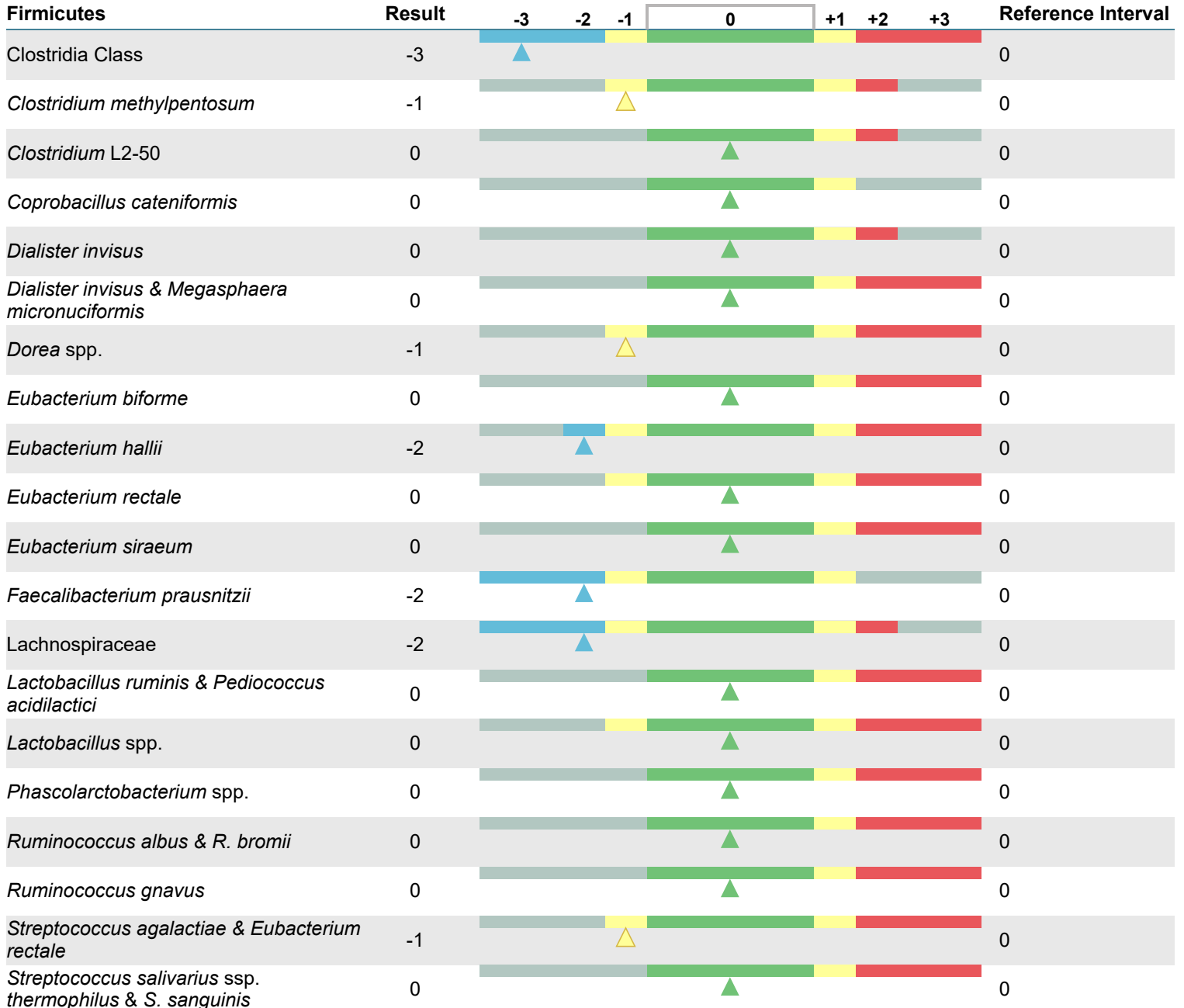
Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.

