UNDERSTANDING & TREATING CHRONIC DIGESTIVE ILLNESSES

A Guide to Digestive Well-Being



Dean C. Kramer, M.D.

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Note to the Reader:

An abridged version of this Digestive Health Guidebook has been created to improve readability by removing footnotes, references, and images found in this edition. To assist with scientific terms used throughout the text, a comprehensive glossary is provided in the Appendix. For those who would like to use the abridged version of the guidebook it can be found at www.kramermedicalclinic.com

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CAROLINE'S CASE HISTORY



The human digestive tract is not just a collection of organs and cells; it is interconnected constellation of ecosystems, where trillions of microorganisms interact within the body to shape health and disease. Caroline's case, which became the inspiration for this guidebook, illustrates the importance of recognizing and working within this ecological framework.

At 45, Caroline — a legal secretary — had suffered for years with chronic digestive symptoms: recurring nausea, abdominal bloating, uncomfortable fullness after meals, excess belching, and irregular bowel habits. Caroline had seen multiple doctors — primary care physicians, gastroenterologists, integrative specialists, psychiatrists — and undergone an exhaustive series of tests: bloodwork, imaging, endoscopies. Every result was considered "normal." She had cycled through an array of diets — lactose-free, glutenfree, low FODMAP, keto, Paleo, and intermittent fasting — none bringing lasting relief. Anti-anxiety and anti-depressant medications were added by mental health consultants which she quickly abandoned due to worsening symptoms.

At the time of her first visit, Caroline was taking four prescription medications and a collection of multiple supplements. Throughout her visit, she expressed her deep sense of frustration and despair.

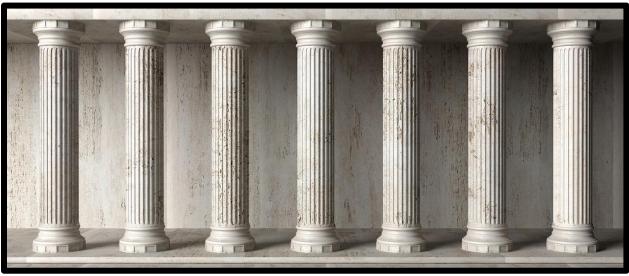
What had been missed in all prior assessments was the role of Caroline's gut's microbial ecology: the dynamic interplay between microorganisms, gut cells, and environmental exposures, including diet. By shifting the clinical focus from isolated organ dysfunction to the broader context of gut-microbe interactions, Caroline's treatment took a more promising turn — and her long-standing symptoms began to improve.

This monograph explores the scientific principles behind such microbial-ecosystem approaches and offers a path of understanding — and hope — for Caroline and the many others who share her struggles.

The next section introduces The Seven Pillars of Digestive Health a comprehensive framework designed to help patients, practitioners, and caregivers understand the key elements necessary for restoring and maintaining digestive well-being. These pillars draw upon the latest insights from microbiome science, nutritional therapy, and integrative medicine, offering a roadmap that emphasizes balance, nourishment, and repair.

By approaching digestive health through these seven interconnected foundations, we aim to provide strategies that can be tailored to individual needs, just as they were in rethinking Caroline's care plan.

Understanding the Seven Pillars of Human Wellness



Health is not a singular or isolated phenomenon; it is the result of a dynamic interplay among biological, environmental, and genetic factors. The remarkable complexity and resilience of the human body in maintaining homeostasis depend on seven fundamental pillars: genetics, metabolism, microorganisms, immunity, nutrients, communication systems (vascular, neural, hormonal), and environmental influences.

These interconnected systems form the foundation of wellness. Disruption in any one pillar can reverberate through the others, increasing the risk of disease. A comprehensive understanding of these systems provides a framework for preventive care and personalized health management.

1. Genetics: The Blueprint of Life

Our genetic inheritance profoundly influences health outcomes. Mitochondrial DNA, passed exclusively through the maternal line, determines the efficiency of cellular energy production and plays a pivotal role in metabolism and aging.¹ Genetic predispositions can also shape an individual's risk for metabolic disorders, autoimmune conditions, and neurodegenerative diseases.

However, genes are not destiny. Epigenetic factors—such as diet, stress, and environmental exposures—can modify gene expression, altering the trajectory of health.² Understanding genetic influences paves the way for personalized medicine and preventive strategies tailored to individual risk profiles.

2. Metabolic Health: The Energy Economy of the Body

Metabolism encompasses the biochemical processes that govern energy production and utilization. A healthy metabolism ensures efficient processing of carbohydrates, fats, and proteins to maintain energy balance. Key factors include insulin sensitivity, mitochondrial function, and hormonal regulation.³ In modern society, sedentary lifestyles and diets rich in ultraprocessed foods have led to a surge in metabolic disorders such as diabetes, obesity, and metabolic-associated steatotic liver disease (MASLD).⁴ Promoting metabolic health through physical activity, nutrient-dense diets, and stress management is essential to preventing chronic illness.

3. Microorganisms: The Invisible Ecosystems Within

The human body is host to trillions of microorganisms—collectively known as the microbiome—which influence digestion, immune response, and even brain function.⁵ The gut microbiota, in particular, plays critical roles in breaking down complex carbohydrates, synthesizing vitamins, and regulating inflammation.⁶

Imbalances in microbial populations, a condition known as dysbiosis, have been associated with irritable bowel syndrome (IBS), depression, autoimmune disease, and more.⁷ Supporting a diverse and balanced microbiome through prebiotic fibers, fermented foods, and cautious antibiotic use is key to maintaining health.⁸

4. Immunity: The Guardian of Health

The immune system acts as the body's defense network, distinguishing between harmful invaders and friendly inhabitants. A well-functioning immune response protects against infection, cancer, and autoimmune reactions.⁹ Chronic inflammation—driven by poor nutrition, stress, pollutants, or microbial imbalance—can impair immune function and increase the risk of conditions such as rheumatoid arthritis, asthma, and Alzheimer's disease.¹⁰ Strengthening immunity involves regular sleep, physical activity, stress management, and sufficient intake of nutrients like vitamin D, zinc, and omega-3 fatty acids.¹¹ **See the section:** *The Biotic Family*)

5. Nutrients: The Building Blocks of Life

Nutrition provides the essential components for cellular function, energy production, and repair. Macronutrients (carbohydrates, proteins, and fats) supply fuel, while micronutrients (vitamins and minerals) enable thousands of metabolic reactions.¹²

Deficiencies—whether from poor diet, malabsorption, or increased physiological demand—can lead to immune dysfunction, cognitive decline, and systemic disease.¹³ Nutrient bioavailability depends on gut health, genetic factors, and dietary composition.¹⁴ A varied, predominantly plant-based diet that meets individual needs supports optimal functioning.

<u>6. Communication Systems: Vascular, Neural, and Hormonal</u> <u>Networks</u>

Health depends on efficient communication between organs and tissues through three primary systems:

 The vascular system, delivering oxygen and nutrients to cells¹⁵

- The nervous system, coordinating responses via neurotransmitters and neural pathways¹⁶
- The endocrine system, regulating metabolism, stress, growth, and reproduction through hormones¹⁷

Disruption in any of these networks—such as poor circulation, neuroinflammation, or hormonal imbalances—can contribute to conditions like hypertension, mood disorders, and metabolic syndrome.¹⁸

For example, a major communication network is between the gut and the brain known as the gut-brain axis. The gut-brain axis involves bidirectional communications between the gut microbiome and the central nervous system.

Gut bacteria produce substances that affect neurotransmitter production that reaches the brain and can impact mood, cognition, and mental health conditions like anxiety and depression.

Regular exercise, cognitive engagement, and dietary choices can help preserve these communication pathways.

7. Environmental Influences (Exposome): The External Forces Shaping Health

Every day, humans interact with a complex array of environmental inputs—air, water, toxins, and psychosocial factors—that shape long-term health.¹⁹ The exposome includes both physical elements (pollutants, endocrine disruptors, allergens) and social determinants (stress, relationships, socioeconomic status).²⁰ Chronic exposure to environmental insults has been linked to systemic inflammation, metabolic dysfunction, and cognitive impairment.²¹ Creating health-supportive environments—clean air and water, access to nature, supportive social networks—can buffer against disease and promote well-being.

A Systems Approach to Health

The seven pillars of health do not operate in isolation. Rather, they form a tightly interwoven web, where imbalance in one area can lead to dysfunction in others. This interconnectivity underscores the importance of a system-based, integrative approach to wellness.

By addressing these foundational elements through preventive care, lifestyle modification, and personalized interventions, individuals can reduce disease risk and optimize their health trajectory. Recognizing the dynamic interplay between genetics, metabolism, microbes, immunity, nutrition, signaling systems, and environment allows for a more precise and sustainable model of health.

A Journey Toward Longevity and Wellness

In the sections that follow, each of the seven pillars will be explored in greater depth. The goal is to empower readers with knowledge and practical strategies for aligning internal biology with external conditions. By integrating principles from genetics, immunology, environmental science, microbiology, and physiology, individuals can chart a path toward lasting health, resilience, and longevity.

REFERENCES:

¹ Douglas C. Wallace, *"Mitochondrial DNA in Evolution and Disease,"* Nature 535, no. 7613 (2016): 498–500, <u>https://doi.org/10.1038/nature18902</u>.

^{1.} Jaenisch, Rudolf, and Adrian Bird. "Epigenetic Regulation of Gene Expression: How the Genome Integrates Intrinsic and Environmental Signals." *Nature Genetics* 33, no. 3 (2003): 245–254. <u>https://doi.org/10.1038/ng1089.</u>

^{2.} Saltiel, Alan R., and Jeffrey M. Olefsky. "Inflammatory Mechanisms Linking Obesity and Metabolic Disease." *Journal of Clinical Investigation* 127, no. 1 (2017): 1–10. <u>https://doi.org/10.1172/JCI92035.</u>

^{3.} Monda, A., de Stefano, M. I., Villano, I., Allocca, S., Casillo, M., Messina, A., Monda, V., Moscatelli, F., Dipace, A., Limone, P., Di Maio, G., La Marra, M., Di Padova, M., Chieffi, S., Messina, G., Monda, M., & Polito, R. (2024). Ultra-Processed Food Intake and Increased Risk of Obesity: A Narrative Review. *Foods (Basel, Switzerland)*, *13*(16), 2627. <u>https://doi.org/10.3390/foods13162627</u>

^{4.} Cryan, John F., and Timothy G. Dinan. "Mind-Altering Microorganisms: The Impact of the Gut Microbiota on Brain and Behaviour." *Nature Reviews Neuroscience* 13, no. 10 (201<u>2): 701–712.</u> <u>https://doi.org/10.1038/nrn3346.</u>

^{5.} Mayer, Emeran A., Rob Knight, and Sarkis K. Mazmanian. "Gut Microbes and the Brain: Paradigm Shift in Neuroscience." *Journal of Neuroscience* 34, no. 46 (2014): 15490–15496. <u>https://doi.org/10.1523/JNEUROSCI.3299-14.2014.</u> ^{6.} Foster, Jane A., and Karen-Anne McVey Neufeld. "Gut–Brain Axis: How the Microbiome Influences Anxiety and Depression." *Trends in Neurosciences* 36, no. 5 (2013): 305–312. <u>https://doi.org/10.1016/j.tins.2013.01.005.</u>

^{7.} Hill, Collins, et al. "Expert Consensus Document: The International Scientific Association for Probiotics and Prebiotics Consensus Statement on the Scope and Appropriate Use of the Term Probiotic." *Nature Reviews Gastroenterology & Hepatology* 11, no. 8 (2014): 506–514. <u>https://doi.org/10.1038/nrgastro.2014.66.</u>

^{8.} Chaplin, David D. "Overview of the Immune Response." *Journal of Allergy and Clinical Immunology* 125, no. 2 (2010): S3–S23. <u>https://doi.org/10.1016/j.jaci.2009.12.980.</u>

^{9.} Furman, David, et al. "Chronic Inflammation in the Etiology of Disease across the Life Span." *Nature Medicine* 25, no. 12 (2019): 1822–1832. https://doi.org/10.1038/s41591-019-0675-0.

^{10.} Calder, Philip C. "Feeding the Immune System." *Proceedings of the Nutrition Society* 72, no. 3 (2013): 299–309.
 <u>https://doi.org/10.1017/S0029665113001286.</u>

^{11.} Gropper, Sareen S., and Jack L. Smith. *Advanced Nutrition and Human Metabolism*. 6th ed. Belmont, CA: Wadsworth, 2013.

^{12.} Bailey, Regan L., Johanna T. Dodd, Johanna M. Gahche, and Paul M. Coates. "Examination of Vitamin Intakes among US Adults by Dietary Supplement Use." *Journal of the Academy of Nutrition and Dietetics* 112, no. 5 (2012): 657–663.e4. https://doi.org/10.1016/j.jand.2012.01.026.

^{13.} Raiten, Daniel J., Christine M. Namasté, Lindsay H. Brabin, Barbara A. Brabin, Kenneth H. Brown, Gail G. Harrison, Janet C. King, et al. "Executive Summary: Biomarkers of Nutrition for Development—Building a Consensus." *American Journal of Clinical Nutrition* 94, no. 2 (2011): 633S–650S.

 ^{14.} Laughlin, M. Harold. "Cardiovascular Response to Exercise." In Principles of Exercise Testing and Interpretation: Including Pathophysiology and Clinical Applications, edited by Karlman Wasserman, 13–31. Philadelphia: Lippincott Williams & Wilkins, 2012.

^{15.} Bear, Mark F., Barry W. Connors, and Michael A. Paradiso. *Neuroscience: Exploring the Brain*. 4th ed. Philadelphia: Wolters Kluwer, 2016.

^{16.} Melmed, Shlomo, et al., eds. *Williams Textbook of Endocrinology*. 13th ed. Philadelphia: Elsevier, 2016.

^{17.} Mendis, Shanthi, Pekka Puska, and Bo Norrving, eds. *Global Atlas on Cardiovascular Disease Prevention and Control*. Geneva: World Health Organization, 2011.

^{18.} Landrigan, Philip J., et al. "The Lancet Commission on Pollution and Health." *The Lancet* 391, no. 10119 (2018): 462–512. https://doi.org/10.1016/S0140-6736(17)32345-0.

^{19.} Steptoe, Andrew, and Michael Marmot. "The Role of Psychosocial Factors in Socioeconomic Inequalities in Health." In *Social Determinants of Health*, edited by Michael Marmot and Richard G. Wilkinson, 2nd ed., 109–127. Oxford: Oxford University Press, 2005. Publisher's page

^{20.} Block, M. L., & Calderón-Garcidueñas, L. (2009). Air pollution: mechanisms of neuroinflammation and CNS disease. *Trends in Neurosciences*, *32*(9), 506–516.

https://doi.org/10.1016/j.tins.2009.05.009

THE CHIMERIC NATURE OF HUMANS

The human body can be likened to the mythological Chimera, a creature composed of a lion, a goat, and a serpent—each with distinct identities but functioning as one being. Likewise, the

human body is a composite organism, cohabited by six different kingdoms of life: human cells and five distinct microbial domains bacteria, viruses, fungi, protozoa, and archaea.

The Mythological Chimera



This new paradigm compels clinicians and individuals alike to consider the entire ecosystem within the body when diagnosing and treating chronic disease. Much like the mythical Chimera, the human organism is a chimeric entity, reliant on multiple kingdoms of life, each contributing distinct capabilities.

Microbes vastly outnumber human cells and are essential for survival. They assist in digesting nutrients, regulating immune function, and even modulating mood and cognition. Without them, life would not be possible.

This synbiotic relationship urges a redefinition of what it means to be human—and what it means to be healthy. Wellness must now

be understood as a cooperative equilibrium among all six domains of life that coexist within the human form.

SECTION ONE

Treating Caroline Required A Different Paradigm

Caroline's previous healthcare providers performed a comprehensive diagnostic workup using standard medical tools: endoscopy, imaging studies, stool analyses, and blood tests. These conventional approaches, while valuable for evaluating organ anatomy and human cellular function, failed to uncover the root cause of her persistent symptoms—and ultimately did not improve her well-being.

A different approach was needed—one that considered not only human cells and organs but also the vast microbial world that coexists within the body. Her symptoms were reinterpreted as signs of dysfunctional digestive ecosystems, also known as intestinal microecological imbalances. This paradigm shift recognizes that health and disease arise not solely from human physiology, but from the complex relationships between host cells, microbial residents, and their shared environment.

Ecosystems Defined

Ecosystems are communities of living organisms interacting with each other and with non-living environmental components,

functioning together as an integrated system.¹ The human digestive tract can be viewed as a vast and dynamic ecosystem one in which body cells and microorganisms interact continuously within defined microenvironments.

In this *Guide*, the digestive tract is considered a collection of interconnected yet distinct ecosystems, each with its own unique structure and microbial inhabitants. These include the oral cavity, esophagus, stomach, small and large intestines, and accessory organs such as the nasal cavity, salivary glands, lungs, pancreas, gallbladder, liver, and appendix.

Each site functions as a specialized microenvironment, influenced not only by its anatomy but also by its microbiology and surrounding conditions. Disruption in one of these interdependent ecosystems can trigger dysfunction across the system, leading to chronic digestive disorders. Understanding digestive health, therefore, requires an appreciation for how each part contributes to the whole.

Modern medical care can no longer separate anatomy and cell biology from microbiology and evolutionary biology. The body is best understood as an integrated eco-biological system.

To unravel the complexities of digestive illness, we must examine how human cells (with their genetic and metabolic functions), microbial organisms, the immune system, nutrient availability, environmental exposures, and two-way signaling networks interact. These interconnected factors help explain how disturbed ecosystems give rise to chronic symptoms—and how restoring balance can become a target for effective therapy.

(See the next section: Redefining Who We Are as Humans)

REFERENCES:

¹ Wang, S., Mu, L., Yu, C., He, Y., Hu, X., Jiao, Y., Xu, Z., You, S., Liu, S.-L., and Bao, H. 2024. "Microbial Collaborations and Conflicts: Unraveling Interactions in the Gut Ecosystem." *Gut Microbes* 16 (1): 2296603. https://doi.org/10.1080/19490976.2023.2296603

REDEFINING WHO WE ARE AS HUMANS



Improving digestive health begins with redefining our understanding of the human body. Rather than seeing the body as a singular biological organism, we must recognize it as a composite of six life forms that live in dynamic balance: the human host and five microbial kingdoms—bacteria, viruses, fungi, protozoa, and archaea.¹

Understanding chronic digestive illness requires a systems-level view of these interconnected ecosystems—beginning in the oral cavity and continuing through the esophagus, stomach, small intestine, and colon.

Yet, digestive health is also shaped by adjacent ecosystems, such as those in the nasal cavity, facial sinuses, middle ear, mastoids, lungs, liver, gallbladder, pancreas, and appendix.² These organs influence, and are influenced by, the microbial and immunologic status of the digestive tract.

A New Perspective

Digestion can no longer be viewed as the exclusive function of human cells and organs. It must be understood as a collaborative process—a complex interplay between human biology, microbial populations, and environmental conditions within distinct ecological zones of the digestive system.³

By recognizing and addressing disturbances within these ecosystems, we can begin to promote healing, digestive health, and overall well-being.

REFERENCES

¹ Narayanan, A., Latika, A., Nair, A., Ajeesh, P., Kumar, N., and Babu, M. "Role of Gut Microbiota in Human Health and Diseases." *Current Nutrition* & Food Science 16 (2020). https://doi.org/10.2174/1573401316999200930130101

² Yoo, S., Jung, S., Kwak, K., and Kim, J. "The Role of Prebiotics in Modulating Gut Microbiota: Implications for Human Health." *International Journal of Molecular Sciences* 25 (2024). <u>https://doi.org/10.3390/ijms25094834</u>

³ Ruan, W., Engevik, M., Spinler, J., and Versalovic, J. "Healthy Human Gastrointestinal Microbiome: Composition and Function After a Decade of Exploration." *Digestive Diseases and Sciences* 65 (2020): 695–705. <u>https://doi.org/10.1007/s10620-020-06118-4</u>

<u>The Body as a Metropolis: Understanding</u> <u>the Role of Microbial Ecosystems in</u> <u>Health and Disease</u>

The state of our health is intimately tied to the diversity, density, functionality, and location of microbial populations within our body. Like a thriving metropolis, the human body consists of numerous "neighborhoods" or ecosystems, each with its own specific microbial community. These microbial communities work Synbiotically with human cells to maintain homeostasis, perform vital functions, and protect against harmful invaders.

Just as a city's health is determined by the stability and cooperation of its neighborhoods, our well-being is determined by the balance and functionality of these microbial ecosystems. When these ecosystems become imbalanced or dysfunctional, the result is often a state of disease, representing a failure of one or more of these internal systems.

Microbial Ecosystems as the "Neighborhoods" of the Body

Each organ system supports a specialized microbial population much like neighborhoods in a city support different functions. The oral cavity initiates digestion and houses both protective and pathogenic microbes. The intestinal tract, especially the colon, is a rich fermentation site for fiber, generating short chain fatty acids, the metabolic *currency* of intestinal well-being. Each site's microbial community plays a vital role in human health and resilience.

The Health of Microbial Ecosystems and Well-Being

A diverse and balanced microbiome enables immune regulation, metabolism, and protection against disease.^{1 2} Low diversity, often from fiber deficient diets or medication overuse, increases vulnerability to dysbiosis-related illnesses like diabetes and inflammatory bowel conditions.

Dysfunctional Ecosystems and Disease: The "Illness of the City"

When microbial communities become unbalanced, referred to as loss of *homeostasis*,—either too few beneficial species or overgrowth of pathogens—the result is systemic dysfunction.³⁻⁵

Just like a decaying neighborhood in a metropolis, different regions of the digestive tract may fall into disrepair, manifesting as

disease. For instance, microbial imbalance and inflammation in the gums can lead to periodontitis; in the esophagus, esophagitis; in the stomach, gastritis; and in the pancreas, pancreatitis. Further downstream, dysfunction in the liver ecosystem may lead to fatty liver disease, while microbial alterations in the appendix or colon may result in appendicitis or diverticulitis.

Chronic inflammation and dysbiosis in the colon and small intestine underlie inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. Even digestive tract malignancies can be an end result of long-standing microbial imbalance and inflammation, as seen in some cases of colorectal cancer.⁶

<u>Inflammation:</u> The Central Role of Inflammation in Digestive Illness: Molecular Markers and Mechanisms

Digestive disorders, from irritable bowel syndrome (IBS) to inflammatory bowel disease (IBD), celiac disease, and nonalcoholic fatty liver disease (NAFLD), share a unifying pathophysiologic thread: *inflammation*.¹ While symptoms differ across conditions—bloating, diarrhea, abdominal pain, ma.labsorption—the underlying biological process frequently centers on the activation of the intestinal immune response.

Over the past two decades, research has identified several key molecular markers that provide both mechanistic insight and clinical utility in tracking intestinal inflammation. Among these are markers of immunity--interleukins such as IL-1² and IL-6,³ tumor necrosis factor alpha (TNF-α),⁴ lipopolysaccharides (LPS),⁵ zonulin,⁶ diamine oxidase (DAO),⁷ and intestinal fatty acid-binding protein (I-FABP).⁸

The intestinal tract is a dynamic interface between the external environment (food, microbes, toxins) and the internal immune system. Normally, the intestinal epithelial barrier, tight junction proteins, mucus layers, and immune tolerance mechanisms maintain a balanced state—allowing nutrient absorption without excessive immune activation. However, when the barrier is compromised or the microbial balance shifts (dysbiosis), the immune system becomes persistently activated. This chronic inflammation damages tissue, impairs digestion, and contributes to systemic disease.⁹

IN.TERLEUKINS: Interleukin-1 (IL-1) is one of the first responders in the inflammatory cascade.² Produced primarily by activated macrophages, it promotes leukocyte recruitment, fever, and the production of other cytokines. Elevated IL-1 levels are seen in active Crohn's disease, ulcerative colitis, and even IBS subtypes characterized by low-grade inflammation.

Interleukin-6 (IL-6) serves as both a pro-inflammatory and antiinflammatory mediator.³ It is secreted by T cells, macrophages, and epithelial cells, contributing to acute-phase responses, B cell differentiation, and CRP (C-reactive protein) production. Chronic overproduction of IL-6 is implicated in IBD pathogenesis and correlates with disease activity and relapse risk.

TUMOR NECROSIS FACTOR ALPHA: Tumor necrosis factor alpha (TNF-α) plays a central role in mediating intestinal inflammation.⁴ Secreted by macrophages, mast cells, and T cells, TNF-α promotes leukocyte adhesion, endothelial activation, and epithelial apoptosis. Its critical role is highlighted by the success of anti-TNF biologics (*like infliximab*) in treating IBD, where they help induce and maintain remission by blocking this potent inflammatory signal.

LIPOPOLYSACCHARIDE: Lipopolysaccharide (LPS), a structural component of Gram-negative bacterial cell walls, acts as a powerful endotoxin.⁵ When gut permeability increases (so-called "leaky gut"), LPS translocates across the epithelial barrier into the body, triggering receptors on immune cells. This activation leads to widespread production of IL-1, IL-6, TNF- α , and other inflammatory mediators, fueling both local and systemic inflammation. Elevated serum LPS levels are linked to metabolic endotoxemia, obesity, insulin resistance, and hepatic inflammation.

ZONULIN: Zonulin is a human protein that modulates intercellular tight junctions in the gut epithelium.⁶ Elevated zonulin levels lead to increased intestinal permeability, facilitating the passage of antigens, toxins, and microbes into the submucosa. Zonulin is upregulated in celiac disease, type 1 diabetes, and several autoimmune disorders, suggesting it plays a pivotal role in barrier dysfunction and inflammation.

DIAMINE OXIDASE: Diamine oxidase (DAO) is an enzyme responsible for degrading dietary histamine in the gut.⁷ Reduced DAO activity or impaired function leads to histamine accumulation, which can exacerbate inflammatory responses and contribute to symptoms like diarrhea, cramping, and bloating. While not a direct inflammatory cytokine, DAO serves as an indirect marker of gut inflammation and permeability, especially in histamine intolerance syndromes.

INTESTINAL FATTY ACID-BINDING PROTEIN (I-FABP)

Intestinal fatty acid-binding protein (I-FABP) is a small cytoplasmic protein abundant in mature enterocytes of the small intestine.⁸ When epithelial cells are injured—due to ischemia, inflammation, or infection—I-FABP is released into the bloodstream. Elevated serum levels provide a sensitive marker of acute intestinal injury, making it a useful tool in conditions like necrotizing enterocolitis, acute mesenteric ischemia, and even monitoring IBD activity.

Whether driven by immune dysregulation, microbial imbalance, genetic susceptibility, or environmental triggers, *inflammation emerges as the shared physiological driver across most digestive illnesses.*¹⁰ Understanding and measuring markers like IL- 1, IL-6, TNF- α , LPS, zonulin, DAO, and I-FABP allows clinicians and researchers to track disease activity, guide treatment, and develop targeted therapies. Moving forward, integrating these molecular insights with dietary, microbial, and lifestyle interventions holds the promise of more personalized and effective management of intestinal inflammatory disorders.

RESOURCES:

Fiocchi, Claudio. "Inflammatory Bowel Disease: Etiology and Pathogenesis." Gastroenterology 115, no. 1 (1998): 182–205. https://doi.org/10.1016/S0016-5085(98)70381-6.

2. Dinarello, Charles A. "Interleukin-1 in the Pathogenesis and Treatment of Inflammatory Diseases." Blood 117, no. 14 (2011): 3720–32. https://doi.org/10.1182/blood-2010-07-273417.

3. Kishimoto, Tadamitsu. "IL-6: From Its Discovery to Clinical Applications." International Immunology 22, no. 5 (2010): 347–52. https://doi.org/10.1093/intimm/dxq030.

4. Feldmann, Marc, and Ravinder N. Maini. "TNF Defined as a Therapeutic Target for Rheumatoid Arthritis and Other Autoimmune Diseases." Nature Medicine 9, no. 10 (2003): 1245–50. https://doi.org/10.1038/nm939.

5. Cani, Patrice D., and Nathalie M. Delzenne. "The Role of the Gut Microbiota in Energy Metabolism and Metabolic Disease." Current Pharmaceutical Design 15, no. 13 (2009): 1546–58. https://doi.org/10.2174/138161209788168164.

6. Fasano, Alessio. "Zonulin and Its Regulation of Intestinal Barrier Function: The Biological Door to Inflammation, Autoimmunity, and Cancer." Physiological Reviews 91, no. 1 (2011): 151–75. https://doi.org/10.1152/physrev.00003.2008.

7. Schwelberger, Hubert G. "Histamine Intolerance: A Metabolic Disease?" Inflamm Res 59 (2010): S219–S221. <u>https://doi.org/10.1007/s00011-010-</u> 2156-1.

8. Derikx, Joep P. M., et al. "New Insight in Loss of Gut Barrier during Major Non-Abdominal Surgery." PLoS One 3, no. 12 (2008): e3954. https://doi.org/10.1371/journal.pone.0003954.

9. Peterson, Loren W., and Daniel Artis. "Intestinal Epithelial Cells: Regulators of Barrier Function and Immune Homeostasis." Nature Reviews Immunology 14, no. 3 (2014): 141–53. https://doi.org/10.1038/nri3608.

10. Honda, Kenya, and Dan R. Littman. "The Microbiota in Adaptive Immune Homeostasis and Disease." Nature 535, no. 7610 (2016): 75–84. https://doi.org/10.1038/nature18848.

ADDENDUM: Not All Inflammation Is Caused by Infection

It is important to make a key distinction here: while all infections cause inflammation, not all inflammation is caused by infection. Infections by bacteria, viruses, or fungi are well-known triggers of inflammation. However, in many chronic digestive diseases, inflammation occurs in the absence of active infection and instead results from immune dysregulation, dietary triggers, environmental insults, or microbial imbalances. Recognizing this difference is crucial. It influences treatment strategies: antibiotics may address infection, but they do little to address non-infectious inflammation—and may even exacerbate it by disturbing the gut microbiome.

REFERENCES:

^{1.} Susan V. Lynch and Oluf Pedersen, "The Human Intestinal Microbiome in Health and Disease," *New England Journal of Medicine* 375, no. 24 (2016): 2369–79. <u>https://doi.org/10.1056/NEJMra1600266</u>.

² DeGruttola, Andrea K., Ethan Low, Luis Mizoguchi, Jun Sun, Jonathan K. Mizoguchi, and Mari Mino-Kenudson. "Current Understanding of Dysbiosis in Disease in Human and Animal Models." *Inflammatory Bowel Diseases* 22, no. 5 (2016): 1137–1150. https://doi.org/10.1097/MIB.00000000000750.

^{3.} Petersen, Charisse, and June L. Round. "Defining Dysbiosis and Its Influence on Host Immunity and Disease." *Cell Microbiology* 16, no. 7 (2014): 1024–1033. <u>https://doi.org/10.1111/cmi.12308.</u>

^{4.} Fasano, Alessio. "Zonulin, Regulation of Tight Junctions, and Autoimmune Diseases." Annals of the New York Academy of Sciences 1258, no. 1 (2012): 25–33. <u>https://doi.org/10.1111/j.1749-</u> 6632.2012.06538.x.

^{5.} Tonetti, Maurizio S., and Thomas E. Van Dyke. "Periodontitis and Atherosclerotic Cardiovascular Disease: Consensus Report of the Joint EFP/AAP Workshop." *Journal of Clinical Periodontology* 40 (2013): S24– S29. <u>https://doi.org/10.1111/jcpe.12047.</u>

^{6.} Wong, Shannon H., and Jun Yu. "Gut Microbiota in Colorectal Cancer: Mechanisms of Action and Clinical Applications." *Nature Reviews Gastroenterology* & *Hepatology* 16, no. 11 (2019): 690–704. <u>https://doi.org/10.1038/s41575-019-0209-8.</u>

^{7.} Sonnenburg, Justin L., and Erica D. Sonnenburg. "The Good Gut: Taking Control of Your Weight, Your Mood, and Your Long-Term Health." *Penguin Press*, 2015.

^{8.} Fasano, Alessio, and Susie Flaherty. *Gut Feelings: The Microbiome and Our Health*. Cambridge, MA: The MIT Press, 2021.

Harvard T.H. Chan School of Public Health. "Alessio Fasano." Accessed April 20, 2025. <u>https://nutrition.hms.harvard.edu/people/alessio-fasano</u>

Dr. Fasano is Professor of Pediatrics at Harvard Medical School and Professor of Nutrition at the Harvard T.H. Chan School of Public Health. He also serves as the Director of the Center for Celiac Research and Treatment at Massachusetts General Hospital. Susie Flaherty is the Director of Communications at the same center.

SECTION TWO

STAGGERING NUMBERS



IT'S HUMBLING TO REALIZE THAT LESS THAN HALF OF THE HUMAN BODY IS ACTUALLY COMPOSED OF HUMAN CELLS



"Because we humans are big and clever enough to produce and utilize antibiotics and disinfectants, it is easy to convince ourselves that we have banished bacteria to the fringes of existence. Don't you believe it. Bacteria may not build cities or have interesting social lives, but they will be here when the Sun explodes. This is their planet, and we are on it only because they allow us to be."

--Bill Bryson

*Bryson, Bill. A Short History of Nearly Everything. New York: Broadway Books, 2003.

Thirty Trillion Body Cells with 22,000 Genes

The Human Microbiome Project (HMP)—a groundbreaking initiative led by the National Institutes of Health (NIH)—brought together over 200 researchers from 80 institutions with the goal of mapping the microbial populations found in healthy adults. Their efforts identified more than 10,000 distinct microbial species inhabiting different regions of the human body.¹

One of the most striking findings of this project is that microbial cells vastly outnumber human cells. While the human body contains approximately 30 trillion human cells, it harbors an estimated 39 trillion microbial cells. These microbes are not passive passengers—they are actively involved in essential physiological processes, including nutrient metabolism, immune system modulation, and protection against pathogens.²

Though precise figures continue to evolve, it is clear that the number of microbial genes far exceeds that of the human genome. Human cells carry roughly 22,000 protein-coding genes, while microbial communities collectively contribute millions of genes. These microbial genes encode enzymes and proteins critical to breaking down complex carbohydrates, synthesizing essential vitamins, and modulating immune responses.³

Humans and their microbiota have co-evolved as a synbiotic system, in which the health of one is deeply dependent on the health of the other. The body provides a stable, nutrient-rich environment for microbial survival, while microbes perform functions the human genome alone cannot accomplish. When this delicate balance is disrupted, a wide range of health complications can result—highlighting the importance of maintaining a diverse, resilient microbiome.⁴

Cohabiting Microbes Contain Over 200 Million Genes

Each microorganism carries genes that encode proteins essential for its survival and its interactions within the host environment. Similarly, human genes regulate bodily processes and help mediate interactions with the external world.⁵

A large-scale study by Dr. Brandon Tierney and colleagues at Harvard Medical School examined the microbiomes of 3,600 adults. Their findings revealed that the human digestive tract alone contains approximately 200 million non-redundant microbial genes.⁶

When bacteriophages—viruses that infect bacteria—are included, the total gene count increases dramatically. These viruses

contribute additional layers of genetic material, potentially adding hundreds of millions of genes to the ecosystem.⁷

Our knowledge, however, about phages is limited since the vast majority of them remain unmapped. It's accurate to say that the expanded gene pool contributed by phages further amplifies the complexity and adaptability of the gut microbiome.

Tierney's team also discovered that the digestive tract contains up to 150,000 unique microbial strains, many with minor genetic variations even within the same species. These differences influence individual responses to diet, susceptibility to illness, immune signaling, and metabolic capacity—offering a clearer picture of why health outcomes vary so widely from person to person.

Together, these findings reinforce a central idea: the human gut is not just a site of digestion—it is a genetically rich constellation of ecosystems whose diversity and integrity are fundamental to health.

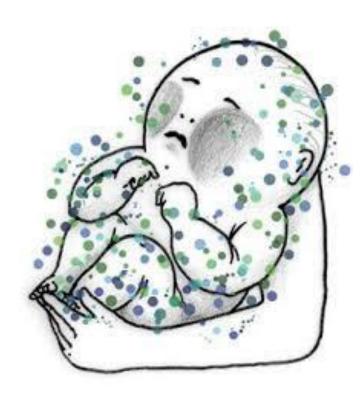
REFERENCES:

 Pasolli, E., Asnicar, F., Manara, S., Zolfo, M., Karcher, N., Armanini, F., et al. "Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle." *Cell* 176, no. 3 (2019): 649–662.e20. <u>https://doi.org/10.1016/j.cell.2019.01.001</u>

- ^{2.} Garud, N. R., and Pollard, K. "Population Genetics in the Human Microbiome." *Trends in Genetics* 35, no. 10 (2019): 852–865. <u>https://doi.org/10.1016/j.tig.2019.10.010</u>
- ^{3.} Scepanovic, P., Hodel, F., Mondot, S., Partula, V., Byrd, A. L., et al. "A Comprehensive Assessment of Demographic, Environmental, and Host Genetic Associations with Gut Microbiome Diversity in Healthy Individuals." *Microbiome* 7 (2019): 130. <u>https://doi.org/10.1186/s40168-019-0747-x</u>
- ^{4.} Singh, N., and Haider, N. "Microbiota, Microbiome, and Retinal Diseases." International Ophthalmology Clinics 62 (2022): 197–214. <u>https://doi.org/10.1097/IIO.00000000000418</u>
- ^{5.} Zimmerman, S., Tierney, B., Patel, C., and Kostic, A. "Quantifying Shared and Unique Gene Content Across 17 Microbial Ecosystems." *bioRxiv* (2022). <u>https://doi.org/10.1101/2022.07.19.500741</u>
- ^{6.} Tierney, B., Yang, Z., Luber, J. M., et al. "The Landscape of Genetic Content in the Gut and Oral Human Microbiome." *Cell Host & Microbe* 26, no. 2 (2019): 283–295.e8. <u>https://doi.org/10.1016/j.chom.2019.07.008</u>
- ^{7.} Shoemaker, W. "A Macroecological Perspective on Genetic Diversity in the Human Gut Microbiome." *bioRxiv* (2022). <u>https://doi.org/10.1371/journal.pone.0288926</u>

SECTION THREE

How Infants Acquire Their First Microbes



Newborns acquire their initial microbiome from their mothers at birth—primarily through exposure to maternal secretions during vaginal delivery. This process introduces the infant to a diverse array of microbial life, including bacteria, viruses, fungi, protozoa, and archaea. Together, these microorganisms and their genetic material form the microbiome, a critical player in early human development.¹

During childbirth, large numbers of maternal microbes colonize the newborn's oral cavity, nasal passages, skin, and digestive tract. These early colonizers contribute to digestion, immune system maturation, and protection against pathogenic invaders. Research suggests that maternal gut microbes, transferred vertically during birth and breastfeeding, may exert the most lasting impact, as they are best suited to colonize and thrive in the infant's gastrointestinal environment.²

Maturation of the Infant's Microbiome

An infant's microbiome undergoes dramatic changes during the first few years of life, shaped by genetics, mode of delivery, feeding practices, antibiotic exposure, and environmental influences.³

- Breastfeeding supports the growth of beneficial microbes like *Bifidobacterium* species, which aid in nutrient absorption and immune development.⁴
- Formula-fed infants tend to have more *Firmicutes* and *Proteobacteria*, which may be associated with altered metabolism and increased gut inflammation.⁵
- Environmental exposures, including interaction with caregivers, siblings, and pets, enhance microbial diversity.⁶

Disruptions to this developmental process—whether from Cesarean delivery, early antibiotic use, or lack of breastfeeding can alter the natural progression of microbial colonization, increasing the risk of microbial dysbiosis and chronic disease later in life.

Long-Term Consequences of Microbial Dysbiosis in Infancy

Early-life dysbiosis, or microbial imbalance, has been associated with an elevated risk of:

- Asthma and allergies
- Type 1 diabetes
- Celiac disease
- Inflammatory bowel disease (IBD)
- Obesity

The First Six Months of Life: A Window of Opportunity

The first six months after birth represent a critical window during which gut microbial colonization shapes the development of the immune and metabolic systems.

- During this time, the infant's gut is exposed to microbe-associated molecular patterns (MAMPs) that trigger key immune responses.⁵
- Interventions such as breastfeeding promotion or probiotic supplementation during this window may prevent or mitigate dysbiosis-related conditions.³

REFERENCES:

 Ferretti, P., Pasolli, E., Tett, A., et al. (2018). "Mother-to-infant microbial transmission from different body sites shapes the developing infant gut microbiome." *Cell Host & Microbe*, 24: 133–145.e5. <u>https://doi.org/10.1016/j.chom.2018.06.005</u>

- ^{2.} Wang, S., Ryan, C., Boyaval, P., et al. (2019). "Maternal vertical transmission affecting early-life microbiota development." *Trends in Microbiology*. <u>https://doi.org/10.1016/j.tim.2019.07.010</u>
- ^{3.} DuPont, H. L., & Salge, M. M. H. (2023). "The importance of a healthy microbiome in pregnancy and infancy." *Antibiotics*, 12. <u>https://doi.org/10.3390/antibiotics12111617</u>
- ^{4.} Stewart, C. J., Ajami, N. J., O'Brien, J. L., et al. (2018). "Temporal development of the gut microbiome in early childhood from the TEDDY study." *Nature*, 562(7728): 583–588. <u>https://doi.org/10.1038/s41586-018-0617-x</u>
- ^{5.} Aires, J. (2021). "First 1000 Days of Life: Consequences of Antibiotics on Gut Microbiota." *Frontiers in Microbiology*, 12: 681427. <u>https://doi.org/10.3389/fmicb.2021.681427</u>
- ^{6.} Wopereis, H., Oozeer, R., Knipping, K., Belzer, C., & Knol, J. "The First Thousand Days—Intestinal Microbiology of Early Life: Establishing a Symbiosis." *Pediatric Allergy and Immunology* 25, no. 5 (2014): 428– 438. <u>https://doi.org/10.1111/pai.12232.</u>

SECTION FOUR

THE LASTING IMPACT OF EARLY LIFETIME EVENTS ON LATER HEALTH--

A FOCUS ON DYSBIOSIS

Recent research has highlighted the lasting influence of early-life microbial exposures on long-term health, with a particular focus on the role of human milk oligosaccharides (HMOs), the infant microbiome, and factors contributing to dysbiosis—a state of microbial imbalance.

Premature Birth and Microbial Colonization

Premature birth (before 37 weeks of gestation) may interfere with the natural progression of microbial colonization that typically occurs during the third trimester. Some researchers propose that fetal exposure to microbes via the placenta or amniotic fluid may help prime the neonatal immune system and prepare the gut for microbial life.¹

This theory challenges the longstanding belief that the womb is sterile. Although debated, studies have detected microbial DNA in placental, amniotic, and fetal tissues, suggesting the possibility of in utero microbial exposure. Some scientists argue this may be the result of contamination, while others suggest that even non-viable microbial fragments may influence fetal development.

In preterm infants, who miss this late-gestation microbial exposure, initial colonization often comes from hospital-associated organisms. Medical interventions, especially antibiotics, can further disrupt microbial development. This early dysbiosis has been linked to greater risks of infection, autoimmune diseases, and metabolic disorders.¹²³

Mode of Delivery: C-Section vs. Vaginal Birth

The mode of delivery significantly influences microbiome composition:

- Vaginal birth exposes infants to beneficial maternal microbes, especially *Lactobacillus* and *Bifidobacterium*, which support immune training and metabolic health.
- Cesarean delivery, in contrast, introduces skin- and hospital-derived microbes.

Infants born by C-section often have reduced microbial diversity and lower colonization with protective species—an imbalance associated with elevated risks for asthma, allergies, obesity, and autoimmune conditions.

Breastfeeding and Human Milk Oligosaccharides (HMOs)

Breast milk is uniquely suited to promote a healthy infant microbiome. It contains over 200 types of human milk oligosaccharides (HMOs)—specialized prebiotic sugars that selectively nourish beneficial bacteria like *Bifidobacterium*.

- HMOs such as 2'-fucosyllactose (2'FL) foster gut integrity, immune development, and resistance to pathogens.
- Formula-fed infants do not receive the same diversity of HMOs, and this absence has been linked to higher

rates of infections, allergies, and inflammation-related disorders.

Bridging the Gap: Formula Supplementation with HMOs

To reduce disparities between formula-fed and breastfed infants, some formulas now include bioengineered HMOs such as 2'FL.

- Clinical trials show that 2'FL-supplemented formulas help establish a gut microbiome more similar to that of breastfed infants.
- These formulas have also been linked to reduced respiratory and gastrointestinal infections, and enhanced immune responses.⁴
- Regulatory agencies including the FDA and EFSA have approved the use of 2'FL in infant nutrition.

The Impact of Early Antibiotic Exposure

Antibiotics, though essential in treating infections, can profoundly disrupt the developing microbiome when used in infancy.

- Early and frequent antibiotic use reduces microbial diversity and allows the overgrowth of opportunistic or resistant organisms.
- These alterations increase susceptibility to inflammatory bowel disease (IBD), obesity, allergies, and even mood disorders.

• The first year of life is especially critical, as the microbiome is highly vulnerable during this formative stage.

Other Factors Contributing to Dysbiosis

- Early introduction of solid foods, especially processed or lowfiber diets, may encourage the growth of pro-inflammatory microbes.
- Environmental toxins such as pesticides and pollutants disrupt gut ecology and promote systemic inflammation.
- The "hygiene hypothesis" suggests that reduced microbial exposure in modern, sanitized environments may impair immune education, increasing the risk of allergies and autoimmune diseases.

Dysbiosis and Immune-Related Diseases

Because the gut microbiome is essential in shaping immune tolerance and inflammation control, dysbiosis in infancy can tilt the immune system toward dysregulation:

- Children with early-life dysbiosis show increased risk for eczema, asthma, type 1 diabetes, and other autoimmune conditions.
- Chronic dysbiosis may perpetuate low-grade systemic inflammation, contributing to disease progression later in life.

CONCLUSION:

The early years of life are foundational for establishing a healthy microbiome that supports lifelong wellness.

Factors such as prematurity, Cesarean birth, lack of breastfeeding, early antibiotic exposure, and poor environmental conditions can disrupt this process, leading to microbial imbalances with longterm consequences.

Interventions that support microbial development include natural childbirth, exclusive breastfeeding, judicious antibiotic use, and fostering diverse microbial exposure. These factors are essential for reducing the burden of dysbiosis-linked diseases. Ongoing research continues to explore strategies to restore and enhance microbial health in early life and beyond.

REFERENCES:

- Aagaard, K., et al. (2014). "The Placenta Harbors a Unique Microbiome." Science Translational Medicine 6 (254): 254ra127. <u>https://doi.org/10.1126/scitranslmed.3008599</u>
- Berger, P. K., et al. (2020). "Human Milk Oligosaccharide 2'-Fucosyllactose Links Feedings at One Month to Cognitive Development at 24 Months." *PLOS ONE* 15(2): e0228323. <u>https://doi.org/10.1371/journal.pone.0228323</u>
- Craft, K. M., & Townsend, S. D. (2018). "The Human Milk Glycome as a Defense Against Infectious Diseases." ACS Infectious Diseases 4(2): 77– 83. <u>https://doi.org/10.1021/acsinfecdis.7b00209</u>

- Goehring, K. C., et al. (2016). "Infants Fed a Formula Containing 2'-Fucosyllactose Have Lower Inflammatory Cytokines." *The Journal of Nutrition* 146(12): 2559–2566. <u>https://doi.org/10.3945/jn.116.236919</u>
- Perez-Muñoz, M. E., et al. (2017). "A Critical Assessment of the 'Sterile Womb' Hypothesis." *Microbiome* 5(1): 48. <u>https://doi.org/10.1186/s40168-017-0268-4</u>
- Puccio, G., et al. (2017). "Effects of Infant Formula with Human Milk Oligosaccharides." J Pediatr Gastroenterol Nutr 64(4): 624–631. <u>https://doi.org/10.1097/MPG.00000000001520</u>
- Stinson, L. F., et al. (2019). "Evidence That the Human Fetus Is Exposed to Bacteria Prior to Birth." *Front Microbiol* 10: 1124. <u>https://doi.org/10.3389/fmicb.2019.01124</u>
- Triantis, V., et al. (2018). "Immunological Effects of Human Milk Oligosaccharides." Front Pediatr 6: 190. <u>https://doi.org/10.3389/fped.2018.00190</u>

SECTION FIVE

THE FIRST THREE ECOSYSTEMS: ORAL CAVITY, ESOPHAGUS, AND STOMACH



The oral cavity, esophagus, and stomach constitute the initial segments of the digestive system, functioning collectively as the body's "food processor." They transform ingested nutrients through physical, chemical, and microbial interactions, preparing them for absorption in the intestines.

Physical Changes

These regions collaborate to modify the size and consistency of ingested food, facilitating efficient absorption further along the digestive tract.

ORAL CAVITY ECOSYSTEM

Chemical Changes

Chemical digestion begins in the oral cavity, where salivary amylase initiates carbohydrate breakdown, and lingual lipase begins fat digestion. This process continues in the stomach, where gastric acid and proteolytic enzymes further degrade proteins and other macromolecules.

ESOPHAGEAL ECOSYSTEM

The esophagus maintains its health and functionality through a complex interplay of components:

- Microbiota: The esophagus hosts a unique microbial community, including bacteria such as *Streptococcus*, *Prevotella*, and *Veillonella*. This composition is influenced by diet, health status, and colonization patterns throughout the digestive tract.
- **Epithelial Cells:** These cells form a protective lining, shielding the esophagus from mechanical damage, pathogens, and chemical injury, while also participating in immune responses.
- Immune Cells: Lymphocytes, macrophages, and dendritic cells patrol the esophageal lining, detecting and responding to potential threats such as pathogens or allergens.
- <u>Mucus</u>: Secreted by esophageal glands, mucus lubricates and protects the lining, trapping microbes and debris to facilitate their removal.
- Enzymes and Antimicrobial Peptides: These secretions aid in the breakdown of ingested materials and provide defense against microbial invasion.

- <u>Nerve Networks</u>: The esophagus is innervated by the enteric nervous system, which manages peristalsis and sphincter control, regulating the flow of material.
- Physical and Chemical Barriers: The upper and lower esophageal sphincters, along with the acidic environment at the stomach junction, serve as barriers that regulate passage and inhibit microbial overgrowth.

Understanding the esophageal ecosystem is crucial for diagnosing and treating conditions such as gastroesophageal reflux disease (GERD), esophagitis, eosinophilic esophagitis, Barrett's esophagus, and esophageal cancers.

GASTRIC ECOSYSTEM

Gastric Acid: A Critical Antimicrobial Protective Secretion

Gastric acid, produced by parietal cells in the stomach lining, plays a vital role in digestion and defense against ingested pathogens. Under normal conditions, this acidic environment neutralizes up to 99.9% of ingested microbes. However, reduced gastric acid levels can increase the risk of microbial migration into the small intestine, potentially leading to conditions such as Small Intestinal Bacterial Overgrowth (SIBO).

Factors that can reduce gastric acid include:

Use of acid-reducing medications

- Autoimmune conditions affecting the gastric lining, such as pernicious anemia
- Helicobacter pylori infection of the stomach
- Surgical procedures that reduce acid-producing cells
- Retrograde bile flow from the small intestine into the stomach

The Stomach: A Dual Role in Digestion and Microbial Defense

The stomach acts as both a digestive organ and an ecological barrier, regulating the entry of nutrients and microbes into the digestive tract. Its combination of gastric acid and enzymes not only breaks down food into absorbable components but also defends against harmful pathogens. This dual role is essential for preventing downstream conditions like SIBO and systemic infections.¹

LESSONS LEARNED FROM

THE TURKEY VULTURE



The turkey vulture, which thrives on decaying meat, provides a compelling example of nature's survival strategies. With a stomach pH often below 1.0—more acidic than battery acid—it can safely digest pathogen-laden meat. This extreme acidity neutralizes harmful bacteria such as *Clostridium*, *Salmonella*, and *Bacillus anthracis*, protecting the bird from intestinal infection.

Similarly, the human stomach's acidic environment serves as a protective barrier, reducing the risk of pathogenic colonization in the small bowel and colon. This cross-species mechanism of microbial control—via extreme gastric acidity—demonstrates nature's tendency to adopt similar solutions across different life forms.

Gastric Acid and Human Health: A Delicate Balance

When the stomach's acid barrier is compromised—due to medications or conditions like hypochlorhydria—the risk of microbial overgrowth increases. Studies link long-term acid suppression therapy to elevated risks of SIBO, *Clostridioides* *difficile* infections, and even pneumonia due to weakened microbial defenses. Reduced acid levels disrupt this gatekeeping function, allowing bacteria from the oral cavity or food to survive and colonize the small intestine.

<u>A Unified Survival Strategy: Duplication Across Life Forms</u>

The vulture's resilience to pathogens underscores the evolutionary value of a highly acidic gastric environment. In humans and other species, gastric acid remains essential to both digestive and immune functions. This strategy—repeated across organisms— highlights nature's preference for effective, conserved survival mechanisms.

Thus, stomach acid functions not only as a digestive agent but also as an evolutionary safeguard against microbial threats, supporting the health of the entire digestive ecosystem. Preserving this gastric barrier is essential for nutrient absorption and microbial balance throughout the gut.

THE SMALL INTESTINE ECOSYSTEM



The adult human small intestine, approximately 22 feet long, is the primary site for digestion and absorption of nutrients, vitamins, minerals, and water. Its function is enhanced by the liver, gallbladder, and pancreas—accessory organs that contribute specialized secretions to aid digestion.

Physical Changes

As partially digested food, now called chyme, enters the small intestine from the stomach, its semi-liquid consistency maximizes surface area for nutrient absorption.

