



Green Health

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a collaborative thinktank of ecologically minded beings
 405 Alberto Way Suite C and Suite 1
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STOOL SCAN

Signal	Lvl	% Imbalance	Notes
<p>Stool Assessment -> Parasitology Protozoans -> Dientamoeba fragilis</p> <p>Transmission: Unknown; often associated with pinworm infection or fecal contamination. Patients will be asymptomatic or present with diarrhea, nausea, and vomiting; abdominal tenderness is possible.</p> <p>There is no consensus as to best clinical practice; goal is eradication of parasite.</p> <p>For more info see www.dpd.cdc.gov/dpdx/HTML/Dientamoeba.htm</p>	6	100	
<p>Stool Assessment -> Digestion and Absorption -> Fecal Fat total -> Long Chain Fatty Acids (LFCAs)</p> <p>These are types of fatty acids present in significant amounts in our diets. Examples include arachidonic acid (AA), which is abundant in saturated fats, and docosahexaenoic acid (DHA), an Omega-3 polyunsaturated fatty acid found in fish oil. Elevated levels suggest malabsorption of fats due to inadequate digestion, since LCFAs must first be broken down into smaller components before they can be absorbed.</p>	8	100	
<p>Stool Assessment -> Digestion and Absorption -> Chymotrypsin</p> <p>Chymotrypsin is a digestive enzyme belonging to a super family of enzymes called serine proteases. It uses an active serine residue to perform hydrolysis on the C-terminus of the aromatic amino acids of other proteins. Chymotrypsin is a protease enzyme that cleaves on the C-terminal phenylalanine (F), tryptophan (W), and tyrosine (Y) on peptide chains. It shows specificity for aromatic amino acids because of its hydrophobic pocket.</p> <p>Low levels correlate with pancreatic insufficiency, hypochlorhdryia, slow transit time. Assess putrefactive SCFAs.</p> <p>Elevated levels rule out false elevations from diarrhea (assess pancreatic elastase 1 levels) and look at microbial overgrowth, lactose intolerance, food sensitivities.</p>	6	98	
<p>Stool Assessment -> Digestion and Absorption -> Pancreatic Elastase 1</p> <p>Pancreatic Elastase (PE) is a simple, noninvasive fecal marker for assessing exocrine pancreatic function.</p> <p>Pancreatic insufficiency may play a role in:</p>	10	97	



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<ul style="list-style-type: none"> • Post-prandial bloating, pain or nausea • Loose or watery stools • Undigested food in the stool • Hypochlorhydria • Food intolerances • Gastroesophageal reflux symptoms <p>Low levels correlate with mild to moderate pancreatic insufficiency. Very low levels correlate with moderate to severe pancreatic insufficiency.</p>			
<p>Stool Assessment -> Individual Commensal Bacteria - > Firmicutes phylum -> Ruminococcus spp Abundance associated with low bacterial gene richness in the gut. Human studies have reported that Ruminococcus spp tend to be more abundant in IBD; active UC, active CD, and ileal CD. Levels are variable in IBS, depending on IBS subtype, with some researchers reporting increased concentrations and some finding decreased amounts. May be more prevalent in autism.</p>	10	96	
<p>Stool Assessment -> Digestion and Absorption -> Fecal Fat total -> Phospholipids Low levels correspond with insufficient dietary fat intake/phospholipid deficiency, and/or impaired gallbladder function. Elevated levels are associated with malabsorption, reduce bile salt resorption, and/or increased mucosal cell turnover.</p>	8	96	
<p>Stool Assessment -> Individual Commensal Bacteria - > Firmicutes phylum -> Pseudoflavonifractor spp Abundance associated with higher bacterial gene richness in the gut.</p>	7	95	
<p>Stool Assessment -> Parasitology Protozoans -> Blastocystis Hominis Watery or loose stools, diarrhea, abdominal pain, anal itching, weight loss, constipation, fatigue, and excess flatulence have been reported in persons with Blastocystis infection. Many people are asymptomatic. The clinical significance of Blastocystis spp. is controversial, although there is increasing evidence that it may be a pathogen in some individuals with symptoms meeting criteria for Irritable Bowel Syndrome. For additional information, see www.dpd.cdc.gov/dpdx/HTML/Blastocystis.htm.</p>	7	91	
<p>Stool Assessment -> Individual Commensal Bacteria - > Firmicutes phylum -> Coprococcus eutactus</p>	2	88	



