



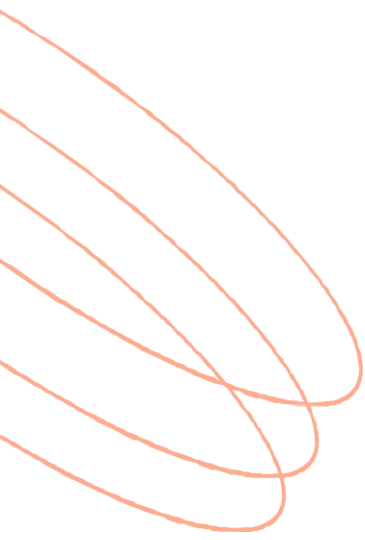
Understanding bacterial gut dysbiosis using a comprehensive microbiome test

Masterclass for clinicians

By Chidozie Ojobor, Ph.D.

Co-founder and Chief Scientific Officer, Vitract

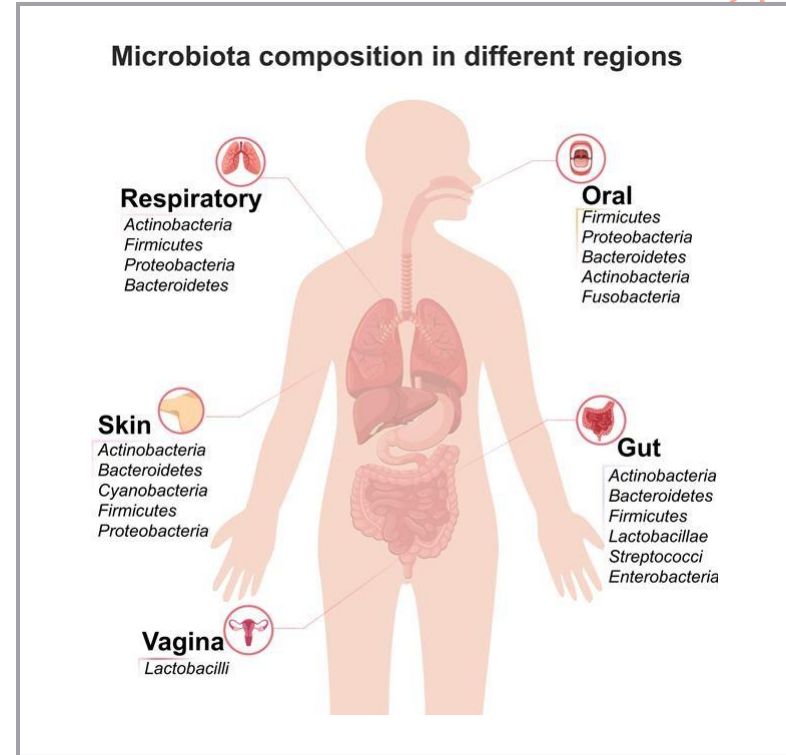


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What you will learn?

- **Benefits of the gut microbiome to health**
- **The Spatial biogeography of the gut microbiota**
- **The concept of gut dysbiosis**
- **Signatures of healthy vs unhealthy gut microbiome**
- **How disease states and colonic oxygen concentration drives dysbiosis**
- **Insights into the role of commensals and pathobionts in health and disease**

The human microbiome is the totality of all microbes, including bacteria, fungi, viruses, protozoa, parasites and their gene functions residing in/on the human body.



The Human Gut Microbiome



The human GI tract contains an abundant and diverse microbial community that gathers more than 100 trillion microorganisms (Thursby and Juge, 2017; Rinninnella *et al*, 2019).



The gut microbiome encodes over 3 million genes, producing thousands of metabolites. The human genome, on the other hand, consists of approximately 23,000 genes (Valdes *et al*, 2018).



The human gut microbiome weighs approximately 2-5 pounds (equivalent to the size of a human brain).

Importance of the Gut Microbiome



Regulates digestion and nutrient metabolism



Maintenance of structural integrity of mucosal barrier



Protection against pathogens.



Immune system regulation



Xenobiotic and drug metabolism



Bile acid metabolism

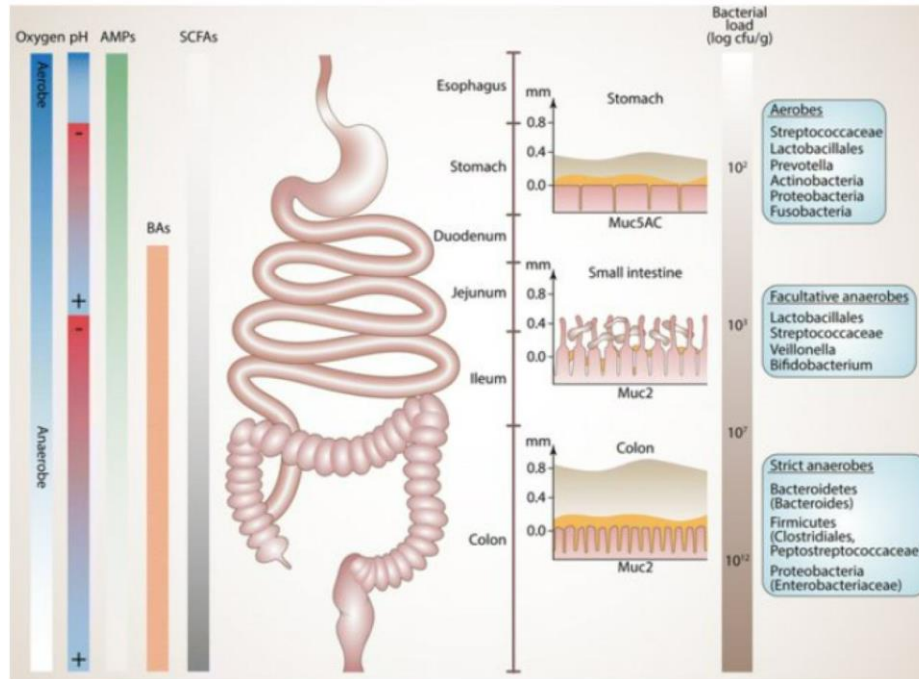


Production of beneficial metabolites such as SCFAs, vitamins, and longevity factors



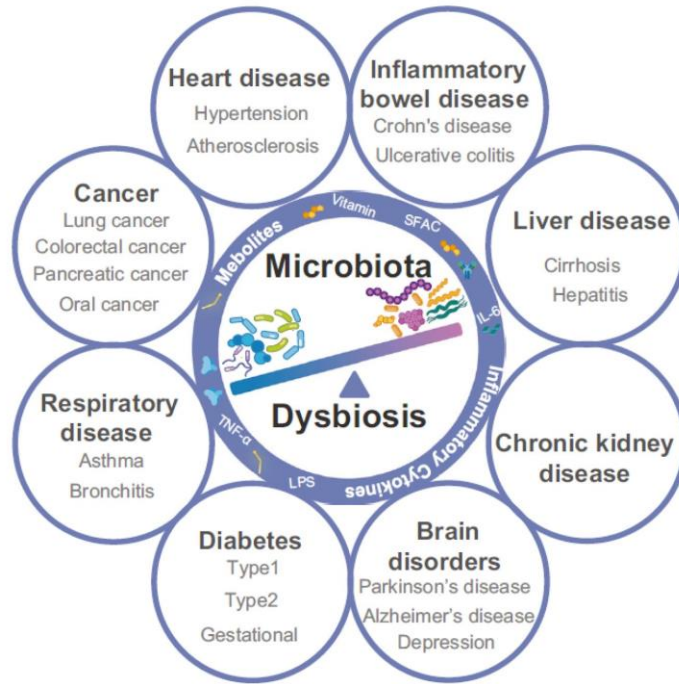
Modulates the gut-brain axis.

