



Order: SAMPLE REPORT



Client #: 12345

Doctor: Sample Doctor
Precision Point
Diagnostics

Patient: Sample Patient

Age: 56

Sex: Female

Sample Collection

Date/Time

Date Collected

12/30/2020

Date Received

12/31/2020

Date Reported

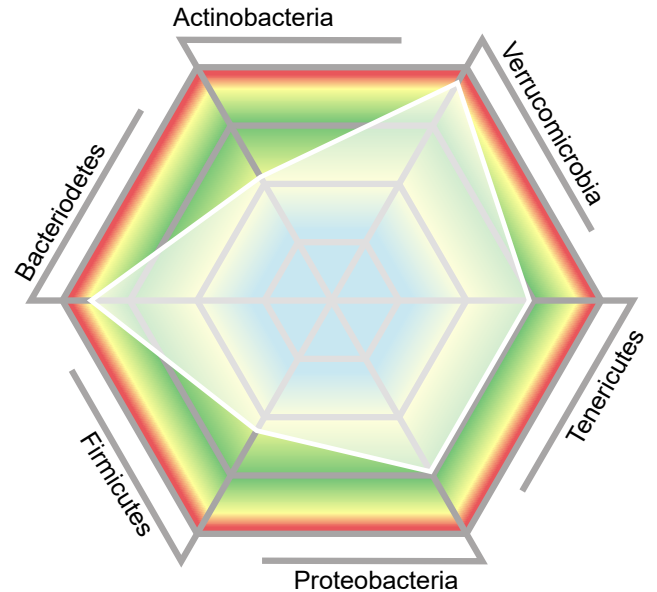
01/01/2021

Specimens Collected

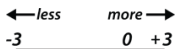
3

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



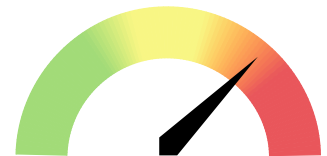
The web image shows the relative diversity and balance among bacteria belonging to the six primary Phyla. The white shaded area represents the patient's results compared to a normobiotic reference population. The center of the web represents less abundance while the outer edges represent more than normobiotic.

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

4



Key Findings

<i>Akkermansia muciniphila</i> , Very High	↑	Vegetable fibers, Abnormal
Bacilli Class, Very Low	↓	<i>Enterobacter cloacae</i> complex, Cultured
<i>Bacteroides zooglooformans</i> , Very High	↑	
<i>Faecalibacterium prausnitzii</i> , Very Low	↓	
<i>Phascolarctobacterium</i> spp., Very High	↑	