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<p>Abundance associated with greater bacterial gene richness in the gut Coprococcus may be less prevalent in autistic children compared to neurotypical children; may be result of intestinal disaccharidase deficiencies common in autism. In IBS, reduced abundance reported (in association with elevated Ruminococcus spp).</p>			
<p>Stool Assessment -> Metabolic Markers -> Bile Acids Bile acids are the final product of cholesterol metabolism in the liver. They cannot be considered solely as a waste product however as they play an important role in fat digestion and absorption. Bile acids become part of bile, the green substance that is secreted by the liver, stored in the gallbladder, and released during digestion. The primary bile acids are chenodeoxycholic acid (CDCA) and cholic acid (CA). These bile acids can be converted into secondary bile acids by anaerobic bacteria, such as Clostridium, Enterococcus and Bacteroides, in the colon. CDCA is converted into lithocholic acid (LCA) and CA is converted into deoxycholic acid (DCA). These secondary bile acids are associated with increased disease risk. An LCA:DCA ratio greater than 1 is associated with increased risk of gallstones, breast cancer, and colorectal cancer. LCA is considered to be most toxic as it inhibits glutathione-S-transferase, an important antioxidant enzyme produced by the body. A diet high in fiber and/or fiber supplementation can help return bile acid results to normal as it absorbs cholesterol and reduces the overall concentrations of secondary bile acids. Probiotic supplements have also been shown to reduce the conversion of primary bile acids to toxic secondary bile acids.</p>	1	85	
<p>Stool Assessment -> Beneficial Bacteria -> Bifidobacterium</p>	10	80	
<p>Stool Assessment -> Parasitology Protozoans -> Entamoeba Entamoeba coli, Entamoeba histolytica and Entamoeba dispar. Transmission: Contaminated food or water, pets, sexual contact. More common in people who live in tropical areas with poor sanitary conditions. It can be a pathogenic amoeba. Several protozoan species in the genus Entamoeba colonize humans, but not all of them are associated with pathology. Entamoeba histolytica is well recognized as a pathogenic amoeba, associated with intestinal and extra-intestinal infections. Only about 10% to 20%</p>	10	80	



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<p>of people who are infected with <i>E. histolytica</i> become sick. A severe form of <i>E. histolytica</i> is associated with stomach pain, bloody stools, and fever (may resemble ulcerative colitis). <i>E. dispar</i> is non-pathogenic. For more info: www.dpd.cdc.gov/dpdx/HTML/IntestinalAmebae.htm</p>			
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Clostridium spp Many of its species are associated with lower bacterial gene richness. Higher Clostridium counts and increased number of Clostridium species reported in autism; vancomycin (which targets Clostridium) improves symptoms in children with late-onset regressive autism.</p>	12	80	
<p>Stool Assessment -> Individual Commensal Bacteria -> Actinobacteria phylum -> Collinsella aerofaciens Lower counts reported in IBS; lower levels may correlate with greater severity of IBS symptoms. Higher concentrations reported in IBD; thought to be result of abnormal host responses to the bacteria. Collinsella spp reported higher in type 2 diabetes.</p>	4	78	
<p>Stool Assessment -> Digestion and Absorption -> Meat and Vegetable Fibers The presence of meat fibers in the stool is an indicator of incomplete digestion, particularly of protein. This may be due to simple reasons including excessive meat consumption, improper chewing of food, or rapid transit time, or it may indicate inadequate stomach acid or pancreatic enzyme production which would need to be addressed with supplementation. Vegetable fibers may be present at abnormally high levels as a result of the same factors influencing meat fiber content.</p>	3	77	
<p>Stool Assessment -> Individual Commensal Bacteria -> Euryarchaeota phylum -> Methanobrevibacter smithii Abundance associated with higher bacterial gene richness in the gut. Lower counts of Methanobrevibacter species reported in human obesity; higher amounts reported in anorexia; in contrast, one study confirmed a positive association with increased BMI and body fat in methanogen-colonized populations. Higher levels linked to IBS-C; reduced levels linked with IBS-D. Methanogens found higher in people with GI inflammation. Breath-testing study, an accepted indirect measure of gut methanogens; although <i>M. smithii</i> is currently considered the dominant methanogenic archaeon in</p>	11	74	