The Spatial biogeography of the gut microbiota



Gorkiewicz and Moschen, 2017

Role of the microbiome in health and disease

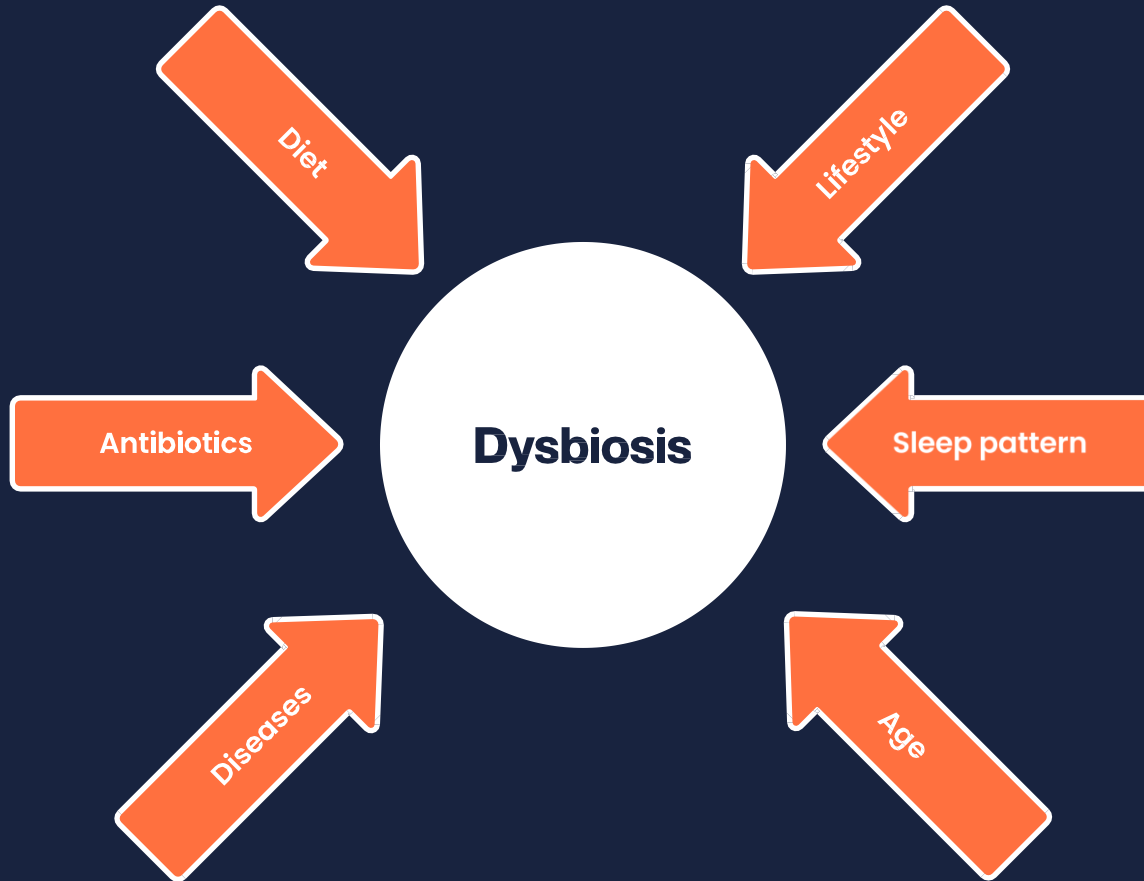


Rinninnella *et al*, 2019

What is Gut Dysbiosis?

- ◆ Dysbiosis is defined by an **imbalance in bacterial composition, unfavorable changes in the bacterial metabolic activities, or changes in bacterial localization** within the gut.
- ◆ Dysbiosis is characterized by a **loss in beneficial bacteria, overgrowth of [potentially] harmful organisms, and a loss in gut diversity (richness and evenness of the microbiota).**
- ◆ The balance in the composition and function of the gut microbiome to favor maintenance and promotion of health is referred to as ***eubiosis***.

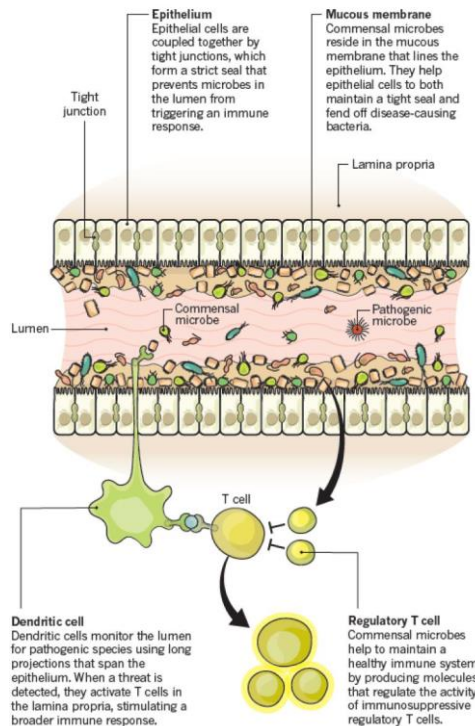
Factors influencing gut dysbiosis



Disease states can drive gut dysbiosis

PICTURE OF HEALTH

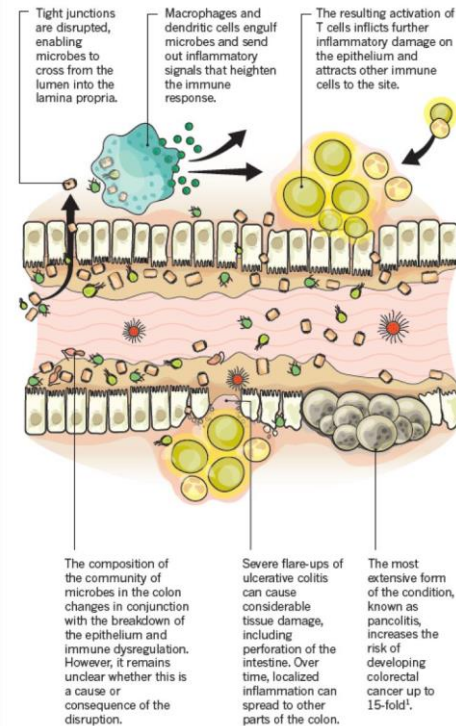
In the healthy colon, the epithelium, immune cells and commensal microbes collaboratively maintain a stable equilibrium that both preserves intestinal health and protects the gut from potential threats.