**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	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i>	-1			▲					0
<i>Streptococcus</i> spp.	0				▲				0
<i>Veillonella</i> spp.	-1			▲					0
Proteobacteria	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Proteobacteria	+3							▲	0
<i>Enterobacteriaceae</i>	0				▲				0
<i>Escherichia</i> spp.	+3							▲	0
<i>Acinetobacter junii</i>	0				▲				0
Tenericutes	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Mycoplasma hominis</i>	0				▲				0
Verrucomicrobia	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<i>Akkermansia muciniphila</i>	0				▲				0

**Microbiome Abundance Information:**

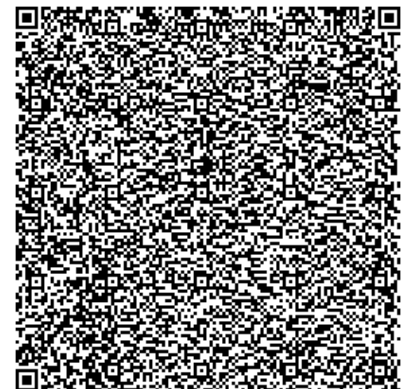
- The GI360™ Microbiome Profile is a focused gut microbiota DNA analysis tool that identifies more than 45 targeted analytes across six phyla using a CE-marked multiplex PCR system. Patient results are compared to a highly defined normobiotic reference population (n > 1,100). The white shadowed web plot 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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Viruses	Result	
Adenovirus F40/41	Negative	<input checked="" type="checkbox"/>
Norovirus GI/GII	Negative	<input checked="" type="checkbox"/>
Rotavirus A	Negative	<input checked="" type="checkbox"/>

Pathogenic Bacteria	Result	
<i>Campylobacter</i> (<i>C. jejuni</i> , <i>C. coli</i> and <i>C. lari</i>)	Negative	<input checked="" type="checkbox"/>
<i>Clostridioides difficile</i> (Toxin A/B)	Negative	<input checked="" type="checkbox"/>
<i>Escherichia coli</i> O157	Negative	<input checked="" type="checkbox"/>
Enterotoxigenic <i>Escherichia coli</i> (EPEC) It/st	Negative	<input checked="" type="checkbox"/>
<i>Salmonella</i> spp.	Negative	<input checked="" type="checkbox"/>
Shiga-like toxin-producing <i>Escherichia coli</i> (STEC) stx1/stx2	Negative	<input checked="" type="checkbox"/>
<i>Shigella</i> (<i>S. boydii</i> , <i>S. sonnei</i> , <i>S. flexneri</i> & <i>S. dysenteriae</i>)	Negative	<input checked="" type="checkbox"/>
<i>Vibrio cholerae</i>	Negative	<input checked="" type="checkbox"/>

Parasites	Result	
<i>Cryptosporidium</i> (<i>C. parvum</i> and <i>C. hominis</i>)	Negative	<input checked="" type="checkbox"/>
<i>Entamoeba histolytica</i>	Negative	<input checked="" type="checkbox"/>
<i>Giardia duodenalis</i> (AKA <i>intestinalis</i> & <i>lamblia</i>)	Negative	<input checked="" type="checkbox"/>

Notes:

Methodology: Multiplex PCR





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Protozoa

Result

Table with 3 columns: Protozoa, Result, and a toggle switch. Rows include Balantidium coli, Blastocystis spp., Chilomastix mesnili, Dientamoeba fragilis, Endolimax nana, Entamoeba coli, Entamoeba hartmanni, Entamoeba histolytica/Entamoeba dispar, Entamoeba polecki, Enteromonas hominis, Giardia duodenalis, Iodamoeba bütschlii, Isospora belli, Pentatrichomonas hominis, and Retortamonas intestinalis.

Cestodes - Tapeworms

Result

Table with 3 columns: Cestodes - Tapeworms, Result, and a toggle switch. Rows include Diphyllbothrium latum, Dipylidium caninum, Hymenolepis diminuta, Hymenolepis nana, and Taenia.

Trematodes - Flukes

Result

Table with 3 columns: Trematodes - Flukes, Result, and a toggle switch. Rows include Clonorchis sinensis, Fasciola hepatica/Fasciolopsis buski, Heterophyes heterophyes, and Paragonimus westermani.

Nematodes - Roundworms

Result

Table with 3 columns: Nematodes - Roundworms, Result, and a toggle switch. Row includes Ascaris lumbricoides.

Notes:

Methodology: Microscopy



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Nematodes - Roundworms

Result

Table with 3 columns: Parasite Name, Result, and Status. Rows include Capillaria hepatica, Capillaria philippinensis, Enterobius vermicularis, Hookworm, Strongyloides stercoralis, and Trichuris trichiura, all marked as 'Not Detected'.

Other Markers

Result

Reference Interval

Table with 4 columns: Marker Name, Result, Status, and Reference Interval. Rows include Yeast, RBC, WBC, Muscle fibers, Vegetable fibers, Charcot-Leyden Crystals, and Pollen, all marked as 'Not Detected'.

Macroscopic Appearance

Result

Reference Interval

Table with 4 columns: Appearance Name, Result, Status, and Reference Interval. Rows include Color (Brown), Consistency (Soft), and Mucus (Negative).

