



PHYSICIAN'S GUIDELINES

Intestinal Dysbiosis: Clinical Approach and Recommendations

INTRODUCTION

The gastrointestinal tract harbors a tremendous diversity of microbial life. These microbes, known collectively as the "microbiome," are directly involved in digestion and immune function, and appear to also play a role in multiple additional human biologic processes [1]. Intestinal dysbiosis refers to an abnormality of the gut microbiota, either due to low microbial diversity, sub-optimal levels of commensal microbes, or an abundance of pathogenic microbes [2].

Alterations to the microbiome have been linked to a variety of disorders, including gastrointestinal disease [3], obesity, diabetes, and even kidney stones.

CLINICAL HISTORY

Patients with intestinal dysbiosis may present with a variety of signs or symptoms, or may have no active clinical indications present in their history or examination.

PRESENTING SYMPTOMS MAY INCLUDE:

- Diarrhea
- Constipation
- Flatulence
- Bloating

PRESENTING SIGNS MAY INCLUDE:

- Obesity
- Abdominal tenderness

RELATED DIAGNOSES MAY INCLUDE:

- Irritable bowel syndrome (IBS)
- Inflammatory bowel disease (IBD): Crohn's disease, ulcerative colitis
- Type II Diabetes
- Prediabetes
- Kidney stones

TESTING

The SmartGut™ clinical test extracts microbial DNA from a stool swab sample and identifies microorganisms associated and inversely associated with health conditions and symptoms. The test yields information about overall microbial diversity and the presence of individual microorganisms. The simple at-home sampling process increases patient usage compliance and ease of regular monitoring.

Reference ranges are based on 897 samples from self-reported healthy individuals from the uBiome database, the largest microbiome database. For more information about the healthy cohort, go [here](#) gutpaper for the publication explaining uBiome's methods underlying this test.

INDIVIDUALS SUITABLE FOR TESTING

- Individuals with chronic gut conditions (e.g., IBD, IBS)
- Individuals experiencing chronic gut symptoms (e.g., gas, bloating, diarrhea)
- Individuals with obesity, diabetes, prediabetes, or kidney stones
- Individuals experiencing no symptoms who seek to monitor their gut microbiome in collaboration with their physician (screening test)
- Individuals with obesity, diabetes, prediabetes, or kidney stones

TEST RESULTS

SmartGut results enable a better understanding of:

- If there are specific pathogens present that might be causing illness
- The balance of commensal and beneficial bacteria that may contribute to symptoms
- Risk factors relating to the microbiome (e.g., diabetes, obesity)

REPORT INFORMATION

MICROBIAL DIVERSITY SCORE

The Microbial Diversity Score (MDS) is a measure of the microorganism richness, evenness, and distinctness in the microbiome. The MDS is classified as "high," "normal," or "low." A high MDS may be an indicator of good health [4] while a low MDS is associated with intestinal dysbiosis [2]. A low MDS has been associated with a variety of health conditions, including diarrhea, inflammatory bowel disease, obesity, and prediabetes [5-7]. Presence of *Alistipes*, *Butyrivibrio*, and *Methanobrevibacter smithii* species are particularly associated with a high MDS [8].

PATHOGENIC MICROORGANISMS

The SmartGut clinical test currently identifies certain pathogenic microorganisms. Presence of one or more of these types of organisms does not necessarily indicate active disease, though they are generally associated with documented clinical patterns.

POTENTIALLY HARMFUL MICROORGANISMS

The SmartGut clinical test provides information about individual microorganisms that appear to be associated with certain health conditions. Presence of these microorganisms may be indicative of poor health. See chart below for specific correlations, and see related treatment guides for further clinical guidance for specific conditions.

POTENTIALLY BENEFICIAL MICROORGANISMS

The SmartGut clinical test provides information about individual microorganisms that appear to be inversely associated with certain health conditions. Lowered levels of these microorganisms may be indicative of poor health. See chart below for specific correlations, and see related treatment guides for further clinical guidance for specific conditions.

TREATMENT APPROACH

The gut microbiome can be altered by making changes to diet and exercise. Ingestion of probiotics and prebiotics may also play a role in correcting dysbiosis. Regular monitoring of gut microbes can assist with patient adherence, provide information about the effectiveness of interventions, and help monitor overall health and disease progression.

IMPROVING MICROBIAL DIVERSITY

Low microbial diversity is generally considered to be associated with poor health. Overall microbial diversity may be encouraged through the addition of a high-fiber diet [9], by increasing physical exercise [10], by increased consumption of fruits and vegetables, and by eating animal-based products (such as meats, eggs, and cheeses) [11].

REDUCING PATHOGENIC AND POTENTIALLY HARMFUL MICROORGANISMS

Presence of certain microorganisms appear to be associated with increased morbidity. Populations of these microorganisms may be decreased through the use of dietary supplements (lactulose, oligosaccharides, and probiotics) [12], increased consumption of polyphenol-rich foods, such as tea and some fruits [13], and by reducing intake of resistant starches and animal products [11].