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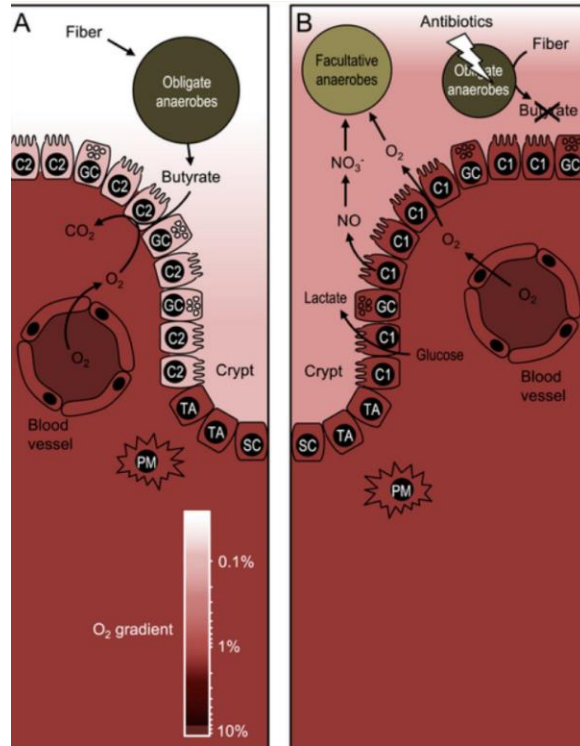
BARRIER BREAKDOWN

In people with ulcerative colitis, factors such as a genetic predisposition, environmental triggers and infection set into motion a cycle of uncontrolled inflammation that wreaks havoc on the intestinal wall.





Colonic aerobiosis drives gut dysbiosis

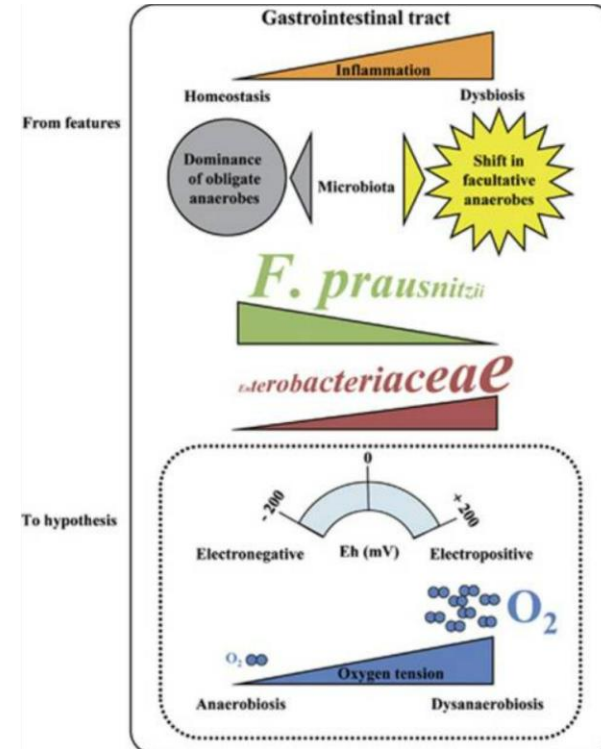


Anaerobiosis of the healthy colon drives the composition of the gut microbiota towards a dominance of obligate anaerobes, while **dysbiosis** is often associated with a sustained increase in the abundance of facultative anaerobic Proteobacteria, indicative of a disruption in anaerobiosis.

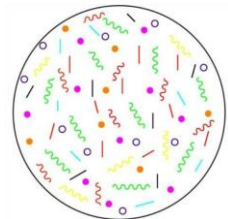




A healthy colon is dominated by obligate anaerobes, whereas **dysbiosis** is often associated with a sustained increase in the abundance of facultative anaerobic bacteria, as seen in conditions such as IBD.

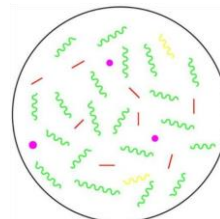


Signatures of a healthy (eubiotic) vs dysbiotic gut



Healthy gut microbiome

- High bacterial diversity
- Production of beneficial metabolites, e.g. SCFAs, vitamins, neurotransmitters, etc.
- Low levels of pathobionts
- Dominance of probiotic bacteria and commensals



Dysbiotic gut microbiome

- Loss of beneficial bacteria
- Overgrowth of pathobionts
- Exogenous pathogen colonization
- Loss of bacterial diversity



Health-promoting VS Disease-associated groups

◆ Bacteria life forms ↪

- Probiotic bacteria, e.g. *Akkermansia*, *Faecalibacterium*, *Roseburia*, etc.
- Commensals, e.g. *Bacteroides*, *Prevotella*, *Veillonella*, *Streptococcus*, etc.
- Pathobionts, e.g. *Desulfovibrio*, *Bilophila*, *Methanobrevibacter*, etc.
- Exogenous pathogens, e.g. *Campylobacter*, *Shigella*, *Vibrio*, etc.
- Gut diversity

Health-promoting groups

Probiotic bacteria
Commensals (localized
correctly in the gut).

Disease-associated groups

Pathobiont overgrowth
Exogenous pathogen
colonization.





Functional insights from gut microbial signatures

♦ Insights into metabolites produced or degraded by microbes



- Short chain fatty acids : Acetate, butyrate, propionate.
- Neurotransmitters : Acetylcholine, GABA, histamine, serotonin, etc.
- B-vitamins : Niacin, Riboflavin, biotin, cobalamine, etc.
- Toxin build-up: LPS, methane, H₂S, ammonia, etc.
- Lactose and oxalate degraders.
- Longevity factors: Myrosinase, urolithin, indoles and phenols, etc.



Dietary interventions that influence the gut microbiota

♦ Dietary recommendations based on bacterial shifts

- Food
- Prebiotics
- Probiotics
- Herbs
- Vitamins and minerals



The Vitract Microbiome Test

- ♦ Vitract microbiome test uses 16s ribosomal RNA (16s rRNA) sequencing to identify all taxonomic groups of bacteria and archaea in the colonic ecosystem of your gut. This test gives you deep insights into:
- Gut diversity (richness and evenness).
 - Health-promoting and disease-associated bacteria implicated in health and disease symptoms.
 - Metabolites produced by gut bacteria and their impact on health/disease.
 - Highly Personalized dietary recommendations to achieve improved gut health.