GI 360 Parasitology Information:

- This test is not designed to detect Cyclospora cayetanensis or Microsporidia spp.
Intestinal parasites are abnormal inhabitants of the gastrointestinal tract that have the potential to cause damage to their host.
There are two main classes of intestinal parasites, they include protozoa and helminths.

Notes:

Methodology: Microscopy, Macroscopic Observation

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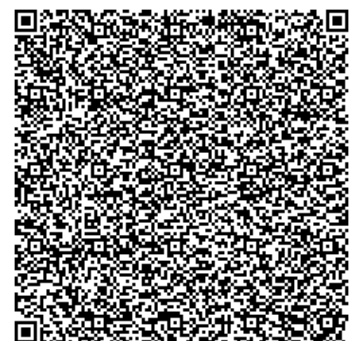
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**Parasitology Information:**

- 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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Table with 7 sections: Pathogenic Bacteria, Imbalance Bacteria, Dysbiotic Bacteria, and Yeast. Each section lists bacterial species, their results (e.g., NG, 2+), and reference intervals. Includes visual progress bars for each result.



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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Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	301	µg/mL		▲		> 200
Fat Stain	None		▲			None – Few
Carbohydrates [†]	Negative			▲		Negative
Inflammation	Result	Unit	L	WRI	H	Reference Interval
Lactoferrin	1.8	µg/mL	▲			< 7.3
Lysozyme*	223	ng/mL		▲		≤ 500
Calprotectin	<5	µg/g	▲			≤ 50
Immunology	Result	Unit	L	WRI	H	Reference Interval
Secretory IgA*	884	mg/dL			▲	30 – 275
Short Chain Fatty Acids	Result	Unit	L	WRI	H	Reference Interval
% Acetate [‡]	65			▲		50 – 72
% Propionate [‡]	20			▲		11 – 25
% Butyrate [‡]	13			▲		11 – 32
% Valerate [‡]	2.3			▲		0.8 – 5.0
Butyrate [‡]	0.70	mg/mL		▲		0.8 – 4.0
Total SCFA's [‡]	5.5	mg/mL		▲		5.0 – 16.0
Intestinal Health Markers	Result	Unit	L	WRI	H	Reference Interval
pH	6.4			▲		5.8 – 7.0
β-glucuronidase*	528	U/L		▲		100 – 1200
Occult Blood	Negative			▲		Negative

**Chemistry Information:**

- Elastase** findings can be used for the diagnosis or the exclusion of exocrine pancreatic insufficiency. Correlations between low levels and chronic pancreatitis and cancer have been reported.

Notes:

RI= Reference Interval, L (blue)= Low (below RI), WRI (green)= within RI, Yellow= moderately outside RI, L or H, H (red)= High (above RI)

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[†]This test has been modified from the manufacturer's instructions and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements.

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Methodology: Elisa, Microscopy, Colormetric, Gas Chromotography, ph Electrode, Guaiac



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Chemistry Information:

- **Fat Stain:** Microscopic determination of fecal fat using Sudan IV staining is a qualitative procedure utilized to assess fat absorption and to detect steatorrhea.
- **Carbohydrates:** The presence of reducing substances in stool specimens can indicate carbohydrate malabsorption.
- **Lactoferrin** and **Calprotectin** are reliable markers for differentiating organic inflammation (IBD) from function symptoms (IBS) and for management of IBD. Monitoring levels of fecal lactoferrin and calprotectin can play an essential role in determining the effectiveness of therapy, are good predictors of IBD remission, and can indicate a low risk of relapse.
- **Lysozyme** is an enzyme secreted at the site of inflammation in the GI tract and elevated levels have been identified in IBD patients.
- **Secretory IgA (sIgA)** is secreted by mucosal tissue and represents the first line of defense of the GI mucosa and is central to the normal function of the GI tract as an immune barrier. Elevated levels of sIgA have been associated with an upregulated immune response.
- **Short chain fatty acids (SCFAs):** SCFAs are the end product of the bacterial fermentation process of dietary fiber by beneficial flora in the gut and play an important role in the health of the GI as well as protecting against intestinal dysbiosis. Lactobacilli and bifidobacteria produce large amounts of short chain fatty acids, which decrease the pH of the intestines and therefore make the environment unsuitable for pathogens, including bacteria and yeast. Studies have shown that SCFAs have numerous implications in maintaining gut physiology. SCFAs decrease inflammation, stimulate healing, and contribute to normal cell metabolism and differentiation. Levels of **Butyrate** and **Total SCFA** in mg/mL are important for assessing overall SCFA production, and are reflective of beneficial flora levels and/or adequate fiber intake.
- **pH:** Fecal pH is largely dependent on the fermentation of fiber by the beneficial flora of the gut.
- **Occult blood:** A positive occult blood indicates the presence of free hemoglobin found in the stool, which is released when red blood cells are lysed.
- **β-glucuronidase** is an enzyme that breaks the tight bond between glucuronic acid and toxins in the intestines. The binding of toxins in the gut is protective by way of blocking their absorption and facilitating excretion.