ENCOURAGING PROLIFERATION OF POTENTIALLY BENEFICIAL ORGANISMS

Presence of certain microorganisms appear to play a beneficial role in health and physiology. Populations of these microorganisms may be increased through the use of dietary supplements (oligosaccharides and probiotics) [14], increased consumption of fruits and cruciferous vegetables [15], and eating a varied animal and plant-based diet [11]. A high-fiber, low-carbohydrate diet may also encourage proliferation of certain beneficial organisms [9], as well as the addition of polyphenol-rich foods [13], seeds such as almonds and pistachio [16], and dark cacao [17].

CLINICAL ASSOCIATIONS

For any health condition with one or more alerts  evaluate patients' symptoms and results accordingly. The table below summarizes the relevant microorganisms that are associated or inversely associated with different clinical conditions.

See the Physician Treatment Guides for further guidance on the following clinical conditions:

- Infections
- Gut Conditions
- Lifestyle & Diet
- Kidney stones

Clinical approach and recommendations

PHYSICIAN'S GUIDELINES

Microorganism	Clinical Conditions													
	Gastrointestinal infections	Diarrhea	Irritable Bowel Syndrome	Inflammatory Bowel Syndrome	Crohn's Disease	Ulcerative Colitis	Constipation	Abdominal Tenderness	Bloating	Flatulenc	Obesity	Type II Diabetes	Prediabetes	Kidney Stones
<i>Akkermansia muciniphila</i>				◆	◆						◆	●		
<i>Alistipes</i>			◆								◆			
<i>Anaerotruncus colihominis</i>	●							●			◆			
<i>Bacteroides fragilis</i>									●					
<i>Barnesiella</i>											◆			
<i>Bifidobacterium</i>			◆	◆		◆								
<i>Butyrivibrio crossotus</i>											◆			
<i>Campylobacter</i>	●	●	●											
<i>Clostridium</i>		●												
<i>Clostridium difficile</i>	●	●												
<i>Collinsella aerofaciens</i>			◆											
<i>Desulfovibrio piger</i>				●										
<i>Dialister invisus</i>					◆									
<i>Escherichia-Shigella</i>	●	●	●	●										
<i>Fusobacterium</i>				●										
<i>Lactobacillus</i>											●	◆		
<i>Methanobrevibacter smithii</i>							●	●			◆			
<i>Odoribacter</i>				◆	◆									
<i>Oxalobacter formigenes</i>														◆
<i>Prevotella</i>					◆									
<i>Roseburia</i>			◆	◆	◆							◆		
<i>Ruminococcus</i>				●	●									
<i>Ruminococcus albus</i>					◆									
<i>Salmonella enterica</i>	●	●	●											
<i>Veilonella</i>			●											
<i>Vibrio cholerae</i>	●	●												
Microbial Diversity				◆	◆						◆		◆	

METHOD

- Patient friendly, at-home sampling process following NIH Human Microbiome Project specifications [18].
 - Takes under 2 minutes (just a swab from toilet paper), simplifying patient sampling process.
- Microorganisms in samples are lysed and the DNA is stabilized in a buffer solution before patient mails to uBiome laboratory.
- Analysis of SmartGut samples is performed using high-throughput bioinformatics, which incorporate phylogenetic algorithms and custom databases specifically developed for microbiome data.
- On average, the sensitivity, specificity, precision, and negative prediction value for the microorganisms on our target list are 99.0%, 100%, 98.9%, and 100%, for the species, and 97.4%, 100%, 98.5%, and 100% for the genera, respectively.

SUMMARY

- The gastrointestinal tract is home to a diverse microbial population, which appears to play a vital role in human health, and in the development and progression of certain symptoms and diseases.
- Disruptions to the intestinal microbiota can lead to intestinal dysbiosis, characterized by diarrhea, constipation, flatulence, obesity, and abdominal tenderness. Dysbiosis is also associated with certain disease conditions: irritable bowel disease, inflammatory bowel disease, type 2 diabetes, prediabetes, obesity, and kidney stones [2,5-7,19].
- The presence or absence of certain microorganisms, as well as overall microbial diversity, appear to contribute to intestinal dysbiosis. Microbial diversity and certain microorganisms appear to be associated with good health, decreased morbidity, and longevity [20].
- Microbial diversity may be encouraged by increasing fiber intake, by increasing physical exercise, and by consumption of fruits and vegetables [11,21].
- Proliferation of pathogenic microorganisms may be discouraged by ingesting prebiotics and probiotics, by consuming polyphenol-rich foods, and by increasing intake of resistant starches and animal products [22].
- Proliferation of beneficial microorganisms may be encouraged by ingesting prebiotics and probiotics, by eating a high-fiber low-carbohydrate diet rich in diverse plant and animal products, and by increasing consumption of polyphenol-rich foods, seeds, and dark cacao [13,16-17].
- Monitoring the intestinal microbiome at regular intervals can assist with patient adherence, provide information about the effectiveness of interventions, and help monitor overall health and disease progression.