Section 1 - Summary



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Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

This is your complete gut microbiome analysis containing condition related findings with food and supplements recommendation to optimize your gut health.

SECTION 1: Summary of your results

0-49 represents **Poor** • 50-79 represents **Needs work** • 80-100 represents **Satisfactory**

Gut Health Score



Your Gut Health Score

Your Gut Health Score is computed based on all the bacteria & archaea enlisted in section 2. Assuming all your bacterial taxa are within optimal ranges, then your score will be 100. For every taxon that is out of range, your score will decrease accordingly to the degree that it deviates from the optimal range

Diversity Score



Your Diversity Score

Your Diversity Score is computed using the Shannon Index, which accounts for the richness and evenness of the species found in your gut. Your score is a percentile value compared to the rest of the people who have taken the Vitract Gut Microbiome Test. Note that apart from diet, other factors such as age, geographical location, genetics, sleep patterns, and antibiotic use, can affect your diversity score

Disclaimer

- This report is not a diagnosis. It is for educational and informational purposes only. 'All associations between your microbiome profile, disease conditions and recommended food suggestions, are based on published peer-reviewed research papers. Note that other factors such as genetics, lifestyle, environment, etc. can contribute to disease or health associations. Always seek the advice of your doctor or healthcare provider for any issues relating to your diagnosis, disease prevention, impairment, symptoms or treatment. This report does not replace the role of your healthcare provider.

Section 2 - Probiotic bacteria



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SECTION 2: Bacteria life forms

Health-associated bacteria

Probiotic bacteria
Commensals

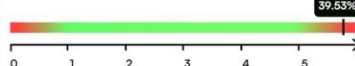
Disease-associated bacteria

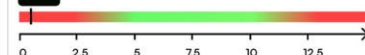
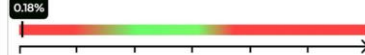
Pathobiont overgrowth
Exogenous pathogens

Probiotic bacteria - 17

Probiotic bacteria are live microorganisms that, when consumed in sufficient quantities, provide health benefits by promoting a balanced and healthy gut microbiota.

Low Optimal High represents bacteria levels.

#	Probiotic bacteria	Implication
1	<i>Akkermansia</i> - 39.53% High Optimal Range (1-5%) 	High Overabundance of <i>Akkermansia</i> can disrupt dynamic balance between mucin secretion and degradation leading to destruction of intestinal barrier and aggravation of conditions such as colitis and colorectal cancer.
2	<i>Bifidobacterium</i> - 0.01% Low Optimal Range (2-5%) 	Low Low amounts of <i>Bifidobacterium</i> can lead to dysbiosis, a microbial imbalance associated with various digestive disorders, including IBS, ulcerative colitis and IBD. Additionally, it can weaken the gut's barrier function, making it more susceptible to harmful pathogen invasion.

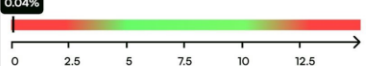
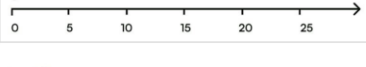
3	<i>Blautia</i> - 0.45% Low Optimal Range (5-10%) 	Low Low levels of <i>Blautia</i> have been reported in adults and children suffering from type 2 diabetes and inflammatory bowel disease (IBD), including Crohn's disease (CD) and ulcerative colitis and also liver cirrhosis. Also, a reduction in the abundance of <i>Blautia</i> has been associated with colorectal cancer and colitis-related cancer.
4	<i>Faecalibacterium</i> - 0.18% Low Optimal Range (>=10%) 	Low Low amounts of <i>Faecalibacterium</i> have been linked to dysbiosis, an imbalance in the gut microbiota. This imbalance is associated with other gastrointestinal disorders such as irritable bowel syndrome (IBS). This reduction can also lead to weakened gut barrier function, making the intestines more susceptible to pathogenic infections and increased inflammation.
5	<i>Lactobacillus</i> - 0% Low Optimal Range (0.01-1%) 	Low Low levels of <i>Lactobacillus</i> can lead to an imbalance in the gut microbiota, which is associated with various gastrointestinal issues, such as diarrhea, irritable bowel syndrome, and inflammatory bowel diseases.

All bacteria optimal ranges in section 2, with the exception of *Dorea*, *Coprococcus*, *Clostridium butyricum*, *Veillonella*, and *Enterococcus faecalis*, are based on the recommendations of Dr. Jason Hawrelak of Probiotic Advisor.

Section 2 - Probiotic (cont'd) & Commensals

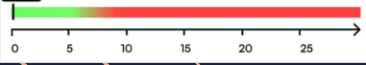
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#	Probiotic bacteria	Implication
6	<i>Roseburia</i> - 0.04% Low Optimal Range (5-10%) 0.04% 	Low Low levels of <i>Roseburia</i> can lead to an imbalance in the gut microbiota, which is associated with various gastrointestinal disorders, including irritable bowel syndrome (IBS) and inflammatory bowel diseases (IBD).
7	<i>Ruminococcus</i> - 0.15% Optimal Optimal Range (0-15%) 0.15% 	Optimal Levels seen are optimal.

Commensals - 74

Gut commensals are microorganisms that coexist with the host in the gastrointestinal tract without causing harm. They contribute to host wellbeing and gut homeostasis.