Microbiome Bacterial Abundance; Multiplex PCR

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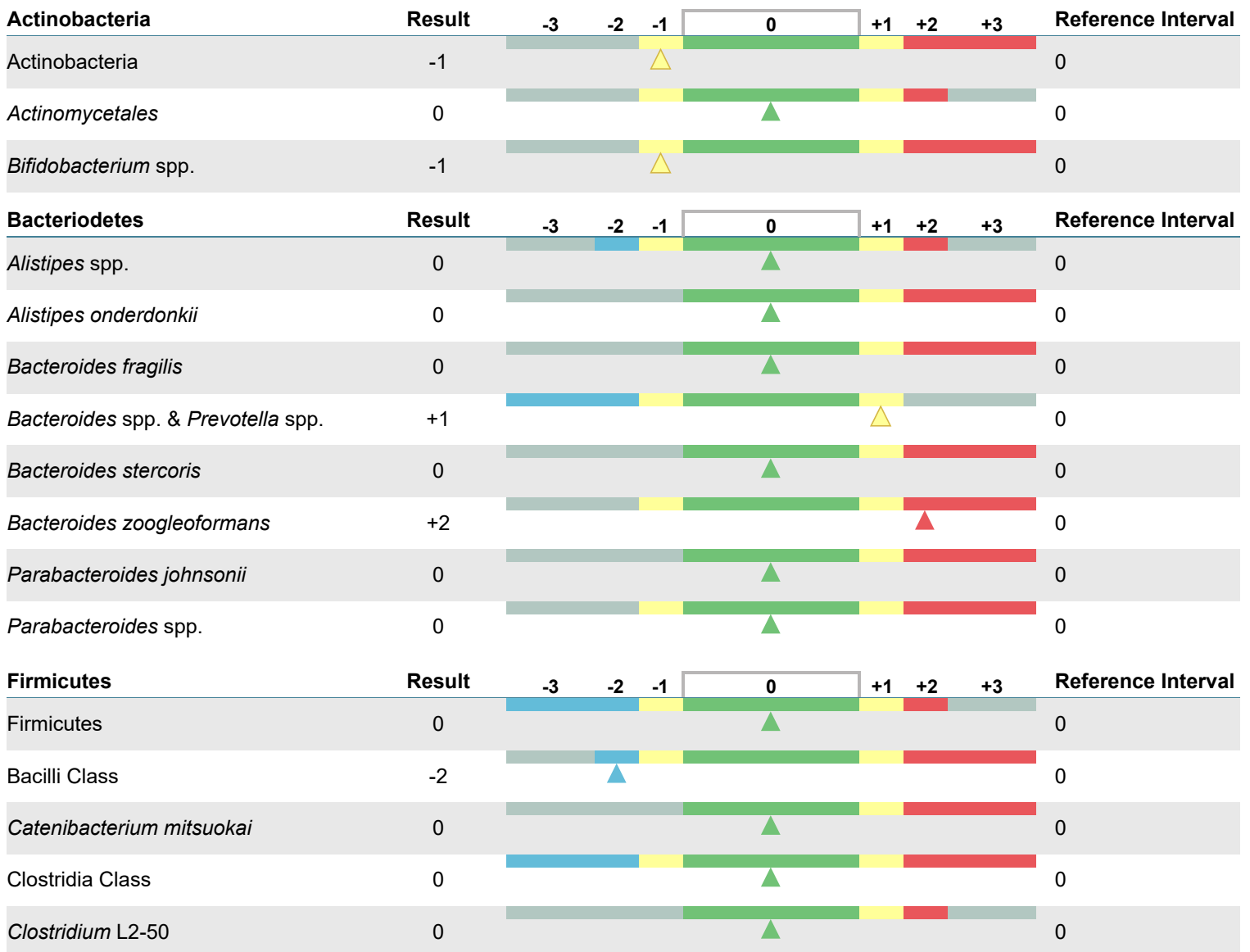
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LEGEND



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.

*This test was developed and its performance characteristics determined in a manner consistent with CLIA requirements. The U. S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for clinical use. The results are not intended to be used as a sole means for clinical diagnosis or patient management decisions.

Methodology: Multiplex PCR



Microbiome Bacterial Abundance; Multiplex PCR

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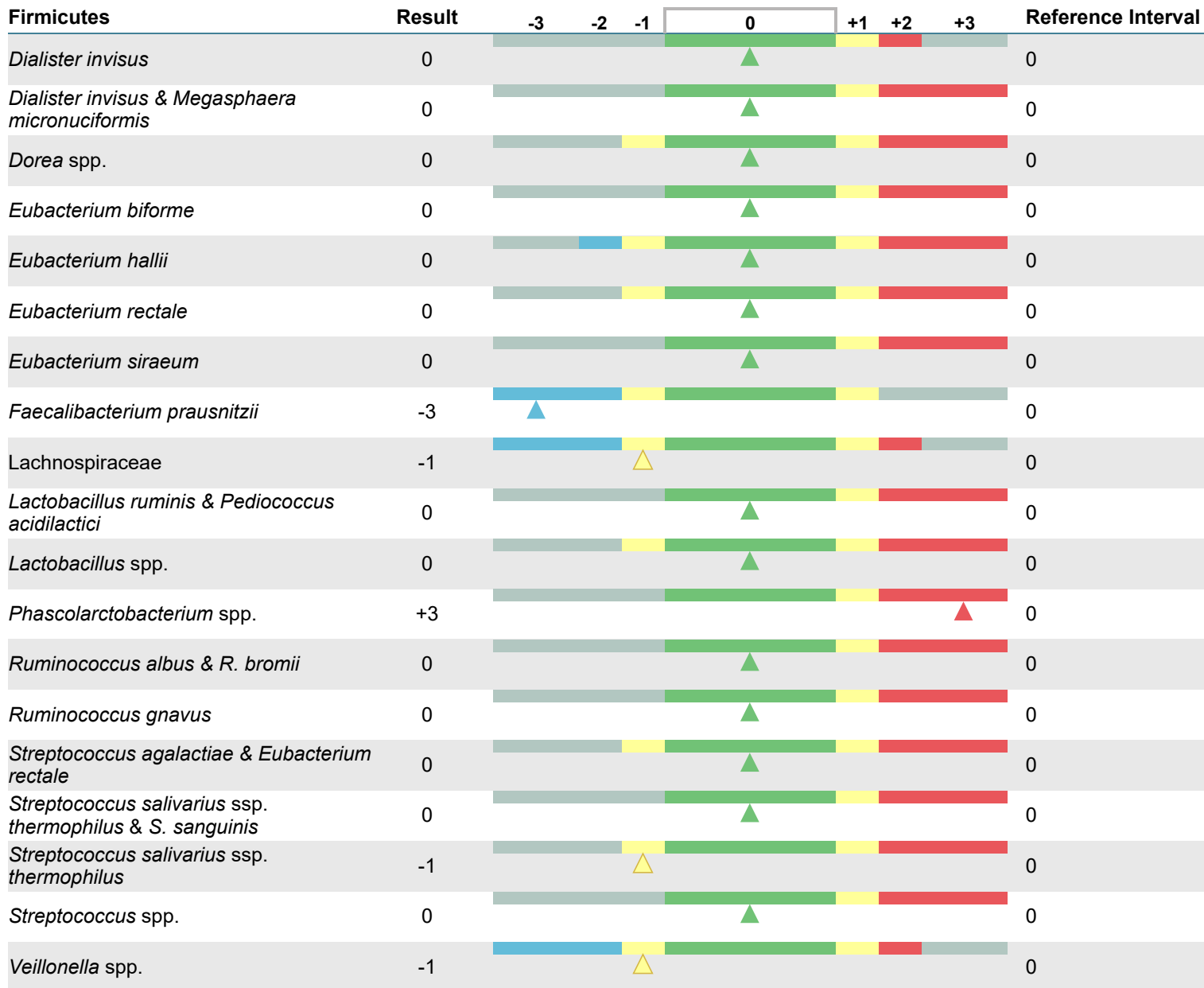
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Specimens Collected 3