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the gut, other methanogenic bacteria may also be contributors to breath methane.			
<p>Stool Assessment -> Individual Commensal Bacteria -> Actinobacteria phylum -> Bifidobacterium spp</p> <p>Abundance associated with higher bacterial gene richness in the gut.</p> <p>Modulates local and systemic immune responses.</p> <p>Abundance lower in IBD.</p> <p>Abundance lower in IBS; low levels also correlate with symptom severity in IBS. Lower levels seen in type 2 diabetes, pediatric allergy, and autism.</p> <p>Increased levels in obese subjects compared to lean/overweight; infants with lower Bifidobacterium may have increased risk for weight gain in childhood. Abundance decreases after weight loss and gastric-bypass surgery.</p>	8	74	
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Roseburia spp</p> <p>Abundance associated with higher bacterial gene richness in the gut.</p> <p>Less abundant in individuals with IBS, particularly constipation-predominant IBS. Counts lower in type 2 diabetics; trending inversely with plasma glucose. Lower in IBD and early-onset rheumatoid arthritis (as part of decreased E. rectale-C. coccoides group).</p>	10	71	
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Faecalibacterium prausnitzi</p> <p>In a healthy gut, represents more than 5% of the total bacterial population and is comprised of only one species.</p> <p>Abundance associated with higher bacterial gene richness in the gut</p> <p>Controls inflammation through inflammatory-cytokine inhibition; lower counts reported in IBD, Crohn's disease, and ulcerative colitis (UC), although increases have been noted.</p> <p>Appears to protect against glucose intolerance and type 2 diabetes; possibly due to anti-inflammatory effects and/or positive effects on insulin resistance status.</p>	9	70	
<p>Stool Assessment -> Parasitology Protozoans -> Giardia lamblia</p> <p>Transmission: Contaminated water, food, or fecal-oral transmission .</p> <p>G. lamblia is the leading cause of intestinal parasitic infection in the US.</p> <p>Patients can be asymptomatic. If symptomatic, will present with acute to chronic diarrhea with bloating, intestinal malabsorption, and steatorrhea. Giardiasis has been associated with agammaglobulinemia, chronic pancreatitis,</p>	1	69	



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<p>achlorhydria, and cystic fibrosis. For more info: www.dpd.cdc.gov/dpdx/HTML/Giardiasis.htm</p>			
<p>Stool Assessment -> Individual Commensal Bacteria -> Bacteroides phylum -> Bacteroides-Prevotella Group Abundance associated with lower bacterial gene richness in the gut Increased levels may be associated with IBD Reduced patterns of Bacteroides reported in IBS and ulcerative colitis Ratio of Bacteroides-Prevotella group to other gut bacteria correlated positively and significantly with plasma glucose</p>	4	64	
<p>Stool Assessment -> Digestion and Absorption -> Protein breakdown products total (Valerate, Isobutyrate, Isovalerate) Products of Protein Breakdown are short chain fatty acids (SCFAs) that come from the bacterial breakdown of protein or their digestion products (amino acids), in the distal colon. They include isovalerate, valerate and isobutyrate. Normal protein digestion is generally completed in the stomach and small intestine, thus only small amounts of protein-derived products of protein breakdown are expected to be in the stool. The SCFAs described more robustly in clinical literature, specifically acetate, butyrate and propionate, are produced by bacterial action on carbohydrates. Though the relationship between gut health and protein fermentation has not been thoroughly investigated, patients with elevated products of protein breakdown should be evaluated for: Common causes of insufficient protein digestion Excessive protein presenting to the colon Excessive protein intake</p>	7	62	
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Butyrivibrio crossotus Abundance associated with higher bacterial richness in the gut. Abundance may help protect against weight gain.</p>	5	62	
<p>Stool Assessment -> Digestion and Absorption -> Steatocrit This is a marker of the total amount of fat found in the stool. It is considered the most accurate method for obtaining this information from a single stool sample. A high steatocrit result is indicative of fat malabsorption and would suggest inadequate secretion of stomach acid, bile, and/or</p>	4	58	