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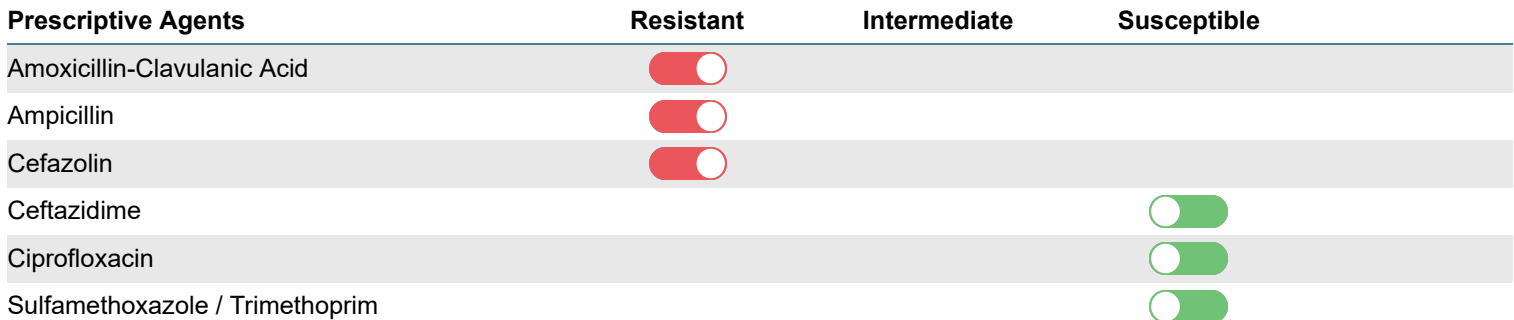
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Enterobacter cloacae complex

Natural Agents**Prescriptive Agents****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.

Bacteroidetes (phylum)

Bacteroidetes 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 Bacteroidetes 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 *Alistipes* 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 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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3755 Illinois Ave.

St. Charles, IL 60174

Patient: Sample Patient

Age: 35

Sex: Female

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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 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 β -lactamases. Isolates may become resistant to all cephalosporins after initiation of therapy. Avoid β -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.

Stool Chemistries**Secretory IgA (sIgA) High**

The concentration of sIgA is abnormally high in this fecal specimen. Secretory IgA represents the first line of defense of the gastrointestinal (GI) mucosa and is central to the normal function of the GI tract as an immune barrier. Elevated fecal sIgA is an appropriate response to antigens such as pathogenic bacteria, parasites, yeast, and viruses. Eradication of the pathogenic microorganisms will bring sIgA back down into the normal range. sIgA may remain elevated up to six weeks after a GI viral infection. Elevated fecal sIgA may also be associated with autoinflammatory conditions such as reactive arthritis and spondyloarthritis. Actively breast-feeding infants may exhibit high fecal sIgA due to high maternal milk content. Consumption of bovine colostrum does not artificially increase fecal sIgA because the assay is specific for human sIgA.

Short Chain Fatty Acids (SCFAs)

The total concentration and/or percentage distribution of the primary short chain fatty acids (SCFAs) are abnormal in this specimen. Beneficial bacteria that ferment non-digestible soluble fiber produce SCFAs that are pivotal in the regulation of intestinal health and function. Restoration of microbial abundance and diversity, and adequate daily consumption of soluble fiber and polyphenols can improve SCFA status.



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Stool Chemistries continued...

The primary SCFAs butyrate, propionate and acetate are produced by predominant commensal bacteria via fermentation of soluble dietary fiber 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 specialized 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. The SCFAs also contribute to a more acidic and anaerobic microenvironment that disfavors dysbiotic bacteria and yeast. Abnormal SCFAs may be associated with dysbiosis (including insufficiency dysbiosis), compromised intestinal barrier function (intestinal permeability) and inappropriate immune and inflammatory conditions.

“Seeding” with supplemental probiotics may contribute to improved production and status of SCFAs, but it is imperative to “feed” the beneficial microbes. Sources of soluble fiber that are available to the microbes include chick peas, beans, lentils, oat and rice bran, fructo- and galacto- oligosaccharides, and inulin.