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Methodology: Multiplex PCR



Microbiome Bacterial Abundance; Multiplex PCR

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	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
Proteobacteria									
Proteobacteria	0				▲				0
<i>Escherichia</i> spp.	0				▲				0
Tenericutes									
<i>Mycoplasma hominis</i>	0				▲				0
Verrucomicrobia									
<i>Akkermansia muciniphila</i>	+2						▲		0

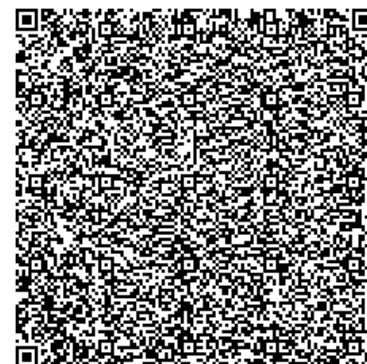


Microbiome Abundance Information:

- 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





GI Pathogens; Multiplex PCR

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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



Parasitology; Microscopy

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Protozoa

Result

<i>Balantidium coli</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Blastocystis</i> spp.	Not Detected	<input checked="" type="checkbox"/>
<i>Chilomastix mesnili</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Dientamoeba fragilis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Endolimax nana</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Entamoeba coli</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Entamoeba hartmanni</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Entamoeba histolytica/Entamoeba dispar</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Entamoeba polecki</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Enteromonas hominis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Giardia duodenalis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Iodamoeba bütschlii</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Isospora belli</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Pentatrichomonas hominis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Retortamonas intestinalis</i>	Not Detected	<input checked="" type="checkbox"/>

Cestodes - Tapeworms

Result

<i>Diphyllobothrium latum</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Dipylidium caninum</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Hymenolepis diminuta</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Hymenolepis nana</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Taenia</i>	Not Detected	<input checked="" type="checkbox"/>

Trematodes - Flukes

Result

<i>Clonorchis sinensis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Fasciola hepatica/Fasciolopsis buski</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Heterophyes heterophyes</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Paragonimus westermani</i>	Not Detected	<input checked="" type="checkbox"/>

Nematodes - Roundworms

Result

<i>Ascaris lumbricoides</i>	Not Detected	<input checked="" type="checkbox"/>
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Notes:

Methodology: Microscopy



Parasitology; Microscopy

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<i>Capillaria hepatica</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Capillaria philippinensis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Enterobius vermicularis</i>	Not Detected	<input checked="" type="checkbox"/>
Hookworm	Not Detected	<input checked="" type="checkbox"/>
<i>Strongyloides stercoralis</i>	Not Detected	<input checked="" type="checkbox"/>
<i>Trichuris trichiura</i>	Not Detected	<input checked="" type="checkbox"/>

Other Markers**Result****Reference Interval**

Yeast	Few	<input type="checkbox"/>	Not Detected – Rare
RBC	Not Detected	<input checked="" type="checkbox"/>	Not Detected – Rare
WBC	Not Detected	<input checked="" type="checkbox"/>	Not Detected – Rare
Muscle fibers	Not Detected	<input checked="" type="checkbox"/>	Not Detected – Rare
Vegetable fibers	Moderate	<input type="checkbox"/>	Not Detected – Few
Charcot-Leyden Crystals	Not Detected	<input checked="" type="checkbox"/>	Not Detected
Pollen	Not Detected	<input checked="" type="checkbox"/>	Not Detected

Macroscopic Appearance**Result****Reference Interval**

Color	Brown	<input checked="" type="checkbox"/>	Brown
Consistency	Soft	<input checked="" type="checkbox"/>	Soft
Mucus	Negative	<input checked="" type="checkbox"/>	Negative

**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. 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



Parasitology; Microscopy

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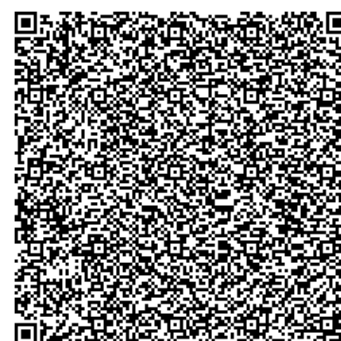
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Parasitology Information:

- 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".





Microbiology

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Pathogenic Bacteria	Result	NG	1+	2+	3+	4+	Reference Interval
<i>Aeromonas</i>	NG	▲					No Growth
<i>Edwardsiella tarda</i>	NG	▲					No Growth
<i>Plesiomonas shigelloides</i>	NG	▲					No Growth
<i>Salmonella</i>	NG	▲					No Growth
<i>Shigella spp.</i>	NG	▲					No Growth
<i>Vibrio cholerae</i>	NG	▲					No Growth
<i>Vibrio</i>	NG	▲					No Growth
<i>Yersinia</i>	NG	▲					No Growth
Imbalance Bacteria	Result	NG	1+	2+	3+	4+	Reference Interval
Beta hemolytic strep, group B	2+			▲			No Growth
<i>Citrobacter freundii</i> complex	1+		▲				No Growth
<i>Comamonas jiangduensis</i>	3+				▲		No Growth
Gamma hemolytic strep	2+			▲			No Growth
Dysbiotic Bacteria	Result	NG	1+	2+	3+	4+	Reference Interval
<i>Enterobacter cloacae</i> complex	3+				▲		No Growth
Yeast	Result	NG	1+	2+	3+	4+	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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Stool Chemistries

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Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	427	µg/mL				> 200
Fat Stain	Few					None – Few
Carbohydrates [†]	Negative					Negative
Inflammation	Result	Unit	L	WRI	H	Reference Interval
Lactoferrin	1.1	µg/mL				< 7.3
Lysozyme*	117	ng/mL				≤ 500
Calprotectin	12	µg/g				≤ 50
Immunology	Result	Unit	L	WRI	H	Reference Interval
Secretory IgA*	60.0	mg/dL				30 – 275
Short Chain Fatty Acids	Result	Unit	L	WRI	H	Reference Interval
% Acetate [‡]	71					50 – 72
% Propionate [‡]	16					11 – 25
% Butyrate [‡]	12					11 – 32
% Valerate [‡]	1.3					0.8 – 5.0
Butyrate [‡]	1.3	mg/mL				0.8 – 4.0
Total SCFA's [‡]	11	mg/mL				5.0 – 16.0
Intestinal Health Markers	Result	Unit	L	WRI	H	Reference Interval
pH	6.2					5.8 – 7.0
β-glucuronidase*	100	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 (optimal), WRI (yellow)= Within RI (not optimal), H (red)= High (above RI)

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†This test has been modified from the manufacturer's instructions and its performance characteristics determined 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 functional 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.