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lipase. Symptoms associated with poor fat digestion and absorption include bloating, flatulence, feelings of fullness, pale and foul-smelling stools, and an 'oil slick' in the toilet water after bowel movements. Treatment may include betaine HCL, digestive enzyme, and bile salt supplements along with a low fat diet and recommendations on reducing transit time e.g. stress reduction and increased fibre in the diet.			
Stool Assessment -> Individual Commensal Bacteria -> Proteobacteria phylum -> Desulfovibrio piger Reported higher in IBD. Sulfate-reducing bacteria higher in constipation-predominant IBS compared with healthy subjects Desulfovibrio spp also found higher in autism. May be lower in obesity.	8	52	
Stool Assessment -> Individual Commensal Bacteria -> Bacteroides phylum -> B. vulgatus Bacteroides spp associated with lower bacterial gene richness in the gut Lower levels of B. vulgatus have been seen in IBS patients in comparison to healthy controls Low relative proportions of B. vulgatus along with high concentrations of Lactobacillus spp observed in the microbiota of obese children when compared to lean B. vulgatus found to be present in significantly higher numbers in stools of severely autistic children when compared to controls	5	52	
Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Anaerotruncus colihominis Abundance associated with higher bacterial gene richness in the gut. Inversely associated with BMI and triglycerides.	8	50	
Stool Assessment -> Digestion and Absorption -> Fecal Fat total -> Cholesterol Low levels correspond with low fat diet. Elevated levels associated with malabsorption, bacterial overgrowth of the small intestine, and/or increased mucosal cell turnover.	3	47	
Stool Assessment -> Inflammation and Immunology -> Fecal secretory IgA Low levels correlate with chronic stress, low immunity, dysbiosis, and/or immunosuppressants. Elevated levels suggest food sensitivities and/or immune response to elimination of pathogenic organisms in the GI tract.	11	44	
Stool Assessment -> Individual Commensal Bacteria -> Bacteroides phylum -> Odoribacter spp	10	41	



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Lower concentrations in humans have been reported in ileal Crohn's and pancolononic ulcerative colitis.			
Stool Assessment -> Individual Commensal Bacteria -> Bacteroides phylum -> Barnesiella spp Higher fecal Barnesiella (two logs difference) associated with protective effect against Vancomycin Resistant Enterococcus in stem cell transplant patients	9	41	
Stool Assessment -> Individual Commensal Bacteria -> Actinobacteria phylum -> Bifidobacterium longum Bifidobacterium longum is a Gram-positive, catalase-negative, rod-shaped bacterium present in the human gastrointestinal tract and one of the 32 species that belong to the genus Bifidobacterium. It is a microaerotolerant anaerobe and considered to be one of the earliest colonizers of the gastrointestinal tract of infants. Abundance associated with higher bacterial gene richness in the gut Abundance decreases with weight loss. Found increased in obese subjects compared to lean/overweight.	10	38	
Stool Assessment -> Parasitology Protozoans -> Cryptosporidium spp Transmission: Fecal contamination of food or water, including swimming pools and municipal water supplies. Patients will be symptomatic or present with diarrhea varying from mild to severe, abdominal cramping, weight loss, anorexia, nausea, vomiting, flatulence, malaise, and mild fever. Most people who have healthy immune systems will recover without treatment. Diarrhea can be managed by drinking plenty of fluids to prevent dehydration. Immunosuppression increases infection severity. See www.dpd.cdc.gov/dpdx/HTML/Cryptosporidiosis.htm for more info.	10	36	
Stool Assessment -> Metabolic Markers -> Beta-Glucuronidase An enzyme produced by certain members of the gut flora including E. coli, Peptostreptococcus, Bacteroides, and Clostridia. Some of these are considered harmless while others are said to be pathogens. A high b-glucuronidase level indicates that toxins, hormones, carcinogens, and drugs which are normally bound to a compound called glucuronide in the liver and then excreted from the body in bowel movements can be freed by b-glucuronidase and reabsorbed into the body where they can contribute to imbalance/toxic overload. Elevated b-glucuronidase levels can be reduced by using supplements including probiotics containing	6	33	