#	Commensals	Implication
1	<i>Alistipes</i> - 0.05% Optimal Optimal Range (0-5%) 0.05% 	Optimal Levels seen are optimal.

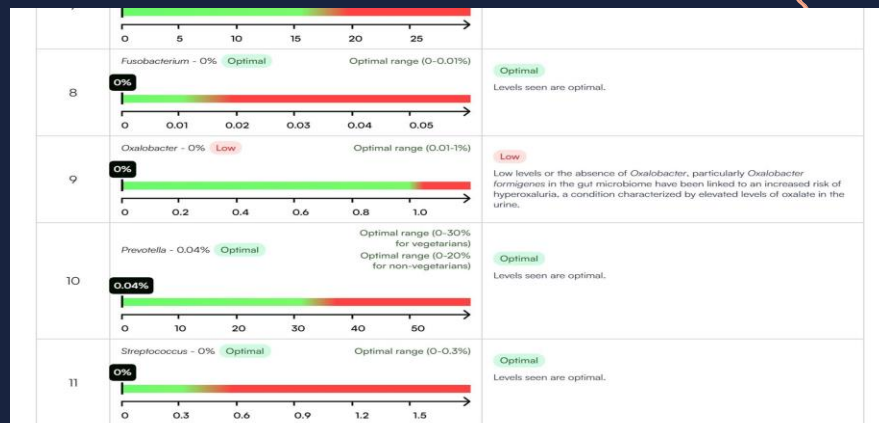
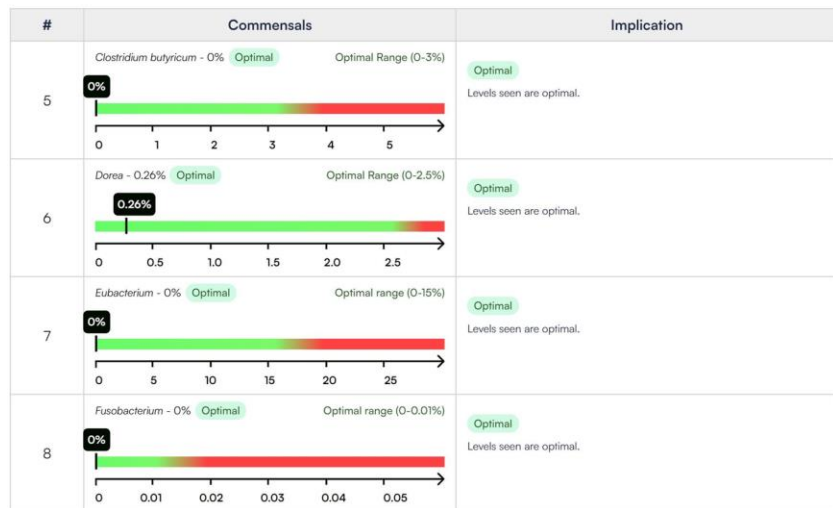
2	<i>Bacteroides</i> - 26.27% High Optimal Range (0-20%) 26.27% 	High Increased levels of certain <i>Bacteroides</i> spp. have been associated with increased mucosal inflammation and the development of colorectal and invasive breast cancer.
3	<i>Bacteroidetes</i> - 40.39% High Optimal Range (0-35%) 40.39% 	High Excessive growth of certain <i>Bacteroidetes</i> species might lead to alterations in the production of polymer-degrading enzymes targeting host cellular components. <i>Bacteroidetes</i> also secrete various proteases, which can destroy human brush border digestive enzymes.
4	<i>Coprococcus</i> - 0.33% Optimal Optimal Range (0-6%) 0.33% 	Optimal Levels seen are optimal.

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Section 2 - Commensals

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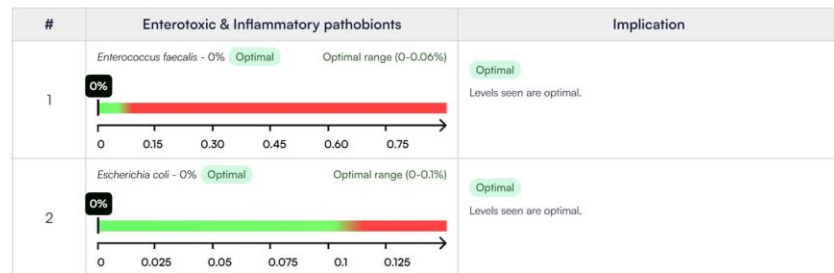
Section 2 - Pathobionts (cont'd) & Exogenous pathogens

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Exogenous pathogens

Detected Not Detected represents bacteria detection.

#	Exogenous pathogens	Implication
1	<i>Campylobacter</i> - 0% Not Detected	Not Detected
2	<i>Shigella</i> - 0% Not Detected	Not Detected
3	<i>Salmonella</i> - 0% Not Detected	Not Detected
4	<i>Staphylococcus</i> - 0% Not Detected	Not Detected
5	<i>Vibrio</i> - 0% Not Detected	Not Detected
6	<i>Yersinia</i> - 0% Not Detected	Not Detected

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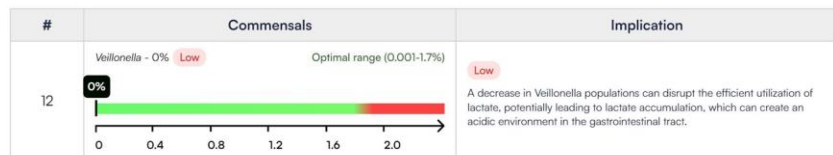
Section 2 - Commensals (cont'd) & Pathobionts (cont'd)

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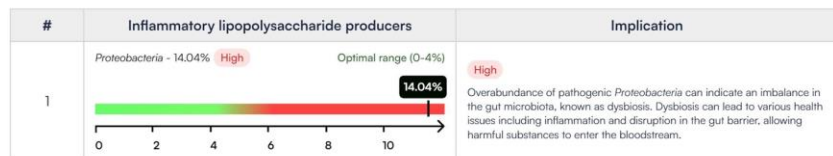
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Pathobionts - 45

Pathobionts are microorganisms that typically reside harmlessly in the gut but have the potential to cause disease under certain conditions or when the host's immune system is compromised. Pathobionts in this test are shown in 4 sub-categories:



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Gut Microbiome Analysis

Comprehensive Analysis, 16s rRNA Sequencing

John Doe | VT1-123DC

SUPPLEMENTARY TABLE 1: Reference bacteria used to compute the metabolite section (section 3) of the test report.

BUTYRATE			
Bacteria name	Taxon ID	Rank	Link
<i>Anaerostipes</i>	207244	Genus	https://journals.asm.org/doi/10.1128/mra.00056-21
<i>Anaerostipes caccae</i>	105841	Species	https://pubmed.ncbi.nlm.nih.gov/15466518/
<i>Blautia</i>	572511	Genus	https://pubmed.ncbi.nlm.nih.gov/38022552/
<i>Butyricicoccus</i>	580596	Genus	https://pubmed.ncbi.nlm.nih.gov/29620502/
<i>Butyricicoccus pullicaecorum</i>	501571	Species	https://pubmed.ncbi.nlm.nih.gov/29620502/
<i>Clostridium</i>	1485	Genus	https://pubmed.ncbi.nlm.nih.gov/32794091/
<i>Clostridium butyricum</i>	1492	Species	https://pubmed.ncbi.nlm.nih.gov/32794091/
<i>Coprococcus</i>	33042	Genus	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9877435/
<i>Coprococcus catus</i>	116085	Species	https://pubmed.ncbi.nlm.nih.gov/32141148/
<i>Coprococcus comes</i>	410072	Species	https://pubmed.ncbi.nlm.nih.gov/32141148/
<i>Eubacterium</i>	1730	Genus	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9877435/
<i>Eubacterium hallii</i>	1263078	Species	https://pubmed.ncbi.nlm.nih.gov/27242734/
<i>Eubacterium rectale</i>	39491	Species	https://pubmed.ncbi.nlm.nih.gov/33790426/
<i>Faecalibacterium</i>	216851	Genus	https://pubmed.ncbi.nlm.nih.gov/19222573/
<i>Faecalibacterium prausnitzii</i>	853	Species	https://pubmed.ncbi.nlm.nih.gov/19222573/
<i>Megasphaera</i>	906	Genus	https://pubmed.ncbi.nlm.nih.gov/14519808/
<i>Roseburia</i>	841	Genus	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9877435/
<i>Roseburia intestinalis</i>	166486	Species	https://pubmed.ncbi.nlm.nih.gov/20105245/
<i>Roseburia inulinivorans</i>	360807	Species	https://pubmed.ncbi.nlm.nih.gov/17012576/
<i>Ruminococcus</i>	1263	Genus	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9877435/
<i>Ruminococcus bromii</i>	40518	Species	https://pubmed.ncbi.nlm.nih.gov/22343308/
<i>Ruminococcus obeum</i>	1263107	Species	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9877435/

Section 3 - Metabolites



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VITAMINS PRODUCERS

The closer your score is to 100, the better.

• Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Vitamin B1 (Thiamin)	24	Serves as a coenzyme in carbohydrate metabolism Cellular growth and repair Essential for the proper functioning of the enteric nervous system
Vitamin B2 (Riboflavin)	73	Aids in the breakdown of carbohydrates, proteins, and fats for energy Antioxidant defense Supports the growth and maintenance of gut epithelial cells
Vitamin B3 (Niacin)	30	Aids metabolism of fats, carbohydrates and proteins Aids in neurotransmitter synthesis Essential for maintaining skin health
Vitamin B5 (Pantothenic Acid)	6	Energy production through metabolism of carbohydrates, proteins, and fats Contributes to the synthesis of acetylcholine Fatty acid and hormone synthesis
Vitamin B6 (Pyridoxine)	19	Essential for the synthesis of neurotransmitters like serotonin, dopamine, and GABA Supports the immune system

Vitamin B7 (Biotin)	30	Fatty acid synthesis Carbohydrate metabolism Cell growth and maintenance of gene expression
Vitamin B9 (Folate)	20	DNA synthesis and repair Metabolism of amino acids Involved in the synthesis of serotonin, dopamine, and norepinephrine
Vitamin B12 (Cobalamin)	5	Supports neurological function Red blood cell formation Energy production
Vitamin K2	2	Essential for proper blood clotting and coagulation Improves bone health Prevents arterial calcification and reduces the risk of atherosclerosis

Reference bacteria can be found on supplementary pages.

Section 3 - Metabolites

Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

TOXIN PRODUCERS

• 0 to 50: Satisfactory • 51 to 74: Needs work • Above 74: High
• 0 to 25: Satisfactory • 26 to 74: Needs work • Above 75: High For Methane
• 0 to 50: Satisfactory • Above 50: Needs work For Trimethylamine (TMA) and Trimethylamine-N-Oxide (TMAO)

The closer your score is to 0, the better.

Metabolites	Percentile score	Impact
Hydrogen sulfide High	100	Increased risk of colorectal cancer Impaired mucin production Bloating and abdominal pain Malodorous breath
Ammonia Satisfactory	38	Disruptions in the intestinal barrier function Inflammation and abdominal pain Neurotoxic effect Gut microbiota disruption
Methane High	84	Abdominal distension or bloating Constipation, cramping and flatulence Increased methane breath
Trimethylamine (TMA) and Trimethylamine-N-Oxide (TMAO) Satisfactory	38	Increased cardiovascular health risk Cognitive function and neurological disorders Inflammation and lipid accumulation in the blood vessels
Lipopolysaccharides (LPS) High	94	Increased inflammation Metabolic dysfunction and insulin resistance Neurological effect Increased contribution to chronic diseases

DETOXIFICATION BIOMARKERS

Scores too close to 0 or 100 are not desirable.

• 26 to 75: Satisfactory • 0 to 25: Needs work • Above 75: High

Metabolites	Percentile score	Impact
Beta glucuronidase Needs work	4	Deconjugation of bile acids Influence the pharmacokinetics of drugs Regulation of physiological estrogen metabolism
LONGEVITY		
The closer your score is to 100, the better.		
• Above 50: Satisfactory • 0 to 50: Needs work		
Metabolites	Percentile score	Impact
Indoles and Phenols Needs work	15	Indole is a precursor for neurotransmitter synthesis Indoles regulates mood and sleep-wake cycles Phenol reduces oxidative stress and inflammation

Reference bacteria can be found on supplementary pages.

Section 3 - Metabolites



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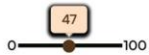
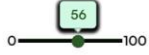
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LONGEVITY

The closer your score is to 100, the better.

• Above 50: **Satisfactory** • 0 to 50: **Needs work**

Metabolites	Percentile score	Impact
Myrosinase Needs work		Anti-cancer potential Antioxidant and anti-inflammatory properties Detoxification of harmful substances
Urolithin Satisfactory		Antioxidant activity Mitochondrial health Muscle health and exercise performance Cellular senescence regulation

LACTOSE AND OXALATE DEGRADERS

The closer your score is to 100, the better.

• Above 50: **Satisfactory** • 0 to 50: **Needs work**

Metabolites	Percentile score	Impact
Oxalate Needs work		Prevention of kidney stone formation Maintain gut microbial balance
Lactose Degradars Needs work		Digestive efficiency and nutrient absorption Production of beneficial metabolites Immune system modulation

Section 4 - Dietary recommendations

Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia **High**, Bacteroides **High**, Bifidobacterium **Low**, Bilophila **High**, Blautia **Low**, Coprococcus **Optimal**, Desulfovibrio **High**, Faecalibacterium