Chemical Changes

Digestion in the small intestine depends on enzymes during a transit time of approximately five hours. While the intestine has limited intrinsic enzymatic capacity, it relies heavily on external secretions:

- Pancreatic Enzymes: These include amylase, lipase, and proteases for the digestion of carbohydrates, fats, and proteins.
- <u>Bile Acids</u>: Produced by the liver and stored in the gallbladder, bile emulsifies fats, facilitating their digestion and absorption.

Microbial Dynamics

While the stomach's acidity eliminates most ingested microbes, some acid-resistant bacteria, such as *Porphyromonas gingivalis*, can survive and reach the small intestine. *P. gingivalis*, linked to periodontitis, has even been detected in colon cancer tissues, suggesting effects beyond the oral cavity. Additionally, bacterial spores resistant to acid and enzymes may reach the small bowel intact.

Bile as an Antimicrobial Agent

Both bile and pancreatic secretions help regulate microbial populations. Bile acids, in particular, have antimicrobial effects that contribute to maintaining gut microbiota balance.

However, the following can impair bile's effectiveness:

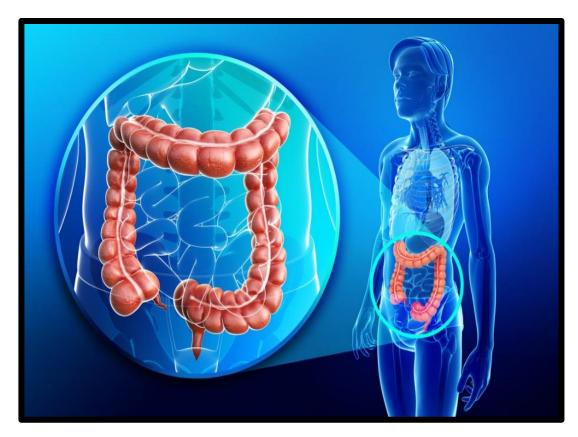
- Cholesterol-lowering drugs
- Gallbladder removal
- Pancreatic insufficiency

Surgeries or diseases affecting secretion pathways

These impairments may contribute to microbial overgrowth as in SIBO and IMO. (See List 5—Factors That Alter the Microbiome.)

Understanding the interplay of physical, chemical, and microbial factors is crucial to appreciating the small intestine's role in both health and disease.

THE COLON: THE MOST COMPLEX ECOSYSTEM IN THE BODY



The colon, or large intestine, is a densely populated microbial ecosystem, hosting trillions of organisms that perform essential functions far beyond waste elimination.

Overview of the Colonic Ecosystem

Approximately 1.5 meters (5 feet) long, the colon contains the densest concentration of microbes in the human body—estimated at up to 38 trillion. This diverse population includes bacteria, archaea, fungi, viruses, and protozoa that form a self-sustaining ecosystem with direct interaction with the host's immune and intestinal cells.

<u>The Compartmentalized Colon:</u> <u>A Splitter's Perspective on Colonic Ecology and Function</u>

The human colon is often described as a uniform tube tasked with absorbing water and storing waste, but this simplistic view overlooks the colon's extraordinary ecological and functional compartmentalization. Just as ecosystems vary by geography and climate, different segments of the colon possess distinct microbial populations, biochemical conditions, and physiological responsibilities.

The cecum, for instance, serves as a fermentation chamber where undigested fibers undergo microbial metabolism, producing shortchain fatty acids (SCFAs) such as acetate, propionate, and butyrate that nourish colonocytes and regulate inflammation. This region maintains a slightly acidic pH, fostering anaerobic fermentation by saccharolytic bacteria like *Bacteroides* and *Faecalibacterium* species.¹

As contents progress toward the transverse and descending colon, shifts occur in substrate availability, bile acid concentration, and microbial diversity. The depletion of easily fermentable fibers allows proteolytic and putrefactive species—such as *Clostridium* and *Fusobacterium*—to dominate, leading to the production of branched-chain fatty acids, ammonia, phenols, and other potentially harmful metabolites.² These shifts may increase luminal pH and contribute to oxidative stress, mucosal inflammation, and epithelial barrier dysfunction.³

Bile acids play a central role in shaping colonic biogeography. Primary bile acids secreted from the liver are transformed by colonic microbes into secondary bile acids like deoxycholic acid and lithocholic acid. While some secondary bile acids exert antimicrobial effects and regulate gut motility, excessive accumulation may promote epithelial injury and colorectal cancer.⁴ Regional variations in bile acid metabolism underscore the importance of spatial context in assessing colonic health.⁵

The rectum, positioned as the colon's final segment, is distinct not only in function but also in its microbial community, exposure to dietary residues, and immune surveillance. It is more frequently colonized by aerotolerant species due to higher oxygen tension and its proximity to the external environment.⁶ This region also exhibits heightened immune cell density and serves as a checkpoint for microbial translocation, inflammation, and antigen sampling.

Neuroenteric signaling further illustrates colonic compartmentalization. The enteric nervous system (ENS) demonstrates regional specificity, with variations in neuronal density, receptor expression, and neurotransmitter activity along the colon.⁷ These neurochemical gradients influence peristalsis, microbial interactions, and visceral sensitivity, reinforcing the concept of a compartmentalized gut-brain interface.

Considering the colon as a patchwork of microenvironments rather than a monolithic organ invites a more precise understanding of gut health. Therapeutic interventions—including fiber supplementation, prebiotics, probiotics, polyphenols and fecal microbiota transplantation—should account for the functional diversity of colonic regions. A "splitter's" perspective emphasizes tailoring interventions to specific ecological niches, rather than applying uniform treatments across heterogeneous terrain.⁸

REFERENCES:

^{1.} Cummings, J. H., and G. T. Macfarlane. "The Control and Consequences of Bacterial Fermentation in the Human Colon." *Journal of Applied Bacteriology* 70, no. 6 (1991): 443–459. <u>https://doi.org/10.1111/j.1365-</u> <u>2672.1991.tb02739.x.</u>

^{2.} Zheng, Wei, Kairui Wang, Yijun Sun, and S. Kuo. "Dietary or Supplemental Fermentable Fiber Intake Reduces the Presence of Clostridium XI in Mouse Intestinal Microbiota: The Importance of Higher Fecal Bacterial Load and Density." PLoS ONE 13 (2018). https://doi.org/10.1371/journal.pone.0205055.

^{3.} Louis, P., and H. J. Flint. "Formation of Propionate and Butyrate by the Human Colonic Microbiota." *Environmental Microbiology* 19, no. 1 (2017): 29–41<u>. https://doi.org/10.1111/1462-2920.13589.</u>

^{4.} Ridlon, J. M., D. J. Kang, and P. B. Hylemon. "Bile Salt Biotransformations by Human Intestinal Bacteria." *Journal of Lipid Research 47, no. 2 (2006): 241–259.* <u>https://doi.org/10.1194/jlr.R500013-</u> JLR200.

^{5.} Devlin, A. S., and E. B. Fischbach. "A Biosynthetic Pathway for a Prominent Class of Microbiota-Derived Bile Acids." *Nature Chemical Biology* 11, no. 9 (2015): 685–690. https://doi.org/10.1038/nchembio.1864.

^{6.} Bassis, C. M., et al. "Analysis of the Upper Respiratory Tract Microbiotas as the Source of the Lung and Gastric Microbiotas in Healthy Individuals." *mBio* 6, no. 2 (2015): e00037-15. <u>https://doi.org/10.1128/mBio.00037-15.</u>

^{7.} Furness, J. B. "The Enteric Nervous System and Neurogastroenterology." *Nature Reviews Gastroenterology & Hepatology* 9, no. 5 (2012): 286–294. <u>https://doi.org/10.1038/nrgastro.2012.32.</u>

^{8.} Zmora, N., et al. "Personalized Gut Mucosal Colonization Resistance to Empiric Probiotics Is Associated with Unique Host and Microbiome Features." *Cell* 174, no. 6 (2018): 1388–1405.e21. <u>https://doi.org/10.1016/j.cell.2018.08.041.</u>

Distinctive Features of the Colonic Environment

1. <u>Anaerobic Conditions</u>: The colon's low-oxygen environment favors obligate anaerobes like *Bacteroides, Firmicutes,* and *Clostridium* species, which generate vital short-chain fatty acids (SCFAs) such as butyrate, acetate, and propionate.

2. Nutrient Supply and Fermentation:

Microbes derive energy by fermenting dietary fibers and resistant starches, producing SCFAs and gases (e.g., methane, hydrogen sulfide), which support nutrition and motility.

3. <u>Metabolic Versatility</u>: The colon acts as a fermentation hub, producing SCFAs, synthesizing vitamins (notably K and B vitamins), detoxifying harmful compounds, and regulating bile acid metabolism.

(**See:** Fermentable Substrates Produce Short-Chain Fatty Acids—The Molecular Currency of Digestive Well-Being.)

The Colon's Role in Systemic Health

- 1. <u>Immune System Education</u>: About 70% of immune cells reside in the gut-associated lymphoid tissue (GALT), where microbial interactions help train the immune system and prevent autoimmunity.
- 2. <u>Gut-Brain Axis</u>: Colonic microbes communicate with the brain via hormonal, neural, and immune pathways. SCFAs like

butyrate help maintain the blood-brain barrier and influence neurotransmitter production.

- 3. <u>Metabolic Regulation</u>: The microbiota modulate host metabolism, influence insulin sensitivity, and regulate fat storage. Dysbiosis has been linked to obesity, type 2 diabetes, and fatty liver disease.
- 4. **Barrier Function and Disease Prevention:** The colon's epithelial barrier blocks pathogens and absorbs beneficial metabolites. Butyrate fuels colonocytes and helps reduce permeability, protecting against "leaky gut."

The Dynamic Interplay of Microbial and Host Factors

The colonic ecosystem's stability depends on microbial-host interactions, including dietary inputs, immune responses, hormone signaling, and bile acid profiles. Disruptions—via antibiotics, illness, or poor diet—can lead to dysbiosis, affecting health broadly.

Clinical Implications of a Dysregulated Colonic Ecosystem

A healthy colon is essential for overall well-being. Dysbiosis has been linked to inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), and colorectal cancer. Systemic disorders—like cardiovascular disease, depression, and neurodegeneration—also correlate with altered colonic microbiota. Therapeutic strategies such as dietary interventions, prebiotics, probiotics, and fecal microbiota transplantation are under investigation.

Future Directions: Understanding the Colonic Microbiome

The colon's complexity demands further study. Advancements in metagenomics, metabolomics, and systems biology are helping uncover how host-microbe interactions impact health, paving the way for personalized, microbiome-based therapies.

CONCLUSION:

The colon is more than a waste-processing organ—it is a vital metabolic and immunological ecosystem. Its ability to digest fiber, support immunity, communicate with the brain, and regulate systemic health underlines its importance. Maintaining this ecosystem is essential for both digestive and overall health. Ongoing research will continue to unveil the colon's pivotal role as the most complex microbial ecosystem in the human body.

The next section explores thirty-six (36) distinct functions that microbes perform for their human host. Many more have yet to be discovered.

REFERENCES:

- Cummings, John H., and Glenn T. Macfarlane. "Role of Intestinal Bacteria in Nutrient Metabolism." *Journal of Parenteral and Enteral Nutrition* 21, no. 6 (1997): 357–65. <u>https://doi.org/10.1177/0148607197021006357.</u>
- Dinan, Timothy G., and John F. Cryan. 2017. "Gut Instincts: Microbiota as a Key Regulator of Brain Development, Ageing and Neurodegeneration." *The Journal of Physiology* 595 (2): 489–503. <u>https://doi.org/10.1113/JP273106.</u>

- Haiser, Henry J., and Peter J. Turnbaugh. 2012. "Is It Time for a Metagenomic Basis of Therapeutics?" *Science* 336 (6086): 1253–55. <u>https://doi.org/10.1126/science.1224396.</u>
- Lloyd-Price, Jason, Gholamali Abu-Ali, and Curtis Huttenhower. 2016.
 "The Healthy Human Microbiome." *Genome Medicine* 8 (1): 51. <u>https://doi.org/10.1186/s13073-016-0307-y.</u>
- Macfarlane, Glenn T., and Sylvia Macfarlane. 2012. "Bacteria, Colonic Fermentation, and Gastrointestinal Health." *Journal of AOAC International* 95 (1): 50–60. <u>https://doi.org/10.5740/jaoacint.SGE_Macfarlane.</u>
- Manichanh, Chaysavanh, Nuria Borruel, Francesc Casellas, and Francisco Guarner. 2012. "The Gut Microbiota in IBD." *Nature Reviews Gastroenterology & Hepatology* 9 (10): 599–608. <u>https://doi.org/10.1038/nrgastro.2012.152.</u>
- Ríos-Covián, David, Patricia Ruas-Madiedo, Abelardo Margolles, Miguel Gueimonde, Carlos G. de los Reyes-Gavilán, and Nuria Salazar. 2016.
 "Intestinal Short-Chain Fatty Acids and Their Link with Diet and Human Health." *Frontiers in Microbiology* 7: 185. <u>https://doi.org/10.3389/fmicb.2016.00185.</u>
- Sender, Ron, Shai Fuchs, and Ron Milo. 2016. "Are We Really Vastly Outnumbered? Revisiting the Ratio of Bacterial to Host Cells in Humans." *Cell* 164 (3): 337–40. <u>https://doi.org/10.1016/j.cell.2016.01.013.</u>
- Sonnenburg, Justin L., and Fredrik Bäckhed. 2016. "Microbiota Interactions as Moderators of Human Metabolism." *Nature* 535 (7610): <u>56–64. https://doi.org/10.1038/nature18846.</u>
- Turnbaugh, Peter J., Ruth E. Ley, Mark A. Mahowald, Vincent Magrini, Elaine R. Mardis, and Jeffrey I. Gordon. 2006. "An Obesity-Associated Gut Microbiome with Increased Capacity for Energy Harvest." *Nature* 444 (7122): 1027–31. <u>https://doi.org/10.1038/nature05414.</u>

Willems, Roel P. J., Karin van Dijk, Johannes C. F. Ket, and Christina M. J. E. Vandenbroucke-Grauls. "Evaluation of the Association Between Gastric Acid Suppression and Risk of Intestinal Colonization with Multidrug-Resistant Microorganisms: A Systematic Review and Meta-analysis." JAMA Internal Medicine 180, no. 4 (2020): 561–571.

https://doi.org/10.1001/jamainternmed.2020.0009.



THE BENEFICIAL ROLE OF MICROBES IN THE LARGE AND SMALL INTESTINES THAT SUPPORT WELL-BEING



Specific strains of microorganisms—particularly those living in the last portions of the small intestine and in the colon—are indispensable to human health and survival. This diverse microbial community, which includes bacteria, fungi, protozoa, viruses, and archaea, contribute to a wide range of essential biological functions. These microbes are deeply integrated into human physiology, assisting in digestion, synthesizing nutrients, modulating the immune system, and defending against pathogens. Their symbiotic relationship with the human host underscores their critical role in maintaining health and preventing disease.

A key mechanism by which intestinal microbes benefit the host is through the chemical process of fermentation. As non-digestible fibers pass through the small intestine and reach the colon, they are fermented by specific members of the microbial population. The chemical fermentation process produces short-chain fatty acids (SCFAs)—sometimes referred to as the microbial "currency" of digestive well-being.

When appropriately nourished, gut microbes generate short chain fatty acids (SCFAs), polyphenols and other bioactive chemicals that influence nearly every organ system in the body. They have enormous numbers of health benefits that are anti-inflammatory, immunoregulatory, anti-obesity, anti-cancer, cardiovascular protective, hepatoprotective, and neuroprotective. Below is a listing of some of the many benefits that the host derives from interaction with select microbes.

Fuel For Colonocytres

Butyrate is the primary energy source for colonocytes accounting for up to 70% of their energy needs, enhancing mucosal integrity and promoting cell survival.¹

Tight Junction Reinforcement

Short-chain fatty acids, particularly butyrate activates pathways that strengthen tight junctions, helping to seal the epithelial barrier.²

<u>Mucus Layer Support</u>

Short-chain fatty acids stimulate the secretion of mucin by goblet cells, maintaining the intestinal mucus barrier and protecting epithelial cells from microbial invasion.³

Ph Modulation

Short-chain fatty acids through the process of fermentation lower the luminal pH and suppress pathogenic bacterial growth, creating an environment favorable for beneficial microbes.⁴

Epithelial Oxygen Regulation

Short-chain fatty acids regulate the consumption of oxygen by lining cells of the digestive tract which helps maintain a low oxygen environment that favors the growth of anaerobic microbes.⁵

T Reg Cell Development

Butyrate and propionate promote the differentiation of regulatory T cells that are critical for suppressing inflammation and autoimmunity.⁶

Cytokine Balance

SCFAs decrease pro-inflammatory cytokines like TNF alpha and IL-6, and increase anti-inflammatory markers like IL-10.⁷

HDAC Inhibition

Histone deacetylase (HDAC) inhibition by butyrate alters gene expression in immune cells thereby reducing inflammation.⁸

Protection Against Intestinal Infections

The short-chain fatty acid, acetate, enhances epithelial defense and immune responses to reduce pathogen burden.⁹

Allergy and Autoimmunity Regulation

Short-chain fatty acids induce Treg cells and suppress hypersensitivity reactions, reduce allergic inflammation and the development of autoimmunity.¹⁰

Colorectal Cancer Protection

Butyrate induces apoptosis and cell cycle arrest in cancerous colonocytes potentially preventing the development of colon cancer.¹¹

Epigenetic Control

Short-chain fatty acids alter chromatin structure by inhibiting HDACs and altering gene transcription.¹²

Appetite Regulation

The short-chain fatty acid propionate stimulates the secretion of satiety hormones such as PYY and GLP-1 from enteroendocrine cells thereby promoting satiety and reducing calorie intake.¹³

Glucose Metabolism and Insulin Sensitivity

Butyrate improves glucose tolerance and insulin sensitivity via its effects on skeletal muscle and adipocytes (fat cells).¹⁴

Lipid Metabolism and Storage of Fat

Butyrate and propionate suppress lipogenesis and promote fatty acid oxidation in liver and fat cells.¹⁵

Blood Pressure Regulation

Propionate interacts with receptors in the kidney to modulate renin and vasodilation which control blood pressure.¹⁶

Nitrogen and Ammonia Detoxification

Butyrate reduces colonic pH which limits the absorption and toxicity of ammonia.¹⁷

<u>Hepatic Function</u>

Short-chain fatty acids regulate fat metabolism in the liver, reducing hepatic steatosis (fatty liver) and inflammation.¹⁸

• Precursor For Longer-Chain Metabolites

Acetate and other short-chain fatty acids are substrates for the production of cholesterol and fatty acids.¹⁹

Enhanced Mineral Absorption

Short-chain fatty acids induce acidification of the colon and enhance the solubility and uptake of minerals like calcium and magnesium.²⁰

More Microbial Stability and Diversity

Short-chain fatty acids support cross-feeding among microbe species, thus promoting a resilient and diverse microbe population.²¹

<u>Gut-Brain Axis Support</u>

Butyrate crosses the blood-brain barrier and influences neurogenesis, neurotransmitter synthesis, and neuroinflammation.²²

Satiety and Food Intake Regulation

Increased short-chain fatty acid levels lead to reduced caloric intake and modulation of brain's appetite centers.²³

<u>Regulation of Bile Acid Synthesis and Composition</u>

Short-chain fatty acids influence gut microbe composition that in turn modifies bile acid profiles.²⁴

Modulation of Colon Transit

Butyrate stimulates serotonin release from enterochromaffin cells enhancing colon peristalsis and influencing bowel regularity.²⁵

Association With Preeclampsia

Women with preeclampsia show altered SCFA profiles, suggesting roles in placental immune regulation.²⁶

Influence on Fertility and Pregnancy Outcomes

Higher short-chain fatty acid levels correlate with healthier reproductive and environments, embryo implantation and pregnancy success.²⁷

Potential Impact On Retinal Health

Butyrate reduces retinal inflammation and protects against oxidative stress in ocular tissues.²⁸

<u>Enhancement of Bone Metabolism Through Butyrate-</u> <u>Mediated Parathyroid Hormone Activation</u>

Butyrate promotes calcium absorption and stimulates osteoblast activity by activating parathyroid hormone.²⁹

<u>Strengthening of Skin Barrier and Reduction of Inflammation</u> <u>Through SCFA-Mediated Keratinocyte Modulation</u>

Short-chain fatty acids improve mitochondrial function and barrier integrity in keratinocytes, reducing skin inflammation.³⁰

<u>Renal Health Support Via SCFA-Mediated Modulation of</u> <u>Energy and Immune Homeostasis</u>

Short-chain fatty acids regulate immune responses in the kidney and protect against inflammation-induced renal injury.³¹

Pancreatic Regulation Through SCFA Effects on Lipid and Glucose Metabolism

Short-chain fatty acids modulate enteroendocrine signaling thus impacting insulin production and pancreatic beta-cell function.³²

Anti-Inflammatory Effects of SCFAs In the Pulmonary System

Butyrate and propionate reduce lung inflammation and promote immune tolerance in models of asthma and acute lung injury.³³

Potential Role In Neurodegenerative Disease Modulation by the Gut-Brain Axis

Short-chain fatty acids modulate microglial activity, reduce neuroinflammation, and may protect against cognitive decline in models of Alzheimer's dementia and Parkinson's disease.³⁴

<u>Attenuation of Atherosclerosis or Reduction In Lipids,</u> <u>Oxidative Stress, and Foam Cell Formation</u>

Propionate reduces arterial plaque burden, foam cell formation, and systemic inflammation, improving cardiovascular outcomes.³⁵

Suppression of Oral Inflammation and Periodontal Disease <u>Progression</u>

Butyrate and acetate reduce gingival inflammation and inhibit pathogenic oral bacteria.³⁶

REFERENCES:

¹ Berni Canani, Roberto, Margherita Di Costanzo, Ludovica Leone, Monica Pedata, Rosaria Meli, and Antonio Calignano. "Potential Beneficial Effects of Butyrate in Intestinal and Extraintestinal Diseases." *World Journal of Gastroenterology* 17, no. 12 (2011): 1519– 1528. <u>https://doi.org/10.3748/wjg.v17.i12.1519.</u>

²Peng, Lu, et al. *"Butyrate Enhances the Intestinal Barrier by Facilitating Tight Junction Assembly via Activation of AMP-Activated Protein Kinase in Caco-2 Cell Monolayers."* Journal of Nutrition 139, no. 9 (2009): 1619–1625. <u>https://doi.org/10.3945/jn.109.104638.</u>

³ Barcelo, A., et al. "Short-Chain Fatty Acids Stimulate Mucin Secretion in Goblet Cells." American Journal of Physiology-Gastrointestinal and Liver Physiology 273, no. 1 (1997): G180–G186.

⁴ Louis, Petra, and Harry J. Flint. "Formation of Propionate and Butyrate by the Human Colonic Microbiota." Environmental Microbiology 19, no. 1 (2017): 29–41. <u>https://doi.org/10.1111/1462-2920.13589</u>

⁵ Byndloss, M. X., Olsan, E. E., Rivera-Chávez, F., Tiffany, C. R., Cevallos, S. A., Lokken, K. L., ... & Bäumler, A. J. (2017). Microbiota-activated PPAR-γ signaling inhibits dysbiotic Enterobacteriaceae expansion. Science, 357(6351), 570–575. <u>https://doi.org/10.1126/science.aam9949</u>

[°] Hamer, Henrike M., et al. "Review Article: The Role of Butyrate on Colonic Function." *Alimentary Pharmacology* & *Therapeutics* 27, no. 2 (2008): 104-119.

['] Macia, L., Tan, J., Vieira, A. T., Leach, K., Stanley, D., Luong, S., Maruya, M., Ian McKenzie, C., Hijikata, A., Wong, C., Binge, L., Thorburn, A. N., Chevalier, N., Ang, S. F., Tam, J., Dalod, M., Bowman, J., Peat, R., Lu, J., ... Mackay, C. R. (2015). Metabolite-sensing receptors GPR43 and GPR109A facilitate dietary fibre-induced gut homeostasis through regulation of the inflammasome. Nature Communications, 6, 6734.

https://doi.org/10.1038/ncomms7734

[°] Vinolo, Marco A. R., Rafael S. Rodrigues, Rafael Nachbar, Fernanda C. C. C. C. de Miranda, Claudia S. Curi, and Rui Curi. "SCFAs Induce Apoptosis in Leukocytes by a GPR43-Dependent Mechanism." Cell Death & Disease 2, no. 10 (2011): e248. <u>https://doi.org/10.1038/cddis.2011.130</u>.

^o Maslowski, K. M., et al. "Regulation of Inflammatory Responses by Gut Microbiota and Chemoattractant Receptor GPR43." Nature 461, no. 7268 (2009): 1282-1286 <u>https://doi.org/10.1038/nature08530.</u>

¹⁰ Trompette, Aurelien, et al. "Gut Microbiota Metabolism of Dietary Fiber Influences Allergic Airway Disease and Hematopoiesis." *Nature Medicine* 20, no. 2 (2014): 159-166. <u>https://doi.org/10.1038/nm.3444</u>

¹¹ Donohoe, Dallas R., Aiping G. Garge, Xiaolun Zhang, Wei Sun, Gary M. O'Connell, Anny M. Bunger, Jiangjiang G. Yang, et al. "The Microbiome and Butyrate Regulate Energy Metabolism and Autophagy in the Mammalian Colon." Cell Metabolism 13, no. 5 (2011): 517–526. <u>https://doi.org/10.1016/j.cmet.2011.02.018</u>

¹² Fellows, Robert, Thomas Denizot, Adam D. Stellato, et al. "Microbiota Derived Short Chain Fatty Acids Promote Histone Crotonylation in the Colon through Histone Deacetylases." Nature Communications 9 (2018):

105. https://doi.org/10.1038/s41467-017-02651-5

¹³Tolhurst, Gwen, Helen Heffron, Elizabeth Lam, Gail Parker, Guang Yang, Daniel Reimann, and Frank Reimann. "Short-Chain Fatty Acids Stimulate Glucagon-Like Peptide-1 Secretion via the G-Protein–Coupled Receptor FFAR2." *Diabetes* 61, no. 2 (2012): 364–371.

https://doi.org/10.2337/db11-1019.

 ¹⁴ Gao, Zhenyang, et al. "Butyrate Improves Insulin Sensitivity and Increases Energy Expenditure in Mice." *Diabetes* 58, no. 7 (2009): 1509-1517. <u>https://doi.org/10.2337/db08-1637.</u>

15

den Besten, Gijs, Koen Venema, Albert van Eunen, Klaske J. Groen, Billy M. Venema, Daniël D. Reijngoud, and Barbara M. Bakker. "The Role of Short-Chain Fatty Acids in the Interplay between Diet, Gut Microbiota, and Host Energy Metabolism." *Journal of Lipid Research* 54, no. 9 (2013): 2325–2340. <u>https://doi.org/10.1194/jlr.R036012.</u>

16

Poll, Brian G., Muhammad Umar Cheema, and Jennifer L. Pluznick. 2020. "Gut Microbial Metabolites and Blood Pressure Regulation: Focus on SCFAs and TMAO." *Physiology* 35 (4): 275–284. <u>https://doi.org/10.1152/physiol.00004.2020.</u>

^{1'} Liu, Yi, Limin Wang, Zhihong Chen, and Mingming Guo. "Butyrate: A Double-Edged Sword for Health?" *Advances in Nutrition* 9, no. 1 (2018): 21–29. <u>https://doi.org/10.1093/advances/nmx009</u>.

18

Li, Yadong, Chenxi Yi, Seyedeh S. Katiraei, Sander Kooijman, Erfei Zhou, Chau K. Chung, Yichuan Gao, Jeroen K. van den Heuvel, Onno C. Meijer, Jan F. P. Berbée, Monique Heijink, Michal Giera, Klaas Willems van Dijk, Albert K. Groen, Patrick C. N. Rensen, and Ya Wang. "Butyrate Reduces Appetite and Activates Brown Adipose Tissue via the Gut-Brain Neural Circuit." *Gut* 67, no. 7 (2018): 1269–1279. <u>https://doi.org/10.1136/gutjnl-2017-314050</u>. ¹⁹ Walsh, Mary E., Andrea E. Sloane, Deon M. Fischer, Guohua Zhu, Dmitriy E. Austad, and Rozalyn M. Anderson. "Short-Chain Fatty Acids and Aging-Associated Inflammation." Journal of Clinical Investigation 125, no. 2 (2015): 681–690.

²⁰ Macfarlane, George T., and Sylvia Macfarlane. "Fermentation in the Human Large Intestine: Its Physiologic Consequences and the Potential Contribution of Prebiotics." *Journal of Clinical Gastroenterology* 45 (2011): S120–S127. <u>https://doi.org/10.1097/MCG.0b013e31822fecfe</u>.

²¹ Zhang, Qian, Shuangshuang Hu, Xiaoyu Zhang, Jianzhong Xiao, Na Li, Heping Zhang, and Wei Chen. "A Positive Role of Short-Chain Fatty Acids on Gut Microbiota and Immune System." *Scientific Reports* 11, no. 1 (2021): 21629.

22

²² Dalile, Benedicte, Amber Van Oudenhove, Ilse Vervliet, and Kristin Verbeke. "The Role of Short-Chain Fatty Acids in Microbiota-Gut-Brain Communication." Nature Reviews Gastroenterology & Hepatology 16, no. 8 (2019): 461–478. <u>https://doi.org/10.1038/s41575-019-0157-3.</u>

²³ Chambers, Edward S., Gary Frost, Douglas J. Morrison, Stephanie M. Cooke, Antonio C. L. Neto, Amandine M. Ouaret, Abigail G. Bewick, et al. "Effects of Targeted Delivery of Propionate to the Human Colon on Appetite Regulation, Body Weight Maintenance, and Adiposity in Overweight Adults." *Gut* 64, no. 11 (2015): 1744–1754. https://doi.org/10.1136/gutjnl-2014-307913.

24

Sayin, Sama I., Andrew Wahlström, Alek Aleksic, Christofer M. Luna, Francois K. Marschall, Thomas G. Mottawea, Vincent P. Perkins, et al. "Gut Microbiota Regulates Bile Acid Metabolism by Reducing the Levels of Tauro-β-Muricholic Acid, a Naturally Occurring FXR Antagonist." *Cell Metabolism* 17, no. 2 (2013): 225–235.

https://doi.org/10.1016/j.cmet.2013.01.003.

²⁵ Buey, Berta, Ana Forcén, Laura Grasa, Elena Layunta, Jose Emilio Mesonero, and Eva Latorre. "Gut Microbiota-Derived Short-Chain Fatty Acids: Novel Regulators of Intestinal Serotonin Transporter." *Life* 13, no. 5 (2023): 1085. <u>https://doi.org/10.3390/life13051085.</u>

²⁶ Yu, Ying, et al. "Short-Chain Fatty Acids Alleviate the Pathogenesis of Preeclampsia by Activating GPR43 and Inhibiting NLRP3 Inflammasome." *Frontiers in Immunology* 13 (2022): 897810.

²⁷ Gudnadottir, Unnur, Justine W. Debelius, Juan Du, Luisa W. Hugerth, Hanna Danielsson, Ina Schuppe-Koistinen, Emma Fransson, and Nele Brusselaers. 2022. "The Vaginal Microbiome and the Risk of Preterm Birth: A Systematic Review and Network Meta-Analysis." Scientific Reports 12: Article 7926.

²⁸ Ciurariu, E., Tirziu, A.-T., Varga, N.-I., Hirtie, B., Alexandru, A., Ivan, C.-S., & Nicolescu, L. (2025). Short-Chain Fatty Acids and the Gut–Retina Connection: A Systematic Review. *International Journal of Molecular Sciences*, 26(6), 2470.

²⁹ Rahman, Md Mahfujur, et al. "The Role of Short Chain Fatty Acids in the Modulation of Bone Metabolism." *Medical Hypotheses* 149 (2021): 110540.

³⁰ Wang, Yaxian, et al. "Butyrate Improves Skin Barrier Function." Journal of Dermatological Science 104, no. 1 (2021): 46-54

³¹ Andrade-Oliveira, Vinicius, et al. "Short-Chain Fatty Acids Regulate the Immune Response and Ameliorate Kidney Injury." *Nature Communications* 6 (2015): 1-15.

³² De Vadder, Filipe, et al. "Microbiota-Produced Short- Chain Fatty Acids Activate Enteroendocrine Cells." *Cell Metabolism* 19, no. 3 (2014): 513-520. ³³ Vinolo, Marco A. R., et al. "Short Chain Fatty Acids Modulate the Inflammatory Response." *Journal of Immunology* 185, no. 10 (2010): 5788-5795.

³⁴ Silva, Yara P., et al. "The Role of Short-Chain Fatty Acids from Gut Microbiota in Gut-Brain Communication." *Frontiers in Endocrinology* 11 (2020): 25.

³⁵ Bartolomaeus, Hendrik, et al. "Short-Chain Fatty Acid Propionate
 Protects from Hypertensive Cardiovascular Damage." *Circulation* 139, no.
 11 (2019): 1407-1421.

36

³⁶ Xiao, Erfei, et al. "Butyrate Reduces Inflammation in Periodontal Ligament Cells." *Journal of Clinical Periodontology* 48, no. 1 (2021): 71-83.

APPETITE REGULATION REVISITED

Among the many health-promoting effects of short-chain fatty acids (SCFAs), one of the most striking is their ability to influence appetite regulation. Specifically, the SCFA propionate activates enteroendocrine L-cells in the distal small intestine and colon, triggering the release of glucagon-like peptide-1 (GLP-1) and peptide YY (PYY)—two hormones that slow gastric emptying, enhance satiety, and reduce food intake.¹ These hormones help the body self-regulate food consumption.

Popular weight-loss and antidiabetic medications such as Ozempic[®], Wegovy[®], Rybelsus[®], and Mounjaro[®] are designed to mimic the actions of GLP-1 and PYY. These drugs have surged in popularity not only for their effectiveness in lowering blood sugar and promoting weight loss, but also for their ability to suppress appetite—essentially invoking the same GLP-1 signaling pathway that healthy gut microbes support naturally.²

While these medications can be life-changing for some, they are expensive, may produce gastrointestinal side effects (including nausea, vomiting, and constipation), and do not correct the underlying dietary and microbial imbalances that often lead to GLP-1 deficiency in the first place.

Controversy exists over whether these drugs may create an unwanted and potentially harmful overgrowth of microbes in the small bowel (*SIBO*) by slowing gut motility (*peristalsis*) and altering nutrient availability. Additionally, they may affect the composition and circulation of bile acids, which are essential for maintaining microbial balance in the small intestine.

In contrast, a fiber-rich, plant-focused diet offers a sustainable, multi-benefit strategy: it feeds the beneficial microbes that produce short chain fatty acids, which in turn activate GLP-1 and PYY through their interaction with G-protein-coupled receptors (GPR41 and GPR43).³

Moreover, diets rich in fruits, vegetables, beans, legumes, whole grains, resistant starches, seeds, and nuts not only stimulate these hormone-releasing pathways but also improve microbial diversity, enhance gut barrier function, and reduce systemic inflammation. When viewed through this lens, the body's natural capacity to regulate appetite through diet and microbial metabolism appears not just elegant, but preferable.

REFERENCES:

^{1.} Chambers, Emma S., et al. "Effects of Targeted Delivery of Propionate to the Human Colon on Appetite Regulation, Body Weight Maintenance and Adiposity in Overweight Adults." *Gut* 64, no. 11 (2015): 1744–1754.

². Nauck, Michael A., and Juris J. Meier. "Incretin Hormones: Their Role in Health and Disease." *Diabetes, Obesity and Metabolism* 20, Suppl 1 (2018): 5–21.

^{3.} Tolhurst, Gareth, et al. "Short-Chain Fatty Acids Stimulate Glucagon-Like Peptide-1 Secretion via the G-Protein–Coupled Receptor FFAR2." *Diabetes* 61, no. 2 (2012): 364–371. <u>https://doi.org/10.2337/db11-1019</u>

Beyond SCFAs: The Microbiome's Metabolic Arsenal and its Impact on Human Health

While SCFAs receive much attention, they are part of a broader suite of bioactive compounds synthesized by gut microbes collectively forming a vast metabolic arsenal. These include:

 Ribosomally synthesized and post-translationally modified peptides (RiPPs): These are a class of antimicrobial and signaling peptides produced by microbial ribosomes and enzymatically altered to yield complex molecules that can modulate host immunity and suppress pathogenic competitors.

<u>See</u>: Arnison, Paul G., et al. "Ribosomally synthesized and posttranslationally modified peptide natural products: overview and recommendations for a universal nomenclature." *Natural Product Reports* 30.1 (2013): 108-160. https://doi.org/10.1039/C2NP20085F

 <u>Neurotransmitters and neuromodulators</u>: Certain gut bacteria produce gamma-aminobutyric acid (GABA), dopamine, serotonin, and acetylcholine, influencing host behavior and cognition through the gut-brain axis.

See: Cryan, John F., and Timothy G. Dinan. "Mind-Altering Microorganisms: The Impact Of The Gut Microbiota On Brain And Behaviour." *Nature Reviews Neuroscience* 13, no. 10 (2012): 701-712. <u>https://doi.org/10.1038/nrn3346</u>

 Bile acid derivatives: Microbial enzymes transform primary bile acids into secondary bile acids, affecting lipid metabolism, host signaling pathways, and intestinal immunity.

<u>See:</u> Ridlon, Jason M., et al. "Consequences Of Bile Salt Biotransformations By Intestinal Bacteria." *Gut Microbes* 7, no. 1 (2016): 22-39. <u>https://doi.org/10.1080/19490976.2015.1127483</u>

 <u>TMAO (Trimethylamine N-oxide)</u>: Generated from microbial metabolism of choline and carnitine, TMAO has been associated with increased cardiovascular risk, though it may also represent a homeostatic adaptation under certain conditions.

See: Yang, Y., et al. "Advancements in the Study of Short-Chain Fatty Acids and their Therapeutic Effects on Atherosclerosis." *Life*

Sciences 369 (2025): 123528. https://doi.org/10.1016/j.lfs.2025.123528

 <u>Vitamins and cofactors</u>: Bacteria in the gut synthesize vitamin K, folate, biotin, and several B vitamins, notably B12—an essential nutrient that humans cannot produce on their own.

See: LeBlanc, Jean Guy, et al. "Bacteria As Vitamin Suppliers To Their Host: A Gut Microbiota Perspective." *Current Opinion in Biotechnology* 24, no. 2 (2013): 160-168. <u>https://doi.org/10.1016/j.copbio.2012.08.005</u>

This expansive biochemical output emphasizes that microbes are not simply assistants to human health; they are active engineers of metabolic balance, immune education, detoxification, nutrient assimilation, and even behavior modulation. As such, they deserve to be recognized as the primary architects of digestive and systemic well-being.

POLYPHENOLS

Polyphenols represent another foundational category of plantderived compounds that influence gastrointestinal and systemic health. They interact intimately with the gut microbiota. While fermentable fibers serve as direct substrates for microbial fermentation and SCFA production, polyphenols often act as modulators—reshaping the microbiota's composition and function.¹

Comparison of Dietary Fiber and Polyphenols

Feature	Dietary Fiber	Polyphenols
Chemical Structure	Polysaccharides (e.g., cellulose, pectins, beta- glucans)	Polyphenolic rings (e.g., flavonoids, phenolic acids)
Digestibility	Indigestible by human enzymes; fermented by gut microbiota	Partially absorbed in small intestine; further metabolized by gut microbiota
Primary Metabolites	Short-chain fatty acids (SCFAs) such as butyrate, acetate, propionate	Phenolic metabolites such as urolithins and flavonoid derivatives
Gut Microbiota Interaction	Feeds SCFA-producing bacteria; increases microbial diversity	Modulates microbial composition; promotes beneficial phenotypes
Physiological Effects	Improves bowel function, regulates glucose and lipid metabolism, lowers cholesterol	Antioxidant, anti- inflammatory, cardioprotective, neuroprotective
Disease Prevention	Reduces risk of colorectal cancer, cardiovascular disease, type 2 diabetes	Associated with reduced risk of cardiovascular, neurodegenerative, and inflammatory diseases
Synergistic Role	Supports microbes that metabolize polyphenols	Enhances microbial pathways for SCFA production
Dietary Sources	Whole grains, legumes, fruits, vegetables, nuts, seeds	Tea, coffee, berries, red wine, cocoa, olive oil, herbs

Polyphenols are structurally diverse secondary plant metabolites characterized by aromatic rings with hydroxyl groups. They include flavonoids, phenolic acids, stilbenes, and lignans, and are commonly found in fruits, vegetables, tea, cocoa, and whole grains. Most polyphenols are poorly absorbed in the small intestine, and a significant portion reaches the colon where microbial enzymes break them down into smaller, bioactive phenolic metabolites.²

These metabolites often exert greater biological activity than their precursors.³

By comparison, dietary fiber consists of non-digestible carbohydrate polymers such as inulin, resistant starch, betaglucans, and pectins. These fibers resist digestion in the small intestine and are fermented in the colon by resident microbiota. The fermentation process results in the production of SCFAs primarily acetate, propionate, and butyrate—which serve as energy substrates for colonocytes, modulate immune responses, and exert anti-inflammatory effects⁴ with different types of fiber yielding different SCFA profiles, influencing host physiology accordingly.⁵

Both polyphenols and dietary fiber modulate the gut microbiota, but in distinct ways. Polyphenols tend to exert selective pressure, inhibiting pathogenic bacteria while promoting beneficial species such as *Bifidobacterium* and *Lactobacillus*.¹

In doing so, they indirectly influence SCFA production by favoring microbial communities that ferment fiber more efficiently. Fiber,

on the other hand, acts directly as a carbon source for saccharolytic bacteria such as *Faecalibacterium prausnitzii* and *Roseburia*, major producers of butyrate.⁵

There is increasing evidence of synergy between polyphenols and fiber. Many polyphenol-rich foods—such as berries, apples, legumes, and whole grains—also contain fiber. Fiber may slow intestinal transit, promoting polyphenol retention in the colon and enhancing microbial transformation.¹

Moreover, some polyphenols bind to fiber matrices, affecting their release and the timing of microbial access. This co-localization supports the emerging view that the health effects of plant-based diets are driven by the complex interplay of dietary constituents and microbial ecology.⁶

In conclusion, while dietary fiber remains the primary driver of SCFA production, polyphenols shape the microbial ecosystem that governs fermentation dynamics. Fiber provides the metabolic fuel; polyphenols refine and direct its combustion. The interplay of these compounds within the gut underscores the importance of whole-plant foods in health promotion, suggesting that a food-first strategy may yield greater microbial and metabolic benefits than isolated supplementation alone.

RESOURCES:

¹ Ozdal, Tülay, et al. "The Reciprocal Interactions between Polyphenols and Gut Microbiota and Effects on Bioaccessibility." *Nutrients* 8, no. 2 (2016): 78. <u>https://doi.org/10.3390/nu8020078.</u> ² Cardona, Fernando, et al. "Benefits of Polyphenols on Gut Microbiota and Implications in Human Health." *The Journal of Nutritional Biochemistry* 24, no. 8 (2013): 1415–1422. https://doi.org/10.1016/j.jnutbio.2013.05.001.

³ Tzounis, Xenofon, et al. "Prebiotic Evaluation of Cocoa-Derived Flavanols in Healthy Humans by Using a Randomized, Controlled, Double-Blind, Crossover Intervention Study." *The American Journal of Clinical Nutrition* 93, no. 1 (2011): 62–72. <u>https://doi.org/10.3945/ajcn.110.000075.</u>

⁴ Koh, Angela, et al. "From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites." *Cell* 165, no. 6 (2016): 1332– 1345. <u>https://doi.org/10.1016/j.cell.2016.05.041.</u>

⁵ Rivière, Aurore, et al. "Bifidobacteria and Butyrate-Producing Colon Bacteria: Importance and Strategies for Their Stimulation in the Human Gut." *Frontiers in Microbiology* 7 (2016): 979. <u>https://doi.org/10.3389/fmicb.2016.00979.</u>

⁶ Baxter, Niel T., et al. "Dynamics of Human Gut Microbiota and Short-Chain Fatty Acids in Response to Dietary Interventions with Three Fermentable Fibers." *mBio* 10, no. 1 (2019): e02566-18. <u>https://doi.org/10.1128/mBio.02566-18.</u>

CONCLUSION: THE MAESTRO OF HUMAN HEALTH

The gut microbiota is the maestro of host physiology. Human survival and vitality depend on microbial metabolism, particularly the fermentation of fiber and select amino acids into SCFAs, the generation of polyphenols and the synthesis of an array of regulatory molecules. As research advances, it becomes increasingly clear that nurturing the digestive tract ecosystems through diet, lifestyle, and judicious medical interventions is not just good practice—it is essential medicine. In subsequent sections, strategies to restore and rejuvenate dysbiotic microbial ecosystems will be explored. These include the use of prebiotics, probiotics, postbiotics, synbiotics and dietary therapies that enhance SCFA production and the production of polyphenols which will support a balanced microbial community.

THE GOOD, THE BAD, AND THE UGLY: MICROBIAL ECOSYSTEMS AT EACH END OF THE DIGESTIVE TRACT



The digestive tract is a complex system of interconnected ecosystems, home to trillions of microorganisms that play pivotal roles in both health and disease. These microbial communities vary significantly along the tract, particularly between the two ends the oral cavity and the colon. Each end presents a contrasting microbial narrative: one often dominated by pathogenic potential and the other by beneficial symbiosis. This section explores "the good, the bad, and the ugly" of these microbial populations, highlighting their diverse roles and their profound implications for human health.

THE ORAL MICROBIAL ECOSYSTEM:

THE BAD AND THE UGLY

The oral cavity teems with a diverse microbial population that performs both beneficial and harmful functions. On the positive side, oral microbes aid in the initial breakdown of food, supported by the enzymatic activity of saliva, thereby assisting nutrient assimilation. However, the benefits of the oral microbiome are frequently overshadowed by its pathogenic potential.

The Bad: Plaque Formation As A Microbial Survival Strategy

Dental plaque is a structured biofilm formed by microbial accumulation on teeth and gum surfaces. This biofilm represents a highly evolved microbial survival mechanism, providing a protective niche where bacteria can thrive, communicate, and exchange genetic material.

While plaque formation is a natural process, it becomes pathogenic when unmanaged. Acid production by plaque bacteria erodes tooth enamel, facilitating the development of dental caries. More concerning is the role of plaque as a reservoir for microbes implicated in gum inflammation and periodontal disease. Oral plaque is essentially "Club Med" for microbes—a sheltered condominium where bacteria share nutrients and genes, while collaborating in the destruction of gum tissue, enamel, and the bony foundations of the face and jaw.^{1,2}

The Ugly: Receding Gums And Periodontal Pockets

If plaque is not removed, it calcifies into tartar, extending beneath the gum line and provoking an immune response. This leads to gingivitis, which, if unchecked, progresses to periodontitis. In this advanced state, the gums recede and form deep periodontal pockets—ideal anaerobic environments where destructive bacteria proliferate. These bacteria release toxins that damage soft tissue, dissolve bone, and perpetuate inflammation in a self-reinforcing loop.

The systemic impact of periodontitis is substantial. Pathogenic microbes and their inflammatory byproducts can enter the bloodstream, traveling to and damaging distant organs such as the heart, liver, brain, and lungs.^{3,4,5}

The Imperative of Controlling Microbial Load

Given the potential for oral microbes to seed distant infections and contribute to systemic inflammation, controlling the microbial load in the mouth is essential for overall health. Effective oral hygiene including regular brushing, flossing, and professional cleanings disrupts the biofilm, reduces microbial colonization, and lowers the risk of both local and systemic illness. Failure to manage the oral microbial burden can contribute to diseases such as endocarditis, pneumonia, and complications in diabetes management.^{4,5}

The Distal Gut Microbiome: The Good

In contrast to the challenges posed by the oral microbiome, the colon harbors a dense and diverse microbial community with overwhelmingly beneficial effects. These colonic microbes play an essential role in digestion, immune modulation, and metabolic regulation. (See: How Humans Rely on Beneficial Microbes)

The Good: Beneficial Functions of Colonic Microbes

As previously noted, colonic microbes are indispensable for breaking down complex carbohydrates and fibers, producing vital short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate. Butyrate, in particular, serves as a key energy source for colonocytes and supports the integrity of the intestinal barrier. It also exhibits potent anti-inflammatory and anti-carcinogenic effects, reducing the risk of inflammatory bowel disease (IBD) and colorectal cancer.^{6,7,8}

These microbes also synthesize essential nutrients, including vitamin K and various B vitamins. They support the host immune system by interacting with gut-associated lymphoid tissue (GALT), helping to discriminate between benign and harmful antigens. In addition, colonic bacteria create a competitive environment that deters colonization by pathogens.^{6,9}

Microbial Diversity and Health

Microbial diversity within the gut is a marker of ecosystem resilience and health. A diverse gut microbiome provides a broad array of metabolic capabilities, enhances barrier function, and supports immune tolerance. Diet, environment, medications, and antibiotics can all influence this diversity. Diets rich in dietary fiber promote the growth of beneficial bacteria that ferment fiber into SCFAs, reinforcing gut health and systemic well-being.¹⁰

Contrasting The Two Ends: The Need For Balance

The oral and colonic microbiomes illustrate the dual nature of microbial life within the digestive tract. The oral microbiome requires vigilant control to prevent disease, while the colonic microbiome thrives when nourished with proper dietary and lifestyle choices. Both ends of the digestive tract underscore the importance of microbial stewardship—nurturing beneficial microbes while suppressing or eliminating those that cause harm.

CONCLUSION:

The microbial ecosystems at the two ends of the digestive tract embody the spectrum of microbial influence on human health. The oral microbiome, though capable of aiding digestion, poses significant risks through its association with dental and systemic diseases. In contrast, the colonic microbiome plays a predominantly beneficial role in energy harvest, immune regulation, and chronic disease prevention. Understanding these opposing dynamics highlights the need for both preventive dental care and dietary practices that foster a healthy gut. Together, they serve as foundational pillars for long-term health and disease prevention.

RESOURCES:

- Belibasakis, Georgios N., and Antonios M. Mylonakis. "Pathogenesis of Bacterial Biofilms in Periodontal Disease." *Journal of Molecular Biology* 427, no. 23 (2015): 3605–3619.
- Hajishengallis, George. "Immunomicrobial Pathogenesis of Periodontitis: Keystones, Pathobionts, and Host Response." *Trends in Immunology* 35, no. 1 (2014): 3–11. <u>https://doi.org/10.1016/j.it.2013.09.001.</u>
- ^{3.} Koren, Omry, et al. "Human Oral, Gut, and Plaque Microbiota in Patients with Atherosclerosis." *Proceedings of the National Academy* of Sciences 108, Supplement 1 (2011): 4592–4598. <u>https://doi.org/10.1073/pnas.1011383107.</u>
- ^{4.} Han, Yiping W., and Shatha Wang. "Mobile Microbiome: Oral Bacteria in Extra-Oral Infections and Inflammation." *Journal of Dental Research* 92, no. 6 (2013): 485–491. <u>https://doi.org/10.1177/0022034513487559.</u>
- ^{5.} Tonetti, Maurizio S., and Iain L. C. Chapple. "Periodontitis and Systemic Disease: Emerging Links and Risks." *Journal of Clinical Periodontology* 47, Supplement 22 (2020): 1–6. <u>https://doi.org/10.1111/jcpe.13292.</u>
- ^{6.} Koh, Ara, Dong-Hyun Kim, Hannah Kim, and Seok-Hwan Choi. "From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites." *Cell* 165, no. 6 (2016): 1332–1345. <u>https://doi.org/10.1016/j.cell.2016.05.041.</u>

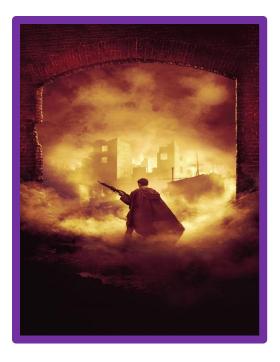
- ^{7.} Louis, Petra, and Harry J. Flint. "Diversity, Metabolism and Microbial Ecology of Butyrate-Producing Bacteria from the Human Large Intestine." *FEMS Microbiology Letters* 294, no. 1 (2009): 1–8. <u>https://doi.org/10.1111/j.1574-6968.2009.01514.x</u>.
- ^{8.} Chen, Jiezhong, Kong-Nan Zhao, and Luis Vitetta. "Effects of Intestinal Microbial–Elaborated Butyrate on Oncogenic Signaling Pathways." *Nutrients* 11, no. 5 (2019): 1026. <u>https://doi.org/10.3390/nu11051026.</u>
- ^{9.} Qin, Junjie, et al. "A Human Gut Microbial Gene Catalogue Established by Metagenomic Sequencing." *Nature* 464, no. 7285 (2010): 59–65. <u>https://doi.org/10.1038/nature08821.</u>
- ^{10.} Lozupone, Catherine A., Jesse I. Stombaugh, Jeffrey I. Gordon, Janet K. Jansson, and Rob Knight. "Diversity, Stability and Resilience of the Human Gut Microbiota." *Nature* 489, no. 7415 (2012): 220–230. <u>https://doi.org/10.1038/nature11550.</u>

SECTION SEVEN

ENEMIES AT THE GATES:

THE MULTILAYERED DEFENSES OF THE GUT AGAINST PATHOGENS AND

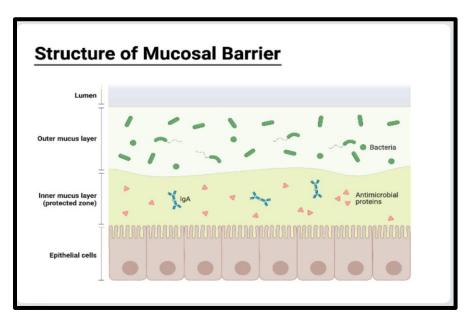
FOREIGN ANTIGENS



The human gut represents a sophisticated barrier and surveillance system designed to protect the host from pathogens and harmful antigens while maintaining a delicate balance with trillions of resident microorganisms. This complex, multilayered defense system incorporates physical barriers, immune responses, and synbiotic relationships with commensal bacteria, each playing a critical role in safeguarding the intestinal ecosystem. However, targeted disruptions to these defenses by toxins, microbes, or foreign antigens can breach the barriers, triggering inflammation and chronic illnesses.