Bacterial Susceptibilities

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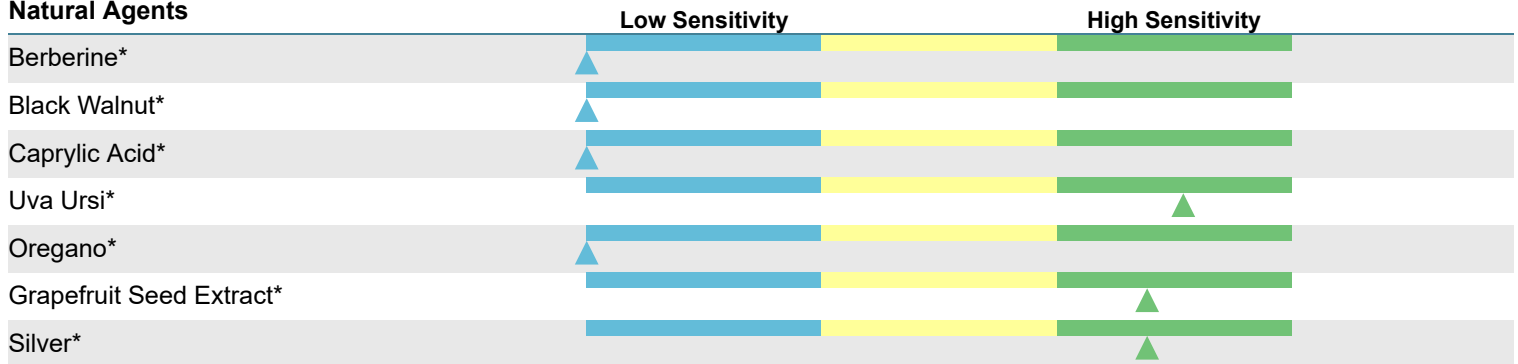
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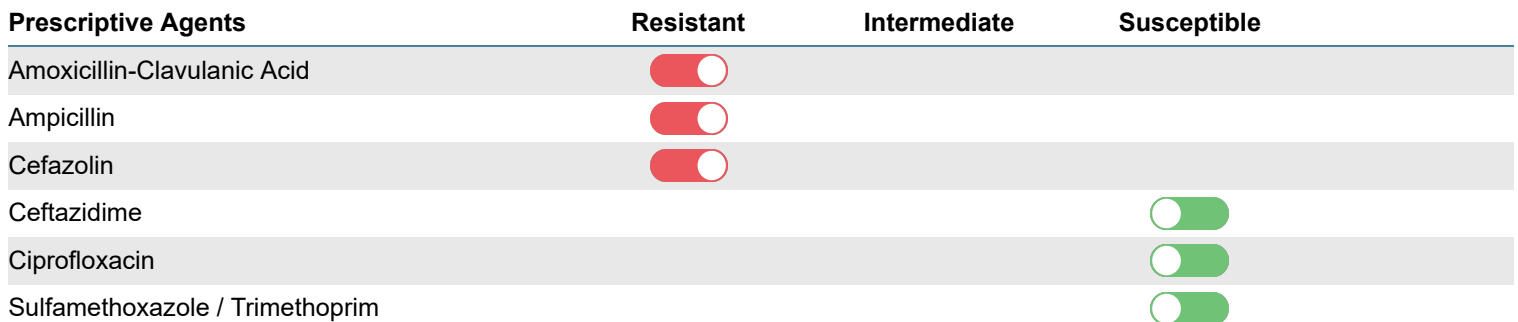
3

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.

↓ *Bifidobacterium* (genus)