Modifiers	Bacteria shifted	Scientific evidence
FOOD		
To include: ginger ¹ , banana ² , Pulses ³ , rye ⁴ , sea weed ⁵ , potatoes ⁶ , oats ⁷ , lingonberries ⁸ , pomegranate ⁹ , chaga (mushroom) ¹⁰ , Konjaku flour ¹¹	Reduce Akkermansia ¹ Reduce Bacteroides ² Increase Bifidobacterium ³ Reduce Bilophila ⁴ Increase Blautia ⁵ Reduce Coprococcus ⁶ Reduce Desulfovibrio ⁷ Increase Faecalibacterium ⁸ Reduce Methanobrevibacter ⁹ Reduce Proteobacteria ¹⁰ Increase Roseburia ¹¹ Increase Akkermansia ¹² Increase Bacteroides ¹³ Reduces Bifidobacterium ¹⁴ Increase Bilophila ¹⁵ Reduces Blautia ¹⁶ Increase Coprococcus ¹⁷ Increase Desulfovibrio ¹⁸ Reduces Faecalibacterium ¹⁹ Reduces Lactobacillus ²⁰ Increase Methanobrevibacter ²¹ Increase Proteobacteria ²² Reduces Roseburia ²³	1. Effect of ginger supplementation on the fecal microbiome in subjects... 2. Fat binding capacity and modulation of the gut microbiota both diets... 3. Effects of banana powder (Musa acuminata Colla) on the composition... 4. Ingesting retrograded rice (Oryza sativa) starch relieves high-fat diet... 5. In vitro fermentation of lupin seeds (Lupinus albus) and broad beans... 6. In Vitro Evaluation of Brown Seaweed Laminaria spp. as a Source of... 7. The effects of fermented rye products on gut microbiota and their... 8. Resveratrol modulates the gut microbiota of cholestasis in pregnant... 9. Ascochylium nodosum polyaccharide regulates gut microbiota meta... 10. Diet Mediate the Impact of Host Habitat on Gut Microbiome and Infl... 11. Potato resistant starch inhibits diet-induced obesity by modifying the... 12. Starch acylation of different short-chain fatty acids and its correspon... 13. Flavonoids from Whole-Grain Oat Alleviated High-Fat Diet-Induced... 14. Agaricus bisporus Polysaccharides Ameliorates Behavioural Deficits... 15. Lingonberries alter the gut microbiota and prevent low-grade inflam... full references for recommendations can be found on supplementary page 12
To avoid: wheat bran ¹ , rice ⁴ , seaweed ⁵ , red wine polyphenols ⁶ , wheat ¹⁵ , maize ¹⁷ , white button mushrooms ¹⁴ , Longan ¹⁶ , d-fructose (sugar) ¹⁷ , rice bran ¹⁸ , soy ²¹ , glucose (sugar) ²³		

PROBIOTICS

To include: Lactobacillus reuteri ¹, Lactobacillus Johnsonii ², Bifidobacterium bifidum ³, Lactobacillus plantarum ⁴, Bacillus coagulans ⁵, Bacillus clausii ⁶, vs#3 ¹⁵, Lactobacillus crispatus ¹⁷, Bacillus amyloquelaciens ¹⁸, Bifidobacterium longum ²⁰

Reduce Akkermansia ¹
Increase Bifidobacterium ⁴
Reduce Bilophila ⁵
Increase Blautia ⁶
Reduce Desulfovibrio ¹²
Increase Faecalibacterium ¹⁵
Increase Lactobacillus ¹⁶
Reduce Methanobrevibacter ¹⁷
Reduce Proteobacteria ¹⁸
Increase Veillonella ²⁰
Increase Akkermansia ²

1. Lactobacillus reuteri DSM 17938 feeding of healthy newborn mice reg...
2. Synbiotic (Lactiplantibacillus pentosus GSK2 and isomalt-oligosac...
3. The Influence of Protein Secretomes of Enterococcus durans on ex vi...
4. Probiotic Lactobacilli Administration Induces Changes in the Fecal Mi...
5. Administration of Aspergillus oryzae suppresses DSS-induced colitis...
6. Bifidobacterium bifidum TMC3115 ameliorates milk protein allergy in...
7. Exopolysaccharides produced by intestinal Bifidobacterium strains ac...
8. Exopolysaccharides from Lactobacillus plantarum YW11 improve imm...
9. Effects of Lactobacillus plantarum and Pediococcus acidilactici co-f...
10. Lactobacillus plantarum-Derived Extracellular Vesicles Modulate Ma...
11. Evaluation of the therapeutic effect and dose-effect of Bifidobacteriu...
12. Effects of Bacillus Coagulans on growth performance, antioxidant c...

Reference bacteria can be found on supplementary pages.

Section 4 - Dietary recommendations

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Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia **High**, Bacteroides **High**, Bifidobacterium **Low**, Bilophila **High**, Blautia **Low**, Coprococcus **Optimal**, Desulfovibrio **High**, Faecalibacterium

Modifiers	Bacteria shifted	Scientific evidence
SUPPLEMENTS	Reduce Akkermansia ¹	1. Enrichment of Food With Tannin Extracts Promotes Healthy Changes...
To include: tannic acid ¹ , Rutin ² , quercetin ³ , polyphenols ⁴ , GABA ¹⁰ , squalamine ¹⁴ , Baicalin ¹⁶ , Dextrin ¹⁹	Reduce Bacteroides ²	2. Effects of Proteases from Pineapple and Papaya on Protein Digestion...
	Reduce Bilophila ⁷	3. Purified rutin and rutin-rich asparagus attenuates disease severity in...
	Reduce Desulfovibrio ¹⁰	4. Dimethyl fumarate reduces the risk of mycotoxins via improving intest...
	Increase Faecalibacterium ¹⁹	5. Structural Insights into Amelioration Effects of Quercetin and Its Glyc...
	Reduce Methanobrevibacter ¹⁴	6. Shen-Ling-Bai-Zhu-San (SL) and SL-Derived Polysaccharide (PL) Am...
	Reduce Proteobacteria ¹⁶	7. A combination of quercetin and resveratrol reduces obesity in high-fa...
	Increase Veillonella ¹⁹	8. Propionate-Producing Consortium Restores Antibiotic-Induced Dysbi...
	Increase Akkermansia ²	9. Glucosamine Ameliorates Symptoms of High-Fat Diet-Fed Mice by B...
	Increase Bacteroides ⁴	10. Taxifolin increased semen quality of Duroc boars by improving out...
	Reduces Bifidobacterium ⁶	11. Reduced obesity, diabetes, and steatosis upon cinnamon and grape...
	Increase Bilophila ⁸	12. Mouse intestinal microbiome modulation by oral administration of a...
	Reduces Blautia ⁹	13. Dietary betaine prevents obesity through gut microbiota-driven micr...
	Increase Coprococcus ¹⁰	14. The antimicrobial resistance pattern of cultured human methanogen...
To avoid: Bromelain ² , disodium fumarate (food additive) ⁴ , Shen Ling Bai Zhu San ⁶ , propionate ⁸ , Glucosamine ⁹ , Taxifolin ¹⁰ , betaine ¹¹ , Bismuth Salts ¹⁶ , cannabinoids ¹⁹ , PreforPro ²⁰	Reduces Lactobacillus ¹⁵	15. Protective effect of baicalin on the regulation of Trex1/Th17 balance...
	Increase Proteobacteria ¹⁶	
	Reduces Roseburia ¹⁸	
	Reduces Veillonella ²⁰	

PREBIOTICS

To include:

To avoid: polydextrose¹, Agavins², Psyllium (Plantago Ovata Husk)³, resistant starch⁴, manno-oligosaccharide⁵, oligofructose-enriched inulin⁶, sialyllactose⁹

Increase Akkermansia¹
Increase Bacteroides²
Reduces Blautia³
Increase Coprococcus⁴
Increase Desulfovibrio⁵
Reduces Faecalibacterium⁶
Reduces Veillonella⁹

1. Dietary Factors and Modulation of Bacteria Strains of Akkermansia m...
2. Assessment of the prebiotic effect of quinoa and amaranth in the hu...
3. Psyllium seed husk regulates the gut microbiota and improves mucos...
4. Potato resistant starch inhibits diet-induced obesity by modifying the...
5. Manno-oligosaccharides from Cassia Seed Gum Attenuate Atheroscl...
6. Additional oligofructose/inulin does not increase faecal bifidobacteria...
7. Anti-inflammatory activity of alkali-soluble polysaccharides from Arcti...
8. Effect of Prebiotic on Microbiota, Intestinal Permeability, and Glycem...
9. Fecal microbiota composition of breast-fed infants is correlated with...

full references for recommendations can be found on supplementary pages

Reference bacteria can be found on supplementary pages.