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<p>Lactobacilli and Bifodobacteria and calcium-D-glucarate, which inhibits b-glucuronidase production. Eating a high fiber diet and including apples, citrus fruits, and cruciferous vegetables (e.g. broccoli, cauliflower), which contain significant amounts of calcium-D-glucarate, can also be helpful.</p>			
<p>Stool Assessment -> Metabolic Markers -> n-Butyrate This short-chain fatty acid (SCFA) is produced as a result of the fermentation of dietary fiber, particularly gums and pectins, by certain bacteria that inhabit the intestines (particularly probiotic bacteria such as Lactobacilli and Bifodobacteria species). A low n-butyrate level may indicate a deficiency of beneficial bacteria. Increasing dietary fiber, particularly in gums and pectins, will help with low levels. A high level suggests a general bacterial overgrowth caused by factors such as low stomach acid or high carbohydrate/fiber diets. In the former case probiotic supplements may be required while in the latter antibiotic therapy, whether drug-based or natural, may be needed. n-Butyrate is the preferred fuel for the cells of the colon, helping to keep them healthy. It helps to regulate the differentiation and proliferation of these cells, and has been associated with a reduced risk of colon cancer. This SCFA is also important for controlling general inflammation of the GI tract since it reduces the production of pro-inflammatory immune chemicals such as tumor necrosis factor-alpha (TNF-a). Recent research has shown that through this mechanism n-butyrate may be helpful in digestive disease such as Crohn's disease and Celiac disease.</p>	3	33	
<p>Stool Assessment -> Inflammation and Immunology -> Calprotectin Fecal calprotectin is a biochemical measurement of the protein calprotectin in the stool. Elevated faecal calprotectin indicates the migration of neutrophils to the intestinal mucosa, which occurs during intestinal inflammation, including inflammation caused by inflammatory bowel disease. Fecal Calprotectin is a marker of gastrointestinal inflammation that is produced by white blood cells (neutrophils) in the gastrointestinal tract, and is used to quantify the degree of inflammation present. Elevated levels suggest low-grade inflammation of the GI tract is present. This could be due to post-infectious</p>	7	32	



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<p>Irritable Bowel Syndrome (IBS), infection, food allergies, polyps, neoplasia, NSAIDS, or IBD in remission. Very elevated levels may correlate with Inflammatory Bowel Disease (IBD), infection, food allergies, NSAID use, polyps, adenomas, colorectal cancer, diverticulitis.</p>			
<p>Stool Assessment -> Individual Commensal Bacteria -> Proteobacteria phylum -> Oxalobacter formigenes Normally present in 46-77% of healthy adults. Unique ability to metabolize oxalates in the gut. Dietary oxalate consumption generally increases O. formigenes abundance in controls, but not stone formers. Colonization with this bacteria may reduce risk of oxalate stone formation, with healthy levels associated with 70% reduced risk of being recurrent calcium-oxalate stone-former.</p>	10	29	
<p>Stool Assessment -> Digestion and Absorption -> Fecal Fat total -> Triglycerides Low levels correspond to low fat intake. Elevated levels suggest incomplete fat hydrolysis due to bile insufficiency, reduced pancreatic function, high fat diet, and/or hypochlorhydria. Most of the fats in our diet are in the form of triglycerides. These are broken down by an efficient digestive system into smaller fragments that can then be absorbed from the small intestine. If higher than normal levels of triglycerides are found in a stool sample it can be a sign that the digestion and/or absorption of fats is insufficient. Since both bile and the enzyme lipase, secreted by the pancreas, are required for fat digestion and absorption high faecal triglycerides may indicate inadequate secretion of these substances. This can result from problems with the liver (where bile is produced), gall bladder (which stores and secretes bile into the small intestine), or the pancreas. High fecal triglycerides can also result from low stomach acid, a high fat diet, or a fast transit time i.e. diarrhea/frequent bowel movements. Symptoms associated with poor fat digestion and absorption include bloating, flatulence, feelings of fullness, pale and foul-smelling stools, and an 'oil slick' in the toilet water after bowel movements. Treatment may include betaine HCL, digestive enzyme, and bile salt supplements along with a low fat diet and recommendations on reducing transit time e.g. stress reduction and increased fibre in the diet.</p>	10	27	