Considered amongst the most beneficial commensal bacteria in the human gut, *Bifidobacterium* spp. are able to degrade monosaccharides, galacto-, manno-, and fructo-oligosaccharides, as well as some complex carbohydrates. Many of the non-digestible oligosaccharides, found as natural components in mother's milk, select for colonization of these species which dominate the infant gut shortly after birth. Bifidobacteria may provide health benefits directly through interactions with the host, and indirectly through interactions with other microorganisms. *Bifidobacterium* spp. take part in production and adsorption of vitamins, such as vitamins K and B12, biotin, folate, thiamine, riboflavin, and pyridoxine. They are also involved in lipid absorption and metabolism, glucose and energy homeostasis, and regulating intestinal barrier function. Although *Bifidobacterium* produce acetate over butyrate, healthy levels of *Bifidobacterium* spp. facilitate colonization of *Faecalibacterium. prausnitzii*. Polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been shown to increase *Bifidobacterium* species. The increased abundance of *Bifidobacterium* species has been associated with amelioration of inflammation. Multiple published studies have suggested that there is an association between obesity and a lower abundance of bifidobacteria. They may also be less abundant in elderly populations, patients with rheumatoid arthritis, and in individuals diagnosed with Alzheimer's disease. Patients with active inflammatory bowel disease (IBD) have a lower abundance of *Bifidobacterium* spp. than patients whose IBD is in remission. Taking a probiotic containing bifidobacteria, lactobacilli, and streptococci might help in controlling ulcerative colitis symptoms and preventing their recurrence. Some *Bifidobacterium* strains have been shown to have beneficial effects in irritable bowel syndrome (IBS). *Bifidobacterium* spp. abundance has been shown to be diminished with IBD and with long term use of macrolide antibiotics. Luminal bifidobacteria is reduced with restriction of fermentable carbohydrates, i.e. a low FODMAP diet. High fat dietary feeding is also associated with reduced abundance of bifidobacteria. Consumption of maize and barley-based whole grain products and red berries, which are comprised of anthocyanins, are known to increase levels of bifidobacteria.

Bacterioidetes (phylum)

Bacterioidetes 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 Bacterioidetes in relation to Firmicutes has been associated with obesity, though this can increase with weight loss and restricted calorie intake.

↑ *Prevotella* (genus)

Prevotella-rich dysbiosis has been associated with insulin-resistance, obesity and hypertension. *Prevotella* have been shown to be significantly decreased in Crohn's disease and Parkinson's disease. High levels of fiber and carbohydrates from fruits and vegetables in a Mediterranean diet have been shown to increase the relative abundance of *Prevotella*.

↑ *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.

Order: SAMPLE REPORT**Client #:** 12345**Doctor:** Sample Doctor
Precision Point
Diagnostics**Patient:** Sample Patient**Age:** 56**Sex:** Female**Sample Collection****Date/Time****Date Collected** 12/30/2020**Date Received** 12/31/2020**Date Reported** 01/01/2021**Specimens Collected** 3**Microbiome Abundance Information continued...****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.

↓ **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.

↑ **Phascolarctobacterium (genus)**

Phascolarctobacterium are in the Firmicutes phylum. *Phascolarctobacterium* can produce short chain fatty acids, including acetate and propionate, and may be associated with metabolic effects and mental state of the host. Patients diagnosed with major depressive disorder had increased levels of these species. Decreased levels of *Phascolarctobacterium* were found to be associated with Crohn's disease, ulcerative colitis and Alzheimer's disease. Consumption of cruciferous vegetables, such as broccoli, increases the abundance of *Phascolarctobacterium* in the gut.

↓ **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.

↓ **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.

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Microbiome Abundance Information continued...

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.

↑ *Akkermansia muciniphila* (genus)

Higher abundance of *Akkermansia muciniphila* has been associated with a milder disease course in newly discovered ulcerative colitis patients. Archaea and *Akkermansia* were significantly more prevalent after weight reduction. A Low FODMAP diet has been shown to decrease the abundance of *A. muciniphila* leading to recommendations against long-term use of such a diet. *A. muciniphila* is a mucolytic specialist that has potent anti-inflammatory effects in part associated with a specific surface coat protein (Amuc- 1100).

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.

Parasitology

Microscopic yeast

Microscopic examination has revealed more yeast in this sample than normal. While small quantities of yeast (reported as rare) may be normal, yeast observed in higher amounts (moderate to many) is considered abnormal. Yeast does not appear to be dispersed uniformly throughout the stool. Yeast may therefore be observed microscopically, but not grow out on culture even when collected from the same bowel movement. Further, some yeast may not survive transit through the intestines rendering it unviable for culturing. Therefore, both microscopic examination and culture are helpful in determining if abnormally high levels of yeast are present. If significant yeast are reported by microscopy, but not by culture, consider the presentation of patient symptoms.

Vegetable fibers

Excessive amounts of vegetable fibers were found in this stool specimen. The presence of vegetable fibers must be considered in conjunction with other parameters such as muscle fibers and Elastase for a proper assessment of maldigestion. Elevated levels of vegetable fibers may be indicative of inadequate chewing or rapid transit time.

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.

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Microbiology continued...

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.

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 (6 - 7.8). Treatment with antimicrobial agents is unnecessary unless bacteria appear under the dysbiotic category.