Section 4 - Dietary recommendations

Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia High, Bacteroides High, Bifidobacterium Low, Bilophila High, Blautia Low, Coprococcus Optimal, Desulfovibrio High, Faecalibacterium

Modifiers	Bacteria shifted	Scientific evidence
LIFESTYLE CHANGES To include: high fiber diet ¹ , nuts ³ , mediterranean diet ⁶ , fibre-rich macrobiotic ma-pi 2 diet ⁹ , moderate-protein moderate-carbohydrate ¹⁶	Reduce Bacteroides ¹ Reduce Bilophila ³ Reduce Coprococcus ⁶ Increase Faecalibacterium ⁹ Increase Veillonella ¹⁶	1. Gut Microbial SNPs Induced by High-Fiber Diet Dominate Nutrition M... 2. Far infrared radiation induces changes in gut microbiota and activate... 3. Pistachio Consumption Alleviates Inflammation and Improves Gut Mi... 4. Interactions between Diet, Bile Acid Metabolism, Gut Microbiota, and... 5. Smoking cessation alters intestinal microbiota: insights from quantitat... 6. Gut Microbiome Composition in Non-human Primates Consuming a... 7. Effects of the dietary protein level on the microbial composition and... 8. Active Smoking Induces Aberrations in Digestive Tract Microbiota of... 9. Modulation of gut microbiota dysbioses in type 2 diabetic patients by... 10. Effect of Whole-Grain Barley on the Human Fecal Microbiota and M... 11. A 90-day subchronic exposure to heated tobacco product aerosol c... 12. The Endotoxemia Marker Lipopolysaccharide-Binding Protein is Red... 13. Metagenomic analyses of alcohol induced pathogenic alterations in... 14. Nuts and their Effect on Gut Microbiota, Gut Function and Symptom... 15. Gut microbiome and metabolome in a non-human primate model of...
To avoid: Far infrared Sauna ² , high-saturated fat diet ⁴ , smoking ⁵ , low protein diet ⁷ , whole grain diet ¹⁰ , Fiber ¹² , alcoholic beverages ¹³ , high saturated milk fat diet ¹⁷	Increase Bacteroides ² Increase Bilophila ⁴ Reduces Blautia ⁵ Increase Coprococcus ⁷ Reduces Faecalibacterium ¹⁰ Increase Methanobrevibacter ¹² Increase Proteobacteria ¹³ Reduces Veillonella ¹⁷	full references for recommendations can be found on supplementary pages



Using the Vitract Microbiome test to understand gut health

-CASE STUDY

Presented by

Chidozie Ojobor, Ph.D.

Co-founder and Chief Scientific Officer, Vitract



Case study profile

- ◆ **General info** – Black female, NYC resident, 102lb
- ◆ **Health Info**
- ◆ **Symptoms** – Joint pain, blood in stool
- ◆ **Conditions** – Leaky gut syndrome, IBS, Sjögren syndrome, ulcerative colitis, Systemic lupus erythematosus.
- ◆ **No food intolerances except to gluten**
- ◆ **Saturated fats** (eat several times daily), **artificial sweeteners** (do not eat), **fruits** (occasionally eat), **vegetables** (eat several times a day), **fermented foods** (rarely eat), **Milk & red meat** (eat daily), **refined carbs, processed foods** (eat occasionally), and **Nuts and grains** (rarely eat).

What should you be looking for in a **gut microbiome test** for this individual?

1

Biomarkers of increased intestinal permeability – Identifying bacteria groups associated with intestinal permeability will give you insights into leaky gut and ulcerative colitis.

2

Drivers of proinflammation – This will give you insights into all the autoimmune disorders (UC, Sjögren syndrome, leaky gut) and symptoms such as joint pain.

3

Drivers of intestinal damage and haemorrhage (such as blood in stool).

Biomarkers of intestinal permeability

◆ Short chain fatty acid producers

- **Butyrate** plays a key role in improving gut barrier integrity and is the primary energy source for colonocytes.
- Butyrate producers include – *Faecalibacterium*, *Roseburia*, *Blautia*, *Anaerostipes*, *Coprococcus*, etc (Seo *et al*, 2020; Zhang *et al*, 2019; Singh *et al*, 2022).
- Butyrate producers are significantly lower in patients diagnosed with **UC** (Xu *et al*, 2020; Varela *et al*, 2013; Yang *et al*, 2023; Weng *et al*, 2021), **IBS** (Rajilic-Stojanovic *et al*, 2011; Nie *et al*, 2021; Gobert *et al*, 2016), **leaky gut** (Vincenzo *et al*, 2024; Ruan *et al*, 2022), **Sjögren syndrome** (Moon *et al*, 2020; Cano-Ortiz *et al*, 2020, de Paiva *et al*, 2016).
- **Mucin activators** enhance mucosal barrier integrity. They include *Akkermansia muciniphila* (Belzer *et al*, 2017), *Faecalibacterium prausnitzii* (Lopez-Siles *et al*, 2017), *Lactobacillus plantarum*, etc.

Drivers of proinflammation

- ◆ **LPS/endotoxin producing bacteria** – Phylum ***Proteobacteria*** with their highly pro-inflammatory lipopolysaccharides (oligosaccharides + lipid A) localized on the outer cell wall of the bacteria (Lin *et al*, 2020; d'Hennezel *et al*, 2017; Mohr *et al*, 2022).
- ◆ **Hydrogen sulfide producing bacteria**. E.g. *Bilophila*, *Desulfovibrio* (Murros, 2022; Buret *et al*, 2022; Peck *et al*, 2019).
- ◆ **Lack of anti-inflammatory bacteria** such as the SCFA producers.

Drivers of intestinal damage and haemorrhage

- ♦ *E. coli* – such as the Shiga-toxin producing, enterohaemorrhagic *E. coli* strain O157:H7 (Vogt *et al*, 2023; Martins *et al*, 2022).
- ♦ Excessive H₂S damages the mucous membrane of the gut epithelium. So, look out for high levels of hydrogen sulfide producers (Buret *et al*, 2022; Rowan *et al*, 2009; Kushkevych *et al*, 2016)

Thank You!



Thank You!

Thank You!

Thank You!

Thank You!