Commensal Bacteria: Protecting their Niche and the Host

Commensal bacteria, the gut's resident microbiota, play a dual role in maintaining health. By occupying niches along the intestinal lining, they outcompete pathogenic microbes, producing antimicrobial compounds like bacteriocins and short-chain fatty acids (SCFAs) such as butyrate, which reinforce the gut barrier¹. Moreover, these microbes modulate the host immune system, promoting regulatory pathways that prevent overactive immune responses². Importantly, they also help regulate the gut's oxygen gradient, ensuring an environment conducive to microbial diversity and barrier health³. These microbial survival strategies protect the host, highlighting a mutualistic relationship.



The Mucus Layer: A Physical and Chemical Shield

The intestinal mucus layer, composed primarily of mucins secreted by goblet cells, serves as a physical barrier that prevents direct contact between luminal microbes and epithelial cells.

In the colon, this layer is stratified, with an inner sterile zone and an outer layer rich in commensal bacteria⁴. In the small intestine, however, the mucus layer is a single, non-stratified layer which is much thinner and less densely organized than the colon mucus. The small intestine mucus layer is more permeable and allows nutrients to pass through while still providing some degree of protection against microbial invasion.

The mucus in the small intestine is constantly being replenished by goblet cells which help minimize bacterial adherence and support the immune response.

Mucins bind to and trap pathogens, facilitating their clearance⁵. Disruption of the mucus barrier—caused by inflammation, infections, or external insults—is associated with increased vulnerability to microbial invasion and gut permeability⁶.

Embedded Immune Cells and Paneth Cell Secretions

Immune cells embedded in the gut epithelium play a frontline role in defense. Paneth cells, located in the crypts of the small intestine, secrete antimicrobial peptides like defensins and lysozyme, targeting invading pathogens⁷. Additionally, immunoglobulin A (IgA), secreted by plasma cells in the lamina propria, binds antigens in the lumen, neutralizing them and preventing their translocation⁸.

Dendritic Cell Surveillance and Monocyte-Macrophage Responses

Dendritic cells extend processes through the epithelial layer into the gut lumen, sampling antigens and presenting them to T cells in Peyer's patches⁹. This mechanism ensures immune surveillance without compromising the epithelial barrier. Meanwhile, monocytes and macrophages act as rapid responders to microbial invasion, releasing pro-inflammatory cytokines like IL-6 and TNF- α to recruit additional immune cells and contain the threat¹⁰.

Tight Junction Proteins: Gatekeepers of Gut Integrity

Tight junction proteins, including occludin, claudins, and zonula occludens, form a dynamic seal between epithelial cells, regulating paracellular permeability¹¹. These proteins are critical for maintaining barrier integrity, and their disruption by toxins, pathogens, or inflammation can lead to increased intestinal permeability, commonly referred to as "leaky gut"¹². This condition facilitates the translocation of antigens and microbes, triggering immune activation.

The Dangers of Repeated or Prolonged Antibiotic Exposure

Antibiotics, though essential in managing bacterial infections, pose significant risks to the gut ecosystem when used repeatedly or for prolonged periods. Once protective commensal microbes have been destroyed, opportunistic organisms such as *Clostridioides difficile* (*C. diff*) and *Candida* species can proliferate, posing significant threats to gut and systemic health.

Depletion of Protective Commensals

Commensal bacteria are integral to maintaining the gut barrier and modulating immune responses. Antibiotics indiscriminately deplete these beneficial microbes, creating a vacuum that opportunistic pathogens like *C. diff* and *Candida* species exploit¹³. *C. diff* produces toxins that damage the gut lining, while *Candida* species, particularly *C. albicans*, can transition from a benign commensal to an invasive pathogen under favorable conditions¹⁴. This fungal overgrowth is associated with mucosal damage, inflammation, and systemic complications known as Candidemia¹⁵.

Proliferation of Resistant and Opportunistic Organisms

Both *C. diff* and *Candida* species thrive in disrupted microbial ecosystems. Antibiotic-resistant *C. diff* strains can cause severe, recurrent colitis, particularly in immunocompromised individuals¹⁶. Similarly, *Candida* species, often resistant to antifungal treatments, form biofilms that protect them from the immune system and therapeutic agents¹⁷. The dual threat of bacterial and fungal overgrowth compounds the risk of gut barrier dysfunction and systemic infections.

The Future of Antimicrobial Modalities

The traditional "shotgun" approach of using broad-spectrum antibiotics contributes to the proliferation of resistant organisms and damages the gut microbiota. There is a growing need to shift toward more targeted therapies. One promising alternative is bacteriophage therapy, which uses viruses that specifically target pathogenic bacteria without harming commensal microbes¹⁸. This precision approach, along with antimicrobial peptides and probiotics, represents a change in basic assumptions in managing infections while preserving gut integrity.

Similar Damage from Cancer Therapies and Other Insults

Beyond antibiotics, other external modalities such as cancer chemotherapy, radiation (both diagnostic and therapeutic), environmental toxins, and contaminated food or water can similarly disrupt gut integrity. These interventions often induce oxidative stress, exacerbating damage to the gut barrier and its immune defenses.

Cancer Chemotherapy and Radiation

Cancer treatments target rapidly dividing cells, including those in the gut epithelium, resulting in mucosal injury and reduced regenerative capacity¹⁹. These treatments also suppress immune responses, increasing susceptibility to infections, including fungal overgrowth.

Radiation-induced oxidative stress is known to damage tight junction proteins, heightening intestinal permeability and the risk of microbial translocation²⁰.

Oxidative Stress and "Baddatives"

Any external insult—such as chronic alcohol consumption, nonsteroidal anti-inflammatory drugs (NSAIDs), heavy metals, or persistent psychological stress—can produce oxidative stress in the gut²¹. In addition, contaminated water, and foreign additives encountered during the growth, manufacturing, packaging, and culinary preparation of foods present significant risks. Examples include pesticide residues, microplastics, preservatives, artificial coloring agents, and emulsifiers²². These substances impair epithelial cell function, disrupt tight junction integrity, and damage mucus-producing goblet cells. Over time, the exposures create an environment conducive to microbial overgrowth, inflammation, and chronic disease.

For instance, certain emulsifiers and synthetic preservatives have been linked to alterations in the gut microbiota, promoting dysbiosis and increasing intestinal permeability²³. Similarly, heavy metals like cadmium and lead found in contaminated water can exacerbate oxidative stress and barrier dysfunction²⁴.

The Consequences of Barrier Loss

Once the protective barrier has been lost or significantly damaged, the host becomes a walking target for bacterial, viral, and fungal infections. Permeating toxins and microbes gain access to the bloodstream, spreading to other organ systems and resulting in multiple systemic illnesses. This breakdown in barrier function also sets the stage for autoimmune diseases, as the immune system encounters and reacts to foreign antigens that would otherwise be confined to the gut lumen. The systemic inflammation triggered by this translocation further exacerbates chronic illnesses, creating a cycle of damage and immune dysregulation.

The Vicious Cycle of Barrier Dysfunction

When the gut's defenses are compromised, a vicious cycle ensues:

1. Loss of Commensal Support: The depletion of beneficial bacteria and the resulting loss of metabolites like butyrate weaken the gut barrier²⁵.

2. **Opportunistic Overgrowth:** Disruption allows opportunistic pathogens like *C. diff* and *Candida* to proliferate unchecked²⁶.

3. <u>Chronic Inflammation</u>: Persistent immune activation against these invaders causes oxidative damage, perpetuating barrier dysfunction and systemic inflammation²⁷.

Immune System Activation and Inflammatory Responses

The gut-associated lymphoid tissue (GALT) is a central player in immune defense. When foreign antigens breach the epithelial barrier, the immune system is activated, resulting in the release of cytokines and chemokines that recruit immune cells to the site of invasion²⁸. While this response is essential for pathogen clearance, dysregulation can lead to chronic inflammation and tissue damage, hallmark features of diseases such as inflammatory bowel disease (IBD)²⁹.

CONCLUSION:

The gut's multilayered defense system is a testament to the complexity of host-microbe interactions. Commensal bacteria, the mucus layer, immune cells, and structural proteins collectively protect the host from external threats while maintaining a Synbiotic environment. However, disruptions to this delicate equilibrium, whether by additives, antibiotics, cancer therapies, or oxidative stress, can lead to inflammation, autoimmune diseases, and systemic illnesses. The future of antimicrobial therapies must move beyond traditional broad-spectrum antibiotics toward targeted solutions such as bacteriophage therapy.

Protecting and restoring gut defenses through judicious therapeutic strategies, mitigating exposure to harmful additives, and promoting gut-supportive measures may offer a pathway to improved health and resilience.

REFERENCES:

- ^{1.} Buffie, C. G., and E. G. Pamer. 2013. "Microbiota-Mediated Colonization Resistance Against Intestinal Pathogens." *Nature Reviews Immunology* 13 (11): 790–801. <u>https://doi.org/10.1038/nri3535.</u>
- ^{2.} Belkaid, Y., and T. W. Hand. 2014. "Role of the Microbiota in Immunity and Inflammation." *Cell* 157 (1): 121–41. <u>https://doi.org/10.1016/j.cell.2014.03.011</u>.
- ^{3.} Litvak, Y., and A. J. Bäumler. 2019. "The Founder Hypothesis: A Basis for Microbiota Resistance, Diversity in Taxa Carriage, and Colonization Resistance Against Pathogens." *PLOS Pathogens* 15 (2): e1007563. <u>https://doi.org/10.1371/journal.ppat.1007563</u>.
- ^{4.} Johansson, M. E. V., M. Phillipson, J. Petersson, A. Velcich, L. Holm, and G. C. Hansson. 2011. "The Inner of the Two Muc2 Mucin-Dependent Mucus Layers in Colon Is Devoid of Bacteria." *Proceedings of the National Academy of Sciences* 108 (39): 4659–65. <u>https://doi.org/10.1073/pnas.1006451107</u>.

- McGuckin, M. A., S. K. Linden, P. Sutton, and T. H. Florin. 2011. "Mucin Dynamics and Enteric Pathogens." *Nature Reviews Microbiology* 9 (4): 265–78. <u>https://doi.org/10.1038/nrmicro2538</u>.
- ^{6.} Van der Post, S., and G. C. Hansson. 2014. "The Role of Mucus in Intestinal Homeostasis." *Mucosal Immunology* 8 (2): 255–66.
- ^{7.} Bevins, C. L., and N. H. Salzman. 2011. "Paneth Cells: Defenders of the Gut." *Nature Reviews Microbiology* 9 (5): 356–68. <u>https://doi.org/10.1038/nrmicro2546.</u>
- ^{8.} Pabst, O. 2020. "IgA and the Intestinal Microbiota: The Importance of Being Specific." *Mucosal Immunology* 13 (1): 12–21. <u>https://doi.org/10.1038/s41385-019-0227-4.</u>
- ^{9.} Rescigno, M. 2011. "Dendritic Cells in Intestinal Homeostasis and Disease." *Nature Reviews Immunology* 11 (7): 468–78. <u>https://doi.org/10.1038/nri2993</u>.
- ^{10.} Bain, C. C., and A. M. Mowat. 2014. "The Monocyte-Macrophage Axis in the Intestine." *Cellular Immunology* 291 (1–2): 41–48. <u>https://doi.org/10.1016/j.cellimm.2014.03.012</u>.
- ^{11.} Turner, J. R. 2009. "Intestinal Mucosal Barrier Function in Health and Disease." *Nature Reviews Immunology* 9 (11): 799–809. <u>https://doi.org/10.1038/nri2653</u>.
- ^{12.} Vancamelbeke, M., and S. Vermeire. 2017. "The Intestinal Barrier: A Fundamental Role in Health and Disease." *Expert Reviews in Gastroenterology & Hepatology* 11 (9): 821–34. <u>https://doi.org/10.1080/17474124.2017.1343143</u>.
- ^{13.} Smits, W. K., D. Lyras, D. B. Lacy, M. H. Wilcox, and E. J. Kuijper. 2016.
 "Clostridium Difficile Infection." *Nature Reviews Disease Primers* 2: 16020. <u>https://doi.org/10.1038/nrdp.2016.20</u>.

- ^{14.} Kullberg, B. J., and M. C. Arendrup. 2015. "Invasive Candidiasis." New England Journal of Medicine 373 (15): 1445–56. <u>https://doi.org/10.1056/NEJMra1315399.</u>
- ^{15.} Calderone, R. A., and W. A. Fonzi. 2001. "Virulence Factors of Candida Albicans." *Trends in Microbiology* 9 (7): 327–35. <u>https://doi.org/10.1016/S0966-842X(01)02094-7</u>.
- ^{16.} Becattini, S., Y. Taur, and E. G. Pamer. 2016. "Antibiotic-Induced Changes in the Intestinal Microbiota and Disease." *Trends in Molecular Medicine* 22 (6): 458–78. https://doi.org/10.1016/j.molmed.2016.04.003.
- ^{17.} Sardi, J. C. O., L. Scorzoni, T. Bernardi, A. M. Fusco-Almeida, and M. J. S. Mendes Giannini. 2013. "Candida Species: Current Epidemiology, Pathogenicity, Biofilm Formation, Natural Antifungal Products, and New Therapeutic Options." *Journal of Medical Microbiology* 62 (Pt 1): 10–24. <u>https://doi.org/10.1099/jmm.0.045054-0</u>.
- ^{18.} Abedon, S. T., P. García, P. Mullany, and R. Aminov. 2017. "Phage Therapy: Past, Present and Future." *Frontiers in Microbiology* 8: 981. <u>https://doi.org/10.3389/fmicb.2017.00981</u>.
- ^{19.} Montassier, E., T. Gastinne, P. Vangay, G. A. Al-Ghalith, S. Bruley des Varannes, S. Massart, and E. Batard. 2015. "Chemotherapy-Driven Dysbiosis in the Intestinal Microbiome." *Alimentary Pharmacology & Therapeutics* 42 (5): 515–28. <u>https://doi.org/10.1111/apt.13302</u>.
- ^{20.} Dahlgren, D., and H. Lennernäs. 2023. "Review on the Effect of Chemotherapy on the Intestinal Barrier: Epithelial Permeability, Mucus and Bacterial Translocation." *Biomedicine & Pharmacotherapy* 164: 114644. <u>https://doi.org/10.1016/j.biopha.2023.114644.</u>
- ^{21.} Pohl, K., P. Moodley, and A. D. Dhanda. 2021. "Alcohol's Impact on the Gut and Liver." *Nutrients* 13 (9): 3170. <u>https://doi.org/10.3390/nu13093170</u>.

- ^{22.} Chassaing, B., O. Koren, J. K. Goodrich, A. C. Poole, S. Srinivasan, R. E. Ley, and A. T. Gewirtz. 2015. "Dietary Emulsifiers Impact the Mouse Gut Microbiota Promoting Colitis and Metabolic Syndrome." *Nature* 519 (7541): 92–96. <u>https://doi.org/10.1038/nature14232</u>.
- ^{23.} Ivanovic, N., and S. Dimitrijevic Brankovic. 2024. "Effects of Food Additives on Gut Microbiota: What's New in 2024." *Microbial Health and Disease* 6: e1106. <u>https://doi.org/10.26355/mhd-202410-1106</u>.
- ^{24.} Camilleri, M. 2019. "Leaky Gut: Mechanisms, Measurement, and Clinical Implications in Humans." *Gut* 68 (8): 1516–1526. <u>https://doi.org/10.1136/gutjnl-2019-318427</u>.
- ^{25.} Kelly, C. J., L. Zheng, E. L. Campbell, B. Saeedi, C. C. Scholz, A. J. Bayless, et al. 2015. "Crosstalk Between Microbiota-Derived Short-Chain Fatty Acids and Intestinal Epithelial HIF Augments Tissue Barrier Function." *Cell Host & Microbe* 17 (5): 662–671. https://doi.org/10.1016/j.chom.2015.03.005.
- ^{26.} Underhill, D. M., and I. D. Iliev. 2014. "The Mycobiota: Interactions Between Commensal Fungi and the Host Immune System." *Nature Reviews Immunology* 14 (6): 405–416. <u>https://doi.org/10.1038/nri3684.</u>
- ^{27.} Neurath, M. F. 2019. "Targeting Immune Cell Circuits and Trafficking in Inflammatory Bowel Disease." *Nature Immunology* 20 (8): 970–979. <u>https://doi.org/10.1038/s41590-019-0433-9</u>.
- ^{28.} White, Z., I. Cabrera, I. Kapustka, and T. Sano. 2023. "Microbiota as Key Factors in Inflammatory Bowel Disease." *Frontiers in Microbiology* 14: 1155388. <u>https://doi.org/10.3389/fmicb.2023.1155388</u>.
- ^{29.} Turner, J. R. 2009. "Intestinal Mucosal Barrier Function in Health and Disease." *Nature Reviews Immunology* 9 (11): 799–809. <u>https://doi.org/10.1038/nri2653</u>.

CONDITIONS ASSOCIATED WITH ABNORMAL INTESTINAL BARRIER FUNCTION



Intestinal barrier dysfunction has been associated with numerous conditions:

- Bacterial and viral infections¹
- Obesity²
- Fatty liver disease³
- Inflammatory bowel disease (IBD)⁴

- Alcohol-induced liver disease⁵
- Cirrhosis⁶
- Pancreatitis⁷
- Diabetes⁸
- Depression⁹
- Neurodegenerative disorders¹⁰
- Cardiovascular disease¹¹

REFERENCES:

¹ Yeoh, Yun Kit, Tao Zuo, Grace Chung-Yan Lui, Fen Zhang, Qin Liu, Amy Y. L. Li, Arthur C. K. Chung, et al. "Gut Microbiota Composition Reflects Disease Severity and Dysfunctional Immune Responses in Patients With COVID-19." *Gut* 70, no. 4 (2021): 698–706. <u>https://doi.org/10.1136/gutjnl-2020-323020</u>.

² Nagpal, Ravinder, T. M. Newman, S. Wang, S. Jain, J. F. Lovato, and H. Yadav. "Obesity-Linked Gut Microbiome Dysbiosis Associated with Derangements in Gut Permeability and Intestinal Cellular Homeostasis Independent of Diet." *Journal of Diabetes Research* 2018 (2018): 3462092. <u>https://doi.org/10.1155/2018/3462092</u>.

³ Kessoku, Takaomi, Kazuhiro Imajo, Takashi Kobayashi, Atsushi Ozaki, Masato Iwaki, Yuki Honda, Kosuke Tanaka, et al. "The Role of Leaky Gut in Nonalcoholic Fatty Liver Disease: A Novel Therapeutic Target." *International Journal of Molecular Sciences* 22, no. 15 (2021): 8161. <u>https://doi.org/10.3390/ijms22158161</u>.

⁴ Turner, Jerrold R. "Intestinal Mucosal Barrier Function in Health and Disease." *Nature Reviews Immunology* 9, no. 11 (2009): 799–809. <u>https://doi.org/10.1038/nri2653</u>. ⁵ Miele, Luca, and Antonio Grieco. "Intestinal Barrier Function and Metabolic/Liver Diseases." *Liver Research* 4, no. 1 (2020): 14–20. <u>https://doi.org/10.1016/j.livres.2020.03.002</u>.

⁶ Fukui, Hiroshi. "Gut-Liver Axis in Liver Cirrhosis: How to Manage Leaky Gut and Endotoxemia." *World Journal of Hepatology* 7, no. 3 (2015): 425–442. <u>https://doi.org/10.4254/wjh.v7.i3.425</u>.

⁷ Pagliari, Daniele, Alessandra Saviano, Elizabeth E. Newton, Maria L. Serricchio, Andrea A. Dal Lago, and Antonio Gasbarrini. "Gut Microbiota–Immune System Cross Talk and Pancreatic Disorders." *Mediators of Inflammation* 2018 (2018): 7946431. https://doi.org/10.1155/2018/7946431.

⁸ Kowalska, Katarzyna, and Michał Wilczyński. "Exploring the Significance of Gut Microbiota in Diabetes: Mechanisms and Therapeutic Potential." *Nutrients* 16, no. 12 (2024): 1938. <u>https://doi.org/10.3390/nu16121938</u>.

⁹ Liu, L., H. Wang, and Y. Zhang. "Gut Microbiota and Its Metabolites in Depression: From Pathogenesis to Treatment." *eBioMedicine* 90 (2023): 104527. <u>https://doi.org/10.1016/j.ebiom.2023.104527</u>.

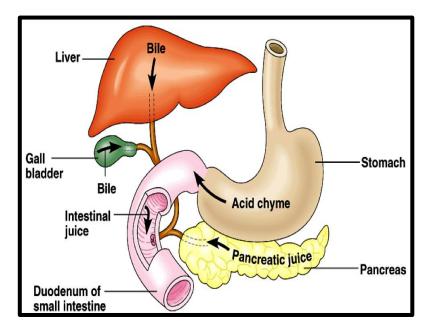
¹⁰ Seguella, Leonardo, and Brian D. Gulbransen. "Enteric Glial Biology, Intercellular Signalling and Roles in Gastrointestinal Disease." *Nature Reviews Gastroenterology & Hepatology* 18, no. 8 (2021): 571–587. <u>https://doi.org/10.1038/s41575-021-00423-7</u>.

¹¹ Lewis, Caitlin V., and W. Robert Taylor. "Intestinal Barrier Dysfunction as a Therapeutic Target for Cardiovascular Disease." *American Journal of Physiology-Heart and Circulatory Physiology* 319, no. 6 (2020): H1227–H1233.

https://doi.org/10.1152/ajpheart.00612.2020.

SECTION EIGHT:

BILE-A MAJOR SECRETION INFLUENCING THE DIGESTIVE TRACT ECOSYSTEMS



MICROBIAL TRANSFORMATION OF BILE ACIDS AND THEIR POTENTIAL EFFECTS ON THE HOST

Bile acids play a key role in digesting fats, absorbing fat-soluble vitamins, and regulating cholesterol levels. They also play a multifaceted role in human health beyond their traditional function of fat digestion.

Bile—More Than A Detergent

Traditionally viewed as a digestive agent for fat absorption, bile plays numerous vital roles in human health, highlighting its multifunctionality and importance. Some of the many functions of bile include the following:

The Role of Bile In Fat Digestion

Bile emulsifies fats in the small intestine, increasing their surface area for easier enzyme access and enhancing absorption by intestinal cells.¹

Bile As a Signaling Molecule

Beyond digestion, bile acids act as signaling molecules, influencing lipid, glucose, and energy metabolism by binding to receptors in various tissues, thus highlighting their therapeutic potential for metabolic disorders.¹

Bile As a Waste Clearance Agent

Bile is essential for excreting waste products like bilirubin and excess cholesterol. In the liver, approximately 500 mg of cholesterol is converted daily into bile acids, underlining bile's role in cholesterol management and cardiovascular health.²

Bile As an Antimicrobial Agent

Bile acids help regulate microbial populations by inhibiting the overgrowth of acid-resistant bacteria that reach the small

intestine, highlighting their importance in preventing Small Intestinal Bacterial Overgrowth (SIBO).

Bile As an Anti-Cancer Secretion

Bile acids influence digestive tract microorganisms and cellular signaling pathways, with emerging evidence supporting a protective role against colon and rectal cancer.³

Microbial Alterations of Bile

Certain microbes can alter bile acids, reducing their efficacy. These transformations include deconjugation, dehydroxylation, dehydrogenation, and epimerization, along with newly discovered amino acid conjugation.⁴

BILE ACID PHYSIOLOGY

After being produced in the liver and released into the small intestine, bile acids encounter a dense population of intestinal microbes. These microbes are not passive bystanders—they actively transform bile through the chemical reactions listed above. These changes significantly affect bile acid structure, reabsorption, and biological activity.

Recently, intestinal fungi have also been shown to modify bile acids, creating novel bile compounds.⁵

The most common change that microbes can carry out when interacting with bile is the chemical process of deconjugation. In the liver, bile acids are typically joined (conjugated) to the amino acids taurine or glycine. Microbes possess enzymes that can reverse this process, removing the amino acids and converting bile acids back to their original forms.⁶

Another chemical transformation carried out by microbes in the gut is dehydroxylation. This reaction leads to the creation of secondary bile acids⁷, such as deoxycholic acid (DCA) and lithocholic acid (LCA). Secondary bile acids can be damaging—they may disrupt cell membranes, increase intestinal permeability (so-called "leaky gut"), and trigger inflammation.

Microbes can also perform additional chemical reactions such as epimerization and dehydrogenation.⁸ Once altered, bile acids may no longer be recognized or efficiently reabsorbed by the body's transport systems, thus causing them to accumulate or act unpredictably.

Scientists speculate that one reason microbes alter the configuration of bile is part of their survival skills allowing them to proliferate more effectively since bile has antimicrobial capability.⁹

New Discoveries

Some microbes have been found that can re-conjugate bile acids with amino acids like phenylalanine or tyrosine—a function that cannot be performed by human liver cells. These novel compounds may affect host tissues in unknown ways.⁹ Altogether, microbial transformations of bile may create over 240 distinct bile acid structures. While some of these may benefit the host—by suppressing pathogens or regulating metabolism—others pose risks. For example, lithocholic acid (LCA) is not only poorly reabsorbed, but also toxic to colon cells. In high concentrations, it may damage DNA and promote colorectal cancer.¹⁰ Chronic exposure to such bile acids may lead to inflammation, barrier dysfunction, and genetic mutations in the colon lining.

Bile acid malabsorption is another adverse outcome. If bile acids aren't properly reabsorbed in the distal ileum (the last section of the small intestine), they can overflow into the colon, where they act as irritants. This can lead to diarrhea, inflammation, and disruption of fluid balance.¹¹ These effects are linked to disorders like irritable bowel syndrome (IBS), bile acid diarrhea (BAD), and inflammatory bowel disease (IBD).

Importantly, not all secondary bile acids are harmful. Some secondary bile acids—such as deoxycholic acid—have been shown to inhibit the germination and growth of Clostridioides difficile spores in the colon, helping to prevent C. difficile colitis.¹² This protective effect highlights the dual nature of secondary bile acids: while some may damage tissues, others may protect the host from infection.

Secondary bile acids, therefore, act as a double-edged sword. The balance between beneficial and harmful effects may be influenced by diet, microbial composition, and host physiology. Further research is needed to determine how this balance can be safely and effectively managed.

CONCLUSION:

Bile acid transformations reflect a complex and ongoing interaction between gut microbes and the host. While some microbial actions support digestion and health, others can contribute to disease. A clearer understanding of these microbial processes may open the door to new treatments for bile-related illnesses. These could include dietary strategies, microbiome-targeted therapies, and pharmaceutical interventions that selectively alter the composition or concentration of bile acids. In some cases—such as bile acid malabsorption—clinical symptoms can be significantly improved with the use of bile acid sequestrants, which bind excess bile acids in the colon and reduce their irritant effects. Continued research will help clarify how best to manage the double-edged nature of microbial bile acid metabolism.

THE EFFECTS OF REMOVING THE GALLBLADDER ON BILE ACID PHYSIOLOGY

Removal of the gallbladder (cholecystectomy) significantly alters bile acid physiology by changing how bile is stored, released, and recycled—leading to various downstream effects on digestion, microbial ecology, and intestinal health.

1. Loss of Bile Storage and Pulsatile Release

The gallbladder serves as a reservoir that concentrates and stores bile between meals. After cholecystectomy, bile produced by the liver flows continuously into the small intestine, even in the absence of food.¹³ This results in loss of controlled, mealstimulated bile delivery, impairing optimal fat digestion and micelle formation.

2. Disruption of Enterohepatic Circulation

Under normal physiology, 95% of bile acids are reabsorbed in the distal ileum (last portions of the small intestine) and returned to the liver via enterohepatic circulation. Without the gallbladder, bile acids circulate more frequently but in smaller, less concentrated amounts, reducing efficiency and altering bile acid pool composition.¹⁴

3. Increased Risk of Bile Acid Malabsorption (BAM)

Continuous bile flow into the colon—especially when bile acids are not efficiently reabsorbed—can overwhelm the colon's absorptive capacity. This leads to diarrhea, gas, and bloating, characteristic of bile acid diarrhea (a type of BAM).¹⁵

4. Alteration of Bile Acid Composition

Bile acids become more deconjugated and transformed into secondary bile acids due to prolonged exposure to gut microbes.¹⁶ This can lead to accumulation of cytotoxic and potentially

carcinogenic bile acids like lithocholic acid (LCA), especially in the colon.

5. Impact on the Gut Microbiome

The antimicrobial action of bile acids affects microbial communities. Changes in bile flow and composition after gallbladder removal may promote dysbiosis, increasing susceptibility to small intestinal bacterial overgrowth (SIBO), colonic inflammation, or C. difficile infection.¹⁷

6. Metabolic Effects

Altered bile acid signaling through FXR and TGR5 receptors can affect glucose and lipid metabolism, possibly increasing risk for insulin resistance or non-alcoholic fatty liver disease (NAFLD).¹⁸

ROLE OF STATINS IN BILE ACID METABOLISM

Statins, widely used to lower cholesterol, also influence bile acid metabolism, primarily because cholesterol is the precursor for all bile acids. Their effects extend beyond cholesterol synthesis to impact bile acid production, pool size, gut microbial interactions, and even gut-liver signaling.¹⁹

<u>1. Inhibition of Cholesterol Synthesis (HMG-CoA Reductase</u> <u>Blockade)</u>

Statins inhibit HMG-CoA reductase, the key enzyme in hepatic cholesterol synthesis. This reduces hepatic cholesterol availability, which is the essential building block for primary bile acid synthesis

(cholic acid and chenodeoxycholic acid). As a result, de novo bile acid production may decrease, especially when statins are used at high doses.²⁰

2. Upregulation of LDL Receptors and Increased Cholesterol Clearance

The liver compensates for statin-induced cholesterol reduction by upregulating LDL receptors, pulling more cholesterol out of the bloodstream. Some of this imported cholesterol is used to synthesize bile acids, which could partially restore bile acid production in a homeostatic feedback loop.²¹

3. Modulation of CYP7A1 and FXR Pathways

The enzyme CYP7A1 catalyzes the rate-limiting step in bile acid synthesis. Statins may indirectly influence CYP7A1 expression through FXR (farnesoid X receptor) and SHP (small heterodimer partner) pathways, which sense bile acid levels and regulate bile acid homeostasis.²² In some cases, statins can enhance CYP7A1 activity, leading to increased bile acid synthesis, especially under cholesterol-depleted states.

4. Changes in Bile Acid Pool Composition

Statins may alter the ratio of primary to secondary bile acids by shifting synthesis and reabsorption patterns. There is some evidence that statins increase hydrophilic bile acids (like ursodeoxycholic acid) and reduce cytotoxic bile acids (like lithocholic acid), which could have protective effects on liver and colon health.

5. Interaction with Gut Microbiota and Enterohepatic Circulation

Changes in bile acid flow, composition, and hydrophobicity affect the intestinal microbiome, which in turn transforms bile acids through deconjugation and dehydroxylation. By modifying the bile acid milieu, statins could indirectly affect microbial composition and related metabolic or inflammatory outcomes.²³

6. Potential Therapeutic Implications

In conditions like non-alcoholic fatty liver disease (NAFLD) or bile acid diarrhea, where bile acid metabolism is dysregulated, *statins* may offer secondary metabolic or anti-inflammatory benefits beyond lipid-lowering.²⁴ However, in rare cases, increased bile acid synthesis could contribute to diarrhea or gastrointestinal discomfort, especially in sensitive individuals.

REFERENCES:

¹ John R. Turner, "Intestinal Mucosal Barrier Function in Health and Disease," *Nature Reviews Immunology* 9, no. 11 (2009): 799–809. <u>https://doi.org/10.1038/nri2653</u>.

² Tess Yntema, Debby P. Y. Koonen, and Folkert Kuipers, "Emerging Roles of Gut Microbial Modulation of Bile Acid Composition in the Etiology of Cardiovascular Diseases," *Nutrients* 15, no. 8 (2023): 1850. <u>https://doi.org/10.3390/nu15081850</u>.

³ H. Ajouz, D. Mukherji, and A. Shamseddine, "Secondary Bile Acids: An Underrecognized Cause of Colon Cancer," *World Journal of Surgical Oncology* 12 (2014): 164. <u>https://doi.org/10.1186/1477-7819-12-164</u>. ⁴ C. Garcia, D. Diez, and V. Garcia-Mediavilla, "Production of New Microbially Conjugated Bile Acids by Human Gut Microbiota," *Biomolecules* 12, no. 5 (2022): 687. <u>https://doi.org/10.3390/biom12050687</u>.

⁵ X. Wei, Y. Deng, Y. Wang, and L. Zhao, "Biotransformation of Chenodeoxycholic Acid by Human Intestinal Fungi and the Agonistic Effects on FXR," *Phytochemistry* 224 (2024): 114162. <u>https://doi.org/10.1016/j.phytochem.2024.114162</u>.

⁶ Máire Begley, Cormac G. M. Gahan, and Colin Hill, "The Interaction between Bacteria and Bile," *FEMS Microbiology Reviews* 29, no. 4 (2005): 625–651. https://doi.org/10.1016/j.femsre.2004.09.003.

 ⁷ Amy S. Devlin and Emily P. Balskus, "Discovery of a Gut Microbial Pathway for Biosynthesis of the Bile Acid Lithocholic Acid," *Journal of the American Chemical Society* 134, no. 7 (2012): 2944–2947.
 <u>https://doi.org/10.1021/ja2110285</u>.

⁸ Ziyuan Song et al., "Taxonomic and Functional Profiles of Bile Acid Transforming Bacteria in the Human Gut," *Gut Microbes* 10, no. 6 (2019): 673–684. <u>https://doi.org/10.1080/19490976.2019.1593782</u>.

⁹ R. A. Quinn et al., "Global Chemical Effects of the Microbiome Include Novel Conjugated Bile Acids," *Science* 369, no. 6509 (2020): 1518–1523. <u>https://doi.org/10.1126/science.aba6148</u>.

¹⁰ Charles Bernstein et al., "Bile Acids as Carcinogens in Human Gastrointestinal Cancers," *Mutation Research/Reviews in Mutation Research* 589, no. 1 (2005): 47–65. https://doi.org/10.1016/j.mrrev.2004.07.006.

¹¹ Michael Camilleri, "Bile Acid Diarrhea: Prevalence, Pathogenesis, and Therapy," *Gut and Liver* 9, no. 3 (2015): 332–339. <u>https://doi.org/10.5009/gnl14397</u>. ¹² Charlie G. Buffie et al., "Precision Microbiome Reconstitution Restores Bile Acid Mediated Resistance to *Clostridium difficile*," *Nature* 517, no.
7533 (2015): 205–208. <u>https://doi.org/10.1038/nature13828</u>.

 ¹³ M. L. Shiffman, "The Role of the Gallbladder in Bile Acid Homeostasis," *Hepatology* 20, no. 6 (1994): 1543–1546.
 <u>https://doi.org/10.1002/hep.1840200623</u>.

¹⁴ Alan F. Hofmann, "The Continuing Importance of Bile Acids in Liver and Intestinal Disease," *Archives of Internal Medicine* 159, no. 22 (1999):
2647–2658. <u>https://doi.org/10.1001/archinte.159.22.2647</u>.

¹⁵ Michael Camilleri, "Bile Acid Diarrhea: Prevalence, Pathogenesis, and Therapy," *Gut and Liver* 9, no. 3 (2015): 332–339. <u>https://doi.org/10.5009/gnl14397</u>.

¹⁶ Jason M. Ridlon et al., "Bile Salt Biotransformations by Human Intestinal Bacteria," *Journal of Lipid Research* 47, no. 2 (2006): 241–259. <u>https://doi.org/10.1194/jlr.R500013-JLR200</u>.

¹⁷ Hadrien Duboc et al., "Connecting Dysbiosis, Bile-Acid Dysmetabolism and Gut Inflammation in Inflammatory Bowel Diseases," *Gut* 62, no. 4 (2013): 531–539. <u>https://doi.org/10.1136/gutjnl-2012-302578</u>.

¹⁸ Tian Li and John Y. L. Chiang, "Bile Acid Signaling in Metabolic Disease and Drug Therapy," *Pharmacological Reviews* 66, no. 4 (2014): 948–983. <u>https://doi.org/10.1124/pr.113.008201</u>.

¹⁹ John Y. L. Chiang, "Bile Acid Metabolism and Signaling in Liver Disease and Therapy," *Liver Research* 1, no. 1 (2017): 3–9. <u>https://doi.org/10.1016/j.livres.2017.05.001</u>.

²⁰ Neil C. Sadler et al., "Metabolomic Profiling of Statin Treatment Reveals Insights into Bile Acid Homeostasis in Mice," *Toxicology and Applied Pharmacology* 280, no. 1 (2014): 140–148. <u>https://doi.org/10.1016/j.taap.2014.07.008</u>. ²¹ Tian Li and John Y. L. Chiang, "Regulation of Bile Acid and Cholesterol Metabolism by PPARs," *PPAR Research* 2009 (2009): 501739. <u>https://doi.org/10.1155/2009/501739</u>.

²² Shigehiko Katsuma et al., "Bile Acids Promote Glucose Metabolism through the TGR5 Receptor in Brown Adipose Tissue," *PLoS ONE* 10, no. 2 (2015): e0116857. <u>https://doi.org/10.1371/journal.pone.0116857</u>.

²³ Annika Wahlström et al., "Bile Acids and the Gut Microbiota: Metabolic Interactions and Implications for Host Health," *Nature Reviews Gastroenterology & Hepatology* 13, no. 7 (2016): 411–425. <u>https://doi.org/10.1038/nrgastro.2016.136</u>.

²⁴ Markus Fuchs, "Non-Alcoholic Fatty Liver Disease: The Bile Acid-Activated Farnesoid X Receptor as an Emerging Treatment Target," *Journal of Lipids* 2012 (2012): 934396. <u>https://doi.org/10.1155/2012/934396</u>.

<u>Section Nine</u> SIBO & IMO



A MISNOMER REFLECTING POLYMICROBIAL DYSBIOSIS

Small Intestinal Bacterial Overgrowth (SIBO) has long been used to describe a condition characterized by excessive bacterial growth in the small intestine, leading to symptoms such as bloating, diarrhea, and abdominal discomfort. Emerging research, however, suggests that this term may be a misnomer, as the condition often involves not just bacteria but a complex interplay of microorganisms, including viruses, protozoa, fungi, and archaea. A more accurate term would reflect this condition, such as *polymicrobial dysbiosis*, (P.D.). The term polymicrobial dysbiosis acknowledges the diverse ecosystem disruptions caused by microorganism which contribute to disease.¹

The Concept of Polymicrobial Dysbiosis

Polymicrobial dysbiosis (P.D.) refers to an imbalance in the microbial populations of the digestive tract that extends beyond bacteria—i.e., the wrong number, in the wrong place at the wrong time. The dysbiosis involves:

- **Bacteria:** Overgrowth of aerobic or anaerobic bacteria that disrupts the delicate balance of microbial populations.²
- <u>Archaea</u>: Methanogenic archaea, such as *Methanobrevibacter smithii*, which is often implicated in methane-dominant breath test results and associated with conditions like chronic constipation.³
- Fungi: Overgrowth of fungal species like Candida that can exacerbate inflammation and gastrointestinal symptoms.⁴
- <u>Viruses</u>: Certain gut-associated viruses that can alter microbial interactions and immune responses.⁵
- <u>Protozoa</u>: Parasites such as *Giardia* that can coexist with bacterial overgrowth, compounding dysbiosis-related symptoms.⁶

This broader understanding shifts the focus from a single bacterial overgrowth to a more complex microbial imbalance.

Shortcomings of The Term S.I.B.O.

As noted, the term "SIBO" implies a purely bacterial etiology, which overlooks the contributions of viruses, protozoa, fungi, and archaea.⁷ It also overlooks the role of polymicrobial interactions in generating symptoms and in progression of disease.⁸

Overemphasis On Breath Tests

- Breath tests primarily measure hydrogen, methane, or hydrogen sulfide gases produced by microbial fermentation. These tests fail to capture the contributions of non-gasproducing organisms, such as fungi, archaea, and viruses.⁹
- In particular, archaea may influence gas profiles, complicating interpretations.¹⁰

Pathophysiology of Polymicrobial Dysbiosis

SIBO implies a singular pathogenic mechanism—bacterial overgrowth—while P.D. encompasses:

- Disrupted microbial diversity.¹¹
- Altered metabolite production (e.g., short-chain fatty acids, bile acids, and toxins).¹²
- Impaired immune regulation and epithelial barrier function.¹³

Treatment Approaches

- Antimicrobial Therapy: Combine antibacterial, antifungal, and antiprotozoal agents based on individual microbiome profiles.¹⁴
- Probiotics and Prebiotics: Restore microbial diversity and support beneficial organisms.¹⁵
- <u>Dietary Interventions</u>: Tailor diets (e.g., low FODMAP or antifungal diets) to temporarily reduce fermentable substrates and address specific dysbiotic patterns.¹⁶

CONCLUSION:

The term "SIBO" oversimplifies a condition that is better understood as polymicrobial dysbiosis, involving a diverse array of microorganisms. Recognizing the contributions of bacteria, archaea, fungi, viruses, and protozoa provides a more comprehensive framework for diagnosis and treatment. Adopting a broader perspective can improve clinical outcomes and advance the understanding of gastrointestinal health.¹⁷

REFERENCES:

- Saffouri, G. B., et al. (2019). Small Intestinal Microbial Dysbiosis Underlies Symptoms Associated With Functional Gastrointestinal Disorders. *Nature Communications*, 10(1), Article 2012. <u>https://doi.org/10.1038/s41467-019-09964-7</u>
- ^{2.} Rao, S. S. C., et al. (2019). Small Intestinal Bacterial Overgrowth: Clinical Features And Therapeutic Management. *Clinical and*

Translational Gastroenterology, 10(10), e00078. https://doi.org/10.14309/ctg.000000000000078

- ^{3.} Shah, A., et al. (2022). Current And Future Approaches For Diagnosing Small Intestinal Dysbiosis In Patients With Symptoms Of Functional Dyspepsia. *Frontiers in Neuroscience*, 16, 830356. <u>https://doi.org/10.3389/fnins.2022.830356</u>
- ^{4.} Erdogan, Aşkın, And Satish S. C. Rao. "Small Intestinal Fungal Overgrowth." *Current Gastroenterology Reports* 17, No. 4 (2015): 16. <u>https://Doi.Org/10.1007/S11894-015-0436-2</u>.
- ^{5.} Norman, J. M., et al. (2015). Disease-specific alterations in the enteric virome in inflammatory bowel disease. *Cell*, 160(3), 447–460. <u>https://doi.org/10.1016/j.cell.2015.01.002</u>
- ^{6.} Scanlan, P. D., & Marchesi, J. R. (2008). Micro-eukaryotic diversity of the human distal gut microbiota: Qualitative assessment using culturedependent and -independent analysis of faeces. *The ISME Journal*, 2(12), 1183–1193. <u>https://doi.org/10.1038/ismej.2008.76</u>
- ^{7.} Cisek, A. A., Szymańska, E., Aleksandrzak-Piekarczyk, T., and Cukrowska, B. 2024. "The Role of Methanogenic Archaea in Inflammatory Bowel Disease—A Review." *Journal of Personalized Medicine* 14, no. 2: 196. <u>https://doi.org/10.3390/jpm14020196</u>
- ^{8.} Mayer, Emeran A., Tidiane Savidge, and R. J. Shulman. "Brain-gut microbiome interactions and functional bowel disorders." *Gastroenterology* 146, no. 6 (2014): 1500–1512. <u>https://doi.org/10.1053/j.gastro.2014.02.037</u>
- ^{9.} Kashyap, P., et al. "Critical Appraisal of the SIBO Hypothesis and Breath Testing: A Clinical Practice Update Endorsed by the European Society of Neurogastroenterology and Motility (ESNM) and the American Neurogastroenterology and Motility Society (ANMS)." *Neurogastroenterology and Motility* 36, no. 3 (2024): e14817. <u>https://doi.org/10.1111/nmo.14817.</u>

- ^{10.} Kunkel, David, Robert J. Basseri, Marc D. Makhani, Kelly Chong, Christopher Chang, and Mark Pimentel. 2011. "Methane on Breath Testing Is Associated with Constipation: A Systematic Review and Meta-Analysis." *Digestive Diseases and Sciences* 56 (6): 1612–18. <u>https://doi.org/10.1007/s10620-011-1590-5</u>
- ^{11.} Park, Y. M., Y. J. Lee, Z. Hussain, Y. H. Lee, and H. Park. 2017. "The Effects and Mechanism of Action of Methane on Ileal Motor Function." *Neurogastroenterology & Motility* 29 (5). <u>https://doi.org/.10.1111/nmo.13077</u>
- ^{12.} Gérard, P. (2013). Metabolism of bile acids by the gut microbiota. *Nature Reviews Gastroenterology & Hepatology*, 10(6), 330–339. <u>https://doi.org/10.1038/nrgastro.2013.112</u>
- ^{13.} Kelly, J. R., et al. (2016). Transferring the blues: Depression-associated gut microbiota induces neurobehavioral changes in the rat. *Journal of Psychiatric Research*, 82, 109–118. <u>https://doi.org/10.1016/j.jpsychires.2016.07.019</u>
- ^{14.} Soares, M., A. Azevedo, R. Ferreira, and M. Pereira. 2019. "The Role of Archaea in Gastrointestinal Diseases." *Gut Microbes* 10 (5): 450–456.
- ^{15.} Rezaie, A., et al. (2017). Hydrogen and methane-based breath testing in gastrointestinal disorders: The North American consensus. *The American Journal of Gastroenterology*, 112(5), 775–784. <u>https://doi.org/10.1038/ajg.2017.46</u>
- ^{16.} Saffouri, G. B., et al. (2019). Small intestinal microbial dysbiosis underlies symptoms associated with functional gastrointestinal disorders. *Nature Communications*, 10(1), Article 2012. <u>https://doi.org/10.1038/s41467-019-09964-7</u>
- ^{17.} Rao, S. S. C., et al. (2019). Small intestinal bacterial overgrowth: Clinical features and therapeutic management. *Clinical and Translational*

Gastroenterology, 10(10), e00078. https://doi.org/10.14309/ctg.0000000000000078

INTESTINAL METHANOGEN OVERGROWTH

(IMO)

Rethinking Methane—From Pathology to Partnership

For years, methane in the gut has been viewed as a clinical red flag—linked to sluggish motility, bloating, and abnormal breath tests. But a broader ecological perspective reveals a more nuanced story: methanogenesis may be less a pathological threat and more a signal of microbial adaptation.

Nature has long employed methanogens to stabilize fermentation. Ruminants—from cows to deer—depend on methane-producing archaea to clear excess hydrogen gas from their rumen, enabling the efficient conversion of fibrous plant matter into usable energy. Without this hydrogen "sink", fermentation would stall.

In the human gut, the same logic may apply. Methanogenesis, particularly by *Methanobrevibacter smithii*, may represent not microbial aggression but a compensatory response following ecosystem disruption—such as antibiotics, infections, or dietary imbalance. These archaea reduce excess hydrogen, modulate redox conditions, and may help fermentative bacteria regain function. Historically, intestinal methanogen overgrowth (IMO)—marked by elevated breath methane—has been interpreted as a pathological finding. However, emerging evidence suggests that *M. smithii*, now recognized as the dominant archaeon in the human intestine, is a normal resident. It is detectable in up to 95% of healthy adults when using sensitive molecular tools such as qPCR and shotgun metagenomics.¹ As a hydrogenotroph, it consumes molecular hydrogen (H₂) and converts it into methane—a process that prevents hydrogen accumulation, which would otherwise inhibit fermentation and contribute to symptoms like bloating or diarrhea.²

Thus, the expansion of methanogens may not cause illness, but rather reflect an adaptive response to dysbiosis—especially when hydrogen-producing bacteria are thriving. Methanogens are notably resistant to antibiotics,³ and in the wake of microbial disruptions, they often flourish in the absence of normal bacterial competitors. This bloom is frequently observed in post-infectious irritable bowel syndrome (IBS), where altered microbiota composition and increased breath methane have been documented.⁴

While increased methane is associated with slower gut transit and constipation-predominant IBS, the direction of causality remains unclear. Methane may not cause the slow transit—it may instead be the result of it, as longer transit times allow methanogens to

accumulate.⁵ Moreover, methanogenesis may serve a protective role by suppressing other potentially harmful gases, such as hydrogen sulfide.⁶

Reframing IMO not as a disease, but as a sign of ecological imbalance—or even as a microbial coping strategy—could reshape treatment approaches. Rather than prioritizing eradication with dual antibiotics like rifaximin and neomycin, we might instead aim to restore balance with prebiotics, probiotics, synbiotics, and postbiotics. In this light, the presence of methanogens becomes a marker of resilience—a microbial effort to restore homeostasis.

REFERENCES:

¹ Dridi, Bechir, Elodie F. Raoult, Didier Drancourt, and Michel Drancourt. "High Prevalence of Methanobrevibacter smithii and Methanosphaera stadtmanae Detected in the Human Gut Using qPCR." *Applied and Environmental Microbiology* 75, no. 20 (2009): 6760–6766. <u>https://doi.org/10.1128/AEM.00743-09.</u>

² Samuel, Buck S., and Jeffrey I. Gordon. "A Humanized Gnotobiotic Mouse Model of Host-Archaeal-Bacterial Mutualism." *Proceedings of the National Academy of Sciences* 103, no. 26 (2006): 10011–10016. <u>https://doi.org/10.1073/pnas.0602187103.</u>

³ Miller, Terry L., and Milton J. Wolin. "Methanogens Are Resistant to Commonly Used Antibiotics." *Antimicrobial Agents and Chemotherapy* 27, no. 2 (1985): 254–257. <u>https://doi.org/10.1128/AAC.27.2.254.</u>

⁴ Jalanka-Tuovinen, Jonna, Airi Salonen, Airi Salojärvi, et al. "Postinfectious Irritable Bowel Syndrome Is Associated with Altered Faecal Microbiota Composition and Mucosal Gene Expression." Gastroenterology 141, no. 4 (2011): 1188–1197.e1. https://doi.org/10.1053/j.gastro.2011.06.046.

⁵ Pimentel, Mark, Dinesh R. Lin, Ruchi Enayati, et al. "Methane, a Gas Produced by Enteric Bacteria, Slows Intestinal Transit and Augments Small Intestinal Contractile Activity." *American Journal of Physiology-Gastrointestinal and Liver Physiology* 290, no. 6 (2006): G1089–G1095. <u>https://doi.org/10.1152/ajpgi.00574.2004</u>.

⁶ Carbonero, Franck, Amanda C. Benefiel, and Hannah R. Gaskins.
"Contributions of the Microbial Hydrogen Economy to Colonic Homeostasis." *Nature Reviews Gastroenterology & Hepatology* 9, no. 9 (2012): 504–518. <u>https://doi.org/10.1038/nrgastro.2012.85.</u>

SECTION TEN

THE IMPORTANCE OF COMMUNICATION BETWEEN THE DIGESTIVE TRACT AND THE BRAIN



THE BRAIN-GUT CONNECTION

MECHANISMS LINKING GUT DYSBIOSIS TO NEUROINFLAMMATION

The intricate relationship between the gut and the brain, often referred to as the gut-brain axis, has garnered significant attention in recent years. Emerging evidence suggests that gut dysbiosis—an imbalance in the gut microbiota—is intricately linked to the pathogenesis of various neuropsychiatric and neurological disorders. Evidence suggests that there exists processes and pathways through which gut dysbiosis contributes to persistent immune activation and increased blood-brain barrier (BBB) permeability, leading to neuroinflammation and the disruption of brain homeostasis.

Gut Dysbiosis and Immune Activation

The human gastrointestinal (GI) tract harbors a complex microbial ecosystem that communicates with the brain through neuroendocrine, immune, and autonomic pathways. Dysbiosis, characterized by an imbalance in this microbial community, can lead to the release of microbial metabolites and cellular components that act as signaling molecules within the gut-brain axis¹. These molecules can activate local gastrointestinal pathways and, upon entering systemic circulation, influence distant organs, including the brain². Notably, gut dysbiosis has been linked to neurological disorders through mechanisms involving activation of the hypothalamic-pituitary-adrenal axis, systemic inflammation, and increased permeability of both the intestinal and blood-brain barriers³.

Increased Blood-Brain Barrier Permeability

The integrity of the BBB is critical for maintaining the brain's microenvironment. Emerging evidence suggests that gut dysbiosis can lead to increased intestinal permeability, allowing microbial products like lipopolysaccharides (LPS) to enter the bloodstream⁴. These endotoxins can disrupt BBB integrity, facilitating the entry of pro-inflammatory cytokines and immune cells into the central nervous system (CNS), thereby promoting neuroinflammation⁵.

Neuroinflammatory Cascade and Brain Homeostasis

Once the BBB is compromised, microbial metabolites and immune cells can access the CNS, triggering a neuroinflammatory cascade⁶. This inflammation disrupts brain homeostasis and has been linked to the development and progression of various neurodegenerative diseases⁷. For instance, microbial dysbiosis leads to a proinflammatory milieu and systemic endotoxemia, contributing to the development of neurodegenerative diseases⁸.