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<p>Stool Assessment -> Inflammation and Immunology -> Eosinophil Protein X (EPX) Eosinophils are involved in a broad range of diseases, including those of inflammatory and neoplastic origin. There is increasing evidence that eosinophils are functionally involved in the pathophysiology of various inflammatory disorders of the gut. Eosinophils contain a number of highly cationic proteins such as eosinophil cationic protein, major basic protein, eosinophil peroxidase, and eosinophil protein X (EPX). These cationic proteins have potent cytotoxic properties and are released from the eosinophils after being activated. Normal levels correlate with no active GI tract inflammation, successful elimination diets. Elevated levels suggest inflammation and/or tissue damage in the GI tract. This could be due to food allergy, protein sensitive enteropathy, helminthic infection, Inflammatory Bowel Disease (IBD), allergic colitis, or GERD.</p>	3	26	
<p>Stool Assessment -> Beneficial Bacteria -> E. Coli</p>	4	26	
<p>Stool Assessment -> Beneficial Bacteria -> Lactobacilli</p>	12	25	
<p>Stool Assessment -> Digestion and Absorption -> Putrefactive Short Chain Fatty Acids (SCFAs) There are three putrefactive SCFAs, valerate, iso-valerate, and iso-butyrate. These SCFAs are the result of the anaerobic (without air/oxygen) fermentation of polypeptides and amino acids (the products of protein digestion) by bacteria in the intestines. Elevated levels can be an indicator of low stomach acid (hypochlorhydria) and/or low secretion of protein-digesting enzymes by the pancreas, poor absorption of protein due to inflammation/damage to the gut lining, rapid transit time, and/or bacterial overgrowth in the small intestine (small intestinal bacterial overgrowth (SIBO)). If high putrefactive SCFAs are found treatment needs to address the underlying cause and may include betaine HCL and or digestive enzyme supplements, nutrients that aid healing of the gut lining, and antibiotic therapy (using drugs or natural alternatives) to eradicate bacterial overgrowth. Low levels correspond with low protein diet.</p>	7	21	
<p>Stool Assessment -> Individual Commensal Bacteria -> Proteobacteria phylum -> Escherichia coli Increased counts reported in inflammatory bowel disease. Increased levels found in diarrhea-predominant IBS. Higher in overweight pregnant women compared to normal weight pregnant women and in women with excessive weight gain during pregnancy.</p>	9	14	