References

1. J.C. Clemente, L.K. Ursell, L.W. Parfrey, R. Knight, *Cell* 148 (2012) 1258–1270.
2. A. Mosca, M. Leclerc, J.P. Hugot, *Front Microbiol* 7 (2016) 455.
3. Q. Aziz, J. Doré, A. Emmanuel, F. Guarner, E.M.M. Quigley, *Neurogastroenterol. Motil.* 25 (2013) 4–15.
4. J.L. Sonnenburg, F. Bäckhed, *Nature* 535 (2016) 56–64.
5. J.Y. Chang, D.A. Antonopoulos, A. Kalra, A. Tonelli, W.T. Khalife, T.M. Schmidt, V.B. Young, *J. Infect. Dis.* 197 (2008) 435–438.
6. G. Musso, R. Gambino, M. Cassader, *Diabetes Care* 33 (2010) 2277–2284.
7. M. Pozuelo, S. Panda, A. Santiago, S. Mendez, A. Accarino, J. Santos, F. Guarner, F. Azpiroz, C. Manichanh, *Sci Rep* 5 (2015) 12693.
8. E. Le Chatelier, T. Nielsen, J. Qin, E. Prifti, F. Hildebrand, G. Falony, M. Almeida, M. Arumugam, J.-M. Batto, S. Kennedy, P. Leonard, J. Li, K. Burgdorf, N. Grarup, T. Jørgensen, I. Brandslund, H.B. Nielsen, A.S. Juncker, M. Bertalan, F. Levenez, N. Pons, S. Rasmussen, S. Sunagawa, J. Tap, S. Tims, E.G. Zoetendal, S. Brunak, K. Clément, J. Doré, M. Kleerebezem, K. Kristiansen, P. Renault, T. Sicheritz-Ponten, W.M. de Vos, J.-D. Zucker, J. Raes, T. Hansen, MetaHIT consortium, P. Bork, J. Wang, S.D. Ehrlich, O. Pedersen, *Nature* 500 (2013) 541–546.
9. C. De Filippo, D. Cavalieri, M. Di Paola, M. Ramazzotti, J.B. Poullet, S. Massart, S. Collini, G. Pieraccini, P. Lionetti, *Proc. Natl. Acad. Sci. U.S.A.* 107 (2010) 14691–14696.
10. N. Mach, D. Fuster-Botella, *J Sport Health Sci* 6 (2017) 179–197.
11. M.L. Heiman, F.L. Greenway, *Mol Metab* 5 (2016) 317–320.
12. K.P. Scott, S.W. Gratz, P.O. Sheridan, H.J. Flint, S.H. Duncan, *Pharmacol. Res.* 69 (2013) 52–60.
13. F. Cardona, C. Andrés-Lacueva, S. Tulipani, F.J. Tinahones, M.I. Queipo-Ortuño, *J. Nutr. Biochem.* 24 (2013) 1415–1422.
14. H.S. Gill, F. Guarner, *Postgrad Med J* 80 (2004) 516–526.
15. F. Li, M.A.J. Hullar, Y. Schwarz, J.W. Lampe, *J. Nutr.* 139 (2009) 1685–1691.
16. M. Ukhanova, X. Wang, D.J. Baer, J.A. Novotny, M. Fredborg, V. Mai, *Br. J. Nutr.* 111 (2014) 2146–2152.
17. N. Hayek, *Front Pharmacol* 4 (2013) 11.
18. Human Microbiome Project Consortium, *Nature* 486 (2012) 207–214.
19. J.M. Stern, S. Moazami, Y. Qiu, I. Kurland, Z. Chen, I. Agalliu, R. Burk, K.P. Davies, *Urolithiasis* 44 (2016) 399–407.
20. E. Biagi, C. Franceschi, S. Rampelli, M. Severgnini, R. Ostan, S. Turrioni, C. Consolandi, S. Quercia, M. Scurti, D. Monti, M. Capri, P. Brigidi, M. Candela, *Curr. Biol.* 26 (2016) 1480–1485.
21. S.F. Clarke, E.F. Murphy, O. O'Sullivan, A.J. Lucey, M. Humphreys, A. Hogan, P. Hayes, M. O'Reilly, I.B. Jeffery, R. Wood-Martin, D.M. Kerins, E. Quigley, R.P. Ross, P.W. O'Toole, M.G. Molloy, E. Falvey, F. Shanahan, P.D. Cotter, *Gut* 63 (2014) 1913–1920.
22. M.S. Desai, A.M. Seekatz, N.M. Koropatkin, N. Kamada, C.A. Hickey, M. Wolter, N.A. Pudlo, S. Kitamoto, N. Terrapon, A. Muller, V.B. Young, B. Henrissat, P. Wilmes, T.S. Stappenbeck, G. Núñez, E.C. Martens, *Cell* 167 (2016) 1339–1353.e21.