Association with Neurological and Psychiatric Disorders

The gut-brain axis plays a pivotal role in regulating neural, endocrine, immune, and humoral pathways. An imbalance in gut microbiota composition has been identified as a critical factor in several disorders, including Alzheimer's disease, schizophrenia, anxiety, depression, epilepsy, migraines, autism, and Parkinson's disease⁹. For example, alterations in gut microbiota have been linked to neuroinflammation and synaptic dysfunction, which are key features in the pathophysiology of these conditions¹⁰.

CONCLUSION:

The bidirectional interactions between the gut and brain underscore the importance of maintaining a balanced gut microbiota for neurological health. Gut dysbiosis leads to persistent immune activation and increased BBB permeability, setting off a cascade of neuroinflammatory events that disrupt brain homeostasis and contribute to the pathogenesis of numerous neuropsychiatric and neurological disorders. Understanding these mechanisms opens avenues for potential therapeutic interventions targeting the gut microbiota to mitigate or prevent these conditions.

REFERENCES:

- Cryan, J. F., & Dinan, T. G. (2012). Mind-Altering Microorganisms: The Impact Of The Gut Microbiota On Brain And Behavior. *Nature Reviews Neuroscience*, 13(10), 701-712. <u>https://doi.org/10.1038/nrn3346</u>
- ^{2.} Sampson, Timothy R., and Sarkis K. Mazmanian. "Control of Brain Development, Function, and Behavior by the Microbiome." *Cell Host & Microbe* 17, no. 5 (2015): 565–576. <u>https://doi.org/10.1016/j.chom.2015.04.011.</u>

- ^{3.} Foster, J. A., Rinaman, L., & Cryan, J. F. (2017). Stress & The Gut-Brain Axis: Regulation By The Microbiome. *Neurobiology of Stress*, 7, 124-136. <u>https://doi.org/10.1016/j.ynstr.2017.03.001</u>
- ^{4.} Braniste, V., et al. (2014). The gut microbiota influences blood-brain barrier permeability in mice. *Science Translational Medicine*, 6(263), 263ra158. <u>https://doi.org/10.1126/scitranslmed.3009759</u>
- ^{5.} Cani, Patrice D., Jacques Amar, Miguel A. Iglesias, Muriel Poggi, Christophe Knauf, Dominique Bastelica, Anne M. Neyrinck, et al. "Metabolic Endotoxemia Initiates Obesity and Insulin Resistance." *Diabetes* 56, no. 7 (2007): 1761–72. <u>https://doi.org/10.2337/db06-1491</u>. <u>pubmed.ncbi.nlm.nih.gov+1jme.bioscientifica.com+1</u>
- ^{6.} Erny, Daniel, Alexander L. Hrabě de Angelis, and Marco Prinz. "Communicating Systems in the Body: How Microbiota and Microglia Cooperate." *Immunology* 150, no. 1 (2017): 7–15.
- ^{7.} Sharon, G., Sampson, T. R., Geschwind, D. H., & Mazmanian, S. K. (2016). The central nervous system and the gut microbiome. *Cell*, 167(4), 915-932. <u>https://doi.org/10.1016/j.cell.2016.10.027</u>
- ^{8.} Qin, J., et al. (2012). A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature*, 490(7418), 55-60.
 <u>https://doi.org/10.1038/nature11450</u>
- ^{9.} Hsiao, E. Y., et al. (2013). Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders. *Cell*, 155(7), 1451-1463. <u>https://doi.org/10.1016/j.cell.2013.11.024</u>
- ^{10.} Valles-Colomer, M., et al. (2019). The neuroactive potential of the human gut microbiota in quality of life and depression. *Nature Microbiology*, 4(4), 623-632. <u>https://doi.org/10.1038/s41564-018-0337-x</u>

SECTION ELEVEN

MICROBE FUNCTIONALITY: <u>A PARADIGM SHIFT</u>

<u>The Limits of Microbial Census: Why Density and Diversity</u> <u>Alone Cannot Define Health or Disease</u>

Over the past two decades, scientific and clinical interest in the human microbiome has grown exponentially. Researchers have mapped the bacterial communities of the skin, mouth, gut, and genitourinary tract, revealing complex ecosystems whose collective gene pool—often called the microbiome—dwarfs the human genome by orders of magnitude. As already pointed out, these discoveries have helped shift medicine's view of the human body from an autonomous entity to a synbiotic "superorganism" cohabiting with trillions of microbes.

In clinical microbiome research and diagnostics, two metrics have received disproportionate attention: density (how many microbes are present) and diversity (how many different types). While these are foundational to understanding community structure, they are inadequate as standalone measures of health or disease. A microbiome can appear dense and diverse on DNA sequencing, and yet be functionally inert, pathogenically active, or systemically destabilizing.¹ Measures of microbial load and alpha diversity (i.e., the number of species present and their relative balance) have been linked to health outcomes across numerous studies. A low-diversity gut microbiome has been associated with obesity, inflammatory bowel disease, and immune dysregulation.²

However, this correlation does not imply causation—and the picture is far more nuanced. For example, patients with Crohn's disease can exhibit elevated microbial density due to blooms of inflammatory microbe species like *Escherichia coli* yet have impaired barrier function and immune tolerance.

Similarly, a person exposed to antibiotics might show reduced diversity, but if the remaining organisms are synbiotic and metabolically active, the microbiome may still fulfill essential health-promoting roles.

In other words, microbial presence does not guarantee microbial performance. To equate the census of organisms with their physiological impact is to mistake structure for function.³

Microbes are not passive residents—they are biochemical powerhouses capable of synthesizing neurotransmitters, detoxifying carcinogens, regulating inflammation, and modulating gene expression in host tissues.⁴

Modern "-omics" tools such as metatranscriptomics, metaproteomics, and metabolomics allow researchers to measure real-time microbial activity. Metatranscriptomics examines which microbial genes are actively transcribed, shedding light on metabolic pathways currently in use.⁵ (See: Microbiome Study Glossary)

Metaproteomics reveals what proteins (enzymes, transporters, virulence factors) are being synthesized. Metabolomics identifies the small molecules—such as short-chain fatty acids, bile acid derivatives, or inflammatory mediators—produced by microbial communities.⁶

These approaches have revealed profound discrepancies between microbial composition and function. In one study, patients with irritable bowel syndrome had gut microbiota that were compositionally similar to controls yet functionally skewed toward gas production and pro-inflammatory metabolites.⁷

Another complexity is that many microbes in the human body exist in latent or dormant states, with minimal gene expression or metabolic activity. These organisms may serve as a functional reserve, reactivating only under specific environmental or immunological conditions. Conversely, a typically "harmless" microbe can become virulent if its gene expression changes in response to environmental cues—such as inflammation, iron availability, or pH shifts.⁸

Thus, the clinical question is not merely "who is there?" but "who is awake?", "who is speaking?", and "what are they saying to the host?"

Overreliance on DNA-based census methods (e.g., 16S rRNA or shotgun metagenomics) can lead to misleading conclusions. A diverse microbiome that is metabolically dormant or producing harmful metabolites can appear "healthy" on paper. Conversely, a seemingly sparse microbiome may be performing critical antiinflammatory or metabolic roles.⁹

Understanding the functional output of microbial communities is essential for identifying therapeutic targets, designing effective probiotics or dietary interventions, monitoring disease progression or response to therapy, and developing personalized microbiome diagnostics.¹⁰

The human microbiome is not a static list of species but a dynamic, context-sensitive metabolic organ. While measures of density and diversity provide a structural overview, they cannot capture the behavioral state of this organ.¹¹

Only then can scientists understand whether microbial inhabitants are serving us, ignoring us, or slowly contributing to our decline.¹²

Inflammation is increasingly viewed not only as a localized immune response but as a systemic signaling state shaped by the microbiome.¹³

It is now evident that microbial shifts are deeply implicated in a range of disorders including cardiovascular, neurodegenerative and metabolic disorders.¹⁴

Metabolomic tools are helping to bridge the gap between microbiome composition and clinical translation of metabolomic data.¹⁵

REFERENCES:

- ^{1.}Biocodex Microbiota Institute. "Diversity or Function: What Defines a Healthy Microbiota." Biocodex Microbiota Institute, March 2025. <u>https://www.biocodexmicrobiotainstitute.com/en/pro/diversity-or-function-what-defines-healthy-microbiota</u>.
- ² Zhang, X., et al. "Metatranscriptomic Analysis Reveals Gut Microbiome Bacterial Genes Associated with Hyperuricemia and Gout." Scientific Reports 15, no. 1 (2025): 93899. https://www.nature.com/articles/s41598-025-93899-1.
- ^{3.}Miller, J. R., et al. "Metatranscriptomics for Understanding the Microbiome in Food and Human Health." Frontiers in Microbiology 16 (2025): 11943699. https://pmc.ncbi.nlm.nih.gov/articles/PMC11943699/.
- ^{4.}Smith, L. M., et al. "Metabolomics in the Analysis of Inflammatory Diseases." NCBI Bookshelf, 2025. <u>https://www.ncbi.nlm.nih.gov/books/NBK402338/</u>.
- ^{5.} Jones, M. B., et al. "Distinguishing between Metabolically Active and Dormant Bacteria in Environmental Samples." Applied and Environmental Microbiology 83, no. 24 (2017): e02646-17. <u>https://pubmed.ncbi.nlm.nih.gov/29098411/.</u>
- ⁶·Wang, Y., et al. "Microbiota in Health and Diseases." Signal Transduction and Targeted Therapy 5, no. 1 (2022): 92. <u>https://www.nature.com/articles/s41392-022-00974-4</u>.
- ^{7.}Lee, S. H., et al. "Diversity, Compositional and Functional Differences between Gut Microbiota of Children and Adults." Scientific Reports 10,

no. 1 (2020): 57734. <u>https://www.nature.com/articles/s41598-020-</u> <u>57734-z</u>.

⁸ Kumar, R., et al. "Exploring the Functional Diversity and Metabolic Activities of the Human Gut Microbiome." Microbiology Spectrum 12, no. 1 (2024): e01599-24.

https://journals.asm.org/doi/10.1128/spectrum.01599-24.

- ⁹ Chen, Y., et al. "Microbiome and Metabolome Features in Inflammatory Bowel Disease." Nature Communications 14, no. 1 (2023): 42788. <u>https://www.nature.com/articles/s41467-023-42788-0</u>.
- ^{10.} Brown, C. T., et al. "Representation of Dormant and Active Microbial Dynamics for Ecosystem Modeling." Applied and Environmental Microbiology 80, no. 16 (2014): 4858–64. <u>https://pmc.ncbi.nlm.nih.gov/articles/PMC3928434/</u>.
- ^{11.} Garcia, S. L., et al. "Microbial Dormancy as an Ecological and Biogeochemical Regulator." Nature Communications 15, no. 1 (2025): 59167. <u>https://www.nature.com/articles/s41467-025-59167-6</u>.
- ^{12.} Li, H., et al. "Metatranscriptomics-Guided Genome-Scale Metabolic Reconstruction of the Human Gut Microbiome." Microbiome 12, no. 1 (2024): 1830.

https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168 -024-01830-z.

 ^{13.} Zhao, L., et al. "Metabolomics Activity Screening of T Cell–Induced Colitis Reveals Anti-Inflammatory Metabolites." Science Signaling 13, no. 658 (2020): abf6584.

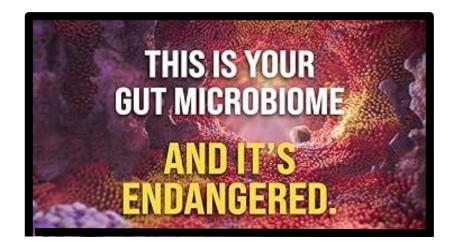
https://www.science.org/doi/10.1126/scisignal.abf6584.

^{14.} Singh, R. K., et al. "Human Gut Microbiota in Health and Disease."
 Frontiers in Microbiology 13 (2022): 999001.
 <u>https://www.frontiersin.org/journals/microbiology/articles/10.3389/fm</u>
 <u>icb.2022.999001/full</u>.

^{15.} Johnson, M. E., et al. "Metabolomics: The Key to Unraveling the Role of the Microbiome in Health and Disease." Frontiers in Neuroscience 16 (2022): 917197.

https://www.frontiersin.org/articles/10.3389/fnins.2022.917.

ENDANGERED MICROBES



The widespread use of antimicrobials in medicine and agriculture has had a profound impact on microbial populations. While antibiotics are lifesaving, they do not distinguish between harmful and beneficial bacteria, leading to collateral damage within digestive ecosystems. This disruption can alter microbial diversity, compromise the gut barrier, and predispose individuals to dysbiosis-related conditions.

Additionally, the modern food supply is laden with chemical additives—herbicides, pesticides, colorants, preservatives, and emulsifiers—that can negatively affect microbial health. Studies suggest that these additives may compromise gut integrity, disrupt microbial composition, and create an environment where pathogenic microbes can thrive unchecked.

Lifestyle Choices And Microbial Health

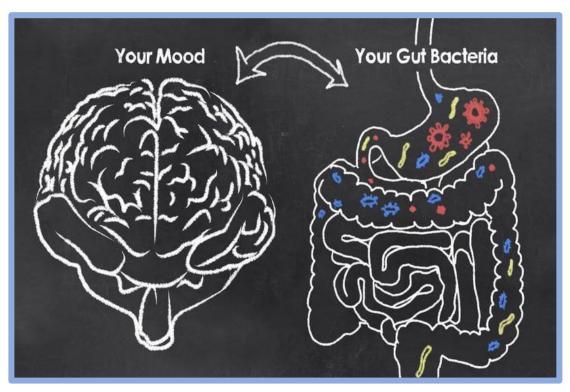
Lifestyle choices play a significant role in shaping the gut microbiome. Alcohol, tobacco, and recreational drug use have been shown to damage beneficial microbes while promoting an inflammatory gut environment. Furthermore, inadequate oral hygiene can contribute to microbial imbalances in the digestive tract. The oral cavity serves as the "headwaters" of the gastrointestinal system, and pathogenic overgrowth here can have downstream consequences, including increased risks of periodontitis, dysbiosis, and systemic inflammation.

The rapid rise in autoimmune illnesses has been impacted by gut microorganisms, genetics, the environment and gut permeability. The evidence has been illustrated best with lupus, type 1 diabetes and multiple sclerosis.¹

REFERENCES:

^{1.} Christovich, Anna, and Xin M. Luo. "Gut Microbiota, Leaky Gut, and Autoimmune Diseases." *Frontiers in Immunology* 13 (2022): 946248. <u>https://doi.org/10.3389/fimmu.2022.946248.</u>

SECTION TWELVE



STRESS AND THE MICROBIOME

Biological, Environmental, and Psychological Stressors:

In healthy adults, various forms of stress—biological, environmental, and psychological—interact with the gut microbiome. Studies utilizing stool samples and assessments of stress across three domains—perceived stress, stressful life events, and biological stress (measured via heart rate variability, specifically reduced respiratory sinus arrhythmia, or RSA)—have revealed significant connections influencing health outcomes and stress resilience.

Gut Microbiome Diversity and Stress:

Research indicates that gut microbial diversity (alpha and beta diversity) varies with individuals' stress levels. Lower perceived stress is associated with greater microbial diversity, often linked to better health outcomes. Conversely, higher stress levels, whether due to psychological perception or biological responses, correlate with distinct changes in microbial composition.

Specific Microbes and Stress Levels:

Certain microbial populations are associated with stress responses. For instance, higher levels of *Escherichia/Shigella* have been linked to increased perceived stress, while lower levels of *Clostridium* correlate with reduced biological stress (RSA). These associations suggest that specific microbial profiles may reflect how the body processes stress.

Microbial Functions and Stress Modulation:

The gut microbiome's ability to produce beneficial compounds like butyrate—a short-chain fatty acid known to reduce inflammation, support brain health, and improve stress resilience—has been noted. Conversely, microbes producing harmful substances like formaldehyde may contribute to cognitive decline. This dual role underscores the microbiome's potential influence on both mental and physical health.

Implications for Stress Management:

These findings suggest that promoting a healthy gut microbiome through diet, probiotics, or other interventions could improve

stress resilience. Identifying specific microbes or microbial functions associated with reduced stress may lead to targeted therapies in the future.

While prior research has focused on clinical populations with stress-related disorders, recent studies uniquely explore stressmicrobiome links in healthy individuals, opening the door to preventive strategies aimed at enhancing resilience before stressrelated conditions develop. Understanding how gut microbes interact with diverse types of stress may help design interventions tailored to individual needs, potentially improving overall wellbeing.

REFERENCES:

Delgadillo, D. R., et al. (2025). Biological, Environmental, and Psychological Stress and the Human Gut Microbiome in Healthy Adults. *Scientific Reports*, 15, 362. <u>https://doi.org/10.1038/s41598-024-77473-9</u>

Dinan, Timothy G., Catherine Stanton, and John F. Cryan. "Psychobiotics: A Novel Class of Psychotropic." *Biological Psychiatry* 74, no. 10 (2013): 720–726. <u>https://doi.org/10.1016/j.biopsych.2013.05.001.</u>

Liu, Xiaofei, Shangqing Cao, and Xuewu Zhang. "Modulation of Gut Microbiota-Brain Axis by Probiotics, Prebiotics, and Diet." *Journal of Agricultural and Food Chemistry* 63, no. 36 (2015): 7885–7895. <u>https://doi.org/10.1021/acs.jafc.5b01864.</u>

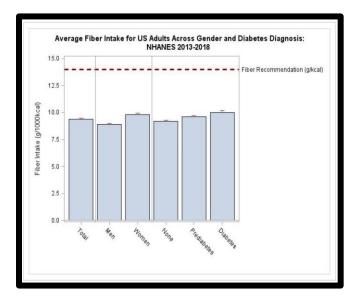
Turnbaugh, Peter J., Ruth E. Ley, Michael A. Mahowald, Vincent Magrini, Elaine R. Mardis, and Jeffrey I. Gordon. "An Obesity-Associated Gut Microbiome with Increased Capacity for Energy Harvest." *Nature* 444, no. 7122 (2006): 1027–31. <u>https://doi.org/10.1038/nature05414.</u>

SECTION THIRTEEN

THE SILENT CRISIS OF FIBER DEFICIENCY IN THE U.S. ADULT POPULATION

LESS THAN 10% OF U.S. ADULTS EAT RECOMMENDED LEVELS OF DIETARY FIBER:

Despite its benefits, dietary fiber intake remains below recommended levels for a large segment of the U.S. population. Specifically, only about 7.4% of adults meet the recommended daily intake of dietary fiber¹.



According to U.S. federal guidelines², the recommended fiber intake is 14 grams of fiber for every 1,000 calories consumed each

day. This translates to approximately 25 grams per day for adult women and 38 grams per day for adult men³. However, current data indicates that the average fiber consumption falls well short of these recommendations, with women consuming about 9.9 grams of fiber per 1,000 calories and men about 8.7 grams per 1,000 calories⁴.

Understanding or adhering to these guidelines poses several challenges. One notable issue is the lack of specificity regarding the type of fiber individuals should consume. Fiber is categorized into several types: soluble, insoluble, fermentable, and non-fermentable, each with distinct functions and health benefits. For example, fermentable fibers contribute to gut health by serving as fuel for beneficial gut bacteria and producing short-chain fatty acids (SCFAs) such as butyrate, while non-fermentable fibers provide bulk and aid in bowel movement without undergoing significant fermentation⁵.

Given this complexity, it is difficult to provide a one-size-fits-all approach to fiber intake. Individual factors such as genetics, gut microbiota composition, metabolic rate, and health status all influence how fiber is processed and utilized in the body. This variability makes it challenging to predict the exact benefit of a specific type or amount of fiber for each person.

The emphasis, therefore, should not be on trying to achieve an exact quantity of fiber or worrying excessively about the proportions of soluble versus insoluble or fermentable versus non-

fermentable fiber. Instead, it is more practical and beneficial to focus on consuming a diverse array of natural fiber sources. This means prioritizing whole foods that are close to their natural state, such as fresh fruits, vegetables, beans, legumes, whole grains, nuts, seeds, polyols, and resistant starches⁶.

Additionally, preparation methods can impact the fiber content and its benefits, underscoring the importance of choosing minimally processed foods.

Natural sources of fiber not only provide a balanced mix of soluble and insoluble types but also come with a variety of vitamins, minerals, and antioxidants that support overall health. This approach helps ensure a more holistic intake of dietary fiber that aligns with the body's varied needs. The use of synthetic fibers or highly processed foods fortified with fiber may not deliver the same comprehensive benefits as naturally fiber-rich foods⁷.

To summarize, while federal guidelines on fiber intake provide a helpful baseline, individuals should strive for a flexible and varied approach to meeting their fiber needs. Incorporating a wide range of natural fiber sources into daily meals and snacks, with a focus on whole, unprocessed foods, can help support digestive health, metabolic function, and overall well-being without the need for precise calculations⁸.

REFERENCES:

¹ McGill, Carla R., Anne Birkett, and Victor L. Fulgonii III. "Healthy Eating Index-2010 and Food Groups Consumed by US Adults Who Meet or Exceed Fiber Intake Recommendations NHANES 2001-2010." *Food & Nutrition Research* 60 (2016). <u>https://doi.org/10.3402/fnr.v60.29977</u>.

² U.S. Department of Agriculture and U.S. Department of Health and Human Services. *Dietary Guidelines for Americans, 2020-2025*. 9th ed. December 2020. <u>https://www.dietaryguidelines.gov</u>.

³ Slavin, Joanne L. "Dietary Fiber and Body Weight." *Nutrition* 21, no. 3 (2005): 411–418. https://doi.org/10.1016/j.nut.2004.08.018.

⁴ Institute of Medicine. *Dietary Reference Intakes for Energy, Carbohydrate, Fiber, Fat, Fatty Acids, Cholesterol, Protein, and Amino Acids*. Washington, DC: National Academies Press, 2005. <u>https://doi.org/10.17226/10490</u>.

 ⁵ Makki, Kiran, Eric C. Deehan, Angela L. Walter, and Fredrik Bäckhed.
 "The Impact of Dietary Fiber on Gut Microbiota in Host Health and Disease." *Cell Host & Microbe* 23, no. 6 (2018): 705–715.
 <u>https://doi.org/10.1016/j.chom.2018.05.012.</u>

⁶ Anderson, James W., Patricia Baird, Rhonda H. Davis Jr., Stephanie Ferreri, Mary Knudtson, Angela Koraym, Valerie Waters, and Christine L. Williams. "Health Benefits of Dietary Fiber." *Nutrition Reviews* 67, no. 4 (2009): 188–205. <u>https://doi.org/10.1111/j.1753-4887.2009.00189.x.</u>

⁷ Weickert, Martin O., and Andreas F. H. Pfeiffer. "Impact of Dietary Fiber Consumption on Insulin Resistance and the Prevention of Type 2 Diabetes." *The Journal of Nutrition* 148, no. 1 (2018): 7–12. <u>https://doi.org/10.1093/jn/nxx008.</u>

⁸ Pandey, Madhurima, Omar AlQassab, Tharinee Kanthajan, Ankit Parikh, Anoop J. Francis, Chithra Sreenivasan, and Maduabuchi Nwosu. "Effectiveness of High-Fiber, Plant-Based Diets in Reducing Cardiovascular Risk Factors Among Middle-Aged and Older Adults: A Systematic Review." *Cureus* 16, no. 8 (2024): e67660. <u>https://doi.org/10.7759/cureus.67660.</u>

CATEGORIES OF FERMENTABLE FOOD ITEMS THAT PRODUCE SHORT-CHAIN FATTY ACIDS (SCFAs) BY INTESTINAL MICROBIAL FERMENTATION

Introduction

The following categories of food items promote SCFA production, with examples provided for clarity. For a comprehensive list of over 100 food products, proceed to the end of the Digestive Health Guide.



<u>Categories of Fermentable Food Items</u> (See List 6)

<u>1. Fruits</u>

Examples: Apples, blueberries, raspberries, strawberries, oranges, and pears.

2. Vegetables

Root vegetables: Sweet potatoes, carrots, and beets.

Cruciferous vegetables: Broccoli, Brussels sprouts, cabbage, and cauliflower.

Alliums: Onions, garlic, leeks, shallots, and chives.

3. Legumes and Beans

Examples: Lentils, chickpeas, black beans, kidney beans, and soybeans.

4. Whole Grains

Examples: Oats, barley, brown rice, whole wheat, and quinoa.

5. Fungi (Mushrooms)

Examples: Shiitake mushrooms, oyster mushrooms, button mushrooms, Reishi mushrooms, and Chaga mushrooms.

<u>6. Nuts</u>

Examples: Almonds, pecans, walnuts, hazelnuts, and pistachios.

7. Seeds

Examples: Chia seeds, flaxseeds, pumpkin seeds, sunflower seeds, and hemp seeds.

8. Resistant Starches

Examples: Cooked and cooled potatoes, cooked and cooled rice, greenish bananas, and greenish plantains.

9. Seaweed

Examples: Nori (red seaweed), wakame (brown seaweed), kombu, dulse, and agar.

10. Human Milk Oligosaccharides (HMOs)

Examples: 2'-Fucosyllactose (2'FL), Lacto-N-neotetraose (LNT), 3'-Sialyllactose (3'SL), and 6'-Sialyllactose (6'SL).

11. Chitin and Chitinous Foods

Examples: Crab shells, shrimp shells, lobster shells, and edible insects.

12. Polyphenol-Rich Foods

Examples: Dark chocolate, green tea, matcha tea, and pomegranates. (See section: Polyphenols)

Maldigestion and Malabsorption of Vitamins and Minerals (1-7)

This widespread deficiency has profound implications, particularly in terms of maldigestion and malabsorption. Both conditions can lead to a gradual depletion of essential vitamins and minerals including the following:

- Calcium
- Phosphorus
- Potassium
- Magnesium
- Folic acid (vitamin B9)
- Vitamin B12
- Iron

In some instances, measuring levels of essential vitamins and minerals in the blood may be part of the diagnostic process.

REFERENCES:

¹ Weaver, Connie M., and Robert P. Heaney, eds. *Calcium in Human Health*. Humana Press, 2006. https://doi.org/10.1007/978-1-59259-961-5.

² He, Feng J., and Graham A. MacGregor. "Beneficial Effects of Potassium on Human Health." *Physiologia Plantarum* 133, no. 4 (2008): 725–735. <u>https://doi.org/10.1111/j.1399-3054.2007.01033.x</u>.

³ Bailey, Lynn B., ed. *Folate in Health and Disease*. 2nd ed. Boca Raton, FL: CRC Press, 2009. <u>https://doi.org/10.1002/9781119946045.ch21</u>.

⁴ Stabler, Sally P. "Vitamin B12 Deficiency." *New England Journal of Medicine* 368 (2013): 149–160. <u>https://doi.org/10.1056/NEJMcp1113996</u>.

⁵ Fairfield, Kathleen M., and Robert H. Fletcher. "Vitamins for Chronic Disease Prevention in Adults: Scientific Review." *JAMA* 287, no. 23 (2002): 3116–3126. <u>https://doi.org/10.1001/jama.287.23.3116</u>.

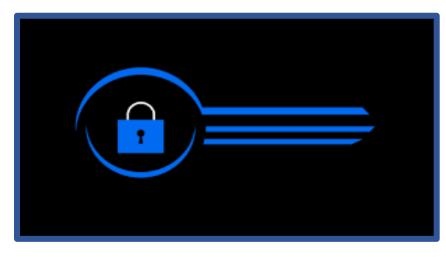
⁶ Fortmann, Stephen P., Beth U. Burda, Christina A. Senger, Jennifer S. Lin, and Evelyn P. Whitlock. "Vitamin and Mineral Supplements in the Primary Prevention of Cardiovascular Disease and Cancer: An Updated Systematic Evidence Review for the U.S. Preventive Services Task Force." *Annals of Internal Medicine* 159, no. 12 (2013): 824–834.

https://doi.org/10.7326/0003-4819-159-12-201312170-00729.

⁷Sesso, Howard D., William G. Christen, Varuna Bubes, Julie P. Smith, Jason MacFadyen, Michael Schvartz, and J. Michael Gaziano.
"Multivitamins in the Prevention of Cardiovascular Disease in Men: The Physicians' Health Study II Randomized Controlled Trial." *JAMA* 308, no.
17 (2012): 1751–1760. <u>https://doi.org/10.1001/jama.2012.14805</u>.

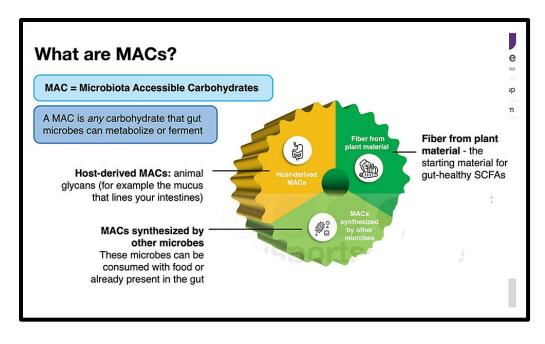
SECTION FOURTEEN

MICROBIAL ACCESSIBLE NUTRIENTS A DEEPER DIVE INTO DIETARY FIBER



HEALTH BENEFITS

Dietary fiber is often heralded as the cornerstone of healthy eating. It is felt to play a pivotal role in maintaining overall health. Dietary fibers are diversified substances that have varied biological effects. They are food substances that escape digestion in the small intestine and reach the large intestine (colon) intact where resident microorganisms partially or completely metabolize them. Dietary fiber is frequently referred to by the acronym MACs (Microbial Accessible Carbohydrates).



Researchers emphasize that "MACs" should not be viewed as a static characteristic of specific dietary components and instead represent the potential metabolic activity associated with carbohydrates that exist in a particular microbiome.¹

Evidence shows that dietary fibers offer a myriad of health benefits, including reducing the risk of chronic diseases such as diabetes, heart disease, and colorectal cancer. **(See the section:** *How Humans Rely on their Microbes*).

Dietary fiber is not just about improving bowel function but is crucial for systemic health and prevention of serious health conditions.

REFERENCES:

¹ Sonnenburg, Erica D., and Justin L. Sonnenburg. "Starving Our Microbial Self: The Deleterious Consequences of a Diet Deficient in Microbiota-Accessible Carbohydrates." *Cell Metabolism* 20, no. 5 (2014): 779–786. <u>https://doi.org/10.1016/j.cmet.2014.07.003.</u>

DIETARY FIBER DEFINED BY

CHEMICAL CHARACTERISTICS

Dietary fibers are commonly divided by subtypes based upon solubility, viscosity, and fermentation properties with health benefits highly correlated with these attributes.

Depending on the solubility of the fiber in water, it can be classified as either soluble or insoluble. Soluble fibers have water holding capacity with high gel forming properties and are readily fermented by digestive tract microorganisms. Common sources of soluble fibers include whole grains (e.g., oats and barley), beans and legumes, the flesh of fruit and vegetables, and seeds (e.g., flaxseeds and chia seeds).

On the other hand, insoluble fibers lack water holding capacity and are less fermentable by microorganisms. Insoluble fibers are typically found in whole-wheat bread, pasta, fruits and vegetable skins, nuts, and seeds.

Many studies on fiber have focused on the benefits of consuming an isolated, single fiber or fiber extract. This is not, however, how humans consume dietary fiber. Plant-predominant foods such as fruits, vegetables, nuts, seeds, legumes, beans, and whole grains are not just one lone source or extract of fiber but may contain a matrix of multiple diverse types of fiber.

SECTION FIFTEEN

UNDERSTANDING THE COMPLEXITIES OF HIGH FIBER SUPPLMENTATION: CHEMISTRY, BENEFITS, AND GOALS

Beyond "High Fiber": Understanding Fermentable and Non-Fermentable Fiber for Optimal Health

The common recommendation to "eat a high-fiber diet" is scientifically imprecise and often misleading. While fiber is an essential component of a healthy diet, not all fiber is created equal. Simply increasing fiber intake without understanding its distinct roles in the body can be ineffective—or even counterproductive.

The Importance of Fiber Selection

Consider natural sources such as leaves, grass, and tree bark. Despite their exceptionally high fiber content, they are nutritionally inadequate for humans because the human body lacks the enzymes necessary to digest and extract nutrients from them. Unlike ruminants such as cows, goats, and deer, which possess specialized gut microbiota and fermentative digestive systems, humans cannot efficiently break down these fibrous materials. Thus, fiber selection must be intentional, prioritizing usable fiber sources rather than indiscriminately increasing total fiber intake.

Fermentable Fiber: Fuel for Gut Microbes

Fiber becomes metabolically useful when it is fermented by gut microbes in the distal small intestine and colon. Fermentable fibers serve as substrates for bacterial metabolism, producing short-chain fatty acids (SCFAs) such as butyrate, acetate, and propionate. These SCFAs play critical roles in gut health, immune function, and metabolic regulation.

Common Sources of Fermentable Fiber:

- Soluble fibers: Found in legumes, oats, barley, bananas, apples, and root vegetables.
- Prebiotic oligosaccharides: Including fructo-oligosaccharides (FOS), galacto-oligosaccharides (GOS), arabinooligosaccharides (AOS), xylo-oligosaccharides (XOS), and inulin.
- **Resistant starches:** Present in cooled potatoes, green bananas, and whole grains.

Since SCFAs derived from fermentation significantly influence gut microbiota, metabolism, and immune function, dietary recommendations should emphasize a high fermentable fiber intake rather than a blanket recommendation to increase fiber without differentiation.

The Role of Non-Fermentable Fiber

Non-fermentable fiber is not without value; rather, it serves a different function. Insoluble fibers, which are non-fermentable, pass through the gut intact and contribute to stool bulk. Some non-fermentable fibers also act osmotically, drawing water into the colon to soften stool and promote regular bowel movements. This mechanical function supports digestion by preventing constipation and maintaining bowel health.

Common Sources of Non-Fermentable Fiber:

- Cellulose and lignin: Found in whole grains, wheat bran, nuts, and many vegetables.
- Certain resistant starches: That escape fermentation.
- Psyllium husk: Which provides both soluble and insoluble properties.

<u>Commercial Strategy: Combining Fermentable and Non-</u> <u>Fermentable Fiber</u>

Food manufacturers, particularly cereal brands, and fiber supplement companies, capitalize on the complementary roles of

fermentable and non-fermentable fiber by incorporating both types into their products. This is reflected in food labeling, which often differentiates between soluble (fermentable) and insoluble (primarily non-fermentable) fiber content.

By balancing these fiber types, products aim to provide stool bulk, improve consistency, and promote fermentation-derived health benefits simultaneously. While this approach can be beneficial, consumers should recognize that not all "high-fiber" foods contribute equally to gut microbial health and SCFA production.

CONCLUSION:

The general advice to eat a "high-fiber diet" is incomplete because it fails to distinguish between fiber that nourishes gut microbes (fermentable fiber) and fiber that primarily adds bulk (nonfermentable fiber). For optimal digestive health, metabolic balance, and microbial support, fiber intake should prioritize fermentable fibers that enhance SCFA production while still incorporating non-fermentable fiber for stool regulation. Understanding this distinction enables individuals to make informed dietary choices that maximize both microbial and physiological benefits.

REFERENCES:

 De Vries, J., Miller, P. E., & Verbeke, K. (2015). Effects Of Cereal Fiber On Bowel Function: A Systematic Review Of Intervention Trials. *World Journal of Gastroenterology*, 21(29), 8952–8963. <u>https://doi.org/10.3748/wjg.v21.i29.8952</u>

- Gill, S. K., Rossi, M., Bajka, B., & Whelan, K. (2021). Dietary Fibre In Gastrointestinal Health And Disease. *Nature Reviews Gastroenterology* & *Hepatology*, 18(2), 101–116. <u>https://doi.org/10.1038/s41575-020-</u> 00375-4
- Harvard T.H. Chan School of Public Health. "Fiber." *The Nutrition Source*. Accessed February 22, 2025. <u>https://www.hsph.harvard.edu/nutritionsource/carbohydrates/fiber/.</u>
- Linus Pauling Institute, Oregon State University. "Dietary Fiber." Accessed February 22, 2025. <u>https://lpi.oregonstate.edu/mic/other-nutrients/fiber.</u>
- McRorie, J. W. (2015). Evidence-Based Approach To Fiber Supplements And Clinically Meaningful Health Benefits, Part 2: What To Look For And How To Recommend An Effective Fiber Therapy. *Nutrition Today*, 50(2), 90–97. <u>https://doi.org/10.1097/NT.0000000000089</u>
- Slavin, J. L. (2005). Dietary Fiber And Body Weight. Nutrition, 21(3), 411–418. <u>https://doi.org/10.1016/j.nut.2004.08.018</u>
- Slavin, Joanne L. "Fiber And Prebiotics: Mechanisms And Health Benefits." *Nutrients* 5, no. 4 (2013): 1417–1435. <u>https://doi.org/10.3390/nu5041417.</u>
- Stephen, A. M., Champ, M. M. J., Cloran, S. J., Fleith, M., van Lieshout, L., Mejborn, H., & Burley, V. J. (2017). Dietary Fibre In Europe: Current State Of Knowledge On Definitions, Sources, Recommendations, Intakes, And Relationships To Health. *Nutrition Research Reviews*, 30(2), 149–190. <u>https://doi.org/10.1017/S095442241700004X</u>
- Wikipedia: The Free Encyclopedia. "Dietary Fiber." Last modified February 18, 2025. <u>https://en.wikipedia.org/wiki/Dietary fiber</u>.

UNIQUE FIBER-LIKE PRODUCTS COMING-OF-AGE

Traditionally, dietary fibers have come from fruits, vegetables, nuts, seeds, whole grains, beans, and legumes. However, there are unique fibers such as resistant starch, potato starch, agricultural and food industry byproducts, seaweed, mushrooms, human milk oligosaccharides, lignin, chitin, and chitosan.

RESISTANT STARCH SOURCES OF RESISTANT STARCH (PER 100 GRAMS OR 1/2 CUP) BROWN RICE BEANS GREEN BANANAS LENTILS 2-4a 3.5g 4.7g 3.4a MUESLI CEREAL OATS POTATOES 3.2g 3.6g 3.6g

Starch is a carbohydrate composed of multiple chains of glucose molecules. Plants synthesize starch during photosynthesis and store it as an energy reserve. When humans consume starchy foods, the body typically breaks down these chains into smaller glucose units to provide energy. However, some starches resist enzymatic digestion in the small intestine and reach the large intestine unchanged or only slightly altered. These are known as "resistant starches" and are classified as a form of dietary fiber. Once in the large intestine, microorganisms ferment resistant starches, producing active metabolites like short-chain fatty acids. Because resistant starches bypass the small intestine, they do not contribute to blood glucose levels.

Studies suggest that early human diets, rich in wild plants, fruits, nuts, seeds, roots, and tubers, provided a high fiber intake, with a sizable portion coming from resistant starches. Estimates indicate that these diets may have provided 75-150 g of total fiber per day.

Potential Side Effects Of Ingesting Resistant Starches

As with other fermentable carbohydrates, consuming resistant starches may increase the production of gases such as carbon dioxide, hydrogen sulfide, and methane. This can lead to side effects including abdominal bloating, distention, and flatulence. To minimize these effects, it is advisable to introduce resistant starches gradually into the diet.

REFERENCES:

- Birt, D. F., Boylston, T., Hendrich, S., Jane, J. L., Hollis, J., Li, L., McClelland, J., Moore, S., Phillips, G. J., Rowling, M., Schalinske, K., Scott, M. P., & Whitley, E. M. (2013). Resistant Starch: Promise For Improving Human Health. *Advances in Nutrition*, 4(6), 587–601. <u>https://doi.org/10.3945/an.113.004325</u>
- Cordain, L., Eaton, S. B., Sebastian, A., Mann, N., Lindeberg, S., Watkins, B. A., O'Keefe, J. H., & Brand-Miller, J. (2005). Origins And Evolution Of The Western Diet: Health Implications For The 21st Century. *The American Journal of Clinical Nutrition*, 81(2), 341–354. <u>https://doi.org/10.1093/ajcn.81.2.341</u>

- Eaton, S. B., Konner, M., & Shostak, M. (1988). Stone Agers In The Fast Lane: Chronic Degenerative Diseases In Evolutionary Perspective. *The American Journal of Medicine*, 84(4), 739–749. <u>https://doi.org/10.1016/0002-9343(88)90113-1</u>
- Keenan, M. J., Zhou, J., McCutcheon, K. L., Raggio, A. M., Bateman, H. G., Todd, E., Jones, C. K., Tulley, R. T., Melton, S., Martin, R. J., & Hegsted, M. (2006). Role of Resistant Starch In Improving Gut Health, Adiposity, and Insulin Resistance. *Advances in Nutrition*, 6(2), 198–205. https://doi.org/10.3945/an.114.007419
- Topping, D. L., & Clifton, P. M. (2001). Short-chain fatty acids and human colonic function: Roles of resistant starch and nonstarch polysaccharides. *Physiological Reviews*, 81(3), 1031–1064. <u>https://doi.org/10.1152/physrev.2001.81.3.1031</u>

POTATO STARCH



Potato starch has gained increasing attention as a dietary supplement. Potato starch is extracted from crushed potatoes and

then dried into a powder form. It should not be confused with potato flour.

Potato starch is a type of resistant starch that is not digested in the stomach or the small intestine and reaches the colon intact¹. Once in the colon, potato starch is fermented by microorganisms, leading to the production of short-chain fatty acids (SCFAs), particularly butyrate.

Butyrate has been found to have beneficial effects on the digestive tract and overall health. By increasing the levels of butyrate, potato starch has the following impacts:

Improvement of Barrier Function: Butyrate serves as a primary energy source for the cells lining the colon, helping to maintain its integrity and function³. A strong barrier function is crucial for preventing pathogens and toxins from entering the tissue and bloodstream. Studies suggest that butyrate can enhance the production of tight junction proteins, which are key components in maintaining the integrity of the digestive tract barrier⁴.

Exertion of Anti-Inflammatory Effects: Butyrate has been shown to possess anti-inflammatory properties⁵. It can decrease the production of pro-inflammatory cytokines⁶. This modulation of the immune response helps prevent and reduce inflammatory diseases in the digestive tract, such as inflammatory bowel disease (IBD)⁷.

Potential Protection Against Cancer: The role of butyrate in cancer protection is linked to its ability to induce programmed cell

death within cancer cells (apoptosis), inhibit cell proliferation, and promote differentiation in the colon⁸. By these mechanisms, butyrate can help prevent the development and progression of colorectal cancer. Additionally, its anti-inflammatory effects contribute to a lower risk of cancer development, as chronic inflammation is a known risk factor for cancer¹⁰.

CONCLUSION:

The intake of potato starch, due to its resistant starch content, can increase the production of butyrate in the colon. This short-chain fatty acid has multiple beneficial effects, including improving intestinal barrier function, exerting anti-inflammatory effects, and potentially offering protection against colorectal cancer. However, the extent of these benefits can depend on numerous factors, including the amount of potato starch consumed, its method of preparation, and the individual's digestive tract microbial composition¹¹.

REFERENCES:

¹ Haenen, D., Souza da Silva, C., Zhang, J., Koopmans, S. J., Bosch, G., van der Meer, I. M., van Arkel, J., & Smidt, H. (2013). Resistant Starch and Its Biological Effects: A Review. *Advances in Nutrition*, 4(6), 587–601. <u>https://doi.org/10.3945/an.113.004325</u>

⁴ Peng, L., Li, Z. R., Green, R. S., Holzman, I. R., & Lin, J. (2009). Butyrate Enhances The Intestinal Barrier By Facilitating Tight Junction Assembly Via Activation of AMP-Activated Protein Kinase In Caco-2 Cell Monolayers. *The Journal of Nutrition*, 139(9), 1619–1625. https://doi.org/10.3945/jn.109.104638

⁵ Birt, D. F., Boylston, T., Hendrich, S., Jane, J. L., Hollis, J., Li, L., McClelland, J., Moore, S., Phillips, G. J., Rowling, M., Schalinske, K., Scott, M. P., & Whitley, E. M. (2013). Resistant Starch: Promise For Improving Human Health. *Advances in Nutrition*, 4(6), 587–601. <u>https://doi.org/10.3945/an.113.004325</u>

⁶ Hamer, H. M., Jonkers, D., Venema, K., Vanhoutvin, S., Troost, F. J., & Brummer, R. J. (2008). Review Article: The Role of Butyrate on Colonic Function. *Alimentary Pharmacology & Therapeutics*, 27(2), 104–119. <u>https://doi.org/10.1111/j.1365-2036.2007.03562.x</u>

⁷Segain, J.-P. et al, "Butyrate Inhibits Inflammatory Responses Through NFκB Inhibition: Implications for Crohn's Disease." *Gut* 47, no. 3 (2000): 397–403. <u>https://doi.org/10.1136/gut.47.3.397</u>

⁸ Topping, D. L., & Clifton, P. M. (2001). Short-Chain Fatty Acids and Human Colonic Function: Roles of Resistant Starch and Nonstarch Polysaccharides. *Physiological Reviews*, 81(3), 1031–1064. <u>https://doi.org/10.1152/physrev.2001.81.3.1031</u>

¹⁰ Louis, P., Young, P., Holtrop, G., & Flint, H. J. (2010). Diversity of Human Colonic Butyrate-Producing Bacteria Revealed By Analysis of The Butyryl-Coa:Acetate Coa-Transferase Gene. *Environmental Microbiology*, 12(2), 304–314. <u>https://doi.org/10.1111/j.1462-2920.2009.02066.x</u>

¹¹ Keenan, M. J., et al., (2006). Role of Resistant Starch In Improving Gut Health, Adiposity, And Insulin Resistance. *Advances in Nutrition*, 6(2), 198–205. <u>https://doi.org/10.3945/an.114.007419</u>

AGRICULTURAL AND FOOD INDUSTRY BYPRODUCTS AS FIBER



Byproducts include skins, seeds and stems of fruits and vegetables which are typically discarded during processing. These byproducts are rich in dietary fiber and other nutrients and can be repurposed into food ingredients. An example might include apple pomace (*figure above*), the leftover material from apple juice production which is high in fiber with pectin being a significant component. Pectin makes up 15% of apple pomace's dry weight. Commercial development of apple pomace for human consumption still requires further research focusing on standard methods of nutrient reporting and human clinical trials.¹

REFERENCES:

¹R. Chris Skinner, Joseph C. Gigliotti, Kang-Mo Ku, and Janet C. Tou. "A Comprehensive Analysis of the Composition, Health Benefits, and Safety of Apple Pomace." *Nutrition Reviews* 76, no. 12 (2018): 893–909. <u>https://academic.oup.com/nutritionreviews/article/76/12/893/5063624</u> ² R. Bhardwaj, P. Gupta, and S. Kumar. "Valorisation of Apple Pomace for the Development of High-Fibre and Antioxidant-Rich Functional Cookies." *Scientific Reports* 14, no. 1 (2024): Article number 12345. <u>https://www.nature.com/articles/s41598-024-77377-8</u>

SEAWEED AS FIBER



Seaweed is a marine alga found in oceans around the world. It is a crucial component of the marine ecosystem but also a valuable nutritional resource for humans. Recent research has demonstrated its potential as a dietary fiber.

Unlike the fibers found in terrestrial plants, the fiber in seaweed has unique properties that contribute to its effectiveness in promoting health. For instance, alginate, a typical soluble fiber found in seaweed such as kelp, in addition to its qualities as a source of fiber, can significantly reduce fat digestion and absorption in the human body¹. This property alone makes seaweed an excellent food for managing weight and combating obesity.

Other benefits of seaweed include the following:

1. Nutrition-Rich:

Seaweed is renowned for its high content of vitamins and minerals and is an excellent source of iodine which is essential for thyroid function. It also contains vitamins A, C, E and K as well as B vitamins. It is rich in antioxidants that help protect cells From Damage.²

2. Source Of Unique Bioactive Compounds

Seaweed contains various bioactive compounds such as fucoxanthin and fucoidans, which have been studied for their anti-inflammatory, antioxidant, and anti-cancer properties³.

3. High In Dietary Fiber

Seaweed has a high dietary fiber content with positive effects on bowel function and its ability to lower blood sugar and cholesterol levels.⁴

4. Heart Health

Regular consumption of seaweed has been found to contribute to cardiovascular health due to its content of omega-3 fatty acids in dietary fiber.⁵

REFERENCES:

¹ Zhou, X., Peng, Z., Liao, Y., Li, D., Xu, S., Wen, Y., Gao, J., Qi, X., Zhang, X., Feng, L., Zhang, H., Hao, X., Wang, Q., Liu, L., & Yang, W. (2023). Weight Reduction Effect Of Alginate Associated With Gut Microbiota And Bile Acids: A Double-Blind And Randomized Trial. *Journal of Functional Foods*, 108, 105774. <u>https://doi.org/10.1016/j.jff.2023.105774</u>

² Teas, J., Pino, S., Critchley, A., & Braverman, L. E. (2004). Variability Of Iodine Content In Common Commercially Available Edible Seaweeds. *Thyroid*, 14(10), 836–841. <u>https://doi.org/10.1089/thy.2004.14.836</u>

³ Holdt, S. L., & Kraan, S. (2011). Bioactive Compounds In Seaweed: Functional Food Applications And Legislation. *Journal of Applied Phycology*, 23(3), 543–597. <u>https://doi.org/10.1007/s10811-010-9632-5</u>

⁴ Jiménez-Escrig, A., & Sánchez-Muniz, F. J. (2000). Dietary Fibre From Edible Seaweeds: Chemical Structure, Physicochemical Properties, And Effects On Cholesterol Metabolism. *Nutrition Research*, 20(4), 585–598. <u>https://doi.org/10.1016/S0271-5317(00)00149-4</u>

⁵ Brown, E. S., Allsopp, P. J., Magee, P. J., Gill, C. I. R., Nitecki, S., Strain, C. R., & McSorley, E. M. (2014). Seaweed and human health. *Nutrition Reviews*, 72(3), 205–216. <u>https://doi.org/10.1111/nure.12091</u>

FUNGUS AS FIBER-MUSHROOMS



Mushrooms have been found to have a low-calorie content and are rich in nutrients, including proteins, vitamins, minerals, and dietary fiber.¹ The fiber in mushrooms is primarily found in their cell walls.

Components of mushrooms can benefit intestinal microorganisms, i.e., acting as prebiotics. (See the section, *Prebiotics*). Mushrooms contain non-digestible components that can be fermented by beneficial microbes promoting their growth and activity. Some of those components include the following:

POLYSACCHARIDES

1. Beta-glucans:

Mushrooms are rich in beta-glucans, a type of polysaccharide that has prebiotic properties. Beta-glucans stimulate the growth of beneficial gut bacteria and enhance the immune response.

2. Chitin:

Chitin is another polysaccharide found in the cell walls of mushrooms. Chitin and its derivative chitosan, have both been shown to have prebiotic effects, promoting the growth of beneficial gut microorganisms.

3. Fungal Polysaccharides:

Mushrooms contain various other polysaccharides that have been demonstrated to have prebiotic effects. These include mannans, xylans, and galactans which can contribute to the growth and activity of microorganisms in the intestinal tract.

Mushrooms have been found to increase the feeling of fullness which can aid in weight management by reducing overall calorie intake.¹ Mushrooms have also been linked with a reduced risk of cardiovascular disease.

Additionally, mushrooms have been associated with reduced risk of type II diabetes and improvement in blood sugar control.

When mushrooms are selected for their fiber content, it is important to consider their variety as diverse types of mushrooms have various levels of fiber. For example, white button mushrooms, shiitake mushrooms, and portobello mushrooms are among those that are particularly high in dietary fiber².

REFERENCES:

¹ Sadler, Michele. 2003. "Nutritional Properties of Edible Fungi." *Nutrition Bulletin* 28 (3): 305–308.

² Fernandez, M. A., Oruna-Concha, M. J., and Ames, J. M. 2017. "Mushrooms: A Rich Source of the Antioxidants Ergothioneine and Glutathione." *Food Chemistry* 233: 429–433. <u>https://doi.org/10.1016/j.foodchem.2017.04.109.</u>

HUMAN MILK OLIGOSACCHARIDES

Human Milk Oligosaccharides (HMOs): A Key Component of Human Breast Milk



Introduction

Human milk provides newborns with essential nutrients tailored to support nerve growth, immunity, and overall development.¹ It contains more than 200 structurally diverse bioactive components and constitutes the third most abundant solid component in human milk after lactose and lipids.²

Human cells lining the gastrointestinal tract do not possess the enzymatic machinery that is required for metabolizing human milk oligosaccharides and thus they can reach the colon intact. Instead, they serve as prebiotics, selectively nourishing beneficial gut bacteria like *Bifidobacterium infantis*.^{3,4} Through fermentation, *B. infantis* metabolizes HMOs to produce short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate, which are critical for:

- Providing energy to intestinal cells
- Enhancing intestinal barrier function
- Supporting immune system development

This fermentation cascade not only provides energy but also plays a role in protecting against pathogens and contributing to the infant's immune and central nervous system development.³ <u>Summary of Health Benefits of HMOs</u>

 Immune Function: HMOs strengthen the immune system, helping reduce inflammation and enhancing pathogen defense.^{3,4}

- Anti-Inflammatory Properties: They mitigate chronic inflammation, potentially reducing the risk of conditions like heart disease and diabetes.⁵
- 3. <u>Pathogen Defense</u>: HMOs block pathogen adhesion to the intestinal lining, preventing infections and promoting gut health.⁶
- 4. <u>Metabolic Health:</u> HMOs improve cholesterol regulation and glucose metabolism, with implications for managing metabolic syndrome and type II diabetes.⁷

Composition of HMOs

Over 200 unique HMOs have been identified, with 2[']fucosyllactose being the most abundant, accounting for 30-50% of total HMOs in breast milk.^{1,2} These sugars profoundly shape an infant's health by establishing a robust microbial ecosystem and promoting intestinal and immune development.