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<p>Reported to increase with weight loss after gastric bypass, correlating negatively with leptin levels.</p>			
<p>Stool Assessment -> Individual Commensal Bacteria -> Bacteroides phylum -> Prevotella spp Abundance associated with lower bacterial gene richness in the gut Has been found higher in IBD, in smokers with (and without) IBD (in association with higher Bacteroides and lower F. prausnitzii), and in type-2 diabetes. Lower levels found in autism. Family Prevotellaceae exhibited a >6-fold increase in obese subjects when compared to the healthy group, with most of the Prevotellaceae sequences belonging to a single-genus, Prevotella.</p>	7	14	
<p>Stool Assessment -> Metabolic Markers -> pH Normally the pH of the stool is slightly acidic due to bacterial fermentation and putrefaction of the intestinal contents. Beneficial bacteria such as Lactobacilli and Bifidobacteria produce large amounts of SCFAs such as n-butyrate which contribute to this slightly acidic intestinal environment and correspondingly slightly acidic stool oh pH 6-7. A stool pH below 6.0 may be the result of a rapid transit time (e.g. diarrhea, loose stools). If this is the case further investigations may be required to determine the cause which could be anything from food allergy or intolerance, bacterial, viral, or parasitic infection, or irritable bowel syndrome (assuming serious bowel disorders have been ruled out previously). A low pH may also be the result of small bowel bacterial overgrowth (SIBO) in which numbers of normal bacteria in the small intestine are present in much higher numbers than normal. This can result from a high carbohydrate diet, low stomach acid (see digestion and absorption markers), or reduced gut immunity, and is common in chronic fatigue syndrome (ME/CFS), fibromyalgia, and irritable bowel syndrome (IBS). For a fast transit time the underlying cause needs to be addressed and treatment therefore varies. SIBO needs to be treated with antibiotic drugs or supplements, or both, and a low carbohydrate diet adopted. The most common causes of a high (alkaline) stool pH are deficiency of beneficial bacteria and therefore SCFAs and a diet that is lacking in fiber. This situation needs to be corrected with probiotic supplements and a high fiber diet as pathogenic microorganisms including bacteria and yeast (e.g. Candida) tend to thrive in an alkaline intestinal environment. Some types of fiber including wheat bran, oat bran, and prebiotics such</p>	1	14	



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as fructooligosaccharides (FOS) help to lower intestinal pH.			
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Lactobacillus spp</p> <p>Abundance associated with higher bacterial gene richness in the gut.</p> <p>Studies have reported altered levels in IBS, with some finding higher concentrations, and others finding lower concentrations.</p> <p>Lower levels reported to correlate with symptom severity in IBS</p> <p>Increased levels seen in obese patients compared to lean controls.</p>	9	3	
<p>Stool Assessment -> Digestion and Absorption -> Fecal Fat total -> Short Chain Fatty Acids (SCFAs)</p> <p>SCFAs are produced from the fermentation of fiber and protein by certain components of the gut microflora. The SCFAs produced from the fermentation of fiber by probiotic bacteria such as Bifidobacteria and Lactobacilli have a range of beneficial effects from serving as a fuel for cells lining the intestine (and the rest of the body) to creating an acidic intestinal environment unfavorable to potential pathogens.</p> <p>Low levels may suggest that the diet is low in fibre and/or protein or there is an imbalance in the gut microflora. High levels might be due to a very high fibre and/or protein diet, small intestinal bacterial overgrowth, or malabsorption.</p>	1	0	
<p>Stool Assessment -> Individual Commensal Bacteria -> Firmicutes phylum -> Veillonella spp</p> <p>Abundance associated with higher bacterial gene richness in the gut</p> <p>Imbalances noted in IBS, although findings are mixed: some studies reported higher concentrations in IBS, in IBS-C, IBS-D; others have reported lower counts, or lower counts weakly correlating with greater symptom severity.</p> <p>Found less abundant in autistic children compared to neurotypical children.</p>	9	0	
<p>Stool Assessment -> Individual Commensal Bacteria -> Fusobacteria phylum -> Fusobacterium spp</p> <p>Although part of normal human gut flora, species of Fusobacterium strongly associated with numerous diseases, including colitis, appendicitis, dental plaque/ periodontal disease, hepatic cirrhosis, and inflammatory bowel disease.</p> <p>Fusobacterium correlates positively with TNF-alpha, suggesting involvement of mucosal inflammation.</p> <p>Obese, older subjects with metabolic syndrome demonstrated increased Fusobacterium as compared to younger subjects.</p>	9	0	
<p>Stool Assessment -> Individual Commensal Bacteria -> Verrucomicrobia phylum -> Akkermansia muciniphila</p>	4	0	



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<p>Dominant mucus-layer species; may represent 3-5% of microbial community in healthy adults. Abundance associated with higher bacterial gene richness in the gut. Plays role glucose homeostasis. Abundance inversely correlated with IBD (both Crohn's and UC) and appendicitis. Abundance inversely correlates with body weight in pregnant women and children. Some have reported decreased <i>A. muciniphila</i> in pre-diabetes and decreased <i>Verrococcocellaceae</i> abundance in T2D and pre-diabetes. Lower in autism.</p>			
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