The Transition to Dietary Fiber

As infants transition to a diverse diet, caregivers face the challenge of replicating the benefits of HMOs. Dietary fiber, much like HMOs, serves as a substrate for beneficial gut microbes, continuing to promote SCFA production and gut health.⁸

HMOs Use In Adults

Recent research has explored HMOs' applications beyond infancy. Studies suggest HMOs may benefit adults by modulating the gut microbiota, reducing inflammation, and enhancing metabolic health.^{13,14} As humans age, the number of *Bifidobacteria* drops steadily particularly in the later years of life. The decline may be associated with an increase risk of inflammation, chronic illnesses and immune dysfunction.

Studies show that 2'FL, the most abundant HMO in human breast milk, boosts *Bifidobacteria* in every age group from infants to older adults. Different age groups had their own dominant Bifidobacteria species that responded to 2'FL. 2'FL also boosted growth of other gut microbes like butyrate producers that support intestinal health and control inflammation.

HMOs are now available in supplement form, with early trials demonstrating safety and potential benefits in conditions such as gastrointestinal disorders.¹⁵

The following is a summary of HMO effects and applications in human adults based on recent research.

Prebiotic Effects on Gut Health

HMOs act as prebiotics, supporting the growth of beneficial gut bacteria such as *Bifidobacterium* and *Lactobacillus* in adults. This modulation of the microbiota improves gut health and may reduce the incidence of intestinal infections.¹⁶

Management of Gastrointestinal Disorders

Supplementation with HMOs such as 2' fucosyllactose (2'-FL) has been shown to improve gut microbe composition without aggravating symptoms in patients with irritable bowel syndrome.¹⁷

Prevention of Intestinal Inflammation

HMOs like 2'-FL may prevent intestinal inflammation by enhancing gut barrier function and modulating gut microbial metabolism. These properties suggest potential therapeutic uses for conditions like colitis.¹⁸

Immune Protection

HMOs impede pathogen attachment epithelial cells, potentially reducing infections from bacteria such as *E. coli* and *Salmonella*. This suggests their role as protective agents against enteric infections in adults.¹⁹

Enhance Barrier Function

HMOs improve gut barrier integrity by increasing beneficial metabolites such as short-chain fatty acids (SCFAs) and regulating inflammatory markers displaying their potential to strengthen the gastrointestinal barrier.²⁰

REFERENCES:

^{1.} Bode, L. (2012). Human Milk Oligosaccharides: Every Baby Needs A Sugar Mama. *Glycobiology*, 22(9), 1147–1162. <u>https://doi.org/10.1093/glycob/cws074</u>

^{2.} Soyyılmaz, B., Mikš, M. H., Röhrig, C. H., Matwiejuk, M., Meszaros-Matwiejuk, A., & Vigsnæs, L. K. (2021). The Mean of Milk: A Review of Human Milk Oligosaccharide Concentrations Throughout Lactation. *Nutrients*, 13(8), 2737. <u>https://doi.org/10.3390/nu13082737</u>

^{3.} Triantis, V., Bode, L., & van Neerven, R. J. J. (2018). Immunological Effects of Human Milk Oligosaccharides. *Frontiers in Pediatrics*, 6, 190. https://doi.org/10.3389/fped.2018.00190 Plaza-Díaz, J., Fontana, L., & Gil, A. (2018). Human Milk
 Oligosaccharides and Immune System Development. *Nutrients*, 10(8),
 1038. <u>https://doi.org/10.3390/nu10081038</u>

^{5.} Rousseaux, A., Brosseau, C., Le Gall, S., & Bouhet, M. (2021). Human Milk Oligosaccharides: Their Effects On the Host and Their Potential As Therapeutic Agents. *Frontiers in Immunology*, 12, 680911. <u>https://doi.org/10.3389/fimmu.2021.680911</u>

 ^{6.} Ryan, J. J., Monteagudo-Mera, A., Contractor, N., & Gibson, G. R.
 (2021). Impact Of 2'-Fucosyllactose On Gut Microbiota Composition In Adults With Chronic Gastrointestinal Conditions: Batch Culture Fermentation Model and Pilot Clinical Trial Findings. *Nutrients*, 13(3), 938. <u>https://doi.org/10.3390/nu13030938</u>

^{7.} Suligoj, T., Schmitt, S., Praznik, W., & Warth, B. (2020). Effects Of Human Milk Oligosaccharides On the Adult Gut Microbiota and Barrier Function. *Nutrients*, 12(9), 2808. <u>https://doi.org/10.3390/nu12092808</u>

^{8.} Roager, H. M., & Dragsted, L. O. (2023). Microbial Metabolites As Modulators of the Infant Gut Microbiome and Host-Microbial Interactions In Early Life. *Gut Microbes*, 15(1), 2192151.

https://doi.org/10.1080/19490976.2023.2192151

^{9.} Button, J. E., et al. (2022). Dosing Synbiotic of Human Milk Oligosaccharides and *B. Infantis* Leads to Reversible Engraftment In Healthy Adult Microbiomes Without Antibiotics. *Cell Host & Microbe*, 30(5), 712–725.e7. <u>https://doi.org/10.1016/j.chom.2022.04.001</u>.

^{10.} Carter, M. M., et al. (2023). A Human Milk Oligosaccharide Alters the Microbiome, Circulating Hormones, Cytokines, and Metabolites In a Randomized Controlled Trial of Older Individuals. *medRxiv Preprint*. <u>https://doi.org/10.1101/2023.08.18.23294085</u>.

^{11.} Elison, E., et al (2016). Oral Supplementation Of Healthy Adults With 2'-O-Fucosyllactose Is Well Tolerated and Shifts the Intestinal Microbiota. *British Journal of Nutrition*, 116(8), 1356–1368. https://doi.org/10.1017/S0007114516003354

^{12.} Barile, D., & Rastall, R. A. (2013). Human Milk and Related
 Oligosaccharides As Prebiotics. *Current Opinion in Biotechnology*, 24(2),
 214–219. <u>https://doi.org/10.1016/j.copbio.2013.01.008</u>

^{13.} Iribarren, C., et al. (2020). Human milk oligosaccharide supplementation in irritable bowel syndrome patients: A parallel, randomized, double-blind, placebo-controlled study. *Neurogastroenterology & Motility*, 32(10), e13920. <u>https://doi.org/10.1111/nmo.13920</u>

^{14.} Schalich, K., et al. (2024). A Human Milk Oligosaccharide Prevents Intestinal Inflammation In Adulthood Via Modulating Gut Microbial Metabolism. *mBio*, 15(4), e00298-24. <u>https://doi.org/10.1128/mbio.00298-24</u>

^{15.} Donovan, Sharon M., et al. "Oral Supplementation of Healthy Adults with 2'-O-Fucosyllactose and Lacto-N-Neotetraose Is Well Tolerated and Selectively Modifies the Gut Microbiota." *The Journal of Nutrition* 146, no. 7 (2016): 1446–1452.

https://doi.org/10.3945/jn.116.230078

^{16.} Elison, E., et al. "Oral Supplementation of Healthy Adults with 2'-O-Fucosyllactose and Lacto-N-Neotetraose Is Well Tolerated and Selectively Modifies the Gut Microbiota." *The Journal of Nutrition* 146, no. 7 (2016): 1446–1452. <u>https://doi.org/10.3945/jn.116.230078.PMC</u>

^{17.} Iribarren, C., et al. "Impact of 2'-Fucosyllactose on Gut Microbiota Composition in Adults with Chronic Gastrointestinal Conditions: Batch Culture Fermentation Model and Pilot Clinical Trial Findings." *Nutrients* 13, no. 11 (2021): 3836. <u>https://doi.org/10.3390/nu13113836</u>.

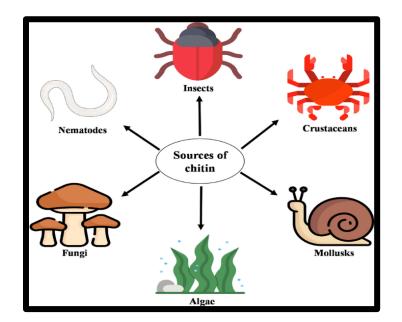
^{18.} Kobata, A., et al. "2'-Fucosyllactose and 3-Fucosyllactose Alleviate Interleukin-6-Induced Intestinal Barrier Dysfunction by Enhancing Tight Junction Integrity." *Nutrients* 15, no. 5 (2023): 10145275. https://doi.org/10.3390/nu150510145275.

^{19.} Coppa, G. V., et al. "Human Milk Oligosaccharides Inhibit the Adhesion to Caco-2 Cells of Diarrheal Pathogens: *Escherichia coli, Vibrio cholerae*, and *Salmonella fyris.*" *Pediatric Research* 59, no. 3 (2006): 377– 382. <u>https://doi.org/10.1203/01.pdr.0000200805.45593.17</u>.

^{20.} Zhang, Y., et al. "2'-Fucosyllactose Alleviates DSS-Induced Ulcerative Colitis via Regulating Gut Microbiota and Enhancing Intestinal Barrier Function." *Journal of Dairy Science* 107, no. 5 (2024): 568.

https://doi.org/10.1016/j.jds.2024.02.005.

CHITIN AND CHITOSAN AS FIBER



CHITIN AND CHITOSAN AS UNIQUE FIBER-LIKE SUBSTANCES

Introduction

Chitin and chitosan are distinct fiber-like compounds gaining recognition for their health-promoting properties when used as dietary fiber.¹⁻³ Despite not being as commonly discussed as traditional dietary fibers, these compounds offer unique advantages due to their chemical structures and physiological effects.

Chitin, a long-chain polymer, serves as a primary structural component in the exoskeletons of crustaceans (e.g., crabs, shrimp, and lobsters), the cell walls of fungi (e.g., mushrooms), and the exoskeletons of insects.^{1,2} Chitosan, derived from chitin, exhibits enhanced water solubility and distinct biochemical properties. This solubility makes chitosan a more versatile ingredient in dietary supplements and food products than chitin.^{2,3}

Health Benefits of Chitin and Chitosan

1. Fat and Cholesterol Binding

A significant benefit of chitin and chitosan lies in their ability to bind fats and cholesterol in the digestive tract. This interaction may help reduce cholesterol levels and support weight management. Research has highlighted their potential in promoting fat excretion and improving lipid profiles, particularly in populations with high cholesterol or obesity concerns.

2. Blood Sugar Regulation

Chitin and chitosan may slow sugar absorption in the digestive tract, leading to a gradual postprandial rise in blood glucose levels.⁴ This modulation could benefit individuals with diabetes or prediabetes, helping to maintain blood sugar control and reduce glycemic variability.⁴

3. Gastrointestinal Health

Like other dietary fibers, chitin and chitosan promote gastrointestinal health by supporting the growth of beneficial gut microbes and improving bowel regularity.^{2,3} Furthermore, the fermentation of chitosan by gut microbiota generates short-chain fatty acids (SCFAs), including butyrate, acetate, and propionate. These SCFAs act as energy sources for colonic cells and possess anti-inflammatory properties, supporting gut barrier integrity and reducing inflammation.

Chitosan Supplements

Chitosan is widely available as an over-the-counter supplement in capsule or tablet form. The powder can be mixed into water, smoothies, or other beverages for easier consumption.

Some functional foods are fortified with chitosan such as health bars or snacks designed for weight management.

Chitosan powder can sometimes be used as a natural thickening agent in soups, sauces, and baked goods. Lesser amounts of

chitosan powder may be sprinkled on cooked or prepared dishes as an additive.

While chitosan itself is not presently in food, its precursor, chitin, is found in shellfish shells and in some mushrooms.

Considerations and Precautions

Despite their potential benefits, the use of chitosan requires caution. Individuals with seafood allergies may need to avoid chitosan derived from crustaceans, as allergenic proteins could remain in these products. Additionally, the quality and source of chitosan supplements vary, potentially influencing their efficacy and safety.³

CONCLUSION:

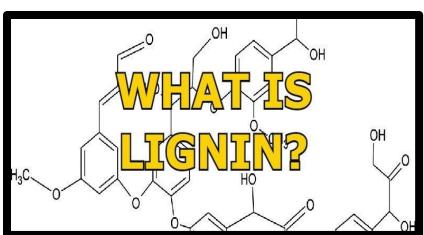
Chitin and chitosan represent an intriguing category of dietary fibers with diverse health benefits, including cholesterol reduction, blood sugar regulation, and gastrointestinal health improvement. However, further research is essential to establish optimal dosages, safety, and practical applications. With consistent quality control and additional studies, these fiber-like compounds may become vital tools in dietary interventions for metabolic and gastrointestinal health.

REFERENCES:

¹ Kumar, M. N. V. (2000). A Review of Chitin and Chitosan Applications. *Reactive and Functional Polymers*, 46(1), 1–27. <u>https://doi.org/10.1016/S1381-5148(00)00038-9</u> ² Rinaudo, M. (2006). Chitin and Chitosan: Properties and Applications. *Progress in Polymer Science*, 31(7), 603–632. <u>https://doi.org/10.1016/j.progpolymsci.2006.06.001</u>

³ Muzzarelli, R. A. A. 2003. "Chitosan as a Dietary Supplement and a Food Technology Agent." *Food Chemistry* 83 (4): 593–599. <u>https://doi.org/10.1016/S0308-8146(03)00104-7</u>.

⁴ Tzeng, H., et al. (2022). Antidiabetic Properties of Chitosan and Its Derivatives. *Marine Drugs*, 20(12), 784. <u>https://doi.org/10.3390/md20120784</u>



<u>LIGNIN</u>

MICROBIAL UTILIZATION OF LIGNIN IN THE HUMAN GUT

Bioconversion By Gut Microbes:

Lignin is a complex organic polymer found in the cell walls of plants and plays a critical role in providing structural support and water transport within various plant tissues. Humans are unable to digest lignin due to lack of specific enzymes. Although unable to digest lignin, humans have certain bacteria in their digestive tract that can break down lignin or its derivatives into smaller, metabolizable compounds that have health benefits including antioxidant, anti-inflammatory, and estrogenic activities. These breakdown products produced by bacteria are known as *lignans*.

Health Implications:

The lignans produced by gut bacteria can influence human health in several ways. For instance, they have been associated with reduced risks of cardiovascular disease, certain types of cancer, and other chronic conditions. The beneficial effects are attributed to their antioxidant properties and their ability to modulate hormone levels and immune responses.

This microbial activity in the human gut shows how dietary components that are indigestible by humans can still have profound effects on health through microbial processing. This interplay between diet, gut microbiota, and health underscores the complexity of the digestive ecosystems and the indirect benefits humans derive from various dietary components.

REFERENCES:

¹Vinardell, M. P., & Mitjans, M. (2017). Lignins and Their Derivatives with Beneficial Effects on Human Health. *International Journal of Molecular Sciences*, 18(6), 1219. <u>https://doi.org/10.3390/ijms18061219</u> ²Solan, Matthew. "The Facts on Fiber." *Harvard Health Publishing*, 1 November 2024. <u>https://www.health.harvard.edu/nutrition/the-facts-on-fiber</u>

³ Rodríguez-García, C., Sánchez-Quesada, C., Toledo, E., Delgado-Rodríguez, M., & Gaforio, J. J. (2019)Naturally Lignan-Rich Foods: A Dietary Tool for Health Promotion? *Molecules*, 2019, 24(5), 917. <u>https://doi.org/10.3390/molecules24050917</u>

SECTION SIXTEEN

LESSONS LEARNED FROM THE TERMITE AND THE COW





THE TERMITE, THE COW, AND THE HUMAN: MICROBIAL PARTNERSHIPS FOR ENERGY EXTRACTION

TERMITES

Termites, which consume wood, rely on a synbiotic relationship with their microbes (primarily *Trichonympha agilis*), a protozoan

that resides in the termite's digestive system and is capable of breaking down cellulose in wood substances into usable energy.^{1,2} This partnership allows termites to thrive on a diet that would otherwise be indigestible.

<u>Cows</u>

Similarly, cows have evolved a specialized fermentation chamber called the rumen. In this chamber, bacteria and other microbes break down fibrous plant materials like grass, hay, and alfalfa into volatile fatty acids (VFAs), primarily acetate, propionate, and butyrate, which the cow absorbs and uses as energy.^{3,4} This symbiosis enables cows to derive energy from fibrous plant materials that humans and other species cannot process.

HUMANS

Humans, by contrast, rely on a different strategy for energy extraction. While carbohydrates, proteins, and fats are primarily digested in the small intestine, the large intestine plays a critical role in processing dietary fibers—complex carbohydrates indigestible by human enzymes. These fibers reach the colon, where they are fermented by intestinal bacteria into short-chain fatty acids (SCFAs), such as butyrate, acetate, and propionate. These SCFAs provide energy, protect against harmful pathogens, and modulate the immune system.^{5,6}

Lessons Learned

1. Symbiosis and Specialized Microbiomes

Each species—termite, cow, and human—relies on specific microorganisms to break down complex substances into simpler forms that can be absorbed and utilized as energy. Both the termite and cow have co-evolved with their microbiomes to digest substances that would otherwise be indigestible.^{1,2,4}

2. Dietary Specificity

Just as termites cannot digest grass and cows cannot digest wood, humans cannot digest cellulose or fibrous plant materials consumed by cows. Each species has evolved to thrive on specific nutrients that their digestive systems and their microbes are equipped to handle.^{3,5}

3. Microbial Contributions to Health

In humans, non-digestible carbohydrates, such as dietary fibers found in fruits, vegetables, nuts, seeds, whole grains, beans, legumes, resistant starches, and human milk oligosaccharides, are critical nutrients for maintaining a healthy intestinal microbiome.^{6,7} The fermentation of these fiber products by intestinal microbes produces SCFAs essential for colonic health, energy production, and immune function. These microbial processes highlight the importance of dietary fiber in maintaining the large intestine's ecosystem.^{5,6}

4. Adaptation to Available Resources

The termite, cow, and human have all adapted to their environments by forming partnerships with microbes that allow them to exploit available resources for energy. This demonstrates the importance of diet in shaping not only the host species but also the microbial communities that contribute to health and survival. It also reinforces the concept that beneficial microbes in the human gut need to be protected and nurtured for intestinal well-being.

CONCLUSION:

This comparison emphasizes that the right nutrients and the right microorganisms are essential for the survival and health of each species. For humans, the inclusion of diverse, fiber-rich foods supports a beneficial microbiome, which in turn promotes overall health and well-being.

REFERENCES:

¹ Breznak, J. A., and A. Brune. "Role of Microorganisms in the Digestion of Lignocellulose by Termites." *Annual Review of Entomology* 39, no. 1 (1994): 453–487. <u>https://doi.org/10.1146/annurev.en.39.010194.002321</u>.

² Brune, Andreas. "Synbiotic Digestion of Lignocellulose in Termite Guts." *Nature Reviews Microbiology* 12, no. 3 (2014): 168–180. <u>https://doi.org/10.1038/nrmicro3182</u>.

³ Russell, J. B. (2001). Factors That Alter Rumen Microbial Ecology. Science, 292(5519), 1119–1122. <u>https://doi.org/10.1126/science.1058830</u> ⁴ Macfarlane, G. T. (2012). Bacteria, Colonic Fermentation, and Gastrointestinal Health. *Journal of AOAC International*, 95(1), 50–60. <u>https://doi.org/10.5740/jaoacint.SGE_Macfarlane</u>

⁵ Koh, A., et al. (2016). From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites. *Cell*, 165(6), 1332–1345. <u>https://doi.org/10.1016/j.cell.2016.05.041</u>

⁶ Silva, Ygor Parladore, Andressa Bernardi, and Rudimar Luiz Frozza. "The Role of Short-Chain Fatty Acids from Gut Microbiota in Gut-Brain Communication." *Frontiers in Endocrinology* 11 (2020): 25. <u>https://doi.org/10.3389/fendo.2020.00025</u>

SECTION SEVENTEEN

CONDITIONS THAT ILLUSTRATE DYFUNCTIONAL DIGESTIVE ECOSYSTEMS

CHRONIC CONSTIPATION

WHAT IS CONSTIPATION?

Chronic constipation is a digestive disorder characterized by infrequent bowel movements, difficulty passing stool, or both. It is commonly defined as having fewer than three bowel movements per week, often accompanied by hard, dry stools that are difficult to pass. While traditionally "normal" bowel function has been defined as having between three bowel movements per week and three bowel movements per day, recent studies¹ suggest that having one to two bowel movements per day may be ideal for maintaining optimal health. Individuals with this frequency often have lower levels of measurable toxins in their bloodstream and typically consume diets higher in dietary fiber.

REFERENCES:

¹ Johnson-Martínez, J. P., Diener, C., Levine, A. E., Wilmanski, T., Suskind, D. L., Ralevski, A., Hadlock, J., Magis, A. T., Hood, L., Rappaport, N., & Gibbons, S. M. (2024). Aberrant Bowel Movement Frequencies Coincide with Increased Microbe-Derived Blood Metabolites Associated with Reduced Organ Function. *Cell Reports Medicine*, 5(7), 101646. <u>https://doi.org/10.1016/j.xcrm.2024.101646</u>

Diagnostic Tests To Establish Causes For Constipation

- <u>Blood Tests</u>: To check for underlying conditions such as hypothyroidism or diabetes.
- <u>Colonoscopy</u>: To examine the colon and rectum for abnormalities.
- <u>Transit studies</u>: To track the movement of stool through the colon using x-ray markers.
- <u>Abdominal imaging studies</u>: CT scans, MRIs, ultrasound exams and capsule endoscopy.
- Breath tests: To identify small intestinal microbial overgrowth and/or excess methane production.

Causes For Constipation

Constipation can result from numerous factors and is often multifactorial in nature:

- Dietary Factors: Low dietary fiber intake, inadequate fluid consumption
- Lifestyle Factors: Sedentary lifestyle, lack of physical activity, use of alcohol, tobacco, and recreational drug
- <u>Medical Conditions</u>: Examples include hypothyroidism, diabetes, and neurological disorders such as Parkinson's disease or multiple sclerosis.
- <u>Medications</u>: Certain medications, including opioids, calcium, iron, aluminum, antihistamines, and some antidepressants are associated with chronic constipation.
- <u>Psychological Factors</u>: Stress, anxiety, and depression
- <u>Structural Issues</u>: Obstructions or abnormalities in the digestive tract, including strictures, adhesions, tumors, radiation damage or rectoceles.
- Pelvic Floor Dysfunction: Pelvic floor dysfunction refers to issues with the coordination of the pelvic floor muscles involved in bowel movements and urination caused by traumatic injury, prior pelvic surgery (hysterectomy or prostatectomy), aging, and/or connective tissue disorders.

- Antibiotics: Recent courses of antibiotics can alter the gut microbiota composition, potentially leading to constipation by disrupting the balance of beneficial bacteria that aid in digestion.
- Colonoscopy or Bowel Irrigation Therapy: A vigorous laxative prep for colonoscopy and/or irrigations administered with irrigation therapies can wash or rinse away critical gut microbes that help control water balance and motility resulting in constipation. In most of these cases, the alteration of bowel motility is limited in duration.

Treatment of Constipation

Treatment strategies for constipation vary depending on the underlying cause and the severity of symptoms. Common treatments include:

- Dietary modifications: Modifications include increasing dietary fiber with ingestion of fruits, vegetables, nuts, seeds, beans, legumes, whole grains, and other fiber-like substances. (See, LIST I at the end of the Digestive Health Guide for high fiber foods and the section in the text on fiber-like products)
- Adequate hydration: Hydration should be achieved primarily with water, drinking 60-80 ounces of fluid (primarily water) every 24 hours--or more under exceptional circumstances like

fever, illness, activity, high ambient temperature, pregnancy, and lactation. (See the section: *Hydration*)

- Lifestyle changes: Changes include regular physical activity, with the establishment of a routine for bowel movements and responding promptly to the urge to defecate.
- Biofeedback therapy: A treatment directed by a specially trained physical therapist who can help the patient retrain the pelvic floor muscles in cases of pelvic floor dysfunction.
- Changing body positioning during defecation: Use a Squatty Potty^{®.} The greater the hip flexion achieved by squatting, the straighter the rectoanal canal will be resulting in less straining to defecate.



Probiotics: Foods containing probiotics can be added as nutrients in the diet and are also available as commercially designed and manufactured supplements. (See the sections: *Probiotics and the section Fermentable Foods).*

- Prebiotics (dietary fiber): Foods containing prebiotics can be added to the diet and are available as commercially designed and manufactured supplements. (See the section: *Prebiotics and the list of high fiber foods at the end of the Digestive Health Guide*)
- Polyphenols: Polyphenols can be found in green tea, fruits, vegetables, coffee, chili peppers, flax seeds, sesame seeds, and whole grains. (See the section: *Polyphenols*)
- <u>Reducing methanogens</u>: Methanogens are microbes found in the class of microorganisms known as archaea. Methanogens produce methane by combining carbon dioxide and hydrogen that accumulates in the intestinal tract. Excessive amounts of methane have been found to reduce gut motility and may be a cause of constipation in some individuals.

Step-Wise Management

In a recent evidence-based study published by the American Gastroenterology Association evaluating management of chronic idiopathic constipation, the following guidelines were recommended (See *Reference 1*):

<u>Step 1</u>: Begin therapy with an increase in dietary fiber. **(See, List 1)**

Step 2: Add psyllium husk powder (Metamucil[®] or Organic Konsyl[®]) to the treatment plan, if needed. Make sure that hydration is adequate when using fiber supplements. Typically, a dose is added to 8 ounces of water, juice, or other favorite beverage.

<u>BRAND</u>	SERVING	DIETARY	<u>SOLUBLE</u>	INSOLUBLE
	<u>SIZE</u>	<u>FIBER</u>	<u>FIBER</u>	<u>FIBER</u>
		grams	grams	grams
KONSYL ^{®*}	1	5	3	2
	rounded			
	tsp			
METAMUCIL®	1-2	3	2	1
	rounded			
	tbsp			

(For exact measurements check product labels).

*Konsyl[®] is a certified USDA Organic all-natural dietary fiber. It does not contain sugar or artificial sweeteners. It is free of colorants, flavor enhancers or artificial additives. It is non-GMO and gluten free and is suitable for vegans and vegetarians. It is free from common allergens like soy and dairy.

<u>Health Benefits of Psyllium Husk Powders in Addition to</u> <u>Relief of Constipation</u>

- A. <u>**Prebiotic action:**</u> Psyllium husk powders promote the growth of beneficial microbes in the intestinal tract. The increase in these microbes reduces inflammation and enhances nutrient absorption.
- B. **<u>Blood sugar regulation</u>**: Psyllium powders slow down the digestion and absorption of carbohydrates. This helps to stabilize blood sugar levels.
- C. <u>Cholesterol reduction</u>: Psyllium husk powders can help lower cholesterol levels by binding to bile acids in the small intestine. The binding of bile reduces the substrate upon which cholesterol is made. This process stimulates the liver to use its cholesterol stores to produce additional bile acids thereby reducing cholesterol levels in the bloodstream.

Step 3: If steps one and two are not adequate, add one or more of the following osmotic laxatives:

- Polyethylene glycol (Miralax[®])
- Magnesium oxide if the individual does not have kidney disease.
- Lactulose. Lactulose is a chemical formulation of fructose that is not digested in the small intestine.

Lactulose comes as a sweet tasting syrup. Increasing or decreasing the dose is done based on response.

Step 4: If steps 1-3 are not adequate, a stimulant laxative using Bisacodyl (Dulcolax[®]), sodium picosulfate or senna derivatives can be added. The first two laxatives are recommended for use for no more than four weeks. Senna derivatives can be used safely for more than four weeks.

Step 5: If steps 1-4 are not adequate, a secretagogue laxative can be added. Secretagogue laxatives increase the secretion of chloride ions from the body into the colon lumen which results in the associated delivery of water into the lumen thus softening the fecal mass and rinsing the colon.

There are several different classes of secretagogue laxatives. They all require a prescription and can be expensive.

- Lubiprostone (Amitiza[®])
- Linaclotide (Linzess[®])
- Prucalopride (Motegrity[®])
- Plecanatide (Trulance[®])

--CAVEAT--

MANAGEMENT OF ALL BUT SIMPLE, SELF LIMITED PERIODS OF CONSTIPATION SHOULD BE DONE UNDER THE SUPERVISION OF A MEDICAL CARE PROVIDER.

NOVEL THERAPY

In selected cases of chronic constipation, especially when associated with low fecal bile acid excretion, the addition of bile salts to the treatment plan has been proposed. Preparations such as ox bile extracts or chenodeoxycholic acid (CDCA) can help augment the colonic bile acid pool, promoting fluid secretion and enhancing motility. Small clinical studies and mechanistic reports suggest that CDCA, a primary bile acid, can increase stool frequency and soften stools by stimulating colonic secretion and transit. Ox bile supplements are also thought to provide exogenous bile acids that similarly promote bowel movements, though controlled trials are limited. For example, Wald discusses the rationale for bile acid supplementation in constipationpredominant irritable bowel syndrome (IBS-C), highlighting that reduced colonic bile acids can contribute to impaired motility and that targeted replacement might benefit a subset of patients. Similarly, Walters et al. have explored the use of bile acid receptor agonists as a novel pharmacologic strategy to treat constipation by mimicking the pro-secretory effects of endogenous bile acids.

While bile salt therapy is not standard first-line treatment, it may be considered under specialist guidance for patients with refractory symptoms and demonstrated bile acid deficiency.

CONCLUSION:

Interventions to correct constipation are still under study. There is increasing recognition that the microbiome and bile acids are integral to gut motility. Overall, understanding these connections helps clinicians approach chronic constipation not just as a bowel habit issue, but as an ecosystem disturbance. By addressing both stool transit and the accompanying microbial and biochemical imbalances, a more comprehensive and effective management of chronic constipation can be achieved.

For persistent or severe cases, a medical care provider should always be consulted.

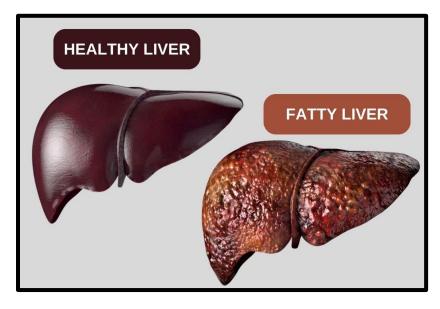
REFERENCES:

- Bharucha, A. E., Pemberton, J. H., and Locke, G. R. "American Gastroenterological Association Technical Review on Constipation." *Gastroenterology* 144, no. 1 (2013): 218–238. <u>https://doi.org/10.1053/j.gastro.2012.10.028</u>.
- Chang, Lin, and Anthony Lembo. "AGA Clinical Practice Update on the Management of Chronic Idiopathic Constipation: Expert Review." *Clinical Gastroenterology and Hepatology* 17, no. 9 (2019): 1774–1784. <u>https://doi.org/10.1016/j.cgh.2019.03.037.</u>
- Jalanka, Jonna, Anne Salonen, Jarkko Salojärvi, Jarmo Ritari, Outi Immonen, Luca Marciani, Penny Gowland, et al. "Effects of Bowel

Cleansing on the Intestinal Microbiota." *Gut* 64, no. 10 (2015): 1562– 1568. <u>https://doi.org/10.1136/gutjnl-2014-307240.</u>

- Lembo, A., and M. Camilleri. "Chronic Constipation." The New England Journal of Medicine 349, no. 14 (2003): 1360–1368. <u>https://doi.org/10.1056/NEJMra020995</u>.
- Rao, Satish S. C., and Jonathan T. Go. "Update on the Management of Constipation in the Elderly: New Treatment Options." *Clinical Interventions in Aging* 5 (2010): 163–171. <u>https://doi.org/10.2147/CIA.S8104.</u>
- Suares, N. C., and A. C. Ford. "Prevalence of, and Risk Factors for, Chronic Idiopathic Constipation in the Community: Systematic Review and Meta-Analysis." *The American Journal of Gastroenterology* 106, no. 9 (2011): 1582–1591. <u>https://doi.org/10.1038/ajg.2011.164</u>.
- Wald, Arnold. "Bile Acids and Bowel Function: Do They Play a Role in Constipation-Associated Irritable Bowel Syndrome?" *Clinical Gastroenterology and Hepatology* 16, no. 4 (2018): 486–487. <u>https://doi.org/10.1016/j.cgh.2017.11.021</u>.
- Walters, Julian R. F., Martin C. Johnston, and Emma Nolan. "Bile Acid Therapeutics for Cholestatic Liver Disease and IBS-C." *Clinical and Translational Gastroenterology* 6, no. 6 (2015): e90. <u>https://doi.org/10.1038/ctg.2015.23</u>.
- Zmora, Niv, Jotham Suez, and Eran Elinav. "You Are What You Eat: Diet, Health, and the Gut Microbiota." Nature Reviews Gastroenterology & Hepatology 16, no. 1 (2019): 35–56. <u>https://doi.org/10.1038/s41575-018-0061-2</u>.

FATTY LIVER DISEASE



The most common form of liver disease in the United States is Metabolic Associated Steatotic Liver Disease (MASLD), formerly known as Non-Alcoholic Fatty Liver Disease (NAFLD).¹ MASLD encompasses a range of liver conditions that affect people who drink little to no alcohol. It is characterized by an excess of fat stored in liver cells and is associated with obesity, insulin resistance, increased fats in the blood (*dyslipidemia*), hypertension and type 2 diabetes.

In its earliest form, there may be no abnormalities found on blood tests and no symptoms. It is frequently first recognized in an imaging study of the abdomen done for some other reason that shows an increased content of fat in the liver.

MASLD can progress to a more severe form known as *steatohepatitis,* which involves liver inflammation and can lead to

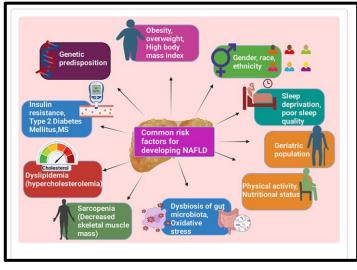
fibrosis (scarring of the liver), cirrhosis, and even liver cancer.^{2,3} In patient with steatohepatitis, blood tests usually show abnormally elevated liver enzyme levels and may also show elevated cholesterol and triglycerides levels and evidence for sugar intolerance (diabetes).

It has been suggested that the prevalence of MASLD has been rising in the United States due to increasing rates of obesity and metabolic disorders.

REFERENCES:

¹ Younossi, Zobair M. (2020). Epidemiology and Natural History of Non-Alcoholic Fatty Liver Disease. *Metabolism* 112: 154259. <u>https://doi.org/10.1016/j.metabol.2020.154259.</u>

² Chalasani, Naga, Zobair Younossi, Joel E. Lavine, Michael Charlton, Kenneth Cusi, Mary E. Rinella, Stephen A. Harrison, Elizabeth M. Brunt, and Arun J. Sanyal. 2018. "The Diagnosis and Management of Nonalcoholic Fatty Liver Disease: Practice Guidance from the American Association for the Study of Liver Diseases." *Hepatology* 67 (1): 328–357. <u>https://doi.org/10.1002/hep.29367.</u>



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The Multiple-Hit Model

Various liver insults appear to contribute to the development of MASLD, primarily through metabolic dysfunction. Here are key factors and insults that have been recognized in the development of MASLD:

Metabolic and Lifestyle Factors

- 1. **Obesity:** Excessive body weight, particularly visceral adiposity, is a significant risk factor. Adipose tissue releases free fatty acids (FFAs) and pro-inflammatory cytokines, contributing to liver fat accumulation.
- Insulin Resistance: A hallmark of MASLD, insulin resistance leads to increased lipolysis (breakdown of fat) and FFAs in the bloodstream, promoting hepatic fat accumulation.
- 3. <u>Type 2 Diabetes Mellitus</u>: Type 2 diabetes is associated with both insulin resistance and hyperglycemia, which exacerbate liver fat accumulation and inflammation.
- 4. **Dyslipidemia:** Elevated levels of triglycerides and low levels of high-density lipoprotein (HDL) cholesterol contribute to hepatic fat accumulation.

Dietary Factors

1. <u>High-Fat Diets</u>: Diets rich in saturated fats and transfats can increase liver fat content. 2. <u>High-Fructose Diets</u>: Excessive fructose intake that promotes liver fat accumulation.

Type: Fructose is a simple sugar, also known as a monosaccharide, similar to glucose.

Sources: Fructose is naturally found in fruits, honey, and root vegetables. It is also a component of table sugar (sucrose), and high-fructose corn syrup found commonly in sugary soda drinks.

Metabolism: Fructose is metabolized primarily in the liver. Unlike glucose, it does not cause a significant increase in blood insulin levels. However, excessive consumption of fructose can lead to increases in triglycerides, insulin resistance and fatty liver.

Genetic Factors

<u>Genetic Predisposition</u>: Variants in genes such as PNPLA3, TM6SF2, and others are associated with increased susceptibility to MASLD.

Epigenetic Modifications: Changes in DNA methylation and histone modification can influence gene expression related to lipid metabolism and inflammation.

Inflammatory and Immune Factors

<u>Chronic Inflammation</u>: Systemic inflammation from obesity and metabolic syndrome contributes to liver inflammation and fibrosis.

Cytokines and Adipokines: Pro-inflammatory cytokines (e.g., TNF- α , IL-6) and adipokines (e.g., leptin, resistin) exacerbate hepatic inflammation and insulin resistance.

Oxidative Stress

<u>Reactive Oxygen Species</u> (ROS): Oxidative stress from ROS can cause cellular damage, lipid peroxidation, and further inflammation in the liver.

Mitochondrial Dysfunction: Impaired mitochondrial function increases oxidative stress and disrupts energy metabolism in liver cells.

Gut-Liver Axis

<u>Gut Dysbiosis</u>: Imbalances in the gut microbiota can influence liver metabolism through the production of metabolites and endotoxins.

Intestinal Permeability: Increased gut permeability (*leaky gut*) allows endotoxins like lipopolysaccharides (LPS) to enter the bloodstream, triggering hepatic inflammation.

Environmental Factors

Toxins and Pollutants: Exposure to environmental toxins such as pesticides, heavy metals, and industrial chemicals can contribute to liver injury and steatosis.

Medications: Certain drugs, including corticosteroids, methotrexate, and tamoxifen, can induce fatty liver.

Hormonal Factors

<u>Sex Hormones</u>: Differences in estrogen and testosterone levels can influence the development and progression of MASLD. Postmenopausal women may be at higher risk due to lower estrogen levels.

Thyroid Hormones: Hypothyroidism can impair lipid metabolism and increase the risk of liver fat accumulation.

Sedentary Lifestyle Factors

Physical Inactivity: Lack of regular physical activity contributes to obesity, insulin resistance, and poor lipid metabolism, all of which are risk factors for MASLD.

Stress and Sleep Disorders

<u>Chronic Stress</u>: Prolonged stress can influence hormonal balance, leading to metabolic disturbances and inflammation.

Sleep Apnea: Obstructive sleep apnea is associated with intermittent hypoxia and systemic inflammation, contributing to liver steatosis and fibrosis.

In summary, MASLD is a multifactorial disease involving a complex interplay of metabolic, genetic, dietary, inflammatory, and environmental factors. Understanding these various liver insults is critical for developing targeted prevention and treatment strategies.

A Balancing Act—Restricting Fructose

Ingestion of fructose has been associated with hepatic steatosis. Achieving a balance between restricting fructose intake and ensuring adequate consumption of dietary fiber, particularly microbial-accessible and fermentable carbohydrates, is crucial for managing Metabolic Associated Steatotic Liver Disease (MASLD).

While fructose has been linked to the worsening of liver steatosis, many fructose-containing foods are also rich in dietary fiber and other beneficial nutrients that support gut health and overall metabolic function. Here is an approach that may help achieve that balance:

<u>1. Prioritize whole fruits and vegetables with lower fructose</u> <u>content:</u>

Opt for fruits and vegetables that are lower in fructose but still rich in fiber, vitamins, and antioxidants. Examples include berries (like strawberries and blackberries), citrus fruits (like oranges and grapefruit), and vegetables such as carrots, leafy greens, and peppers. These foods provide dietary fiber and beneficial phytochemicals with less impact on fructose levels. (*Refer to List 5*)

2. Portion Control:

For higher fructose fruits like apples, pears, and grapes, consume them in moderation. Smaller portions will provide the benefits of fiber without excessive fructose intake.

3. Emphasize Non-Fructose Fiber Sources:

<u>Whole Grains</u>: Include whole grains such as oats, barley, quinoa, and brown rice, which are excellent sources of dietary fiber without contributing to fructose intake. These grains are rich in fermentable fibers that promote the production of short-chain fatty acids (SCFAs), which are beneficial for liver health.

Legumes: Beans, lentils, and peas are high in fiber and low in fructose, making them ideal for supporting gut health and improving insulin sensitivity without exacerbating MASLD.

Include Fructo-Oligosaccharides (FOS) and Other Prebiotic Fibers:

FOS, inulin, and other prebiotic fibers found in foods like onions, garlic, leeks, and asparagus can nourish beneficial gut bacteria and promote SCFA production without contributing significantly to fructose intake. These fibers are particularly important in maintaining gut health and reducing inflammation.

Supplementation: If dietary intake is insufficient, consider prebiotic fiber supplements that are low in fructose but support gut microbiota and overall metabolic health.

<u>4. Monitor and adjust dietary intake based on individual</u> tolerance:

Individuals with MASLD may vary in their tolerance to fructose. Keeping a food diary and monitoring liver function tests can help identify personal triggers and tolerable levels of fructose intake.

<u>Gradual Introduction</u>: Slowly reintroduce or adjust high-fiber foods that contain moderate levels of fructose to assess tolerance. This approach allows the body to adapt and helps identify foods that are beneficial versus those that might aggravate the condition.

5. Focus On Fiber-Rich, Low-Fructose Processed Foods Avoid Added Sugars:

Limit processed foods with added sugars, especially those sweetened with high fructose corn syrup, agave syrup, or similar sweeteners. Instead, focus on fiber-rich, low-fructose alternatives that can support gut health without worsening liver fat.

6. Read Labels

Pay attention to food labels to identify hidden sources of fructose and opt for products that are higher in dietary fiber but lower in sugars.

7. Incorporate Fermented Foods and Probiotics in the Diet

Fermented foods like yogurt, kefir, sauerkraut, and kimchi can support a healthy gut microbiome, which is beneficial for those with MASLD. These foods often contain beneficial probiotics that work synergistically with prebiotic fibers to improve gut health and metabolic function.

• **Combination with Fiber:** Combining fermented foods with high-fiber diets enhances the production of SCFAs, which are crucial for maintaining gut and liver health.

Balance with Overall Dietary Patterns

Mediterranean Diet: Consider adopting a Mediterraneanstyle diet, which emphasizes fruits, vegetables, whole grains, legumes, nuts, and healthy fats. This diet naturally balances fiber intake while minimizing added sugars and refined carbohydrates.

8. Avoid high-glycemic foods:

Reduce or eliminate foods with a high glycemic index, as these can worsen insulin resistance and promote liver fat accumulation. High

glycemic foods are so named because they are rapidly absorbed in the small intestine, unlike low glycemic foods such as dietary fibers, which are digested more slowly and pass into the large intestine (colon) for further processing

<u>A Word Of Explanation—Differences Between *Fructose* And *Fructooligosaccharides*</u>

Fructose is a monosaccharide (simple sugar) that is highly soluble and sweet. It is naturally found in fruits, honey, and some vegetables and is a key component of sucrose (table sugar) and high fructose corn syrup.

On the other hand, fructooligosaccharides (FOS) is a prebiotic consisting of between 3 and 10 fructose molecules linked together. Fructooligosaccharides are complex carbohydrates and are classified as *dietary fibers*. They are naturally found in foods like onions, garlic, asparagus, chicory root and bananas.

Fructose and fructooligosaccharides also differ in digestion and absorption. Fructose is rapidly absorbed in the small intestine and metabolized by the liver. Excess consumption of fructose may lead to metabolic issues like insulin resistance, fatty liver disease, and increased triglycerides.

Fructooligosaccharides, however, are not digested by human enzymes in the small intestine. They are fermented by bacteria (mainly *Bifidobacteria* and *Lactobacilli*) in the colon producing short chain fatty acids (SCFAs) like butyrate, acetate and propionate which support gut and systemic health.

Fructooligosaccharides act as prebiotics promoting a healthy microbiome—fructose, however, does not.

The physiologic effects of fructose and fructooligosaccharides likewise differ. Fructose provides energy quickly as it is rapidly absorbed from the small intestine but has adverse metabolic effects as noted before. Fructooligosaccharides, however, enhance gut health by providing nourishment to gut microbes and producing short-chain fatty acids. Short-chain fatty acids improve gut barrier integrity, reduce inflammation, and regulate immune responses.

CONCLUSION:

Achieving the right balance in the diet for those with MASLD involves careful selection and moderation of fructose-containing foods, prioritizing those that provide significant dietary fiber and other health benefits. By focusing on low-fructose, high-fiber foods, incorporating prebiotic and probiotic sources, and adjusting intake based on individual tolerance, individuals with MASLD can support both their liver health and overall metabolic function.

This balanced approach, combined with regular monitoring, and personalized dietary adjustments, can help manage MASLD while still providing the necessary nutrients to maintain a healthy digestive system and overall well-being.

Accepted Trials Of Therapy For MASLD

Lifestyle Modifications

• Diet and Exercise: Weight loss through calorie restriction and increased physical activity remains a cornerstone of MASLD management. The Mediterranean diet has been shown to improve liver histology and metabolic parameters.¹

<u>Coffee:</u>

Reduced risk of MASLD: Systematic reviews have found that coffee consumption is significantly associated with a lower risk of developing metabolic associated steatotic liver disease. compared to those who did not drink coffee.²⁻³

Impact on Liver Fibrosis:

Among patients with MASLD, coffee consumption has been linked to a reduction in liver fibrosis (scarring)³⁻⁴. These findings highlights coffee's potential role not only in preventing MASLD but also in ameliorating more severe progression of the disease.

These studies collectively suggest that coffee can offer protective effects against the development and progression of fatty liver disease. The suggested amount to consume is between 2 to 4 cups (i.e., 12 to 24 ounces) per day.³⁻⁴

PHARMACOTHERAPY

Pioglitazone: A PPAR-gamma agonist that improves insulin sensitivity and reduces hepatic steatosis and inflammation. It is particularly effective in patients with MASLD.⁵

<u>Vitamin E:</u> An antioxidant that has shown benefits in non-diabetic adults with MASLD, improving liver histology by reducing oxidative stress and inflammation.⁶

<u>GLP-1 Receptor Agonists</u>: Medications like liraglutide and semaglutide have shown promise in reducing liver fat content and improving liver histology in MASLD patients by enhancing insulin secretion and reducing appetite.⁷

<u>SGLT2 Inhibitors</u>: Drugs such as empagliflozin help reduce liver fat and fibrosis by promoting glucose excretion and improving insulin sensitivity.⁸

FXR Agonists: Obeticholic acid, an FXR agonist, has shown potential in reducing liver fibrosis and improving histological features in MASLD.⁹

<u>Statins:</u>

Statins, primarily used to lower cholesterol levels, have shown potential benefits in the management of Metabolic Associated Steatotic Liver Disease (MASLD), formerly known as Non-Alcoholic Fatty Liver Disease (NAFLD). The current evidence suggests that statins can be beneficial in the management of MASLD, primarily through their effects on reducing liver inflammation, slowing fibrosis progression, and lowering cardiovascular risk. Their safety profile in MASLD patients is also well-established. While the data is promising, longer-term studies are still needed to fully understand the extent of *statins'* benefits in this context.

Several studies and clinical trials have provided evidence supporting the role of *statins* in MASLD:

1. Reduction in Liver Fat and Inflammation:

Mechanism: Statins have been shown to reduce liver inflammation and fat accumulation through their cholesterol-lowering effects and by improving endothelial function.

Evidence: Statin therapy has been associated with significant improvements in liver enzyme levels (e.g., ALT, AST) in patients with MASLD. This suggests a reduction in liver inflammation and in hepatic fat content.¹⁰

2. Decreased Risk of Cardiovascular Events:

<u>Cardiovascular Benefits</u>: Since MASLD is often associated with an increased risk of cardiovascular disease (CVD), *statins*' cardiovascular benefits are particularly relevant.

Evidence: Studies have shown that *statins* reduce the risk of cardiovascular events in MASLD patients, which is crucial

given that cardiovascular disease is a leading cause of mortality in this population.¹¹

3. Potential Reduction in Fibrosis (scarring of the liver) Progression:

Mechanism: Some evidence suggests that *statins* may reduce the progression of liver fibrosis, a critical aspect of MASLD that can lead to more severe liver conditions like cirrhosis.

Evidence: Studies have found that patients with MASLD on *statins* had a lower progression of fibrosis compared to those not on *statins*, though this effect was more pronounced in patients with early-stage disease.¹²

4. Improvement in Overall Liver Health:

Liver Enzymes: Statins have been associated with reductions in liver enzymes, suggesting (*but not proving*) improved liver health.

Evidence: Studies report that long-term *statin* use was associated with lower rates of liver-related complications and a lower incidence of liver cancer in MASLD patients.¹³

5. Safety Profile:

Concerns: Initially, there were concerns about the potential liver toxicity of *statins*, particularly in patients with underlying **liver disease.**

Evidence: Large-scale studies have shown that *statins* are safe in patients with MASLD and do not increase the risk of liverrelated adverse effects. Large-scale studies have demonstrated that *statins* are safe for patients with Metabolic Dysfunction-Associated Steatotic Liver Disease (MASLD) and do not increase the risk of liver-related adverse effects. The American Association for the Study of Liver Diseases (AASLD) guidelines endorse the use of *statins* in MASLD patients, particularly when there is an indication for cardiovascular disease prevention.¹⁴

RESMETIROM

The FDA recently approved *Rezdiffra*[®] (Resmetirom), developed by Madrigal Pharmaceuticals, as the first medication specifically for patients with moderate to advanced liver fibrosis caused by (MASLD). Resmetirom has been shown to effectively reduce liver fat and improve fibrosis in a sizable portion of patients.

Resmetirom works by partially activating thyroid hormones which increases liver fat breakdown and reduces lipid buildup. In trials, 24-36% of patients on Resmetirom saw fibrosis improve by at least one stage without worsening MASLD, compared to only 9-13% in the placebo group.¹⁵

The drug also led to significant improvements in liver enzymes and cholesterol levels. The most common side effects were diarrhea

and nausea, with some patients having to be monitored for potential liver toxicity and gallbladder issues.

REFERENCES:

¹ Sofi, Francesco, Francesca Cesari, Rosanna Abbate, Gian Franco Gensini, and Alessandro Casini. 2008. "Adherence to Mediterranean Diet and Health Status: Meta-Analysis." *BMJ* 337: a1344. <u>https://doi.org/10.1136/bmj.a1344.</u>

² Wijarnpreecha, Karn, Charat Thongprayoon, and Patompong Ungprasert. 2017. "Coffee Consumption and Risk of Nonalcoholic Fatty Liver Disease: A Systematic Review and Meta-Analysis." *European Journal of Gastroenterology & Hepatology* 29 (2): e8–e12. <u>https://doi.org/10.1097/MEG.00000000000776</u>

³ Niezen, Sebastian, Manaav Mehta, Z. Gordon Jiang, and Elliot B. Tapper. "Coffee Consumption Is Associated with Lower Liver Stiffness: A Nationally Representative Study." *Clinical Gastroenterology and Hepatology* 20, no. 9 (September 2022): 2032–2040.e6. <u>https://doi.org/10.1016/j.cgh.2021.09.042.</u>

⁴ Kositamongkol, C., et al. (2021). Coffee Consumption and Non-alcoholic Fatty Liver Disease: An Umbrella Review and a Systematic Review and Meta-Analysis. Frontiers in Pharmacology, 12, 786596. <u>https://doi.org/10.3389/fphar.2021.786596</u>

⁵ Bril, F., & Cusi, K. (2017). Management of Nonalcoholic Fatty Liver
Disease in Patients with Type 2 Diabetes: A Call to Action. Diabetes Care,
40(3), 419-430. <u>https://doi.org/10.2337/dc16-1787</u>

⁶ Di Pietrantonio, D., Pace Palitti, V., Cichelli, A., & Tacconelli, S. (2024). Protective Effect of Caffeine and Chlorogenic Acids of Coffee in Liver Disease. *Foods*, *13*(14), 2280. <u>https://doi.org/10.3390/foods13142280</u> ⁷ Newsome, Philip N., et al. "A Placebo-Controlled Trial of Subcutaneous Semaglutide in Nonalcoholic Steatohepatitis." *New England Journal of Medicine* 384, no. 12 (2021): 1113–1124. <u>https://doi.org/10.1056/NEJMoa2028395</u>.

⁸Zhou, P., et al. (2023). Effects Of SGLT2 Inhibitors on Hepatic Fibrosis and Steatosis: A Systematic Review And Meta-Analysis. *Frontiers in Endocrinology*, 14, 1144838.

https://doi.org/10.3389/fendo.2023.1144838

⁹ Boursier, Jérôme, et al. "The Severity of Nonalcoholic Fatty Liver Disease Is Associated with Gut Dysbiosis and Shift in the Metabolic Function of the Gut Microbiota." *Hepatology* 63, no. 3 (March 2016): 764–775. <u>https://doi.org/10.1002/hep.28356</u>.

¹⁰ Pu, K., & Shi, Y. (2016). Efficacy and Safety of Statin Treatment for Nonalcoholic Fatty Liver Disease: A Meta-Analysis of Randomized, Controlled Trials. *Hepatology*, 63(2), 424–432. <u>https://doi.org/10.1002/hep.28356</u>

¹¹ Athyros, Vasilios G., Konstantinos Tziomalos, Thomas D. Gossios, Theodora Griva, Panagiotis Anagnostis, Konstantinos Kargiotis, Efstathios D. Pagourelias, Eleni Theocharidou, Asterios Karagiannis, and Dimitri P. Mikhailidis. "Safety and Efficacy of Long-Term Statin Treatment for Cardiovascular Events in Patients with Coronary Heart Disease and Abnormal Liver Tests in the Greek Atorvastatin and Coronary Heart Disease Evaluation (GREACE) Study: A Post-Hoc Analysis." *The Lancet* 376, no. 9756 (December 4, 2010): 1916–1922. <u>https://doi.org/10.1016/S0140-6736(10)61272-X.</u>

¹² Ekstedt, Mattias, Lennart E. Franzén, Ulrik L. Mathiesen, Marika Holmqvist, Rolf Bendtsen, Göran Bodemar, and Stergios Kechagias.
"Statins in Non-Alcoholic Fatty Liver Disease and Chronically Elevated Liver Enzymes: A Histopathological Follow-Up Study." *Journal of Hepatology* 47, no. 1 (2007): 135–141.
https://doi.org/10.1016/j.jhep.2007.02.013. ¹³ Biyao Zou, Michelle C. Odden, and Mindie H. Nguyen, "*Statin* Use and Reduced Hepatocellular Carcinoma Risk in Patients with Nonalcoholic Fatty Liver Disease," *Clinical Gastroenterology and Hepatology* 21, no. 2 (2023): 435-444.e6, <u>https://doi.org/10.1016/j.cgh.2022.01.057</u>.

¹⁴ Rinella, Mary E., Brent A. Neuschwander-Tetri, Mohammad Shadab Siddiqui, Manal F. Abdelmalek, Stephen Caldwell, Diana Barb, David E. Kleiner, and Rohit Loomba. "AASLD Practice Guidance on the Clinical Assessment and Management of Nonalcoholic Fatty Liver Disease." *Hepatology* 77, no. 5 (May 2023): 1797–1835. <u>https://doi.org/10.1097/HEP.00000000000323</u>.

¹⁵ Karim, Gres, and Meena B. Bansal. "Resmetirom: An Orally Administered, Small-Molecule, Liver-Directed, β-Selective THR Agonist for the Treatment of Non-Alcoholic Fatty Liver Disease and Non-Alcoholic Steatohepatitis." *touchREV Endocrinology* 19, no. 1 (2023): 60-70. <u>https://doi.org/10.17925/EE.2023.19.1.60</u>

Surgical Interventions

Bariatric Surgery: Effective in patients with severe obesity, bariatric surgery significantly reduces liver fat, inflammation, and fibrosis, offering a potential cure for MASLD in this population.¹



REFERENCES:

¹ Lassailly, Guilhem, Romain Caiazzo, David Buob, Maxime Pigeyre, Hélène Verkindt, Jean Labreuche, Vincent Raverdy, et al. "Bariatric Surgery Provides Long-term Resolution of Nonalcoholic Steatohepatitis and Regression of Fibrosis." *Gastroenterology* 159, no. 4 (2020): 1290-1301.e5. <u>https://doi.org/10.1053/j.gastro.2020.06.006</u>.

² Mummadi, Raghavendra R., et al. "Bariatric Surgery Reverses Liver Fibrosis in Patients with Nonalcoholic Steatohepatitis: A Meta-Analysis." *Clinical Gastroenterology and Hepatology* 19, no. 5 (2021): 1112–1121.e6. <u>https://doi.org/10.1016/j.cgh.2020.06.064</u>.

IRRITABLE BOWEL SYNDROME (IBS)



A Multifaceted Disorder of Dysfunctional Intestinal Ecosystems

Definition: Irritable bowel syndrome (IBS) is a prevalent gastrointestinal disorder characterized by chronic abdominal pain and altered bowel habits, including diarrhea, constipation, or a mixture of both^{1,2} along with symptoms of bloating, abdominal distention, flatulence and pain. But beyond these symptoms lies a

deeper and more integrative understanding: IBS represents the systemic manifestations of an "internal climate crisis" with dysregulation of the digestive tract beyond just the colon. IBS represents a dysfunction of one or more of the interconnected and interdependent digestive ecosystems. The bowel dysfunction is characterized by the following:

Dysbiosis: The term "dysbiosis" represents microbial imbalance and is one of the features of irritable bowel syndrome. Patients with irritable bowel syndrome often exhibit reduced microbial diversity and significant alterations in the composition of their gut microbes.

Studies have shown that irritable bowel syndrome patients also tend to have lower levels of beneficial bacteria, such as Lactobacillus and Bifidobacterium, and an overgrowth of potentially harmful microbes³.

Intestinal Permeability: Translocation of luminal antigens, bacteria, and toxins into and through the intestinal wall occurs in irritable bowel syndrome, triggering immune responses and precipitating inflammation. Studies have demonstrated that IBS patients, particularly those with diarrhea-predominant IBS, exhibit an increased intestinal permeability compared to healthy controls⁴.

Depletion of Short Chain Fatty Acids (SCFAs): Short chain fatty acids, primarily produced by the fermentation of dietary fibers by gut bacteria, play a critical role in maintaining gut health. SCFAs

such as butyrate, propionate, and acetate, serve as energy sources for the lining cells of the colon and have anti-inflammatory properties. However, IBS patients often show depletion of these beneficial metabolites, potentially contributing to gut dysbiosis and inflammation^{5,6}.

Inflammation: While irritable bowel syndrome has traditionally been considered non-inflammatory, emerging evidence points to low-grade inflammation in the gut as a contributing factor. Studies have shown that irritable bowel syndrome patients often exhibit elevated levels of pro-inflammatory cytokines and immune cells in their intestinal lining^{7,8}. This subtle inflammatory response can disrupt gut function and can contribute to the characteristic symptoms of irritable bowel syndrome, such as pain and altered bowel habits.

Altered Bile Salt Metabolism: Bile salts, which are needed for the digestion and absorption of fats, also play a significant role in maintaining intestinal micro-balance and signaling within the gutbrain axis. Altered bile salt metabolism has been implicated in the pathophysiology of irritable bowel syndrome, particularly in diarrhea-predominant IBS.

An excess of bile salts can lead to increased water secretion and motility, contributing to diarrhea. Additionally, bile salts can influence gut microbe composition, promoting the growth of certain bacterial species while inhibiting others. This dysregulation can exacerbate symptoms and perpetuate a cycle of gut dysfunction.

Studies have shown that patients with irritable bowel syndromediarrhea variants often have abnormal bile acid profiles, suggesting that therapeutic modulation of bile acids might be beneficial for symptom management⁹⁻¹².

Gut Hypersensitivity and Altered Gut-Brain Communication

Irritable bowel syndrome is often marked by an overly sensitive digestive tract and abnormal bowel movements, sometimes referred to as "visceral hypersensitivity." Those with IBS may experience pain or discomfort from normal digestive processes that would not usually cause symptoms in others. This heightened sensitivity is a term implying that nerves in the digestive tract are overreacting to normal sensations like gas production or movement of the gut (peristalsis) sometimes scientifically described as "central sensitization and altered neural processing of gut signals"¹³.

A key player in IBS, therefore, is the gut-brain axis, the communication network between the digestive tract and the brain. When that two-way communication becomes altered, it can lead to increased pain signals, irregular motility (movement) and a range of digestive symptoms.

CONCLUSION:

The evolving understanding of irritable bowel syndrome highlights its multifactorial origins, encompassing dysbiosis, low-grade inflammation, increased gut permeability, depletion of short chain fatty acids, altered bile salt metabolism, and dysregulated gutbrain communication. These insights underscore the complexity of irritable bowel syndrome and the necessity for a comprehensive approach to its management, integrating diet, attention to microbe composition, and psychological interventions to restore the balance of the digestive system.

REFERENCES:

^{1.} Alexander C. Ford et al., "Irritable Bowel Syndrome," The Lancet 396, no. 10263 (2020): 1675–1688, <u>https://doi.org/10.1016/S0140-6736(20)31548-8</u>.

^{2.} Ami D. Sperber et al., "Global Prevalence of Irritable Bowel Syndrome According to Rome III or IV Criteria: A Systematic Review and Meta-Analysis," Clinical Gastroenterology and Hepatology 19, no. 4 (2021): 665– 676.e3, <u>https://doi.org/10.1016/j.cgh.2020.02.029</u>.

^{3.} Julien Tap et al., "Identification of an Intestinal Microbiota Signature Associated with Severity of Irritable Bowel Syndrome," Gastroenterology 152, no. 1 (2017): 111–123.e8,

https://doi.org/10.1053/j.gastro.2016.09.049.

^{4.} Michael Camilleri, "Leaky Gut: Mechanisms, Measurement and Clinical Implications in Humans," Gut 68, no. 8 (2019): 1516–1526, <u>https://doi.org/10.1136/gutjnl-2019-318427.</u> ^{5.} Qian Sun et al., "Short-Chain Fatty Acids in Irritable Bowel Syndrome: Relevance, Mechanisms, and Therapeutic Potential," Nutrients 11, no. 8 (2019): 1964,

^{6.} José Luiz Fachi et al., "Butyrate Protects Mice from Clostridium Difficile– Induced Colitis Through an HIF-1–Dependent Mechanism," Cell Reports 27, no. 3 (2019): 750–761.e7,

https://doi.org/10.1016/j.celrep.2019.03.054.

^{7.} Lena Öhman and Magnus Simrén, "Pathogenesis of IBS: Role of Inflammation, Immunity and Neuroimmune Interactions," Nature Reviews Gastroenterology & Hepatology 17, no. 2 (2020): 100–116,

^{8.} Lu Zhang et al., "Immune Activation in IBS: Can Neuroimmune Signaling Be Targeted?" Clinical Gastroenterology and Hepatology 20, no. 4 (2022): 882–892,

^{9.} Michael Camilleri, "The Role of Bile Acids in the Pathogenesis of Irritable Bowel Syndrome," Liver Research 5, no. 4 (2021): 1–8,

^{10.} Catherine J. Black et al., "Bile Acids and the Microcirculation: New Insights into an Old Problem," Gastroenterology 159, no. 5 (2020): 1687– 1695,

^{11.} Julian R.F. Walters et al., "Managing Bile Acid Diarrhoea," Therapeutic Advances in Gastroenterology 14 (2021): 1–8,

^{12.} Hélène Duboc et al., "Connecting Dysbiosis, Bile Acid Dysmetabolism and Gut Inflammation in Inflammatory Bowel Diseases," Gut 62, no. 4 (2013): 531–539, <u>https://doi.org/10.1136/gutjnl-2012-302578.</u>

^{13.} Lukas Van Oudenhove et al., "Abnormal Regional Brain Activity During Rest and (Anticipated) Gastric Distension in Functional Dyspepsia and the Role of Anxiety: A H(2)(15)O-PET Study," American Journal of Gastroenterology 105, no. 4 (2010): 913–924, <u>https://doi.org/10.1038/ajg.2010.39.</u>

GASTROPARESIS

Introduction

Gastroparesis is a chronic disorder characterized by delayed gastric emptying without mechanical obstruction. It leads to symptoms such as nausea, vomiting, early satiety, bloating, and abdominal discomfort. The condition disrupts normal stomach motility, impacting the ability of the stomach to pass its contents into the small intestine in a timely manner. The causes of gastroparesis are diverse, and its diagnosis and treatment require a multifaceted approach.

Causes of Gastroparesis

Gastroparesis has several known causes, although in many cases, it remains idiopathic (without a clear cause). Some of the major known causes include:

 Diabetes: One of the most well-established causes of gastroparesis, particularly in long-term diabetes, is autonomic neuropathy, which impairs the vagus nerve. High blood sugar levels damage nerves, leading to delayed gastric emptying.

2. <u>Post-surgical</u>: Gastroparesis can develop after surgeries that involve the stomach or vagus nerve, such as fundoplication or gastric bypass, which can inadvertently damage the nerves responsible for gastric contractions.

3. <u>Neurologic</u>: Neurological conditions like Parkinson's disease, multiple sclerosis, and strokes can interfere with autonomic function, leading to delayed gastric emptying.

4. <u>Autoimmune</u>: Autoimmune diseases like scleroderma or systemic lupus erythematosus (SLE) can damage nerves and muscles in the digestive system, disrupting stomach motility.

5. <u>Medications</u>: Certain medications, such as opioids, tricyclic antidepressants, and anticholinergics, are known to slow gastric motility, exacerbating gastroparesis symptoms.

6. <u>Infections</u>: Viral infections, particularly post-viral syndromes, can trigger gastroparesis. Herpes simplex virus and Epstein-Barr virus have been implicated in delayed gastric emptying.

7. <u>Endocrine and metabolic conditions</u>: Conditions like hypothyroidism can slow overall metabolic rate, affecting gastric motility.

8. <u>Connective Tissue Disorders</u>: Ehlers-Danlos syndrome (EDS), a disorder affecting collagen, has been linked to gastroparesis due to weakened connective tissues that affect motility.

9. <u>Eating Disorders</u>: Anorexia nervosa and bulimia can alter gastric function and result in delayed gastric emptying due to malnutrition or recurrent vomiting.

10. <u>Chemotherapy and Radiation</u>: These cancer treatments, particularly in the abdominal region, can damage nerves and muscles controlling gastric motility.

11. <u>Duodeno-Gastric Reflux of Bile</u>: Gastroparesis may predispose patients to bile reflux due to disrupted gastric emptying and impaired coordination of the pyloric valve, allowing bile to flow back into the stomach.

12. <u>Chronic H. pylori Infection</u>: Long-term infection with *Helicobacter pylori* can damage the stomach lining and disrupt motility. Chronic infection may contribute to gastroparesis.

13. <u>Archaeal Influx from Periodontitis</u>: Recent research has suggested that microbes from the oral cavity, such as *Porphyromonas gingivalis*, and even archaea in individuals with periodontitis, may enter the stomach and contribute to delayed gastric emptying.

Diagnostic Techniques

Diagnosing gastroparesis involves ruling out mechanical obstructions and identifying delayed gastric emptying using various tests:

1. <u>Gastric Emptying Scintigraphy</u>: The gold standard test, where the patient consumes a meal labeled with a small amount of radioactive material, and imaging tracks how fast the stomach empties its contents. 2. <u>Wireless Motility Capsule (SmartPill®)</u>: This device records data as it travels through the digestive system, providing information about transit times in the stomach, small intestine, and colon.

3. <u>Endoscopy</u>: Upper endoscopy helps rule out structural causes of delayed gastric emptying, such as pyloric stenosis or tumors, though it cannot diagnose gastroparesis directly.

4. <u>Antroduodenal Manometry</u>: This test measures the pressure and motor function of the stomach and duodenum, identifying abnormalities in muscle contractions.

5. **Breath Testing:** This non-invasive test measures gas release after consuming a labeled meal to evaluate gastric emptying.

Treatment Options:

While there is no cure for gastroparesis, management focuses on alleviating symptoms and improving gastric motility:

1. <u>Dietary Modifications</u>: Patients are often advised to eat small, frequent meals that are low in fat, which can slow gastric emptying. Pureed or liquid diets are sometimes recommended.

2. Medications:

 Prokinetics: Drugs like metoclopramide and domperidone stimulate stomach contractions and improve gastric emptying.

- Anti-nausea medications: Medications like ondansetron or promethazine are used to relieve nausea and vomiting.
- Erythromycin: Although an antibiotic, erythromycin acts as a motilin receptor agonist and enhances gastric motility.

3. <u>**Gastric Electrical Stimulation:**</u> In patients with severe, medication-refractory gastroparesis, an implanted device may stimulate the stomach muscles, although its effectiveness is variable.

4. <u>Botox Injections</u>: Botox injections into the pyloric sphincter have been explored to reduce gastric outlet resistance and improve emptying. However, studies show that this treatment may not be efficacious for many patients.

^{5.} <u>Surgical Interventions</u>: For severe cases, surgical options like pyloroplasty (widening the pylorus) or a feeding jejunostomy (bypassing the stomach) may be considered.

6. Emerging Therapies:

 Ghrelin and Motilin Agonists: These agents are currently under investigation for their potential to enhance gastric motility.

- Stem Cell Therapy: Research is exploring the use of stem cells to repair damaged nerves and muscles involved in gastroparesis.
- Neuromodulation: Transcutaneous vagal nerve stimulation is being investigated as a non-invasive technique to improve gastric motility and reduce symptoms.

CONCLUSION:

Gastroparesis is a complex condition with multifactorial causes, ranging from diabetes and autoimmune disorders to infections and surgical complications. Diagnosis involves a range of imaging and motility studies to confirm delayed gastric emptying. While current treatment options focus on managing symptoms, ongoing research into novel therapies like stem cell therapy and motilin agonists offers hope for more effective interventions. Managing gastroparesis requires a comprehensive approach, combining dietary modifications, pharmacological treatments, and, in some cases, surgical options to improve quality of life.

By understanding the diverse causes and personalized treatment options, patients and healthcare providers can work together to mitigate the often debilitating effects of gastroparesis.

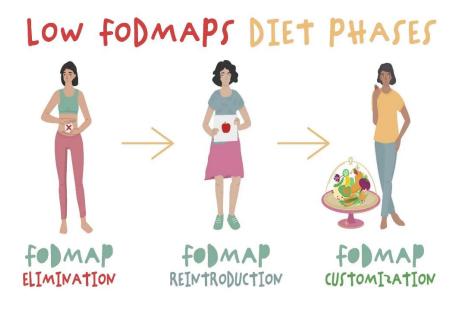
REFERENCES:

1. El Halabi, Maan, and Henry P. Parkman. "2023 Update on the Clinical Management of Gastroparesis." *Expert Review of Gastroenterology &*

Hepatology 17, no. 5 (2023): 431–441. https://doi.org/10.1080/17474124.2023.2196404.

SECTION EIGHTEEN

WHY THE LONG-TERM USE OF THE LOW FODMAP DIET MAY NOT PROMOTE DIGESTIVE HEALTH



While the low FODMAP diet has gained popularity for its effectiveness in alleviating symptoms such as bloating, distention, flatulence, and abdominal pain in conditions like irritable bowel syndrome (IBS), there are potential risks associated with its long-term use. The diet, which restricts fermentable carbohydrates (FODMAPs) such as fructans, galacto-oligosaccharides, and polyols, works by reducing fermentation in the gut, thereby decreasing the production of gases that can contribute to discomfort. However, this symptom relief can come at a cost to long-term gut health.

<u>The Role of Fermentable Carbohydrates</u>: As noted previously, fermentable carbohydrates (like prebiotic fibers) are essential for the production of short-chain fatty acids (SCFAs), particularly butyrate, which is produced when beneficial gut bacteria ferment dietary fibers. SCFAs are crucial for:

- Maintaining the integrity of the gut lining,
- Reducing inflammation,
- Supporting immune function,
- Regulating metabolism.

By restricting fermentable carbs on a prolonged low FODMAP diet, SCFA production decreases, weakening these protective functions and leaving the gut more vulnerable to inflammation, infections, and even long-term metabolic and immune dysfunction.

Shift from Fermentation to Harmful Byproducts:

When the gut microbiota is deprived of fermentable carbohydrates, it shifts to other nutrient sources, particularly proteins.

<u>Gut inflammation</u>: The fermentation of proteins in the gut produces byproducts that can irritate the gut lining and contribute to inflammation. Studies have shown that metabolites such as ammonia and hydrogen sulfide are associated with inflammation due to their cytotoxic effects.^{1,2}

Disruption of the gut barrier: A reduction in short-chain fatty acids (SCFAs), particularly butyrate, compromises the gut's barrier function, contributing to a "leaky gut" and increased systemic inflammation.³ Butyrate is essential for maintaining the integrity of the epithelial barrier and modulating immune responses.⁴

Increased risk of colon cancer: Ammonia and hydrogen sulfide produced during protein fermentation have been linked to an increased risk of colorectal cancer.⁵ These compounds can damage colonocytes and promote carcinogenic pathways.⁶

Worsened microbiome diversity: Diets low in fermentable carbohydrates, such as the low FODMAP diet, can lead to a decrease in beneficial bacterial species and reduced microbial diversity, which is critical for gut health and resilience against disease.⁷

REFERENCES:

¹ Magee, E. A., Richardson, C. J., Hughes, R., and Cummings, J. H. "Contribution of Dietary Protein to Sulfide Production in the Large Intestine: An In Vitro and In Vivo Study." *American Journal of Clinical Nutrition* 72, no. 6 (2000): 1488–1494. <u>https://doi.org/10.1093/ajcn/72.6.1488</u>

² Louis, P., and Flint, H. J. "Formation of Propionate and Butyrate by the Human Colonic Microbiota." *Environmental Microbiology* 19, no. 1 (2017): 29–41. <u>https://doi.org/10.1111/1462-2920.13589</u> ³ Kelly, C. J., et al. "Crosstalk Between Microbiota-Derived Short-Chain Fatty Acids and Intestinal Epithelial Cells Regulates the Intestinal Barrier." *Nature Communications* 6 (2015): 8023.

⁴ Hamer, H. M., et al. "The Role of Butyrate on Colonic Function." *Alimentary Pharmacology & Therapeutics* 27, no. 2 (2008): 104–119.

⁵ Attene-Ramos, Matias S., Elizabeth D. Wagner, H. Rex Gaskins, and Michael J. Plewa. "Hydrogen Sulfide Induces Direct Radical-Associated DNA Damage." *Molecular Cancer Research* 5, no. 5 (May 2007): 455–459. <u>https://doi.org/10.1158/1541-7786.MCR-06-0439.</u>

⁶ Louis, P., and Flint, H. J. "The Gut Microbiota, Bacterial Metabolites and Colorectal Cancer." *Nature Reviews Microbiology* 12, no. 10 (2014): 661– 672.

⁷ Halmos, E. P., et al. "A Diet Low in FODMAPs Reduces Symptoms of Irritable Bowel Syndrome." *Gastroenterology* 146, no. 1 (2014): 67–75. <u>https://doi.org/10.1053/j.gastro.2013.09.046</u>

Short-Term Gain, Long-Term Pain:

In the short term, a low FODMAP diet can offer relief by reducing bloating, distention, flatulence, and pain. However, the long-term restriction of fermentable carbohydrates can shift the gut ecosystem from producing health-promoting SCFAs to generating potentially harmful branched chain fatty acids and toxic byproducts. This can lead to chronic gut inflammation, reduced gut barrier integrity, and increased susceptibility to disease a shortterm gain in symptom relief but long-term pain in the form of gut dysfunction and systemic health problems.

Balancing the Low FODMAP Diet:

Given these risks, it is crucial that the low FODMAP diet be used only as a temporary measure. Patients should work with healthcare professionals to reintroduce fermentable fibers gradually once symptoms are under control. This phased approach helps restore SCFA production and gut health, allowing for symptom management without sacrificing long-term well-being.

Reintroducing Fermentable Carbohydrates:

The low FODMAP diet is designed to be a short-term intervention, typically lasting 4-6 weeks, to reduce gut symptoms like bloating, distention, pain, and flatulence. However, after this period of symptom relief, it is crucial to gradually reintroduce fermentable carbohydrates to restore gut health and avoid the potential longterm harms discussed earlier. Here is how the reintroduction process works:

Phase 1: Identification of Tolerance Levels

After the initial restrictive phase, specific FODMAP groups (such as oligosaccharides, disaccharides, monosaccharides, and polyols) should be reintroduced one at a time. This allows for identification of which types of fermentable fibers the individual can tolerate without triggering symptoms. This phase helps to discern personal sensitivity to particular FODMAPs and ensures that only necessary restrictions are maintained longterm¹.

Phase 2: Gradual Reintroduction

Once tolerance levels are established, gradually increase the intake of tolerated FODMAPs over several weeks. Starting with lesser amounts and slowly building up helps beneficial gut bacteria acclimate and prevents sudden fermentation that could lead to symptom flare-ups. Reintroducing foods such as garlic, onions, and whole grains in moderate quantities is essential for supporting the microbiota and SCFA production.²

Phase 3: Diversification of Fiber Sources

In this phase, the goal is to restore gut microbial diversity by diversifying the types of prebiotic fibers in the diet. Include a variety of high-fermentable fibers such as inulin (found in chicory root), fructo-oligosaccharides (from bananas, asparagus), and resistant starches (from cooled potatoes, green bananas). These fibers support the production of short-chain fatty acids (SCFAs) like butyrate, which are crucial for gut health, immune function, and maintaining the gut barrier.

Phase 4: Maintenance and Monitoring

Once a broad range of FODMAPs has been successfully reintroduced, the focus shifts to maintaining balance. Individuals should regularly consume a wide range of fermentable fibers to keep SCFA production high and prevent harmful shifts in the microbiota toward protein fermentation and the production of branched-chain fatty acids (BCFAs). Regular monitoring of symptoms ensures that reintroduced foods do not exceed tolerance thresholds, but the key is to avoid unnecessary long-term restriction of beneficial fibers³.

FURTHER NUANCES OF GUT HEALTH

The Balance Between SCFAs and BCFAs:

As previously mentioned, SCFAs such as butyrate, acetate, and propionate play crucial roles in gut health by regulating inflammation, supporting the gut barrier, and modulating immune responses. When fermentable carbohydrates are restricted, protein fermentation can increase, leading to the production of branched-chain fatty acids (BCFAs) such as isobutyrate and isovalerate. BCFAs are associated with gut inflammation and can disrupt the balance of the microbiota, leading to a shift toward harmful bacterial species⁴.

<u>"Leaky Gut" and Immune Dysfunction:</u>

Prolonged restriction of fermentable carbohydrates can impair the integrity of the gut barrier. Among the short-chain fatty acids (SCFAs), butyrate plays a particularly important role in maintaining the tight junctions between intestinal cells, thereby preserving proper permeability and preventing the passage of harmful microbial products, such as lipopolysaccharides (LPS), into the bloodstream—a condition often referred to as *"leaky gut."* This compromised barrier function can trigger systemic inflammation and has been associated with various chronic diseases, including autoimmune disorders, obesity, and metabolic syndrome.⁵ To reduce the risk of *leaky gut*, it is essential to support adequate SCFA production by ensuring sufficient intake of fermentable fibers.

Impact on Microbiome Diversity:

The diversity of the gut microbiome is critical for overall health. The low FODMAP diet, by restricting fermentable fibers, can lead to a reduction in microbial diversity. Studies have shown that long-term fiber restriction decreases populations of beneficial bacteria such as *Bifidobacteria* and *Lactobacillus*, which are important for maintaining immune function, preventing inflammation, and producing SCFAs⁶. Restoring a diverse array of prebiotic fibers helps to promote a resilient and diverse microbiome.

Gut-Brain Axis and Mental Health:

Emerging research highlights the connection between the gut microbiome and mental health through the gut-brain axis. SCFAs, particularly butyrate, are involved in modulating the release of neurotransmitters such as serotonin and GABA, which play a role in mood regulation. A lack of fermentable fibers can reduce SCFA production, potentially contributing to mood disorders such as anxiety and depression⁷.

Ensuring an adequate intake of fermentable fibers supports both gut health and mental well-being.

Long-Term Risks of Protein Fermentation:

Shifting the primary energy source in the gut from carbohydrates to proteins over the long term can have deleterious effects. Protein fermentation produces ammonia, hydrogen sulfide, indoles, branched chain fatty acids, and phenols, which are toxic to gut epithelial cells and have been linked to colorectal cancer⁸. Furthermore, protein fermentation generates metabolites that can increase gut permeability, leading to chronic inflammation. These risks highlight the importance of balancing nutrient sources and maintaining adequate intake of fermentable carbohydrates⁹.

REFERENCES:

^{1.} Halmos, Emma P. et al. "Reintroduction of FODMAPs After a Low-FODMAP Diet in Patients with IBS: A Randomized Controlled Trial." *Journal of Gastroenterology and Hepatology* 35, no. 3 (2020): 377–385.

^{2.} McIntosh, Kathleen et al. "FODMAPs, Prebiotics, and Gut Health: The Reintroduction Phase." *Nutrients* 12, no. 10 (2020): 3201.

^{3.} Staudacher, Helen M. et al. "Fermentable Carbohydrate Reintroduction in Irritable Bowel Syndrome Patients Following a Low FODMAP Diet." *Gut Microbes* 10, no. 4 (2019): 493–501.

^{4.} Sonnenburg, Justin L., and Erica D. Sonnenburg. "Dietary Fiber and the Gut Microbiota: Translating Science to Practice." *Cell Metabolism* 30, no. 5 (2019): 867–874.

^{5.} Parada Venegas, Daniela et al. "Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases." *Journal of Cellular Physiology* 234, no. 10 (2019): 17058–17067. ^{6.} Wilson, Benjamin C. et al. "The Super-Donor Phenomenon in Fecal Microbiota Transplantation." *The American Journal of Clinical Nutrition* 111, no. 1 (2020): 142–151.

 ^{7.} Silva, Yvonne P., Carol B. Bernardi, and Francieli C. Frozza. "The Role of Short-Chain Fatty Acids from Gut Microbiota in Gut-Brain Communication." *Frontiers in Endocrinology* 11 (2020): <u>https://doi.org/10.3389/fendo.2020.00025</u>

^{8.} Louis, Petra, and Harry J. Flint. "Formation of Phenolic and Indole Compounds by Anaerobic Bacteria in the Human Colon." *Gut Microbes* 13, no. 1 (2022): 1847621.

^{9.} Sonnenburg, Erica D., and Justin L. Sonnenburg. "Starving Our Microbial Self: The Deleterious Consequences of a Diet Deficient in Microbiota-Accessible Carbohydrates." *Cell Metabolism* 20, no. 5 (2014): 779–786. <u>https://doi.org/10.1016/j.cmet.2014.07.003</u>

SECTION NINETEEN

INTRODUCING FIBER START LOW, GO SLOW



Use Caution When Increasing Fiber

Avoid increasing your fiber intake too quickly, as this can lead to side effects such as abdominal bloating, distention, excess gas, and abdominal pain. Plant-based fibers should be gradually introduced to allow the digestive tract to adapt to the metabolic byproducts produced by gut microorganisms. These byproducts include gases like methane, carbon dioxide, and hydrogen sulfide, which can stretch the walls of the digestive tract and cause discomfort.

Initially, the digestive tract may be hypersensitive to this stretching when fiber is first introduced. However, with time, the digestive system may adapt and reach a new, more comfortable baseline. This adaptation process can take months, especially for individuals whose diets previously contained minimal amounts of dietary fiber.

THE CONSEQUENCES OF NEGLECTING BENEFICIAL MICROBES



The Microbial Forest Of The lleum And Colon

The last portion of the small intestine, the ileum, along with the large intestine (colon), can be likened to a thriving forest.

A flourishing forest is characterized by a rich array of plants, flowers, bushes, vines, trees, grass, and other vibrant vegetation. Similarly, the diverse community of trillions of microorganisms inhabiting the ileum and colon forms a *microbial forest* consisting of thousands of distinct species, strains, and sub-strains—some scientists saying as many as 10,000 different species.

As with any living ecosystem, this *microbial forest* requires a consistent energy source to sustain its growth and balance. The primary energy sources for intestinal microbial communities include dietary fiber, polyphenols, human milk oligosaccharides (HMOs), and resistant starches. These substrates undergo fermentation by gut microbiota, producing among other things, short-chain fatty acids (SCFAs) such as butyrate, acetate, and propionate, which are crucial for maintaining intestinal health and function.

Beyond microbial-derived SCFAs, intestinal epithelial cells (IECs) utilize several other key energy sources:

- **<u>Glutamine</u>**: A vital amino acid fuel for enterocytes, glutamine supports mucosal growth, tight junction maintenance, and epithelial repair, particularly under stress or injury.
- <u>Glucose</u>: Small intestinal cells, such as enterocytes, rely on glucose absorbed directly from the diet as an important energy source, essential for nutrient absorption and epithelial turnover.
- Ketone Bodies: Under conditions like fasting or low carbohydrate intake, ketone bodies such as βhydroxybutyrate serve as alternative fuels for intestinal cells, especially when SCFA availability is reduced.
- Long-Chain Fatty Acids (LCFAs): While not primary energy sources for colonocytes, absorbed LCFAs provide energy to intestinal smooth muscle, immune cells, and some epithelial cells when circulating systemically.
- Other Amino Acids: Amino acids like aspartate and glutamate contribute to energy production under certain conditions, though they are less prominent compared to glutamine in intestinal metabolism.

 Microbial Metabolites: Beyond SCFAs, gut microbes produce lactate, succinate, and other intermediates that may enter host metabolic pathways, offering additional, albeit minor, energy sources.

REFERENCES:

- Xiong, Ruo-Gu, Dan-Dan Zhou, Si-Xia Wu, Si-Yu Huang, Adila Saimaiti, Zhi-Jun Yang, Ao Shang, Cai-Ning Zhao, Ren-You Gan, and Hua-Bin Li. "Health Benefits and Side Effects of Short-Chain Fatty Acids." *Foods* 11, no. 18 (2022): 2863. <u>https://doi.org/10.3390/foods11182863</u>.
- ^{2.} Zhao, Y., et al. "A systematic review and meta-analysis of clinical trials on the effects of glutamine supplementation on intestinal barrier function." *Frontiers in Nutrition* 11 (2024): 11471693.
- ^{3.} Smith, J., et al. "Dietary and metabolic effects on intestinal stem cells in health and disease." *Cell Metabolism* 33, no. 3 (2025): 123-135.
- ^{4.} Lee, H., et al. "Not Just an Alternative Energy Source: Diverse Biological Functions of Ketone Bodies." *Cell Metabolism* 34, no. 2 (2023): 234-245.
- ^{5.} Chen, L., et al. "Long-chain fatty acids and their role in intestinal health." *Journal of Nutritional Biochemistry* 85 (2024): 108456.
- ^{6.} Wang, X., et al. "Effects of glutamine, glutamate, and aspartate on intestinal barrier function and amino acid metabolism." *Frontiers in Veterinary Science* 10 (2023): 1202369. <u>https://doi.org/10.3389/fvets.2023.1202369.</u>
- ^{7.} Johnson, M., et al. "Microbial fiber metabolism supporting colonic epithelial homeostasis." *Trends in Microbiology* 31, no. 2 (2023): 123-134.

"Leaky Gut" and Immune Dysfunction:

Prolonged restriction of fermentable carbohydrates can impair the integrity of the gut barrier. Among the short-chain fatty acids (SCFAs), butyrate plays a particularly important role in maintaining the tight junctions between intestinal cells, preserving proper permeability, and preventing the passage of harmful microbial products, such as lipopolysaccharides (LPS), into the bloodstream—a condition often referred to as "leaky gut." This compromised barrier function can trigger systemic inflammation and has been associated with various chronic diseases, including autoimmune disorders, obesity, and metabolic syndrome.

While dietary fiber is a key player in supporting SCFA production and gut health, it is not the only factor involved in maintaining controlled permeability. Other dietary components, such as polyphenols—plant-derived compounds with antioxidant and antiinflammatory properties—also help strengthen the intestinal barrier by modulating tight junction proteins and reducing oxidative stress. Additionally, during infancy, human milk oligosaccharides (HMOs) play a crucial role in shaping the gut microbiota and enhancing mucosal defenses, laying the foundation for lifelong gut integrity. Together, these diverse nutritional components highlight the importance of a varied and balanced diet in promoting gut health and preventing the onset of leaky gut– associated diseases



WHAT HAPPENS WHEN MICROBES ARE STARVED OF NUTRIENT SUBSTANCES "PLAN "B"

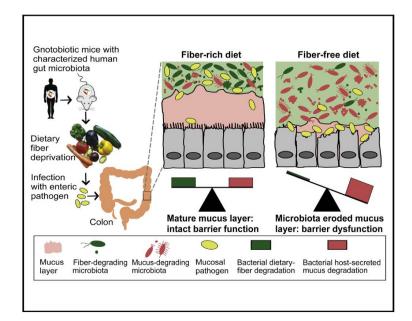
During periods of nutrient deficiency, microbes in the lower intestines adapt by sourcing alternative sources to support their survival and function:

- Fermentation of other sources: As part of natural cellular turnover, dead cells from the intestinal lining are sloughed off and replaced with new ones. These sloughed cells, along with remnants of dead microbes destroyed in the upper digestive tract by gastric acid, pepsin, bile, and pancreatic enzymes, provide nutrients for surviving microbes in the lower gut¹.
- Protein fermentation: In the absence of fermentable carbohydrates, some bacteria turn to protein fermentation for energy, a process that can produce beneficial compounds but also harmful byproducts that may compromise gut health.
- Mucin degradation: Certain bacteria, known as mucolytic bacteria, can break down mucins—glycoproteins that form the mucus lining of the gut—when dietary fiber is lacking. *Akkermansia muciniphila*, a prominent mucolytic bacterium that makes up about 3% of the gut microbiome, thrives in the mucus layer, aiding mucosal health.

In the absence of dietary fiber as a source of energy, *Akkermansia*, and other colonic mucus degrading bacteria, can degrade the mucin lining resulting in the release of substrates that support the activity of other bacteria, like *Alistipes* species which is butyrogenic. These interactions ultimately stimulate pathways to produce butyrate to keep the host lining cells alive.

Without butyrate producing bacteria, this secondary butyrate production pathway can help maintain gut homeostasis, supporting mucosal integrity and modulating inflammation. This compensatory response underscores the resilience of the gut ecosystem, where different microbes can adapt their roles to maintain critical functions, even in the absence of specific microbial populations.

Plan B, however, may result in excessive mucin degradation weakening the gut barrier, increasing permeability, and allowing toxins, pathogens, and food antigens to penetrate, which may trigger immune responses and inflammation².



<u>Change In Microbe Population Due To Fiber Deficiency and</u> <u>Antibiotic Exposure</u>:

When a diet chronically lacks fiber or when antibiotics are frequently used, significant changes occur in the microbiota. Fiberdegrading bacteria decline, and antibiotic-resistant strains may proliferate, disrupting the ecosystem's health and balance. Antibiotics, in particular, when given repeatedly can have a devastating effect on the microbiome. In a BBC interview, Professor Gautam Dantas, Professor of Laboratory and Genomic Medicine, Washington University School of Medicine explains³:

"We know that the more diverse our digestive tract bacteria population is, the better. But every course of antibiotics disrupts this population because antibiotics are not targeted enough to only kill the pathogenic bacteria causing the infection. Instead, they go after all bacteria in our digestive tracts, and there is collateral damage."

"Think of a forest where you are trying to get rid of one weed infection; the way we deploy antibiotics is to carpet-bomb the forest, killing the good and the bad."

"Studies examining the microbiomes of people who have undergone antibiotic treatment after an infection reveal that while microbiome diversity often recovers within a few months, some individuals, however, may never regain certain beneficial bacterial species."

REFERENCES:

¹Derrien, Muriel, Elaine E. Vaughan, Caroline M. Plugge, and Willem M. de Vos. "Akkermansia muciniphila gen. nov., sp. nov., a Human Intestinal Mucin-Degrading Bacterium." *International Journal of Systematic and Evolutionary Microbiology* 54, no. 5 (2004): 1469–1476. <u>https://doi.org/10.1099/ijs.0.02873-0</u>

² Desai, Mahesh S. et al,"A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility." *Cell* 167, no. 5 (2016): 1339–1353.e21. <u>https://doi.org/10.1016/j.cell.2016.10.043</u> ³ Dantas, Gautam. "Do Antibiotics Really Wipe Out Your Digestive Tract Bacteria?" Interview by BBC, August 28, 2023. <u>https://www.bbc.com/future/article/20230825-do-antibiotics-really-</u> wipe-out-your-gut-bacteria

<u>A Focus On Plant Based Nutrients Rather Than Animal</u> <u>Based Proteins</u>

Plant based proteins are often regarded as "incomplete" because many single plant foods lack one or more of the nine essential amino acids in the proportions needed by the human body. However, this view is outdated and misleading. Two principles address this concern: dietary variety and total daily intake.

First, when plant-based foods are consumed in combination—such as grains with legumes (e.g., rice and beans)—they complement each other's amino acid profiles, resulting in a complete protein intake. Second, the human body maintains an amino acid pool and does not require every meal to contain all essential amino acids simultaneously.¹ As long as total intake across the day is adequate, amino acid balance is maintained.

Evidence from the natural world further illustrates this concept. Some of the largest land mammals—elephants, rhinos, hippos, and gorillas—thrive entirely on plant matter. They obtain all essential amino acids by consuming a high volume and wide variety of plantbased foods. In addition, many herbivores host robust gut microbiota that ferment fibrous material and synthesize amino acids and vitamins, which are then absorbed.² Although humans are not strict herbivores, human physiology is capable of extracting and utilizing essential amino acids from wellplanned plant-based diets. Numerous health organizations, including the American Dietetic Association, affirm that appropriately structured vegetarian and vegan diets are nutritionally adequate for all stages of life.^{3,4,5}

Unlike animal protein, which is often high in sulfur-containing amino acids, plant protein is generally accompanied by fiber and phytochemicals that support beneficial gut flora and protective metabolic pathways.

In summary, plant protein is not only sufficient—it offers metabolic advantages when consumed in a diverse and fiber-rich dietary pattern.

REFERENCES:

- ^{1.} Young, Vernon R., and Peter L. Pellett. "Plant Proteins in Relation to Human Protein and Amino Acid Nutrition." The American Journal of Clinical Nutrition 59, no. 5 Suppl (1994): 12035–1212S.
- ² Barabási, Albert-László, et al. "Herbivorous Giants and Microbial Symbiosis: Digestive Strategies in Elephants, Rhinos, and Hippos." Annual Review of Ecology, Evolution, and Systematics 52 (2021): 123– 146.
- ^{3.} American Dietetic Association. "Position of the American Dietetic Association: Vegetarian Diets." Journal of the American Dietetic Association 109, no. 7 (2009): 1266–1282.
- ^{4.} Academy of Nutrition and Dietetics. "Vegetarian Dietary Patterns for Adults: A Position Paper of the Academy of Nutrition and Dietetics."

Journal of the Academy of Nutrition and Dietetics 125, no. 3 (2025): 345–360.

Toxic Metabolic Byproducts of Protein Fermentation in the Gut and Their Carcinogenic Potential

While dietary proteins are essential for human nutrition, excessive or unbalanced intake—especially when not paired with fermentable plant based carbohydrates—can lead to the generation of harmful metabolites in the colon. In the absence of sufficient plant based fiber, gut microbiota shift toward protein fermentation, degrading amino acids into potentially toxic compounds.

Among the key toxic byproducts of animal protein fermentation are:

Ammonia – Ammonia raises colonic pH and can damage epithelial cells, impairing barrier function and promote inflammation.¹

Indoles and Skatole – Derived from the fermentation of tryptophan. These exert cytotoxic and genotoxic effects on the intestinal lining. While some indole derivatives are beneficial in small quantities, others potentially lead to cancer.²

<u>Phenols and p-Cresol</u> – Formed from tyrosine and phenylalanine. These metabolites disrupt mitochondrial function and epithelial cell turnover, and may contribute to DNA damage.³ **Hydrogen Sulfide (H**₂**S)** – Produced from sulfur-containing amino acids such as cysteine and methionine. In high concentrations, H₂S impairs mitochondrial respiration, inhibits butyrate oxidation, and damages DNA. It is increasingly recognized as a potential contributor to colorectal cancer.⁴

Branched-Chain Fatty Acids (BCFAs) – Such as isobutyrate and isovalerate, formed from valine, leucine, and isoleucine. While not directly toxic, they are often markers of excessive protein fermentation and may indicate dysbiosis.⁵

CONCLUSION:

Dietary patterns should aim to balance animal based protein intake with fermentable plant based fiber products to protect gut health and reduce cancer risk.⁶

REFERENCES:

^{1.} Windey, Karen, Kristin De Preter, and Kristin Verbeke. "Relevance of Protein Fermentation to Gut Health." *Molecular Nutrition & Food Research* 56, no. 1 (2012): 184–196.

^{2.} Bansal, Tarun, et al. "Tryptophan Metabolism by Gut Microbiota and Its Role in Brain Function." *International Journal of Molecular Sciences* 23, no. 11 (2022): 6094.

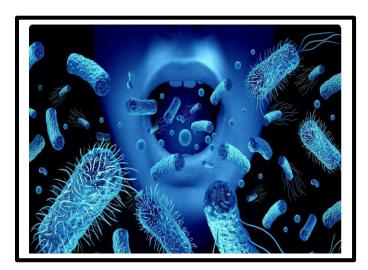
^{3.} Smith, Elizabeth A., and Margaret A. Macfarlane. "Formation of Phenolic and Indolic Compounds by Anaerobic Bacteria in the Human Large Intestine." *Microbial Ecology* 33, no. 3 (1997): 180–188. ^{4.} Carbonero, Franck, et al. "Microbial Hydrogen Sulfide Production in the Gastrointestinal Tract: Implications for Health and Disease." *Current Opinion in Clinical Nutrition and Metabolic Care* 15, no. 6 (2012): 586–592.

^{5.} Davila, Anne-Marie, et al. "Intestinal Luminal Nitrogen Metabolism: Role of the Gut Microbiota and Consequences for the Host." *Pharmacological Research* 68, no. 1 (2013): 95–107.

^{6.} O'Keefe, Stephen J.D. "Diet, Microorganisms and Their Metabolites, and Colon Cancer." *Nature Reviews Gastroenterology & Hepatology* 13, no. 12 (2016): 691–706.



DIGESTIVE TRACT



ORIGINS OF ORAL PATHOLOGY

From birth, the oral cavity is exposed to a constant influx of foreign substances, maintaining it in a pro-inflammatory state. These substances include nutrients, medications, toxins, food additives, and over 770 distinct species of microorganisms.¹ The host immune system manages these exposures, most of which are harmless, though some are pathogenic. With each breath, meal, or drink, billions of microbes—including bacteria, fungi, archaea, viruses, and protozoa—enter the mouth, contributing to the dynamic oral ecosystem.

Microbial Attachments

Once microorganisms enter the oral cavity, their primary objective is to locate "safe havens" for attachment, survival, and replication. These havens include tooth surfaces, gums, the tongue, the mucosal lining, and the gingival sulci (subgingival spaces between gums and teeth).

Microbes utilize specialized structures like pili and fimbriae to adhere to these surfaces, establishing a foothold in the oral environment.

Dental Plaque: The Origin of Periodontal Disease

Microorganisms secrete extracellular polymeric substances (EPS), forming a biofilm called plaque. This sticky protective layer anchors microbes to oral surfaces and shields them from threats such as saliva, enzymes, antibodies, antibiotics, and the host's immune system. Plaqlue accumulates on the teeth and at and below the gum line.

Plaque functions as both a physical barrier and a microbial community, facilitating communication, resource sharing, and genetic exchange that enhance microbial resilience.² If plaque remains undisturbed, it can calcify into tartar (calculus), which requires professional removal through irrigation and debridement.³

During plaque formation, microbial byproducts damage tooth enamel, gum tissues, and supporting bone structures, necessitating continuous control measures to prevent dental and periodontal diseases.⁴

Controlling Microbial Overgrowth in the Oral Cavity

The oral cavity employs several natural defense mechanisms, including antimicrobial peptides in saliva, mechanical cleansing through chewing and swallowing, and immune responses. These defenses help limit microbial overgrowth.

Effective oral hygiene practices—such as brushing with fluoride toothpaste, flossing, using interdental brushes, and periodic dental cleanings—are essential to mitigate plaque buildup and prevent oral inflammation and decay.^{5,6}

The Swallowing of Microorganisms

The number of bacteria in saliva has been calculated to be 100 million (10⁸) bacteria per milliliter.⁷ Studies confirm that adults swallow about 1,000 (10³) milliliters of saliva every 24 hours.⁷ Thus, (10⁸ x 10³) equals 100 billion microbes reaching the stomach every 24 hours—a staggering number. This number may be significantly more in individuals with oral pathology, including gingivitis, dental decay, or periodontitis.

The Oral "Arms Race"

A perpetual battle exists in the oral cavity between microbial colonization and the body's defense mechanisms. Dental restorations—such as cavity fillings, crowns, and root canals—symbolize past battles where microbes temporarily overcame host defenses.

Challenges in Plaque Control

Many individuals fail to adopt sufficient plaque control measures. While brushing is critical, it alone is insufficient; significant plaque often remains even after several minutes of brushing.⁸ This underscores the need for a comprehensive oral hygiene routine.

STRATEGIES FOR EFFECTIVE ORAL HYGIENE

BRUSHING

- Brush at least twice daily using a fluoride containing toothpaste for at least two minutes each time.
- Oscillating or sonic toothbrushes are at least ten times more effective than manual toothbrushes for removing plaque.



FLOSSING

 Floss daily (ideally after each meal and at bedtime) to remove plaque and food particles between teeth and along the gumline. If flossing is only done once a day, it should be at bedtime. Dental tape can be particularly effective for tightly spaced teeth.



WATER IRRIGATION

 Water flossers, like Water Pik,[®] dislodge debris and reduce plaque, especially for individuals with braces or dental implants.



INTERDENTAL BRUSHES

 These small brushes clean between teeth where floss and toothbrushes may not reach. They are particularly useful for braces, bridges, and implants.



MOUTHWASHES



Mouthwash is not a substitute for brushing and flossing but can serve as an adjunctive therapy that enhances oral hygiene by reducing microbial load, delivering therapeutic agents, and reaching areas that may be inaccessible with a toothbrush or floss. Its effectiveness depends on its active ingredients, the condition being treated, and its use in combination with other hygiene practices.

Types of Mouthwashes: Advantages and Disadvantages

Cautionary Note on Mouthwash Use:

Although mouthwashes are widely marketed as long-lasting solutions for oral hygiene, their actual efficacy may be overstated. **Commercial advertisements often suggest that these products can** eliminate pathogenic oral microbes for up to 24 hours. However, this claim is highly questionable, as dental plaque is continuously produced by microbial communities that reside in protected niches—such as below the gum line, within periodontal pockets, and in the microscopic crevices of dental surfaces—areas largely inaccessible to rinsing agents. These resilient microbial populations can persist and proliferate despite the temporary antimicrobial effects of mouthwash. Therefore, while mouthwashes may offer transient benefits such as reducing oral malodor or delivering topical fluoride, they should not be viewed as substitutes for mechanical plaque control through regular brushing, flossing and visits to a dental professional for dental cleanings. A balanced perspective is warranted, recognizing that mouthwash can be a

useful adjunct but not a standalone solution for maintaining oral health.

1. Chlorhexidine Gluconate (Prescription):

Chlorhexidine gluconate is a potent antimicrobial agent commonly prescribed for the management of severe gingivitis, periodontal disease, or following dental surgeries.¹ While highly effective, its use requires careful adherence to professional instructions due to potential side effects such as tooth staining, altered taste perception, and mucosal irritation.

2. Essential Oils (Over-the-Counter, OTC):

Essential oils such as menthol, thymol, and eucalyptol—found in many widely available mouthwashes (e.g., Listerine^{®)}—possess antimicrobial and anti-inflammatory properties.² These formulations provide modest reductions in plaque and gingival inflammation and are generally well tolerated, with fewer side effects than prescription agents.

3. Cetylpyridinium Chloride (OTC):

CPC is a quaternary ammonium compound with antibacterial activity, incorporated into various OTC mouthwashes (e.g., Crest Pro-Health[®], Colgate Total[®]) to help reduce plaque accumulation and gingivitis. While less potent than prescription antimicrobials, CPC-containing products offer a useful adjunct for daily oral hygiene.

4. Hydrogen Peroxide (OTC):

Hydrogen peroxide is an oxygen-releasing antiseptic with

antibacterial properties and mild tooth-whitening effects.³ It is particularly appealing for individuals seeking additional cosmetic benefits while also reducing anaerobic bacterial load.

SELF-SCALING

 With proper technique, individuals can practice self-scaling, though professional scaling is necessary for thorough tartar removal.



REFERENCES:

- ^{1.} Van Strydonck, Dirk A. C., M. F. Timmerman, D. E. Slot, U. Van der Velden, and G. A. Van der Weijden. "Chlorhexidine Mouthrinse in the Prevention of Dental Caries: A Systematic Review." *Journal of Dental Research* 91, no. 5 (2012): 426–432.
- ^{2.} Berchier, C. E., et al. "The Efficacy of Essential Oil Mouthwashes in Preventing Plaque and Gingivitis: A Systematic Review." *Journal of Clinical Periodontology* 35, no. 2 (2008): 277–85.

^{3.} Li, Yiming. "The Role of Hydrogen Peroxide in Oral Health: A Review." Journal of Dentistry 39, no. 8 (2011): 585–92.

PROFESSIONAL DENTAL CARE

Regular dental cleanings and scaling, ideally more frequently than every six months for high-risk individuals, are critical for managing plaque and tartar.



A LIFELONG COMMITMENT TO PLAQUE CONTROL

Plaque formation is continuous, making its control a lifelong commitment essential for oral health and overall well-being. A comprehensive approach—including daily oral hygiene practices and professional care—significantly reduces the risk of dental and gum diseases while promoting long-term digestive health¹. Ng, E., and J. K. F. Suen. "Oral Health: The First Step to Well-Being." *Medicina* 55, no. 10 (2019): 676. <u>https://doi.org/10.3390/medicina55100676.</u>

DENTAL PLAQUE

THE ORIGIN OF TEETH AND GUM DISEASE



Gum disease, dental cavities, and halitosis share a fundamental cause: an abnormal microbial load in the oral cavity. The mouth is home to a diverse microbial ecosystem, but an imbalance in this community—often favoring pathogenic organisms—can lead to significant oral health problems. Proper oral hygiene, including brushing, flossing, water flushing, scaling, mouthwashes and regular dental visits, remains the cornerstone of maintaining a healthy oral environment.

Microbial Imbalance and Oral Health Problems

The oral cavity serves as an entry point to the digestive and respiratory tracts and is constantly exposed to external microbial invaders. It also hosts billions of resident microbes, many of which form biofilms on teeth, gums, and the tongue. While a balanced microbial community is essential for oral health, an overgrowth of pathogenic species can contribute to:

- 1. <u>Gum Disease</u> (Periodontitis and Gingivitis): Pathogens such as *Porphyromonas gingivalis, Tannerella forsythia,* and *Treponema denticola* are associated with chronic gum inflammation, tissue destruction, and eventual tooth loss.¹
- Dental Cavities (Caries): Bacteria like Streptococcus mutans and Lactobacillus spp. metabolize dietary sugars into acids, which erode enamel and cause cavities.²
- 3. <u>Halitosis</u> (Bad Breath): Volatile sulfur compounds (VSCs) produced by anaerobic bacteria such as *Fusobacterium nucleatum* and *Prevotella intermedia* contribute to unpleasant odors.³

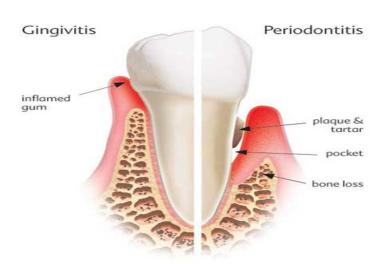
Addressing these issues requires strategies to control microbial growth.

ORAL PATHOLOGY

Diseases Of Epidemic Proportions

As of 2015, the global burden of untreated oral conditions affected 3.5 billion people, representing half of the world's population. Among these, 538 million individuals suffered from severe gum (periodontal) disease¹.

In the United States, the Centers for Disease Control and Prevention (CDC) reported that gum disease (periodontitis) affected 42% of adults over the age of thirty². By age sixty-five, 70% of adults experienced mild to severe periodontitis. These figures have continued to rise alongside population growth and an aging demographic.



Introduction To Periodontal Disease

Periodontal disease is a chronic inflammatory condition initiated by microbial pathogens that destroy the structure of supporting teeth. In addition to the loss of clinical attachment, periodontal disease is characterized by gingival bleeding, gum recession, and the development of periodontal pockets. As the disease progresses, tooth mobility and loss may occur if left untreated. Tooth loss can lead to chewing dysfunction, speech alterations, compromised nutritional status, and a decline in personal quality of life.

PERIODONTAL DISEASE FOLLOWS A CONTINUM

- Gingivitis
- Receding Gums
- Formation of Periodontal Pockets
- Periodontitis
- Local and systemic spread

INFLAMMATION AND GUM DISEASE

(Gingivitis: An Early Stage of Gum Disease)



Gingivitis is characterized by reddening of the gums at the margin between the teeth and gums, swelling of the gum tissue, and bleeding with brushing and/or flossing. Gingivitis is treatable and reversible with vigorous oral hygiene measures.³ Untreated gingivitis, however, may progress to deeper levels of inflammation—periodontitis.

Dr. Iain Chapple, professor of periodontology and head of research at the Institute of Clinical Sciences of the University of Birmingham in the United Kingdom, makes the following point:

"It is time for a paradigm shift: we must control gingivitis and not wait until periodontitis develops. . . There is the need to focus attention on the prevention of periodontitis and, therefore, adequately treat gingivitis, a previous stage of the disease characterized by inflammation and bleeding gums."

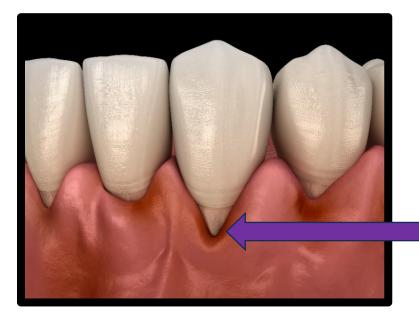
REFERENCES:

¹ GBD 2015 Disease and Injury Incidence and Prevalence Collaborators. (2016). "Global, Regional, and National Incidence, Prevalence, and Years Lived With Disability for 310 Diseases and Injuries, 1990–2015: A Systematic Analysis for the Global Burden of Disease Study 2015." *The Lancet*, 388(10053), 1545–1602. <u>https://doi.org/10.1016/S0140-</u> <u>6736(16)31678-6</u>

² Eke, P. I., et al. (2018). "Periodontitis in U.S. Adults: National Health and Nutrition Examination Survey 2009–2014." *Journal of the American Dental Association*, 149(7), 576–588.e6. https://doi.org/10.1016/j.adaj.2018.04.023 ³ van der Weijden, F. A., & Slot, D. E. (2015). "Efficacy of Homecare Regimens for Mechanical Plaque Removal in Managing Gingivitis: A Meta-Review." *Journal of Clinical Periodontology*, 42(Suppl 16), S77–S91. <u>https://doi.org/10.1111/jcpe.12359</u>

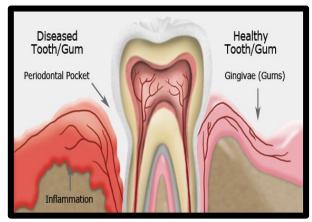
RECEDING GUMS

In response to inflammation, gums pull away from the tooth exposing the root. This process is known as receding gums.



As gums pull away, they form a pocket between the gum and the tooth. These pockets become *incubators* for the proliferation of millions— and frequently billions—of microorganisms.

PERIODONTAL POCKETS



Microbes within periodontal pockets can damage local tissues and destroy the attachments of the tooth to the jawbone resulting in loss of teeth. Failure to control the proliferation of microbes in the gum surfaces leads to deeper levels of gum inflammation, i.e., periodontitis.

Diagnosing Gum Disease: The dentist or dental hygienist can measure the depth of periodontal pockets around each tooth using a special dental ruler. The depth correlates with the severity of infection. The dentist or dental hygienist can also note whether the gum tissue below the gum line is inflamed enough to cause bleeding, i.e., bleeding on probing (B.O.P.).

A Second form of Periodontitis-- Apical Periodontitis

Apical periodontitis is an infection that originates *inside the tooth*, specifically in the pulp tissue at its center. This is where the tooth's nerve and blood supply live. When bacteria invade this area often because of a deep cavity (decay) or trauma to the tooth—the pulp becomes inflamed or dies. The infection can then spread through the root canal system to the tip (apex) of the root and into the jawbone.

The result is a localized infection at the root tip, causing pain when biting, sensitivity to pressure, or swelling in the surrounding area. Unlike periodontitis, apical periodontitis doesn't begin in the gums but within the tooth itself.

Feature	Periodontitis	Apical Periodontitis
Origin	Outside the tooth—begins in the gums	Inside the tooth—begins in the pulp
Cause	Microbial biofilm around gums and root surfaces	Deep decay, trauma, or cracked tooth
Pathology	Loss of gum attachment and bone support	Infection and inflammation at the root tip
Common Signs	Red, bleeding, receding gums; loose teeth	Pain when chewing, swelling, abscess formation
Dental Exam Findings	Periodontal pocketing, bleeding on probing	Pain to percussion, visible infection on X-ray
Treatment	Deep cleaning, possible gum surgery	Root canal therapy or tooth extraction
Specialist Involved	Periodontist	Endodontist

Key Differences Between the Two Conditions

How These Conditions Are Treated?

Treating Periodontitis

Treatment focuses on removing bacterial deposits from the gums and tooth surfaces. This may involve:

- Professional cleaning and deep scaling below the gumline
- Use of antimicrobial rinses or localized antibiotics
- Gum surgery to reduce deep pockets
- Maintenance with excellent home care—brushing, flossing, and regular checkups

Treating Apical Periodontitis

Because the infection is deep inside the tooth, cleaning the outside won't help. Treatment usually involves:

- A root canal, where a dentist or endodontist cleans out the infected pulp tissue and seals the tooth
- In some cases, tooth extraction if the damage is too extensive
- Antibiotics may be used if the infection has spread

Why Understanding the Difference Matters

Both periodontitis and apical periodontitis can lead to tooth loss, but they follow very different paths. Misunderstanding these conditions can lead to delays in treatment or the wrong kind of care. For example, using mouthwash might help reduce gum bacteria in periodontitis but is not particularly helpful for apical periodontitis, which requires internal treatment.

Also important to note: one can have both conditions at the same time. For example, a person with long-standing gum disease may also develop a cavity that leads to apical infection. Proper dental evaluation, including X-rays and probing, is essential to distinguish the two.



Dangers Of Periodontitis:

One of the major pathogenic organisms that cause periodontitis is *Porphymonas gingivalis (Pg). Pg* is a virulent organism resistant to antibiotics. *Pg* also can resist destruction by stomach acid and can avoid being destroyed by the human immune system.

Major virulence factors of *Pg* are protein dissolving chemicals (proteinases) contained in vesicles that *Pg* expresses from its

surface. These chemicals are known as "gingipains"¹. The production of gingipains is unique to *Pg*.

Gingipains participate in the ability of the organism to adhere to and colonize lining tissues, coagulate blood, breakdown red blood cells, and disrupt the protective immune response.

Systemic Dissemination of Porphyromonas gingivalis and Its Presence in Distant Organs

Porphyromonas gingivalis (Pg), a Gram-negative anaerobe and key pathogen in periodontal disease, has been increasingly implicated in systemic pathologies due to its ability to translocate from the oral cavity to distant organs via spread through the blood stream. Studies have demonstrated its presence in several non-oral tissues, where it contributes to chronic inflammation, immune dysregulation, and tissue-specific pathogenesis.

<u>1. Brain</u>

Pg has been identified in the hippocampus and cortex of patients with Alzheimer's disease. Gingipain proteases produced by Pg are neurotoxic and contribute to tau hyperphosphorylation and neurodegeneration.²⁻⁶

2. Heart

Pg has been found in cardiac tissues of individuals with atherosclerosis and infective endocarditis. It promotes myocardial fibrosis and may elevate the risk of atrial fibrillation.^{7,8,9}

3. Liver

Pg DNA has been detected in liver tissue in animal models, where it induces hepatic inflammation and steatosis, possibly contributing to metabolic associated steatotic liver disease (MASLD).¹⁰

4. Pancreas

Pg has been detected in pancreatic tissues and is associated with inflammation and oncogenesis in pancreatic cancer.¹¹

5. Placenta and Amniotic Fluid

Pg has been isolated from placental tissues, amniotic fluid, and the chorioamnion, and is implicated in adverse pregnancy outcomes including preterm birth and fetal growth restriction.¹²

6. Joints

Pg DNA has been found in synovial fluid of patients with rheumatoid arthritis. It contributes to autoantigen generation through citrullination and may trigger autoimmune pathways.¹³

7. Lungs

Pg has been recovered from the respiratory tract in cases of aspiration pneumonia and chronic bronchitis. It contributes to biofilm formation and local immune disruption.¹⁴

REFERENCES:

¹ Li, N. (2011). "Gingipains From *Porphyromonas gingivalis*—Complex Domain Structures Confer Diverse Functions." *European Journal of Microbiology and Immunology*, 1(1), 41–58. <u>https://doi.org/10.1556/EuJMI.1.2011.1.7</u>

² Li, R., Wang, J., Xiong, W., Luo, Y., Feng, H., Zhou, H., Peng, Y., He, Y., & Ye, Q. (2024). "The Oral-Brain Axis: Can Periodontal Pathogens Trigger the Onset and Progression of Alzheimer's Disease?" *Frontiers in Microbiology*, 15, Article 1358179. <u>https://doi.org/10.3389/fmicb.2024.1358179</u>

³ Wu, H., et al. (2022). "The Periodontal Pathogen *Fusobacterium nucleatum* Exacerbates Alzheimer's Pathogenesis Via Specific Pathways." *Frontiers in Aging Neuroscience*, 14, Article 912709. <u>https://doi.org/10.3389/fnagi.2022.912709</u>

⁴ Dominy, S. S., et al. (2019). "*Porphyromonas gingivalis* in Alzheimer's Disease Brains: Evidence for Disease Causation and Treatment With Small-Molecule Inhibitors." *Science Advances*, 5(1), eaau3333. <u>https://doi.org/10.1126/sciadv.aau3333</u>

⁵ Wei, S., et al. "Outer Membrane Vesicles Enhance Tau Phosphorylation and Contribute to Cognitive Impairment." *Journal of Cellular Physiology* 235, no. 6 (2020): 4843–4855.

⁶ Gong, T., et al. (2022). "Outer Membrane Vesicles of *Porphyromonas gingivalis* Trigger NLRP3 Inflammasome and Induce Neuroinflammation, Tau Phosphorylation, and Memory Dysfunction in Mice." *Frontiers in Cellular and Infection Microbiology*, 12, Article 925435. https://doi.org/10.3389/fcimb.2022.925435

⁷ Iwai, T. et al. "Involvement of Porphyromonas gingivalis in the development of atherosclerosis in apoE-deficient mice." Oral Microbiology and Immunology 20, no. 5 (2005): 318–23.

⁸ Shunsuke Miyauchi et al., "Atrial Translocation of *Porphyromonas gingivalis* Exacerbates Atrial Fibrosis and Atrial Fibrillation," *Circulation* 151, no. 12 (2025): 992–996,

https://doi.org/10.1161/CIRCULATIONAHA.124.071310.

⁹ Shunsuke Miyauchi et al., "Periodontitis and the Outcome of Atrial Fibrillation Ablation: *Porphyromonas gingivalis* Is Related to Atrial Fibrillation Recurrence," *Journal of Cardiovascular Electrophysiology* 32, no. 5 (2021): 1240–1250, <u>https://doi.org/10.1111/jce.14952.</u>

¹⁰ Yoneda, M. et al. "Involvement of A Periodontal Pathogen, *Porphyromonas Gingivalis* On The Pathogenesis of Non-Alcoholic Fatty Liver Disease." *BMC Gastroenterology* 12 (2012): 16. <u>https://doi.org/10.1186/1471-230X-12-16.</u>

¹¹ Fan, X. et al. "Human Oral Microbiome and Prospective Risk For Pancreatic Cancer: A Population-Based Nested Case–Control Study." *Gut* 67, no. 1 (2018): 120–127.

¹² Fardini, Y. et al. "Transmission of diverse oral bacteria to murine placenta: evidence for the oral microbiome as a potential source of intrauterine infection." Infection and Immunity 78, no. 4 (2010): 1789–96. <u>https://doi.org/10.1128/IAI.01395-09.</u>

¹³ Mikuls, T. R. et al. *"Porphyromonas gingivalis* and Disease-Related Autoantibodies In Individuals at Increased Risk of Rheumatoid Arthritis." *Arthritis & Rheumatism* 65, no. 4 (2013): 854–63.

¹⁴ Kholy, K. E., Genco, R. J., and Van Dyke, T. E. "Oral Infections And Cardiovascular Disease." *Trends in Endocrinology & Metabolism* 26, no. 6 (2015): 315–21.

Treatment Methods For Gum Disease:

The treatment of periodontal disease may be done by a dentist or a periodontist, i.e., a dentist who specializes in the diagnosis and treatment of gum diseases.

The goal of treatment is to thoroughly clean the pockets around the teeth to prevent damage to the surrounding gum tissue and bone and to remove the biofilm of plaque on the teeth and gums.

The removal of plaque and tartar by dental professionals is usually prescribed for initial stages of periodontitis. The more advanced stages may require deep scaling of teeth beneath the gum line, gum surgery to reduce bacterial deposits beneath the gums and other specialized techniques to reduce the microbial load in the tissue.

Vigorous personal oral hygiene routines are critical for preventing the accumulation of microorganisms in the mouth. Regular brushing and flossing along with the use of interdental brushes and the use of mouth rinses can reduce the risk of developing teeth and gum disease.

THE DANGERS OF SIMPLE SUGARS

Impact on Oral Health

One of the primary threats to oral health is the presence of simple sugars in the mouth, which can be metabolized by microbes like *Streptococcus mutans*. These bacteria convert sugars into acids,

leading to tooth decay and gum disease. Effective strategies to reduce the contact of sugars with these microbes are essential for preventing oral-dental pathology.

Strategies for Reducing Sugar Impact

Simple sugars such as those found in candy, soda, and other sugary foods provide an ideal substrate for the bacteria Streptococcus mutans and similar bacteria. When these bacteria metabolize sugars, they produce lactic acid as a byproduct. This acid demineralizes tooth enamel, leading to dental decay and contributes to the inflammation of gum tissues, which can result in gingivitis and periodontitis.

Avoiding Sugary Foods and Confections

One effective strategy to combat this problem is to limit the intake of sugary foods and beverages. Particularly avoiding sticky confections like gumdrops and caramels or prolonged contact with sugar-containing mints and gum. These types of confections provide a prolonged supply of sugar for bacteria, thereby increasing the risk of acid production and subsequent tooth decay.

Use of Sugar Substitutes

Using sugar substitutes such as xylitol can also be beneficial. Unlike simple sugars, xylitol is not metabolized by *S. mutans*, thereby reducing acid production. Xylitol-containing gums and mints can stimulate saliva flow, which helps to wash away food particles and neutralize acids in the mouth.

THE ROLE OF SALIVA

<u>The Dangers Associated with Reduced Salivary Flow Bathing</u> <u>the Teeth and Gums</u>

As pointed out earlier in this Digestive Health Guide, those who wear dentures, use Invisalign[®] appliances, have dental braces, wear night guards, or any other dental device that shields their teeth create barriers that prevent the teeth and gums from being adequately bathed in antimicrobial saliva—a natural defense that helps control microbial proliferation in the mouth. When the protective effect of saliva is diminished, it can lead to a proinflammatory environment, increasing the risk of oral infections, gum disease, and even systemic illnesses.

Saliva production can also be reduced in those individuals taking antihistamines, or in those who have undergone salivary gland surgery, head, and neck radiation therapy, received chemotherapy, or had autoimmune conditions like Sjogren's sicca syndrome.

Reduced saliva production impairs the mouth's ability to manage harmful microbes, leading to significant oral pathologies and potentially contributing to broader health issues.

THE DANGERS OF MICROBE TRANSMIGRATION



In addition to localized gum and teeth damage, transmigration of microbes from periodontal pockets can take place. This movement of pathogenic organisms from the mouth to adjacent tissues can cause inflammation and infection.

Adjacent tissues that may be affected by extensive exposure to pathogenic microorganism include Eustachian tubes that drain the middle ear, nasal cavity which drains facial sinuses, lacrimal ducts that drain tears from the eyes, salivary glands, and tonsillar tissue.

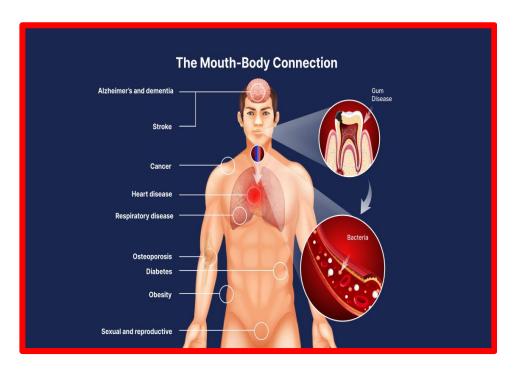
Signs And Symptoms of Adjacent Spread: Signs and symptoms of microbe transmigration to adjacent tissues may include recurrent sinus inflammation, nasal pathology, salivary gland dysfunction,

headaches, earaches, facial pain, loss of hearing, chronic sore throat, and burning mouth and tongue.

Spread Through Blood And Lymph Tissue: In addition to nearby movement of microorganisms, oral cavity microorganisms can pass into the bloodstream and lymph tissues allowing the microbes to travel throughout the body and infect pacemakers, heart valves, joint implants, catheters, implanted drug delivery devices, and more.

Spread By Swallowing Microbes: Billions of microorganisms that are produced every 24 hours in periodontal pockets are also swallowed, potentially causing symptoms like chronic sore throat, chest pain, heartburn, difficulty swallowing, nausea, vomiting, stomach pains, overgrowth of microbes in the small intestine, malabsorption, vitamin deficiencies, diarrhea and/or constipation, abdominal bloating, abdominal distention, eructation, flatulence, and weight loss.

SECTION TWENTY-ONE ASSOCIATIONS OF ORAL CAVITY DISEASE WITH OTHER BODY ILLNESSES



Numerous chronic conditions in the body have been <u>associated</u> with oral cavity inflammation including the following: cardiovascular disease,^{1,2} neurologic disease,³ bone disease,⁴⁻⁵ liver disease,⁶⁻⁸ cancer,⁹⁻¹¹ kidney disease ¹²⁻¹³ lung disease,¹⁴⁻¹⁵ Alzheimer's dementia, ¹⁶⁻¹⁸ Rheumatoid arthritis,¹⁹ COVID outcomes,²⁰⁻²¹ macular degeneration,²² adverse outcomes of pregnancy,²³ benign prostatic hyperplasia,²⁴ skin diseases, ²⁵ and cryptogenic ischemic stroke before the age of 50.²⁶

REFERENCES

Cardiovascular Disease

^{1.} Sanz, M., et al. "Periodontitis and Cardiovascular Diseases: Consensus Report." *Journal of Clinical Periodontology* 47, no. 3 (2020): 268–288. <u>https://doi.org/10.1111/jcpe.13189.</u> ^{2.} Castillo, A. "Periodontitis and Cardiovascular Disease: Consensus Report." *Journal of Clinical Periodontology* 47, no. 3 (2020). <u>https://doi.org/10.1111/jcpe.13189.</u>

Neurologic Disease

^{3.} Li, X. "Neuroinflammation: A Distal Consequence of Periodontitis." Journal of Dental Research 101, no. 12 (2022): 1441–1449.

Bone Disease

- ^{4.} Jayusman, P. "Overview on Postmenopausal Osteoporosis and Periodontitis: Therapeutic Potential of Phytoestrogens Against Alveolar Bone Loss." *Frontiers in Pharmacology* 14 (2023).
- Yu, B. "Osteoporosis and Periodontal Diseases—An Update on Their Association and Mechanistic Links." *Periodontology 2000* 89, no. 1 (2021): 99–113.

Liver Disease

- ^{6.} Gao, Y. "Porphyromonas gingivalis Exacerbates Alcoholic Liver Disease by Altering Digestive Tract Microbiota Composition and Host Immune Response in Mice." *Journal of Clinical Periodontology* 50, no. 9 (2023): 1056–1067.
- ^{7.} Costa, F. O. "Periodontitis in Individuals with Liver Cirrhosis: A Case-Control Study." *Journal of Clinical Periodontology* 46, no. 10 (2019): 991– 998.
- ^{8.} Han, P. "Interaction Between Periodontitis and Liver Diseases." *Biomedical Reports* 5, no. 3 (2016): 267–276.

Cancer

- ^{9.} Nasiri, K. "Periodontitis and Progression of Gastrointestinal Cancer: Current Knowledge and Future Perspective." *Clinical and Translational Oncology* 25 (2023): 2801–2811.
- ^{10.} Janati, A. "Periodontal Disease as a Risk Factor for Sporadic Colorectal Cancer: Results from COLDENT Study." *Cancer Causes & Control* 33, no. 3 (2022): 463–472.
- ^{11.} Jingru, Y. "Poor Dental Health and Risk of Pancreatic Cancer: A Nationwide Registry-Based Cohort Study in Sweden, 2009–2026." *British Journal of Cancer* 127 (2022): 2133–2140.

Kidney Disease

- ^{12.} Ling, L. "Periodontitis Exacerbates and Promotes the Progression of Chronic Kidney Disease Through Oral Flora, Cytokines, and Oxidative Stress." *Frontiers in Microbiology* 12 (2021): 663426.
- ^{13.} Sharma, P. "Association Between Periodontitis and Mortality in Stages 3–
 5 Chronic Kidney Disease: NHANES III and Linked Mortality Study." *Journal of Clinical Periodontology* 43, no. 2 (2016): 104–113.

Lung Disease

- ^{14.} Bansal, M. (2013). Potential role of periodontal infection in respiratory disease—A review. *Journal of Medicine and Life, 6*(3), 244–248.
- ^{15.} Xiong, K. "Research on the Association Between Periodontitis and COPD." International Journal of Chronic Obstructive Pulmonary Disease 18 (2023): 1937–1948.

Alzheimer's Dementia

^{16.} Na, H. S., Jung, N. Y., Song, Y., Kim, S. Y., Kim, H. J., Lee, J. Y., & Chung, J. "A Distinctive Subgingival Microbiome in Patients with Periodontitis and Alzheimer's Disease Compared with Cognitively Unimpaired Periodontitis Patients." *Journal of Clinical Periodontology* 51, no. 1 (2024): 43–53.

- ^{17.} Wu, D., & Yang, Y. "The Link Between Periodontitis and Alzheimer's Disease—Emerging Clinical Evidence." *Dentistry Review* 3, no. 1 (2023): 100071.
- ^{18.} Kanagasingam, S., Chukkapalli, S. S., Welbury, R., Singhrao, S. K., & Crean, S. J. "Porphyromonas gingivalis is a Strong Risk Factor for Alzheimer's Disease." *Journal of Alzheimer's Disease Reports* 4, no. 1 (2020): 501–511.

Rheumatoid Arthritis

¹⁹ Kobayashi, T., & Yoshie, H. "Periodontitis and Periodontopathic Bacteria as Risk Factors for Rheumatoid Arthritis: A Review of the Last 10 Years." *Japanese Dental Science Review* 59 (2023): 263–272.

COVID-19 Outcomes

²⁰ Marouf, N., Cai, W., Said, K. N., Daas, H., Diab, H., Chinta, V. R., & Alazawi, W. (2021). "Association Between Periodontitis and Severity of COVID-19 Infection: A Case–Control Study." *Journal of Clinical Periodontology*, 48(4), 483–491. <u>https://doi.org/10.1111/jcpe.13435</u>

²¹ Al-Maweri, S. A., Halboub, E., Al-Soneidar, W. A., & Al-Sufyani, G. A.
"The Impact of Periodontal Disease on the Clinical Outcomes of COVID-19: A Systematic Review and Meta-Analysis." *BMC Oral Health* 23, no. 1 (2023): 658.

Macular Degeneration

²² Pachiappan, A., & Muthukkaruppan, V. "Invasion of Human Retinal Pigment Epithelial Cells by Porphyromonas gingivalis Leading to Vacuolar/Cytosolic Localization and Autophagy Dysfunction In Vitro." *Scientific Reports* 10, no. 1 (2020): 7468.

Adverse Pregnancy Outcomes

²³ Nannan, M., & Xue, L. "Periodontal Disease in Pregnancy and Adverse Pregnancy Outcomes: Progress in Related Mechanisms and Management Strategies." *Frontiers in Medicine* 9 (2022): 842814.

Benign Prostatic Hyperplasia

²⁴ Wang, S.-Y., and J. Zhang. "Porphyromonas gingivalis in Oral–Prostate Axis Exacerbates Benign Prostatic Hyperplasia via IL-6/IL-6R Pathways." *Military Medical Research*, 2024.

<u>Skin Diseases</u>

²⁵ Di Stefano, M., Alessandro Polizzi, S. Santonocito, Alessandra Romano, T. Lombardi, and G. Isola. "Impact of Oral Microbiome in Periodontal Health and Periodontitis: A Critical Review on Prevention and Treatment." *International Journal of Molecular Sciences* 23, no. 9 (2022): 5142. https://doi.org/10.3390/ijms23095142.

Cryptogenic Ischemic Stroke

²⁶ Leskelä, J., Niskanen, M., Pohjasvaara, T., Kautiainen, H., & Erkinjuntti, T. "Periodontitis, Dental Procedures, and Young-Onset Cryptogenic Stroke." *Journal of Dental Research* 103, no. 5 (2024): 494–500. https://doi.org/10.1177/00220345241232406.

HAS A CAUSAL RELATIONSHIP BETWEEN PERIODONTITIS AND OTHER CHRONIC SYSTEMIC DISEASES BEEN SCIENTIFICALLY ESTABLISHED?

The inflammatory mediators released during periodontal infections, such as cytokines and prostaglandins, can enter the

bloodstream, contributing to systemic inflammation and promoting the development of systemic health complications.

A comprehensive view grading the strength and certainty of the scientific evidence of the bidirectional association between periodontitis and non-communicable system illnesses shows there to be varying degrees of association but low to very low degrees of certainty proving periodontitis as a potential risk factor for system illnesses and *vice a versa*.

Bidirectional relationships mean that the existence of one condition might influence the severity or progression of the other. In 2016, a source related to periodontal measures reported 57 systemic conditions hypothetically associated with periodontitis[.]

Cardiovascular, diabetes and adverse pregnancy outcomes provided abundant evidence. Other diseases included anemia, liver disease, dyspepsia and ankylosing spondylitis.

These disorders are caused by a mix of genetic, physiological, environmental, and behavioral factors. Tobacco use, physical inactivity, a poor diet, and excessive alcohol consumption all contribute to metabolic alterations such as hypertension, obesity, hyperglycemia, and hyperlipidemia. The methodology, quality and scope of the findings, however, resulted in a wide range of results and recommendations making it hard to identify the most relevant high quality data for arriving at an evidence-based disease. In 2016, Monsarrat and coworkers conducted a search related to periodontal medicine and reported that 57 systemic conditions have hypothetically been associated with periodontitis[.] Only in 9 conditions was the evidence for association moderate to strong.¹

Associations, thus, <u>do not</u> equate to causation, and the precise relationships between oral cavity inflammation and physical ailments in other parts of the body remain incompletely understood and, at times, contentious.

REFERENCE:

Monsarrat, Pierre, Jean-Louis Blaizot, Jean-Pierre Kémoun, Jean-Pierre Ravaud, Philippe Nabet, Jean-Marc Sixou, and Philippe Vergnes. 2016. "Clinical Research Activity in Periodontal Medicine: A Systematic Mapping of Trial Registrations." *Journal of Clinical Periodontology* 43 (5): 390–400. <u>https://doi.org/10.1111/jcpe.12534</u>.



GENERAL RECOMMENDATIONS MOUTH



SELECTING THE RIGHT TOOTHBRUSH

Brush with either a sonic or oscillating toothbrush. Both are superior to brushing manually with a bristle toothbrush. Two leading brands of electronic toothbrushes are Sonicare[®] and Oral B[®]. The Sonicare[®] brush operates by sonic technology and the Oral B[®] by oscillation.



When comparing sonic and oscillating toothbrushes, both offer unique advantages depending on oral health needs and preferences of the purchaser.

Sonic Toothbrush Advantages

1. <u>High Vibrational Speed</u>: Sonic toothbrushes, like Sonicare[®], typically vibrate at an extremely high frequency, often up to 31,000 strokes per minute. This high-speed vibration can effectively break up plaque and remove food particles.

Sonic toothbrushes have been shown to be highly effective in reducing plaque and improving gingival health due to their high vibrational speed. A systematic review highlighted the efficacy of

sonic toothbrushes in improving oral health compared to manual brushing.¹

- 2. Fluid Dynamics: The rapid movement of the bristles in sonic toothbrushes creates dynamic fluid forces that can reach areas beyond where the bristles physically touch, potentially improving cleaning in hard-to-reach areas like between teeth and along the gumline.
- 3. <u>Gentle on Gums</u>: Research indicates that sonic toothbrushes are gentler on gums compared to oscillating toothbrushes, making them an excellent choice for individuals with sensitive gums or those prone to gum recession.
- 4. <u>Variety of Modes</u>: Many sonic toothbrushes come with multiple brushing modes, such as sensitive, whitening, or gum care, allowing users to customize their brushing experience.
- 5. <u>Effective Plaque Removal</u>: Studies have shown that sonic toothbrushes can be highly effective at reducing plaque and improving gum health over time.
- Whitening Effect: Some users report that the high-frequency vibrations of sonic brushes help to reduce surface stains on teeth, leading to a whitening effect.

REFERENCE:

¹ Dhir, Sangeeta, and Ankur Gupta. 2018. "Efficacy of Oscillating–Rotating Toothbrush (Oral-B) on Periodontal Health – A 4-Week Controlled Clinical and Microbiologic Study." *Journal of the International Clinical Dental Research Organization* 10 (3): 121–126.

OSCILLATING TOOTHBRUSH ADVANTAGES

- Rotating-oscillating Action: Oscillating toothbrushes, such as those made by Oral-B[®], feature a rotating and oscillating head that moves back and forth in a circular motion. This action is particularly effective at dislodging plaque from the surface of the teeth.¹
- 2. <u>Smaller Brush Head</u>: The smaller, round brush head of an oscillating toothbrush can be easier to maneuver around each tooth, allowing for more precise cleaning, especially in hard-to-reach areas like molars.
- 3. <u>Affordability</u>: Oscillating toothbrushes are often more affordable than sonic toothbrushes, making them a cost-effective option for many users.
- 4. Effective for Plaque and Gingivitis: Research has shown that oscillating toothbrushes can be particularly effective at reducing plaque and gingivitis, sometimes even outperforming manual, and sonic brushes in clinical studies.

- 5. <u>Variety of Brush Heads</u>: Oscillating toothbrushes often have a variety of interchangeable brush heads designed for diverse needs, such as sensitive teeth, deep cleaning, or orthodontic care.
- 6. **Pressure Control:** The use of pressure sensors in oscillating toothbrushes helps in preventing over-brushing, which can damage enamel and gums.

REFERENCE:

Yaacob, M. (2019). "Powered Versus Manual Toothbrushing for Oral Health." Cochrane Database of Systematic Reviews, 12(1), CD002281. https://doi.org/10.1002/14651858.CD002281.pub3

Brush your tongue or use a tongue scraper every time you brush your teeth.



- Change the tip of the sonic or oscillating toothbrush at one-tothree-month intervals.
- Do not share a toothbrush with another person.
- Do not store your toothbrush in the open near your toilet to avoid contamination of your toothbrush from aerosolized waste in the toilet water upon flushing. Close the toilet lid before flushing.
- Use interdental brushes after meals.





PREVENTING SELF RE-INFECTION IN THE AGE OF COVID



Soaking the toothbrush in hydrogen peroxide between uses may offer benefits in reducing the microbial load, including viruses, and potentially lowering the risk of self-infection or crosscontamination during acute COVID-19. Here is a detailed look at this practice:

Benefits of Using Hydrogen Peroxide on Toothbrushes

Antimicrobial Properties: Hydrogen peroxide (H_2O_2) is known for its broad-spectrum antimicrobial properties. It can effectively kill bacteria, viruses, and fungi, making it a useful disinfectant for various surfaces, including toothbrushes. Research shows that hydrogen peroxide can inactivate a wide range of pathogens,

including those that might be present in the oral cavity during an active COVID-19 infection.

Preventing Re-infection: During acute COVID-19, the virus can be present in the mouth and nasal passages. Toothbrushes can harbor these pathogens, potentially leading to self-reinfection or prolonging the illness if not properly sanitized. By soaking the toothbrush in hydrogen peroxide, one can reduce the viral load on the toothbrush, minimizing the risk of re-exposure to the virus.

How To Use Hydrogen Peroxide For Toothbrush Disinfection

Solution Preparation:

- Use a 3% hydrogen peroxide solution, which is commonly available in pharmacies.
- Pour enough solution into a small cup to fully submerge the toothbrush head.

<u>Soaking:</u>

- After brushing, rinse the toothbrush with water to remove any toothpaste residue.
- Submerge the toothbrush head in the hydrogen peroxide solution for at least 1 minute. Some recommendations suggest soaking for up to 10 minutes for thorough disinfection.

Rinsing:

• After soaking, rinse the toothbrush thoroughly with water before the next use to remove any residual hydrogen peroxide.

<u>Storage:</u>

• Store the toothbrush in an upright position and allow it to air dry. Avoid covering the toothbrush or storing it in a closed container, as this can create a moist environment conducive to microbial growth.

CONCLUSION:

Using hydrogen peroxide to soak your toothbrush between uses can be a beneficial practice, especially during an acute COVID-19 infection, to reduce the risk of self-reinfection and maintain better oral hygiene. This simple step, along with other preventive measures, can help mitigate the spread of pathogens within the household.

For more detailed guidance and research, consult sources such as the Centers for Disease Control and Prevention (CDC) and National Institutes of Health (NIH).

SECTION TWENTY-THREE

GENERAL RECOMMENDATIONS

EYES AND NOSE



- Only use steroid containing nasal inhalers, eye drops and oral inhalers when recommended by a healthcare provider.
- Minimize the use of nasal decongestants.
- Avoid piercings of the nose that can serve as an entry point for pathogens.



- Contact lens wearers should consider wearing daily replaceable contact lenses when possible.
- Apply moisturizing eyedrops without preservatives before going to sleep and upon awakening.



• Avoid the placement of cosmetic jewelry in the eyebrows.



Minimize eye cosmetics such as mascara, artificial lashes, glitter, and eyeliners, which block the natural secretions of glands surrounding the eyelashes.

SECTION TWENTY-FOUR





Every organ in the body requires water to function properly. It makes up 50 to 70% of the body weight of an adult human and is needed to survive. Water is required to get rid of waste products that accumulate in the body. It helps maintain normal body temperature. It lubricates joints and protects sensitive tissues.

The United States National Academy of Sciences, Engineering and Medicine recommends a daily intake of 3 to 4 liters of fluids for men (90-120 ounces) and 2 to 3 liters for women (60-90 ounces). These recommendations include, not just water, but other foods and beverages that contain water.

The amount of water to drink, however, may vary based on several factors including the following:

Age and gender

- Exercise: Activities that cause substantial amounts of sweating require increased water intake to cover the losses.
- Environment: Hot and humid environmental conditions increase fluid requirements as does altitude.
- <u>State of health</u>: Losses from fever, vomiting, diarrhea, require fluid replacement. Increased fluid intake is therapeutic for those with urinary tract infections and kidney stones.
- Breast feeding: Breast feeding requires increased fluid intake to remain hydrated.

There are multiple ways to maintain hydration. Non-alcoholic beverages like tea, coffee, sports drinks, soft drinks, and lemonade have a water content of 95-100%. Soups like mushroom soup, cream soups, and chicken noodle soup have a water content between 80% and 95%. Dairy products have varying degrees of water content, for example, whole milk (90%), yogurt (85%), ice cream (65%), and cheese (60%). (See: List 4)

Hydration is fundamental to maintaining cellular function, metabolic processes, and toxin elimination. While water contributes to hydration, the quality of water—including its chemical composition, microbial content, and filtration methods can impact overall health, microbiome balance, and detoxification pathways.

Distilled water, particularly when microfiltered, ozonated, and free from contaminants, offers a unique set of benefits, especially for individuals seeking to minimize exposure to unwanted chemicals, bacteria, and heavy metals.

Benefits of Hydration with Distilled Water

1. Purity: Free from Contaminants and Microbial Load

Distilled water, such as *Parents Choice® Distilled Water* (Walmart), undergoes steam distillation, which removes:

- Heavy metals (e.g., lead, arsenic, mercury).
- Inorganic minerals that may contribute to kidney stones or arterial calcification.
- Chlorine, fluoride, and other disinfection byproducts.

 Pathogenic bacteria, viruses, and parasites that may be present in tap water.¹

Ozonation and activated charcoal filtration further enhance microbial safety by oxidizing bacteria and removing volatile organic compounds (VOCs).²

2. Reduction of Chemical Load in the Body

Tap water often contains trace amounts of pharmaceutical residues, pesticides, industrial solvents, and endocrine-disrupting chemicals.³ Distilled and ozonated water minimizes exposure to these contaminants, reducing oxidative stress, inflammation, and potential endocrine disruptions.⁴

3. Improved Detoxification and Kidney Function

Distilled water has zero total dissolved solids, meaning it does not introduce extra solutes that the kidneys must filter. This reduces the burden on the kidneys and may help prevent kidney stone formation, especially for individuals prone to calcium oxalate stones.⁵ Adequate hydration with low-residue water helps flush out toxins, metabolic waste, and inflammatory byproducts from the liver, kidneys, and lymphatic system.⁶

4. Protection Against Microbiome Disruption

Tap water may contain chlorine, chloramine, and fluoride, which have antimicrobial properties and can disrupt the gut and urinary microbiome.⁷ Microfiltered and distilled water lacks these chemicals, making it gentler on gut flora and bladder microbiota.⁸

5. Reduction in Acid Load and Metabolic Waste

Distilled water is neutral to slightly acidic (pH ~6.5) but does not contribute to metabolic acidity the way mineral-heavy or highsulfate waters might.⁹ This can be beneficial for individuals managing acidic conditions, such as uric acid kidney stones, gout, or metabolic acidosis.¹⁰

Addressing Concerns About Mineral Deficiency

A common critique of distilled water is that it lacks essential minerals (e.g., calcium, magnesium, and potassium). However, the human body should obtain required minerals from food, not water.¹¹

Most municipal water supplies in the U.S. contain about 50 mg of sodium chloride (salt) per 8-ounce glass of tap water. The American Heart Association advises an intake of sodium up to 2,300 mg per day. If one were to rely on water as their primary sodium source, they would need to consume 46 glasses of water a day.

CONCLUSION:

Hydration with high-purity, ozonated, microfiltered, and distilled water offers multiple health benefits, including reduced exposure

to toxins, improved kidney function, enhanced detoxification, and protection of the microbiome.

Distilled water is a safe and effective hydration option, especially for those seeking minimal chemical and bacterial load.

REFERENCES:

- ^{1.} John Fawell and Mark J. Nieuwenhuijsen, "Contaminants in Drinking Water," *British Medical Bulletin* 68, no. 1 (2003): 199–208, <u>https://doi.org/10.1093/bmb/ldg027.</u>
- Li, Xiaojun, et al. "Ozonation for Drinking Water Treatment: A Review." Environmental Science and Pollution Research 29, no. 23 (2022): 34209–34229.
- ^{3.} Mark J. Benotti et al., "Pharmaceuticals and Endocrine Disrupting Compounds in U.S. Drinking Water," *Environmental Science & Technology* 43, no. 3 (2009): 597–603, <u>https://doi.org/10.1021/es801845a.</u>
- ^{4.} Manuela Silva et al., "Emerging Contaminants in Drinking Water: A Review," *Water* 10, no. 6 (2018): 756, <u>https://doi.org/10.3390/w10060756.</u>
- ^{5.} Elaine M. Worcester and Fredric L. Coe, "Calcium Kidney Stones," New England Journal of Medicine 363, no. 10 (2010): 954–963, <u>https://doi.org/10.1056/NEJMcp1001011.</u>
- ^{6.} Pietro M. Ferraro et al., "Dietary Intake and the Risk of Recurrent Kidney Stones," *American Journal of Clinical Nutrition* 102, no. 1 (2015): 155–165
- ^{7.} Alexander, James W. "Suppression of Bacterial Growth in Water Systems with Chlorine." *Journal of Infectious Diseases* 187, no. 7 (2003): 1147–1152.

- ^{8.} William G. Wade, "The Oral Microbiome in Health and Disease," *Pharmacological Research* 69, no. 1 (2013): 137–143, <u>https://doi.org/10.1016/j.phrs.2012.11.006.</u>
- ^{9.} Bouche, C., et al. "The pH of Drinking Water and Its Effect on Human Health." *Hydrology Research* 45, no. 2 (2014): 206–217.
- ^{10.} Khashayar Sakhaee and Orson W. Moe, "Uric Acid and the Progression of Kidney Disease," *Journal of the American Society of Nephrology* 26, no. 8 (2015): 1716–1721,
- ^{11.} Robert P. Heaney, "Drinking Water and Bone Health," *Nutrition Reviews* 64, no. 3 (2006): 116–120,

SECTION TWENTY-FIVE

DRINKING CLEAN WATER



Municipally supplied tap water, even in highly regulated regions, contains numerous contaminants—some known, others

unidentified or emerging. While public water systems undergo routine treatment to meet health and safety standards, they are not designed to remove every trace contaminant. Studies have shown that tap water can carry residual pharmaceutical compounds, agricultural runoff chemicals, industrial byproducts, and microbial agents, including bacteria and viruses, some of which are unmonitored or poorly understood.¹

The most cautious and comprehensive approach to water purification combines distillation followed by carbon filtration. This multi-step process provides exceptionally clean water by targeting both inorganic and organic contaminants.

Understanding Distillation and Condensation

Distillation works by boiling water into vapor, thereby separating it from many contaminants that cannot vaporize, such as heavy metals, salts, and most microbes.² This vapor is then cooled and condensed back into liquid form, leaving behind the non-volatile impurities. This process, however, does not effectively remove all organic compounds, particularly volatile organic compounds (VOCs) that can evaporate alongside water molecules.³ Therefore, while distilled water (sometimes simply called "condensed water") is free from many harmful substances, it can still carry traces of certain chemical pollutants.

Why Add Carbon Filtration?

To address the limitations of distillation, carbon filtration is often used as a second step. Activated carbon is highly porous and has an exceptional capacity to adsorb VOCs, pesticides, chlorine byproducts, and other small organic molecules that might pass through distillation.⁴ This dual process—distillation followed by carbon filtration—produces water that is nearly free of both inorganic and organic contaminants, making it one of the cleanest and safest forms of drinking water available.

Does Ozonation Play a Role?

Ozonation is a separate water treatment process that uses ozone gas (O_3), a potent oxidizer, to disinfect water by killing bacteria, viruses, and protozoa.⁵ While highly effective for disinfection, ozonation does not remove inorganic contaminants such as salts or metals, nor does it physically remove organic material—it only chemically alters or destroys certain biological and chemical compounds. Importantly, ozonation is not part of the distillationcondensation process, though it may be used in municipal water treatment plants or advanced bottled water production systems.

Summary

Although municipal water supplies are generally safe for most populations, they inherently contain trace contaminants from a wide range of sources, including pharmaceuticals, industrial waste, and microbial agents. For those seeking the cleanest possible drinking water, distilled water passed through carbon filtration offers a robust solution, effectively eliminating most inorganic, microbial, and organic pollutants. Notably, Walmart's Parent's Choice bottled water is an example of distilled, carbon-filtered, and ozonated water, providing a commercially available option for highly purified drinking water. Understanding each purification method's strengths and limitations—particularly how distillation, carbon filtration, and ozonation differ—helps make informed decisions about water choices.

REFERENCES:

1. Snyder, Shane A., Paul Westerhoff, Yeomin Yoon, and David L. Sedlak. "Pharmaceuticals, Personal Care Products, and Endocrine Disruptors in Water: Implications for the Water Industry." *Environmental Engineering Science* 20, no. 5 (2003): 449–469.

https://doi.org/10.1089/109287503768335931.

2. U.S. Environmental Protection Agency. "Water Health Series: Filtration Facts." EPA, 2005. https://www.epa.gov/sites/default/files/2015-09/documents/2005_09_14_consumer_factsheets_filtration.pdf.

3. Fawell, John, and Mark Nieuwenhuijsen. "Contaminants in Drinking Water: Environmental Pollution and Health." *British Medical Bulletin* 68, no. 1 (2003): 199–208. <u>https://doi.org/10.1093/bmb/ldg027.</u>

4. Ahmad, Maqsood, Rajesh Kumar, and Sheik Abdullah. "Activated Carbon: Preparation, Characterization, and Applications—A Review." Journal of Industrial and Engineering Chemistry 27 (2015): 1–12.

5. Langlais, Béatrice, David A. Reckhow, and Deborah R. Brink. Ozone in Water Treatment: Application and Engineering. Chelsea, MI: Lewis Publishers, 1991.

SECTION TWENTY-SIX DIETARY MEASURES



With every day we live and every meal we eat, we influence the great microbial organ inside us--for better or for worse.

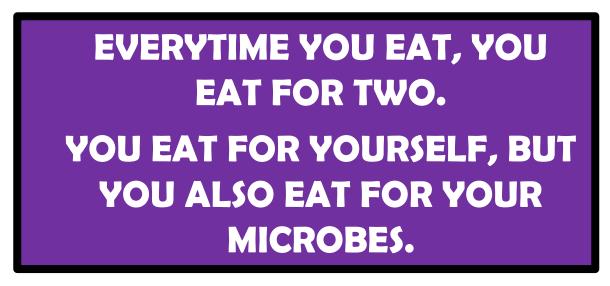
--Giulia Enders

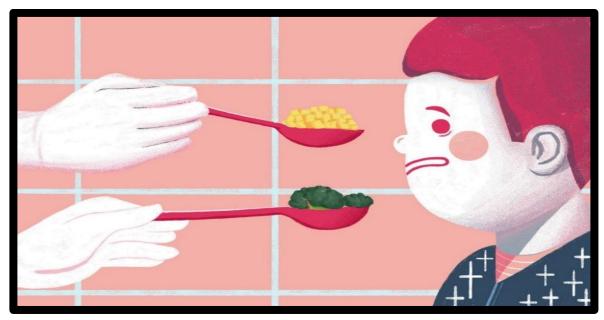
Every time you eat or drink, you are either feeding disease or fighting it.

--Heather Morgan

THE COMPLEXITIES OF FEEDING OURSELVES AND OUR MICROBIAL GUESTS

When we eat, we eat for two. We are not just nourishing ourselves, but we are also feeding trillions of beneficial microorganisms that live in the digestive tract.





Choosing Dietary Fiber Wisely: A Cornerstone Of Digestive and Systemic Health

Food choices are among the most powerful determinants of human health. While modern diets high in refined sugars and fats are metabolized rapidly in the upper digestive tract—mainly in the small intestine—their excess often overwhelms metabolic needs and is stored in adipose tissue, leading to systemic disorders such as obesity, type 2 diabetes, atherosclerosis, and fatty liver disease¹.

In contrast, a diet rich in plant-based dietary fiber takes a slower journey through the gastrointestinal tract, conferring benefits not only to the human host but to the trillions of microbes residing in the colon. This relationship is central to maintaining intestinal integrity, regulating metabolism, and preventing chronic disease².

Unlike sugars and fats that are readily broken down and absorbed in the small intestine, dietary fiber resists enzymatic digestion and proceeds into the large intestine as unprocessed residue³. It is here, in the colon, that a unique partnership unfolds. Colonic microbes ferment the fiber, producing short-chain fatty acids (SCFAs) such as butyrate, acetate, and propionate. (See the section: *How Human Rely on Beneficial Microbes in Their Intestines*). These SCFAs are not waste products but essential metabolites that feed colonocytes, maintain mucosal barrier integrity, reduce inflammation, modulate the immune response, and even influence systemic processes including mood, satiety, and glucose regulation⁴.

Not all fiber is created equal. Fermentable fibers, including inulin, fructooligosaccharides (FOS), and galactooligosaccharides (GOS), serve as prebiotics—selectively feeding beneficial microbes such as Bifidobacterium and Faecalibacterium prausnitzii⁵ (See List I). Non-fermentable fibers, such as cellulose and lignin, add bulk to stool and help promote regular bowel movements. Ideally, a diet includes both types to optimize digestive health, maintain microbial diversity, and support the structure and function of the gastrointestinal tract⁶.

A chronic deficiency in dietary fiber alters the composition and function of the gut microbiota, leading to *dysbiosis*. This imbalance disrupts the production of SCFAs, compromises the epithelial barrier, and promotes systemic inflammation. Over time, this can contribute to the development of not only metabolic diseases but also immune-mediated disorders, colorectal cancer, and neurodegenerative conditions⁷.

Modern diets, often stripped of fiber due to processing, fail to provide the substrates necessary for microbial fermentation and resilience⁸.

Choosing dietary fiber is not merely a matter of digestive comfort—it is a foundational strategy for sustaining long-term health. A fiber-rich, plant-focused diet provides the metabolic groundwork for microbial-host cooperation, systemic homeostasis, and chronic disease prevention. By nourishing both ourselves and our synbiotic microbiota, we foster a resilient internal ecosystem that supports nearly every aspect of health.

REFERENCES:

¹ Ludwig, David S., and Cara B. Ebbeling. "The Carbohydrate-Insulin Model of Obesity: Beyond 'Calories In, Calories Out." *JAMA Internal Medicine* 178, no. 8 (2018): 1098–1103. <u>https://doi.org/10.1001/jamainternmed.2018.2933.</u>

² Sonnenburg, Erica D., and Justin L. Sonnenburg. "The Ancestral and Industrialized Gut Microbiota and Implications for Human Health." *Nature Reviews Microbiology* 17, no. 6 (2019): 383–390. <u>https://doi.org/10.1038/s41579-019-0191-8.</u>

³ Slavin, Joanne. "Dietary Fiber and Body Weight." *Nutrition* 21, no. 3 (2005): 411–418. <u>https://doi.org/10.1016/j.nut.2004.08.018.</u>

⁴ Parada Venegas, Daniela, et al. "Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases." *Frontiers in Immunology* 10 (2019): 277. <u>https://doi.org/10.3389/fimmu.2019.00277.</u>

⁵ Slavin, Joanne. "Fiber and Prebiotics: Mechanisms and Health Benefits." Nutrients 5, no. 4 (2013): 1417–1435. <u>https://doi.org/10.3390/nu5041417.</u>

⁶ Makki, Kassem, et al. "The Impact of Dietary Fiber on Gut Microbiota in Host Health and Disease." *Cell Host & Microbe* 23, no. 6 (2018): 705–715. <u>https://doi.org/10.1016/j.chom.2018.05.012.</u> ⁷ Deehan, Emily C., and Jens Walter. "The Fiber Gap and the Disappearing Gut Microbiome: Implications for Human Nutrition." *Trends in Endocrinology & Metabolism* 27, no. 5 (2016): 239–242. <u>https://doi.org/10.1016/j.tem.2016.03.001.</u>

⁸ Martens, Eric C., et al. "Diet-Microbiota Interactions and Their Implications for Healthy Living." *Cell Host & Microbe* 17, no. 5 (2015): 603–616.

A Work In Progress

The composition of the intestinal microbiome changes over time. As species of microbes wax and wane in response to the host's aging, diet, lifestyle, physical activity, drugs, antibiotic use, toxins, pollutants, and contaminants in the environment, the care and feeding of the microbe population changes.

Feeding the body and its microbiome always remains a work in progress, requiring continuous attention and adjustment.

SECTION TWENTY-SEVEN

The Chronic Erosion of Biological Barriers and Borders: A Pathway to Chronic Illness

Human health is sustained by a series of intricate protective systems that defend the body against toxins, foreign antigens, and microbial invaders. These systems include physical barriers such as the skin, epithelial linings, and endothelial junctions, as well as cellular and molecular defenses that coordinate immune responses. Among the most critical of these interfaces are the gut lining and the blood-brain barrier (BBB), which act as selective gates between internal physiology and the external environment.

Over time, however, the structural integrity and regulatory precision of these systems gradually erode—a process accelerated by aging, genetic susceptibility, environmental insults, microbial imbalance, and nutritional deficiencies.

The decline in barrier function is part of a broader physiological phenomenon known as *"immunosenescence"*, characterized by the gradual deterioration of the immune system. This includes not only a reduction in immune surveillance and repair capacity but also a diminished ability to regulate inflammation and distinguish self from non-self.

As individuals age, immune cells experience functional exhaustion, T-cell diversity declines, and chronic low-grade inflammation termed *"inflammaging"*—becomes a prominent internal feature.¹

The gut is among the earliest and most vulnerable interfaces to exhibit signs of compromise. Under normal conditions, the intestinal barrier is composed of tightly connected epithelial cells, mucus layers, antimicrobial peptides, and immunoglobulin A (IgA). Collectively, these components form a semi-permeable boundary that permits nutrient absorption while excluding pathogens and harmful antigens. However, factors such as microbial dysbiosis, nutrient deficiency, chronic stress, certain medications (e.g., NSAIDs and proton pump inhibitors), and environmental toxins can impair this barrier. The resulting increase in intestinal permeability—often referred to as "leaky gut"—permits microbial components (e.g., lipopolysaccharides), food antigens, and other immunostimulatory molecules to enter the circulation, where they activate the immune system and perpetuate systemic inflammation, often in the absence of overt infection.²

Systemic extraintestinal symptoms may be experienced with bone and joint pain, skin rashes, and dysfunctions in organs such as the liver, heart, brain, and kidneys—many of which are classified as autoimmune illnesses.

Parallel to gut barrier dysfunction is the breakdown of the bloodbrain barrier. The BBB is a specialized structure composed of endothelial cells, astrocytic foot processes, and pericytes that regulates the passage of substances from the blood into the central nervous system (CNS). When intact, the BBB protects neural tissue from toxins, pathogens, and peripheral inflammatory signals. With age, however, this barrier becomes more porous, permitting neurotoxic substances and immune cells to infiltrate the brain. The resulting neuroinflammation is increasingly implicated in the development of neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease.³

Recent studies have uncovered the presence of microplastics in human brain tissue. Research led by Matthew Campen at the

University of New Mexico reported that microplastic concentrations in the brain have increased by approximately 50% over the past eight years, with levels significantly higher than those found in the liver or kidneys. Notably, individuals with dementia had up to ten times more microplastics in their brains compared to those without such diagnoses. While causation remains unconfirmed, these findings underscore the possibility that environmental toxins can breach the BBB and accumulate in neural tissue, potentially exacerbating neurodegenerative processes.⁴

The transition from youth to senescence unfolds gradually over decades, paralleling the natural stages of human development. During infancy and adolescence, the immune system is highly adaptive and responsive. Nutritional needs are met through maternal transfer (*in utero* and via breastfeeding), and the microbiome is shaped by early-life exposures.

In early adulthood, peak physiological performance is achieved particularly in support of reproduction and survival. But beyond the reproductive prime, the human body enters a slow and often silent decline. Systems deteriorate gradually: vision and hearing fade, bone and muscle mass diminish, cardiac and renal reserves shrink, reproductive capacity declines, and hepatic detoxification weakens.⁵

This trajectory is neither purely accidental nor wholly predetermined. It is molded by cumulative exposures: microbial diversity or depletion, nutrient sufficiency or deficiency, drug use, sedentary lifestyle, chronic stress, radiation, pollutants, and xenobiotics. These variables interact with genetic and epigenetic programming to determine whether the body's defenses remain resilient or become increasingly permeable to harm.⁶

Ultimately, chronic illnesses such as autoimmune disease, metabolic syndrome, cancer, and neurodegeneration may not stem solely from pathogens or genetic mutations. Rather, they can arise from the systemic failure of protective barriers. These diseases reflect a breakdown in the body's ability to maintain compartmentalization—a core principle of biological organization.

In this view, aging is not merely the passage of time, but the cumulative effect of breaches: in physical boundaries, immune regulation, and metabolic stability. Preventing or mitigating chronic illness may, therefore, require not only the targeting of pathogens or pathways but also the preservation of biological borders, the nurturing of the microbiome, the reduction of toxic exposures, and support for the body's natural rhythms.

REFERENCES:

¹Fülöp, Tamas, et al. "Immunosenescence: Molecular Mechanisms and Diseases." *Signal Transduction and Targeted Therapy* 8, no. 1 (2023): 1– 27. <u>https://doi.org/10.1038/s41392-023-01451-2.</u>

² Franceschi, Claudio, et al. "Inflammaging and 'Garb-aging'." *Trends in Endocrinology & Metabolism* 28, no. 3 (2017): 199–212. https://doi.org/10.1016/j.tem.2016.09.005. ³ Campen, Matthew J., et al. "Bioaccumulation of Microplastics in Decedent Human Brains." *Nature Medicine* 31, no. 2 (2025): 180–186. <u>https://doi.org/10.1038/s41591-024-03453-1.</u>

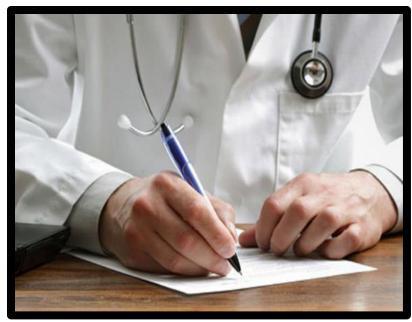
⁴ Identify Microplastics in Brain Tissue from Dementia Patients." *UNM Health Sciences Newsroom*, March 11, 2025.

https://hscnews.unm.edu/news/unm-scientist-devises-new-way-toidentify-microplastics-in-brain-tissue-from-dementia-patients.

⁵ Campen, Matthew J., et al. "Bioaccumulation of Microplastics in Decedent Human Brains." *Nature Medicine* 31, no. 2 (2025): 180–186. <u>https://doi.org/10.1038/s41591-024-03453-1.</u>

⁶ Franceschi, Claudio, et al. "Inflammaging and 'Garb-aging'." *Trends in Endocrinology & Metabolism* 28, no. 3 (2017): 199–212. <u>https://doi.org/10.1016/j.tem</u>

SECTION TWENTY-EIGHT RESTORING AND REJUVENATING STRATEGIES FOR DYFUNCTIONAL INTESTINAL ECOSYSTEMS



IDENTIFY THOSE WHO ARE AT INCREASED RISK:

Genetics: The first step requires identification of those individuals who are at highest risk. This begins with a detailed family history searching for significant genetic factors that may play a role in intestinal microecological imbalance such as obesity¹.

Age: The gut microbiota varies with age. Microbial diversity increases from infancy to adulthood and then decreases after age 70. Changes in diet and the immune system occur as well with advancing age. Older adults typically have a decrease in beneficial bacteria after age 70 such as *Bifidobacteria* and an increase in potentially harmful microorganisms. Ages, therefore, of 0 to 3 years and over the age of 70 are considered substantial risk factors.²

Diet: For decades, dietary recommendations have focused on calories, macronutrient ratios, and food pyramids underappreciating the fact that over 50% of the body cells were made up of microbes rather than human cells with microbes playing a critical role in digestion, immune function, and metabolic health. These traditional dietary models, however, based on calorie counting and macronutrient ratios are no longer adequate.

Intestinal well-being requires a focus on microbiome support, immune resilience, and environmental influences. Achieving digestive well-being is now felt best accomplished by implementing nutrient rich diets of fermentable fiber, reducing harmful additives, promoting short chain fatty acid production, recognizing potential harm to the microbiota from drugs and toxins, and supporting immune defenses.

This understanding is crucial for developing personalized strategies that optimize gut function and overall health, ultimately shifting from a reactive medical approach to a preventative and restorative paradigm.

Diet shapes the intestinal ecosystem and is a major factor that alters the intestinal microbiota. The typical "Western diet" is associated with chronic low-grade inflammation, metabolic disease, and obesity. Diets rich in saturated fats are known to alter the gut microbiota by increasing lipopolysaccharides (LPS) and trimethylamine-N-oxide (TMAO) with decreasing concentrations of short-chain fatty acids. The consumption of high-fat, high sugar, and low-fiber foods with excessive food additives (ultraprocessed) and reduced intake of polyphenols, fermented foods, and probiotics are, therefore, considered high-risk factors.³

Geographic region: adults fecal microbiota differ related to geographical and cultural traditions. For example, the intestinal microbiome of populations in the United States differ significantly from those in South America.⁴ Poor hygiene, environmental pollution, inadequate food intake, and nutritional deficiencies are considered substantial risk factors.

Intrauterine Maturation, Mode Of Delivery, Early Life Nutrient Sources:

Research suggests that colonization and formation of microbes may begin prior to birth. The type of delivery (vaginal or Cesarean section) may, likewise, affect composition of the infant's gut microbiota. The pregnant mother's diet, obesity status, smoking status, and use of antibiotics during pregnancy have also been cited as major determinants of initial microbe colonization. Other factors affecting colonization include pre-pregnancy and gestational comorbidities, use of antibiotics or other medications during pregnancy, use of illicit or recreational drugs, smoking or alcohol consumption during pregnancy, Cesarean section delivery, and lack of breast-feeding. All are considered substantial risk factors and have been previously discussed. **Stress:** Stress affects intestinal microbes. Studies in both animals and humans have shown a decrease in *Lactobacillus* and *Bifidobacterium* and an increase in pathogenic microorganisms due to an increase in stress related catecholamine secretions. Stress, therefore, is considered a substantial risk factor.⁵

Exposure to Xenobiotics: Xenobiotics (exogenous substances) are synthetic chemicals, including drugs, pesticides, food additives, and other contaminants. They are capable of inhibiting or promoting bacterial growth and altering bacterial metabolism thus affecting the virulence of enteric bacteria. Microbes can metabolize and bioaccumulate xenobiotics thereby altering their activity or toxicity. Exposures to antibiotics, pesticides, food additives and other pollutants are thus considered substantial risk factors.⁶

Current and Previous Infections:

Infections are among the most direct causes of intestinal microbial imbalances. Opportunistic pathogens may migrate to other infection sites owing to decrease body resistance or immune function.

Other factors: Other substantial risk factors include lack of exercise, and gastrointestinal surgery.

REFERENCES:

¹ Goodrich, Julia K., Jillian L. Waters, Angela C. Poole, Jessica L. Sutter, Omry Koren, Ran Blekhman, Marcus Beaumont, et al. "Human Genetics Shape the Gut Microbiome." *Cell* 159, no. 4 (2014): 789–799. https://doi.org/10.1016/j.cell.2014.09.053.

² Guigoz, Yves, Joël Doré, and Emmanuel J. Schiffrin. "The Inflammatory Status of Old Age Can Be Nurtured from the Intestinal Environment." *Current Opinion in Clinical Nutrition and Metabolic Care* 11, no. 1 (2008): 13–20. <u>https://doi.org/10.1097/MCO.0b013e3282f2bfdf.</u>

³ Beam, Amanda, Elizabeth Clinger, and Mary E. Hao. "Effect of Diet and Dietary Components on the Composition of the Gut Microbiota." *Nutrients* 13, no. 8 (2021): 2795. <u>https://doi.org/10.3390/nu13082795.</u>

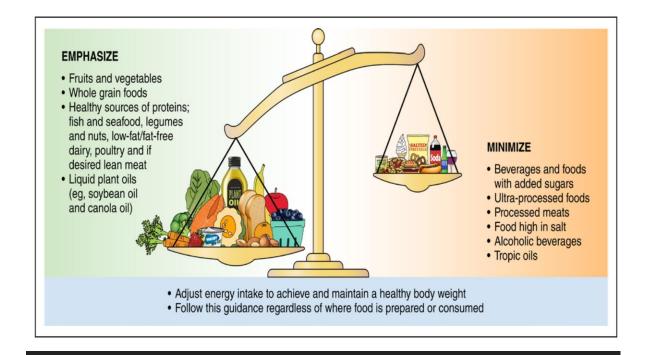
⁴ Yatsunenko, Tanya, Federico E. Rey, Mark J. Manary, Indi Trehan, Maria Gloria Dominguez-Bello, Monica Contreras, Magda Magris, et al. "Human Gut Microbiome Viewed Across Age and Geography." *Nature* 486, no. 7402 (2012): 222–227. <u>https://doi.org/10.1038/nature11053.</u>

⁵ Galli, Jennifer D., Michael J. Nason, and Michael T. Bailey. "The Structures of the Colonic Mucosa-Associated and Luminal Microbial Communities Are Distinct and Differentially Affected by a Prolonged Murine Stressor." *Gut Microbes* 5, no. 6 (2014): 748–760. <u>https://doi.org/10.4161/19490976.2014.972241</u>.

⁶ Lindell, Anna E., and Andrew L. Goodman. 2022. "Multimodal Interactions of Drugs, Natural Compounds and Pollutants with the Gut Microbiota." *Nature Reviews Microbiology* 20 (7): 431–443.

EAT A PLANT--PREDOMINANT DIET

LET YOUR DIET BE YOUR PHARMACY



<u>The Mediterranean Diet as a Comprehensive Source of</u> <u>Cellular and Microbial Substrates</u>

The Mediterranean Diet has long been associated with improved cardiovascular health, reduced cancer risk, and enhanced longevity. More recently, research has highlighted its role in supporting not only human cellular function but also gut microbial diversity and metabolic output.¹ Rich in polyphenols, unsaturated fats, dietary fibers, and fermented foods, this dietary pattern provides a wide range of substrates for both host cells and commensal microbes.²

Polyphenols, found abundantly in olives, grapes, and various herbs, are metabolized by colonic microbiota into bioactive phenolic compounds. These metabolites contribute to the maintenance of gut barrier integrity, modulation of inflammation, and protection against oxidative stress.³

In addition, the fiber content of legumes, fruits, and whole grains found in the Mediterranean diet fuels the fermentation processes of saccharolytic bacteria, leading to the generation of short-chain fatty acids (SCFAs) such as butyrate, acetate, and propionate. These SCFAs support colonocyte health, regulate immune function, and serve as systemic metabolic signals.⁴

Moreover, the inclusion of naturally fermented foods—such as yogurt, kefir, kimchi, Kombucha tea, tempeh and more introduces live microbial strains that may transiently colonize the gut and exert probiotic effects. This combination of prebiotic and probiotic components makes the Mediterranean diet an inherently synbiotic dietary model.⁵

Finally, the balance of omega-3 and omega-6 fatty acids derived from fish, nuts, and olive oil contributes to anti-inflammatory lipid signaling and membrane fluidity, further enhancing both immune modulation and cellular resilience.⁶ The Mediterranean diet, therefore, does more than nourish the host—it also nurtures the gut microbiota. This emphasis on fiber, fermented foods, and plant polyphenols enhances microbial diversity and resilience. Our microbial partners are necessary for full access to many of the diet's health promoting effects, especially the transformation of polyphenols and fiber into bioactive metabolites. In this way, the Mediterranean diet stands as both a nutritional and symbiotic template for long-term health.

RESOURCES:

^{1.} De Filippis, F., Pellegrini, N., Vannini, L., et al. (2016). High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. *Gut*, 65(11), 1812–1821. <u>https://doi.org/10.1136/gutjnl-2015-309957</u>

^{2.} Davis, C., Bryan, J., Hodgson, J., & Murphy, K. (2015). Definition of the Mediterranean Diet; a literature review. *Nutrition*, 31(7–8), 932–939.

^{3.} Del Rio, D., Rodriguez-Mateos, A., Spencer, J. P., Tognolini, M., Borges, G., & Crozier, A. (2013). Dietary (Poly) Phenolics In Human Health: Structures, Bioavailability, and Evidence of Protective Effects Against Chronic Diseases. *Antioxidants & Redox Signaling*, 18(14), 1818–1892. <u>https://doi.org/10.1089/ars.2012.4581</u>

^{4.} Makki, K., Deehan, E. C., Walter, J., & Bäckhed, F. (2018). The Impact Of Dietary Fiber On Gut Microbiota In Host Health And Disease. *Cell Host & Microbe*, 23(6), 705–715. <u>https://doi.org/10.1016/j.chom.2018.05.012</u>

^{5.} Marco, M. L., Heeney, D., Binda, S., Cifelli, C. J., Cotter, P. D., Foligné, B., ... & Hutkins, R. (2017). Health Benefits of Fermented Foods: Microbiota and Beyond. *Current Opinion in Biotechnology*, 44, 94–102. <u>https://doi.org/10.1016/j.copbio.2016.11.010</u> ^{6.} Simopoulos, A. P. (2002). The importance of the ratio of omega-6/omega-3 essential fatty acids. *Biomedicine & Pharmacotherapy*, 56(8), 365–379. <u>https://doi.org/10.1016/S0753-3322(02)00253-6</u>

GREEN MEDITERRANEAN DIET



A more recent modification of the Mediterranean diet has been the introduction of the *green Mediterranean diet*.¹ The green Mediterranean diet causes more substantial compositional changes in the microbiome compared to the Mediterranean diet.

The green Mediterranean diet incorporates a higher intake of plant-based foods and reduction in red meat as well as the introduction of daily polyphenol-rich green tea.

Microbe composition and diversity improved on the green Mediterranean diet and were linked with positive alterations in both body weight and cardiometabolic indicators.¹

REFERENCES:

¹ Rinott, Ehud et. al. 2022. "The Effects of the Green-Mediterranean Diet on Cardiometabolic Health Are Linked to Gut Microbiome Modifications: A Randomized Controlled Trial." *Genome Medicine* 14 (1): Article 29.

EAT A WIDE VARIETY OF PLANT BASED FOODS



1. **Diversity of Fiber Sources:** Consuming a variety of fiber types, such as inulin, pectin, cellulose, and hemicellulose, nourishes different microbial communities. **(See Section:** *Commercially Available Products that Act as Prebiotics)*

Each type of fiber is fermented by specific microbes, leading to the production of different beneficial metabolites most particularly short-chain fatty acids (SCFAs).¹⁻²

- 2. Fermentable Carbohydrates: The diet should include a range of fermentable carbohydrates (prebiotics) like fructans (inulin), oligosaccharides (found in legumes and certain vegetables), and resistant starches (present in foods like "greenish" bananas and cooked-and-cooled potatoes) to support the growth of various beneficial microbes such as *Bifidobacteria* and *Lactobacilli*. (See the Section: Commercially Available Products that Act as Prebiotics)
- 3. **Personalized Nutrition:** The gut microbiome varies significantly among individuals, so a personalized approach to fiber intake is required. This involves adjusting fiber types and amounts based on individual digestive responses and gut microbiota composition.
- 4. <u>Functional Benefits</u>: Different fibers provide different health benefits. For example, inulin and fructo-oligosaccharides (FOS) are known for their ability to promote the growth of *Bifidobacteria*, which can enhance gut immune function¹. On the other hand, fibers like pectin and guar gum help in stimulating hormoneproducing cells that control hunger, satiety, and insulin secretions².

<u>"Eat the Rainbow": Fiber and Phytochemical Diversity for</u> <u>Microbial Resilience</u>

"Eat the rainbow" is more than just a colorful dietary slogan—it's a scientifically grounded strategy to nourish the gut microbiota through a broad spectrum of fibers, polyphenols, and phytonutrients found in multicolored plant foods. Each pigment signals the presence of unique bioactive compounds that interact with the gut microbiome in distinct ways.

Broad-Spectrum Dietary Fiber Strategy

A diverse array of fibers—soluble, insoluble, fermentable, resistant starches, and more—each serve as selective fuel for different bacterial species. For example, pectin from apples, inulin from onions, arabinoxylans from whole grains, and resistant starches from cooked-and-cooled potatoes all support different metabolic pathways and bacterial niches. Limiting fiber intake to only a few types—such as from oat bran or wheat cereal—may restrict microbial diversity and impair the resilience of the gut ecosystem. In contrast, a broad-spectrum fiber intake promotes microbial cross-feeding, increases the production of beneficial short-chain fatty acids (SCFAs), and fosters ecosystem stability.^{1,2}

Color as a Proxy for Phytochemical Variety

Each color in fruits and vegetables represents a different class of phytochemicals:

- Purple and blue (e.g., eggplant, blueberries) are rich in anthocyanins, which exhibit antioxidant and anti-inflammatory properties and promote growth of *Akkermansia* and *Bifidobacterium*.
- <u>Red</u> (e.g., red peppers, tomatoes) contains lycopene and ellagic acid, associated with protection against oxidative stress and enhanced SCFA production.

- <u>Green</u> (e.g., spinach, broccoli) offers chlorophyll, sulforaphane, and folate, supporting detoxification pathways and microbial diversity.
- **Orange and yellow** (e.g., carrots, squash) provide carotenoids like beta-carotene, which modulate gut immunity and barrier integrity.

These bioactive compounds often act as microbial modulators, enhancing beneficial taxa and suppressing pathogens. Their synergy with dietary fibers helps improve intestinal health beyond basic nutrition.³

Refined Microbial Nutrition Advice

Refining the traditional advice to "eat more fiber" into guidance that encourages fiber diversity and phytochemical richness reflects emerging research. Studies now show that not only the amount but the variety of plant foods consumed strongly correlates with gut microbial diversity and health outcomes.⁴

Consuming 30 or more different plant-based foods per week is now considered a clinical target for microbiome diversity, as emphasized in initiatives like the American Gut Project.

In essence, eating the rainbow translates to feeding the widest possible range of beneficial microbes. This promotes a robust and adaptable microbiota—one better equipped to support immunity, digestion, and inflammation control across a range of physiological challenges.

REFERENCES:

¹ Ranaivo, Harimalala, F. Thirion, C. Béra-Maillet, et al. "Increasing the Diversity of Dietary Fibers in a Daily-Consumed Bread Modifies Gut Microbiota and Metabolic Profile in Subjects at Cardiometabolic Risk." *Gut Microbes* 14 (2022).

² Jensen, Nick, Maria X. Maldonado-Gomez, Nithya Krishnakumar, et al. "Dietary Fiber Monosaccharide Content Alters Gut Microbiome Composition and Fermentation." *Applied and Environmental Microbiology*, 2024. <u>https://doi.org/10.1128/aem.00964-24.</u>

³ Dingeo, Giulia, Alex Brito, H. Samouda, M. Iddir, Michael R. La Frano, and T. Bohn. "Phytochemicals as Modifiers of Gut Microbial Communities." *Food & Function*, 2020

⁴ Fu, Jiongxing, Yan Zheng, Ying Gao, and Wanghong Xu. "Dietary Fiber Intake and Gut Microbiota in Human Health." *Microorganisms* 10 (2022). <u>https://doi.org/10.3390/microorganisms10122507.</u>

Categories of Fermentable Food Items Include the Following:

(See List I for a detailed list of high fiber containing foods)

<u>1. Fruits</u>

Examples: Apples, blueberries, raspberries, strawberries, oranges, and pears.

2. Vegetables

- Root Vegetables: Sweet potatoes, carrots, and beets.
- Cruciferous Vegetables: Broccoli, Brussels sprouts, cabbage, and cauliflower.
- Alliums: Onions, garlic, leeks, shallots, and chives.

3. Legumes and beans

Examples: Lentils, chickpeas, black beans, kidney beans, and soybeans.

4. Whole Grains

Examples: Oats, barley, brown rice, whole wheat, and quinoa.

5. Fungi (Mushrooms)

Examples: Shiitake mushrooms, oyster mushrooms, button mushrooms, Reishi mushrooms, and Chaga mushrooms.

<u>6. Nuts</u>

Examples: Almonds, pecans, walnuts, hazelnuts, and pistachios.

7. Seeds

Examples: Chia seeds, flaxseeds, pumpkin seeds, sunflower seeds, and hemp seeds.

8. Resistant Starches

Examples: Cooked and cooled potatoes, cooked and cooled rice, greenish bananas, and greenish plantains.

9. Seaweed

Examples: Nori (red seaweed), wakame (brown seaweed), kombu, dulse, and agar.

10. Human Milk Oligosaccharides (HMOs)

Examples: 2'-Fucosyllactose (2'FL), Lacto-N-neotetraose (LNT), 3'-Sialyllactose (3'SL), and 6'-Sialyllactose (6'SL).

11. Chitin and Chitinous Foods

Examples: Crab shells, shrimp shells, lobster shells, and edible insects.

12. Polyphenol-Rich Foods

Examples: Dark chocolate, green tea, matcha tea, and pomegranates.

POLYOLS

BIOCHEMICAL FORMATION, FERMENTATION, AND DIETARY SOURCES

Introduction

Polyols, also known as sugar alcohols are a class of organic compounds derived from carbohydrates. Polyols are widely used in the food industry as low-calorie sweeteners. They are also naturally synthesized in the body through metabolic pathways.

Fermentation of Polyols by Gut Microbiota

Polyols that escape digestion and absorption in the small intestine enter the colon, where they undergo fermentation by the gut microbiota. The fermentation process primarily involves bacteria, that metabolize polyols into short-chain fatty acids (SCFAs), gases (hydrogen, carbon dioxide, and methane), and organic acids. The extent and efficiency of fermentation depend on the specific polyol and the composition of the gut microbiome. The two polyols, sorbitol and mannitol, are poorly absorbed in the small intestine, leading to osmotic effects that may cause gastrointestinal discomfort when consumed in excessive amounts. These polyols are fermented by colonic bacteria, producing SCFAs such as acetate, propionate, and butyrate, which contribute to gut health by serving as energy sources for colonocytes and modulating inflammatory responses.¹

Xylitol, another commonly used polyol, is less fermentable than sorbitol or mannitol, but it can still be metabolized by certain bacterial species to short chain fatty acids.²

Dietary Sources of Polyols

Polyols occur naturally in a variety of fruits and vegetables, including apples, pears, peaches, cherries, mushrooms, and cauliflower. However, the most significant dietary sources of polyols are processed foods that use these compounds as sweeteners, humectants, and texturizers. The food industry frequently employs polyols such as sorbitol, mannitol, xylitol, erythritol, and maltitol in sugar-free products, including chewing gums, candies, baked goods, and diabetic-friendly foods.³

Erythritol, a polyol with a lower caloric value than other sugar alcohols, is unique in that it is almost entirely absorbed in the small intestine and excreted unchanged in urine, minimizing its fermentation and gastrointestinal side effects. Due to its excellent tolerability, erythritol is widely used in low-calorie diets.⁴ Polyols are also available as dietary supplements, particularly in formulations aimed at improving gut health and glycemic control. Inositol supplements, for example, are commonly used for their roles in insulin signaling and ovarian function, particularly in managing polycystic ovary syndrome (PCOS).⁵

CONCLUSION:

Polyols play a significant role in both human metabolism and nutrition. They are synthesized in the body through enzymatic pathways that regulate glucose metabolism and cellular function. As dietary components, polyols contribute to sugar reduction strategies, offering lower-calorie alternatives in processed foods and supplements.⁶ While beneficial in moderate amounts, excessive consumption can lead to gastrointestinal discomfort due to their osmotic effects and fermentation in the colon. Understanding the metabolism, fermentation, and sources of polyols provides valuable insights into their applications in both health and disease.

REFERENCES:

¹ Slavin, Joanne. "Dietary Fiber and Satiety." *Nutrition Bulletin* 29, no. 1 (2004): 5-11.

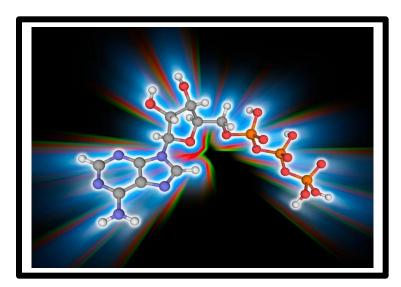
² Salli, Katja, et al. "Xylitol's Health Benefits beyond Dental Health: A Comprehensive Review." *Nutrients* 11, no. 8 (2019): 1813.

³ Livesey, Geoffrey. "Health Potential of Polyols as Sugar Replacers, with Emphasis on Low Glycaemic Properties." *Nutrition Research Reviews* 16, no. 2 (2003): 163-191. ⁴ Grembecka, Małgorzata. "Sugar Alcohols—Their Role in the Modern World of Sweeteners: A Review." *European Food Research and Technology* 242, no. 5 (2016): 603-617.

⁵ Unfer, Vittorio, et al. "Myo-Inositol and D-Chiro-Inositol in Polycystic Ovary Syndrome: A Review on Their Physiological and Clinical Effects." *International Journal of Endocrinology* 2016 (2016): 1-10.

⁶ Borges, N.A., Ferreira, D.C., de Brito, J.S., et al. "Is there a role for polyols in colonic health?" *Journal of Functional Foods* 68 (2020): 103912.

FERMENTATION PRODUCES SHORT CHAIN FATTY ACIDS—THE MOLECULAR CURRENCY OF DIGESTIVE WELL BEING



Short-chain fatty acids (SCFAs)—acetate, propionate, butyrate, isobutyrate, valerate, and caproate—are one of the key metabolic byproducts of microbial fermentation in the digestive tract. These molecules serve as a primary energy source for intestinal cells, regulate immune responses, and support metabolic homeostasis.

SCFAs are primarily produced from dietary fiber and select amino acids with their synthesis depending on cooperative microbial interactions, including quorum sensing and cross-feeding mechanisms.¹

Modern environmental and lifestyle factors can disrupt SCFA production, contributing to dysbiosis and gastrointestinal disorders. Recent research has also identified SCFAs—especially butyrate—as critical regulators in the prevention and control of digestive tract cancers, including colorectal cancer.²

SCFA Production and Microbial Fermentation

SCFA synthesis is primarily driven by the fermentation of dietary fiber (e.g., resistant starches, inulin, and pectin) and select amino acids (e.g., glutamate, lysine, and threonine) by gut bacteria.⁸ The production process includes:

- 1. <u>Substrate Breakdown</u>: Gut bacteria enzymatically degrade complex carbohydrates and proteins into fermentable intermediates.
- 2. <u>Metabolic Conversion</u>: Pyruvate, derived from glycolysis, undergoes various microbial metabolic pathways to produce

SCFAs through processes like the Wood-Ljungdahl pathway and the Stickland reaction.⁸

3. <u>Microbial Cooperation</u>: SCFA production involves cross-feeding, where metabolic byproducts from one microbial species fuel another's fermentation. This interaction is modulated through quorum sensing, ensuring optimal SCFA synthesis.⁹

Key SCFA-Producing Bacteria

Butyrate: Faecalibacterium prausnitzii, Eubacterium rectale, Roseburia spp.⁹

Propionate: *Bacteroides spp.* (via the succinate pathway) and *Lachnospiraceae* (via the acrylate pathway)⁹

Acetate: Bifidobacteria and *Prevotella spp.⁹

SCFAs and the Prevention of Digestive Tract Cancers

Recent studies indicate that SCFAs, particularly butyrate, play a protective role against digestive tract cancers, particularly colorectal cancer:

 Induction of Apoptosis in Cancer Cells: Butyrate induces programmed cell death in colorectal cancer cells through histone deacetylase (HDAC) inhibition, leading to the reactivation of tumor suppressor genes and the suppression of oncogenic pathways.

- <u>Regulation of Cell Proliferation</u>: SCFAs help maintain normal epithelial turnover by promoting the differentiation of colonocytes while inhibiting uncontrolled proliferation, a hallmark of cancer.
- Modulation of Inflammation: Chronic inflammation is a key driver of colorectal cancer. Butyrate reduces the expression of pro-inflammatory cytokines like IL-6 and TNF-α while enhancing anti-inflammatory pathways mediated by IL-10.
 - **Enhancement of Gut Barrier Function:** By strengthening the intestinal epithelial barrier, SCFAs reduce the translocation of bacteria and endotoxins that could trigger inflammatory carcinogenesis.
 - **Alteration of Tumor Microenvironment:** SCFAs influence the metabolic environment of the gut, shifting it away from conditions that favor cancerous growth. Lower colonic pH resulting from SCFA fermentation inhibits secondary bile acid synthesis, which has been linked to colorectal carcinogenesis.
- Impact on DNA Damage and Repair Mechanisms: Butyrate plays a role in maintaining DNA integrity by promoting repair mechanisms and reducing oxidative stress, thereby lowering mutation rates in intestinal epithelial cells.

CONCLUSION:

SCFAs are essential to intestinal well-being and systemic health. Their production relies on microbial fermentation of dietary substrates, which is influenced by numerous lifestyle and environmental factors. Emerging evidence suggests that beyond their role in gut health, SCFAs may have significant cancerpreventative properties, particularly in colorectal cancer.

Understanding the factors that enhance or impair SCFA synthesis is crucial for harnessing their full therapeutic potential in digestive and systemic disease prevention.

REFERENCES:

- Liu, Mingyue, et al. "Role of Short-Chain Fatty Acids in Host Physiology." Animal Models and Experimental Medicine (2024). <u>https://doi.org/10.1002/ame2.12464</u>.
- ^{2.} Mirzaei, Rasoul, et al. "Role of Microbiota-Derived Short-Chain Fatty Acids in Cancer Development and Prevention." *Biomedicine & Pharmacotherapy* 139 (2021): 111619. <u>https://doi.org/10.1016/j.biopha.2021.111619</u>.
- ^{3.} Fusco, W., et al. "Short-Chain Fatty Acid-Producing Bacteria: Key Components of the Human Gut Microbiota." *Nutrients* 15, no. 9 (2023): 2211. <u>https://doi.org/10.3390/nu15092211</u>.
- ^{4.} Tan, Jian, et al. "The Role of Short-Chain Fatty Acids in Health and Disease." Advances in Immunology 121 (2014): 91–119. <u>https://doi.org/10.1016/B978-0-12-800100-4.00003-9</u>.

- ^{5.} Carretta, M. D., et al. "Participation of Short-Chain Fatty Acids and Their Receptors in Gut Inflammation and Colon Cancer." *Frontiers in Physiology* 12 (2021): 662739. https://doi.org/10.3389/fphys.2021.662739.
- ^{6.} Mi-Young Son and Hyun-Soo Cho, "Anticancer Effects of Gut Microbiota-Derived Short-Chain Fatty Acids in Cancers," *Journal of Microbiology and Biotechnology* 33, no. 7 (2023): 849–856, <u>https://doi.org/10.4014/jmb.2301.01031</u>.
- ^{7.} Yao, Yao, et al. "The Role of Short-Chain Fatty Acids in Immunity, Inflammation and Metabolism." *Critical Reviews in Food Science and Nutrition* 62, no. 1 (2020): 1–12. <u>https://doi.org/10.1080/10408398.2020.1854675</u>.
- ^{8.} Blaak, E., et al. "Short Chain Fatty Acids in Human Gut and Metabolic Health." *Beneficial Microbes* 11, no. 5 (2020): 411–455. <u>https://doi.org/10.3920/BM2020.0057</u>.
- ^{9.} Wang, Ling-Yun, et al. "Short-Chain Fatty Acids: Bridges Between Diet, Gut Microbiota, and Health." *Journal of Gastroenterology and Hepatology* (2024). <u>https://doi.org/10.1111/jgh.16619</u>.

AVOID ULTRA-PROCESSED FOODS



Ultra-processed foods are industrially formulated food products made entirely or mostly from substances extracted from foods, derived from food constituents, or synthesized in laboratories from food substrates or other organic sources such as flavor enhancers, colorants, and additives used to impart sensory properties. These foods typically contain little or no whole foods and are characterized by elevated levels of sugar, fat, salt, and chemical additives. Examples include sugary drinks, packaged snacks, reconstituted meat products, and pre-prepared frozen meals.

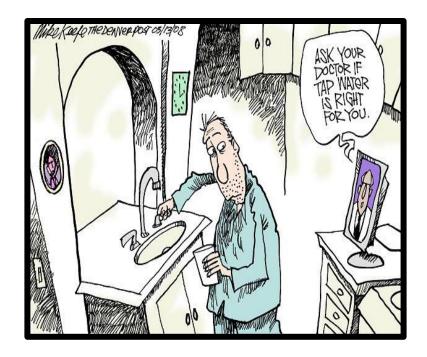
Ultra-processed foods are designed to be convenient, highly palatable, and shelf-stable, often at the expense of nutritional quality. Studies suggest that this group of food increases the risk of intestinal inflammation and activation of the immune system.¹

REFERENCE:

¹ Maki, K.A., Sack, M.N. & Hall, K.D. Ultra-processed foods: increasing the risk of inflammation and immune dysregulation?. *Nat Rev Immunol* 24, 453–454 (2024). <u>https://doi.org/10.1038/s41577-024-01049-x</u>

AVOID TOXINS AND CONTAMINANTS IN WATER--

DRINK DISTILLED WATER



Municipally supplied tap water, even in highly regulated regions, contains numerous contaminants—some known, others unidentified or emerging. While public water systems undergo routine treatment to meet health and safety standards, they are not designed to remove every trace contaminant. Studies have shown that tap water can carry residual pharmaceutical compounds, agricultural runoff chemicals, industrial byproducts, and microbial agents, including bacteria and viruses, some of which are unmonitored or poorly understood.¹

The most cautious and comprehensive approach to water purification combines distillation followed by carbon filtration. This multi-step process provides exceptionally clean water by targeting both inorganic and organic contaminants.

Understanding Distillation and Condensation

Distillation works by boiling water into vapor, thereby separating it from many contaminants that cannot vaporize, such as heavy metals, salts, and most microbes.² The vapor is then cooled and condensed back into liquid form, leaving behind the non-volatile impurities. This process, however, does not effectively remove all organic compounds, particularly volatile organic compounds (VOCs) that can evaporate alongside water molecules.³ Therefore, while distilled water (sometimes simply called "condensed water") is free from many harmful substances, it can still carry traces of certain chemical pollutants.

Why Add Carbon Filtration?

To address the limitations of distillation, carbon filtration is often used as a second step. Activated carbon is highly porous and has an exceptional capacity to adsorb VOCs, pesticides, chlorine byproducts, and other small organic molecules that might pass through distillation.⁴ This dual process—distillation followed by carbon filtration—produces water that is nearly free of both inorganic and organic contaminants, <u>making it one of the cleanest</u> <u>and safest forms of drinking water available.</u>

Does Ozonation Play a Role?

Ozonation is a separate water treatment process that uses ozone gas (O_3), a potent oxidizer, to disinfect water by killing bacteria, viruses, and protozoa.⁵ While highly effective for disinfection,

ozonation does not remove inorganic contaminants such as salts or metals, nor does it physically remove organic material—it only chemically alters or destroys certain biological and chemical compounds. Importantly, ozonation is not part of the distillationcondensation process, though it may be used in municipal water treatment plants or advanced bottled water production systems.

Summary

Although municipal water supplies are generally safe for most populations, they inherently contain trace contaminants from a wide range of sources, including pharmaceuticals, industrial waste, and microbial agents. For those seeking the cleanest possible drinking water, distilled water passed through carbon filtration offers a robust solution, effectively eliminating most inorganic, microbial, and organic pollutants. Notably, Walmart's Parent's Choice[®] bottled water is an example of <u>distilled</u>, <u>carbon-filtered</u>, and <u>ozonated water</u>, providing a commercially available option for highly purified drinking water.

Understanding each purification method's strengths and limitations—particularly how distillation, carbon filtration, and ozonation differ—helps consumers make informed decisions about their water consumption.

REFERENCES:

^{1.} Snyder, Shane A., Paul Westerhoff, Yeomin Yoon, and David L. Sedlak. "Pharmaceuticals, Personal Care Products, and Endocrine Disruptors in Water: Implications for the Water Industry." *Environmental Engineering* *Science* 20, no. 5 (2003): 449–469. https://doi.org/10.1089/109287503768335931.

^{2.} U.S. Environmental Protection Agency. "Water Health Series: Filtration Facts." EPA, 2005. https://www.epa.gov/sites/default/files/2015-09/documents/2005_09_14_consumer_factsheets_filtration.pdf.

^{3.} Fawell, John, and Mark Nieuwenhuijsen. "Contaminants in Drinking Water: Environmental Pollution and Health." *British Medical Bulletin* 68, no. 1 (2003): 199–208. <u>https://doi.org/10.1093/bmb/ldg027</u>.

^{4.} Ahmad, Maqsood, Rajesh Kumar, and Sheik Abdullah. "Activated Carbon: Preparation, Characterization, and Applications—A Review." *Journal of Industrial and Engineering Chemistry* 27 (2015): 1–12. <u>https://doi.org/10.1016/j.jiec.2014.10.002</u>.

^{5.} Langlais, Béatrice, David A. Reckhow, and Deborah R. Brink. *Ozone in Water Treatment: Application and Engineering*. Chelsea, MI: Lewis Publishers, 1991.

AVOID ALCOHOL



Alcohol use is a leading cause of disease and death worldwide. The perspective that alcohol-related diseases are solely caused by tissue damage done by alcohol metabolites has evolved to include

the multiple adverse effects of alcohol on digestive tract microbe populations.^{1,2}

Alcohol Causes Increased Gut Permeability:

Scientists have demonstrated that alcohol can cause an increase in pathogenic bacteria and an increase in intestinal permeability commonly referred to as "leaky digestive tract." As shown before, increased permeability of the digestive tract lining facilitates translocation of microorganisms, toxins, and food antigens into the body. The flow of these substances from the digestive tract through a permeable digestive tract lining into the vascular system and to the liver has been proposed as a major factor in the cause of liver diseases.³

Alcohol Causes Damage To The Liver

Damage to the liver may include fat accumulation in the liver (alcohol induced fatty liver disease), liver cell inflammation (alcohol-related hepatitis), tissue scarring (fibrosis), advanced scarring (cirrhosis) and liver cancer (hepatocellular carcinoma).

Alcohol Damages Organs Beyond The Liver

Alcohol has also been proven to have a significant adverse effect on multiple organ systems including the liver⁴, and brain⁵, in addition to the intestinal microbiome⁶. Now evidence shows that alcohol not only lacks beneficial effects on heart health but can be harmful⁷.

There Is No Safe Amount of Alcohol To Drink

For many years, stakeholders have heavily promoted the use of alcohol as beneficial for heart disease. All recent evidence points to the conclusion that alcohol ingestion should be totally avoided when possible. There are no defined safe limits for alcohol.

In 2022, the World Heart Federation published a policy brief debunking the notion that alcohol was beneficial for heart health stating, "Contrary to popular opinion, alcohol is not good for the heart".⁸ The report points out that some studies that previously showed cardiovascular benefits from drinking alcohol were flawed.

Recent research points out that many chronic conditions are linked to alcohol usage. Studies have now found that alcohol consumption may accelerate genetic aging, shrink brain tissue, and increase the risk of cardiovascular disease.

Dr Carina Ferreira-Borges, acting Unit Lead for Noncommunicable Disease Management and Regional Advisor for Alcohol and Illicit Drugs in the World Health Organization Regional Office for Europe states the following:

"We cannot talk about a so-called safe level of alcohol use. It does not matter how much you drink – the risk to the drinker's health starts from the first drop of any alcoholic beverage. The only thing that we can say for sure is that the more you drink, the more harmful it is – or, in other words, the less you drink, the safer it is.⁸"

REFERENCES:

¹ Day, Andrew. "Gut Microbiome Dysbiosis in Alcoholism: Consequences for Health and Recovery." *Frontiers in Cellular and Infection Microbiology* 12 (March 3, 2022). <u>https://doi.org/10.3389/fcimb.2022.840164</u>.

² Engen, Patrick A., Sean J. Green, Robert M. Voigt, et al. "The Gastrointestinal Microbiome: Alcohol Effects on the Composition of Intestinal Microbiota." *Alcohol Research* 37, no. 2 (2015): 223–36. <u>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4590619/</u>.

³ Nicoletti, Andrea, Francesca R. Ponziani, Maria Biolato, et al. "Intestinal Permeability in the Pathogenesis of Liver Damage: From Non-Alcoholic Fatty Liver Disease to Liver Transplantation." *World Journal of Gastroenterology* 25, no. 33 (September 7, 2019): 4814–34. <u>https://doi.org/10.3748/wjg.v25.i33.4814</u>.

⁴ Subramaniyan, Vijaya, Sathesh Chakravarthi, Ravindran Jegasothy, et al. "Alcohol-Associated Liver Disease: A Review on Its Pathophysiology, Diagnosis, and Drug Therapy." *Toxicology Reports* 8 (2021): 376–95. <u>https://doi.org/10.1016/j.toxrep.2021.02.010</u>.

 ⁵ Anya Topiwala, Klaus P. Ebmeier, Thomas Maullin-Sapey, and Thomas E. Nichols, "No Safe Level of Alcohol Consumption for Brain Health: Observational Cohort Study of 25,378 UK Biobank Participants," *NeuroImage: Clinical* 35 (2022): 103066, <u>https://doi.org/10.1016/j.nicl.2022.103066</u>.

⁶ White, Brian A., Gabriel P. Ramos, and Sunanda Kane. "The Impact of Alcohol in Inflammatory Bowel Diseases." *Inflammatory Bowel Diseases* 28, no. 3 (March 2022): 466–73. <u>https://doi.org/10.1093/ibd/izab089</u>.

⁷ Biddinger, Kathryn J., Carl A. Emdin, Maria E. Haas, et al. "Association of Habitual Alcohol Intake with Risk of Cardiovascular Disease." *JAMA Network Open* 5, no. 3 (2022): e223849.

https://doi.org/10.1001/jamanetworkopen.2022.3849.

⁸ Arora, Megha, Ahmed ElSayed, Benedikt Beger, et al. "The Impact of Alcohol Consumption on Cardiovascular Health: Myths and Measures." *Global Heart* 17, no. 1 (2022): 45. <u>https://doi.org/10.5334/gh.1132</u>

AVOID ALL FORMS OF TOBACCO INCLUDING E-CIGARETTES (VAPING)



THE HARMFUL EFFECTS OF TOBACCO USE ON THE DIGESTIVE TRACT

Tobacco use remains a significant public health issue and is wellrecognized for its detrimental impact on the respiratory and

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cardiovascular systems. However, tobacco use has a pervasive effect on the digestive tract as well.

<u>1. Oral Cavity</u>

The mouth serves as the initial point of contact for tobacco toxins, which include nicotine, tar, polycyclic aromatic hydrocarbons (PAHs), and reactive oxygen species (ROS). Tobacco use is strongly associated with oral diseases such as periodontitis, oral leukoplakia, and oral cancers. Smoking and smokeless tobacco products contribute to microbial dysbiosis in the oral cavity, shifting the balance towards pathogenic bacterial species like *Porphyromonas gingivalis* and *Fusobacterium nucleatum*.

Nicotine and other toxins reduce salivary flow, leading to dry mouth (xerostomia) and impaired clearance of food debris and bacteria, which exacerbate periodontal disease¹.

2. Esophagus

Tobacco use is a major risk factor for esophageal cancer². It also exacerbates gastroesophageal reflux disease (GERD), which, if chronic, can lead to a precancerous condition known as Barrett's esophagus and to an increased risk of cancer.

Recent studies suggest that the carcinogenic components of tobacco, including nitrosamines, may directly damage the esophageal mucosa and contribute to the malignant transformation of epithelial cells³. The association between smoking and achalasia, a motility disorder of the esophagus, has also been documented⁴.

3. Stomach

The gastric lining is sensitive to the detrimental effects of tobacco, as evidenced by its role in promoting peptic ulcer disease⁵. Nicotine stimulates gastric acid secretion and impairs the production of protective mucus, predisposing the stomach to ulceration⁶. Additionally, smoking has been shown to delay gastric emptying, contributing to dyspeptic symptoms. Tobacco also has been found to have a synergistic effect with *Helicobacter pylori* infection, exacerbating the inflammatory response and increasing the risk of gastric cancer⁷.

4. Small Intestine

Tobacco use affects the small intestine by altering its motility and permeability. Nicotine has been found to disrupt the tight junctions between enterocytes, contributing to increased intestinal permeability⁸. This disruption can lead to malabsorption and nutrient deficiencies.

Smoking also is associated with an increased risk of Crohn's disease, an inflammatory bowel disease (IBD) that predominantly affects the small intestine⁹.

Nicotine alters the immune response and microbial composition, promoting a pro-inflammatory environment¹⁰.

5. Large Intestine

The large intestine is also adversely affected by tobacco use. Smoking has been linked to an increased risk of colorectal polyps and colorectal cancer¹¹. The carcinogenic effects are mediated through the induction of oxidative stress, DNA damage, and changes in gut microbiota composition¹².

Studies have shown that smokers harbor a gut microbiome profile distinct from non-smokers, with a reduction in beneficial bacteria like *Faecalibacterium prausnitzii* and an increase in proinflammatory species¹³. These alterations may contribute to the development of colorectal cancer and inflammatory conditions like ulcerative colitis¹⁴.

6. Pancreas and Liver

Tobacco use significantly increases the risk of pancreatic cancer¹⁵. The pathophysiologic mechanisms involved include the activation of pro-carcinogenic pathways, such as the K-ras oncogene, and the promotion of chronic pancreatitis, a known precursor to cancer¹⁶.

In the liver, smoking has been associated with metabolic associated fatty liver disease (MAFLD), formerly referred to as nonalcoholic fatty liver disease (NAFLD) and its progression to steatohepatitis¹⁷. Nicotine can promote hepatic lipid accumulation and inflammation through its effects on adipokines and insulin resistance¹⁸.

7. Summary

The adverse effects of tobacco on the digestive tract are extensive, ranging from microbial dysbiosis in the oral cavity to carcinogenesis in the large bowel. The complex interplay between tobacco toxins, host immunity, and the resident microbiota creates a pro-inflammatory and carcinogenic environment throughout the digestive tract. Efforts to reduce tobacco use and promote cessation are critical in preventing these harmful outcomes.

REFERENCES:

1. Marttila, E., et al. "Tobacco-Induced Oral Dysbiosis and Its Role in Periodontal Disease." Journal of Periodontology 92, no. 3 (2021): 453– 467.

2. Lagergren, J., et al. "Smoking and Esophageal Cancer: Mechanistic Insights and Future Perspectives." Cancer Epidemiology, Biomarkers & Prevention 28, no. 12 (2019): 1853–1858.

3. Chen, X., et al. "Nitrosamines in Tobacco and Esophageal Cancer Risk." Cancer Letters 483 (2020): 25–33.

4. "Esophageal Motility Disorders." Diseases of the Esophagus 35, no. 5 (2022): doac010.

5. Salvo, E. M., et al. "Peptic Ulcer Disease in Smokers: An Update on Management and Prevention." World Journal of Gastroenterology 25, no. 38 (2019): 5377–5389.

6. Tan, S., et al. "Smoking and Gastric Cancer: Mechanistic Insights." Oncotarget 11, no. 27 (2020): 2610–2618. 7. Kondo, Y., et al. "Helicobacter Pylori Infection, Smoking, and Their Synergistic Effects on Gastric Carcinogenesis." Gut Microbes 13, no. 1 (2021): 177–187.

8. Basson, A., et al. "Nicotine's Role in Modulating Small Intestinal Permeability." Journal of Gastroenterology and Hepatology 36, no. 4 (2021): 652–660.

9. Cosnes, J., et al. "Smoking and Crohn's Disease: What Are the Mechanisms?" Inflammatory Bowel Diseases 25, no. 6 (2019): 969–978.

10. Peyrin-Biroulet, L., et al. "Tobacco and IBD: A Double-Edged Sword." Nature Reviews Gastroenterology & Hepatology 18 (2021): 240–252.

11. Giovannucci, E., et al. "Smoking and Colorectal Cancer: Epidemiological and Molecular Considerations." Gastroenterology 158, no. 6 (2020): 1402–1415.

12. Blaut, M., et al. "Gut Microbiota and Colorectal Cancer: Mechanistic Insights from Human and Animal Models." Gut Microbes 14, no. 1 (2022): 193–207.

13. Usyk, M., et al. "The Effect of Tobacco on the Gut Microbiome and Colorectal Health." Gut Microbes 12, no. 1 (2021): 1–12.

14. Lin, J. N., et al. "Smoking and Ulcerative Colitis: Epidemiological Insights." American Journal of Gastroenterology 115, no. 7 (2020): 1135– 1142.

15. Park, Joo-Hyun, et al. "Smoking Cessation and Pancreatic Cancer Risk in Individuals With Prediabetes and Diabetes: A Nationwide Cohort Study." Journal of the National Comprehensive Cancer Network 21, no. 11 (2023): 1149–1155.e3.

16. Han, Xiao, et al. "Effect of Smoking Cessation on the Likelihood of Pancreatitis and Pancreatic Cancer." Tobacco Induced Diseases 22 (2024).

17. Xu, Jiatong, et al. "Cigarette Smoke Contributes to the Progression of MASLD: From the Molecular Mechanisms to Therapy." Cells 14, no. 3 (2025): Article 221.

18. Hamer, Henrike M., David Jonkers, Koen Venema, Frans J. Troost, and Daisy M. Jonkers. "The Role of Butyrate on Colonic Function." Alimentary Pharmacology & Therapeutics 27, no. 2 (2008): 104–119.

19. den Besten, Gijs, Kees van Eunen, Alex Groen, Klaske Venema, Daan Reijngoud, and Barbara Bakker. "The Role of Short-Chain Fatty Acids in the Interplay between Diet, Gut Microbiota, and Host Energy Metabolism." Journal of Lipid Research 54, no. 9 (2013): 2325–2340.

20. Louis, Petra, and Harry J. Flint. "Diversity, Metabolism and Microbial Ecology of Butyrate-Producing Bacteria from the Human Large Intestine." FEMS Microbiology Letters 294, no. 1 (2009): 1–8.

21. Canani, Roberto Berni, Margherita Di Costanzo, Ludovica Leone, Monica Pedata, Rosaria Meli, and Antonio Calignano. "Potential Beneficial Effects of Butyrate in Intestinal and Extraintestinal Diseases." World Journal of Gastroenterology 17, no. 12 (2011): 1519–1528.

22. Louis, Petra, and Sylvia H. Duncan. "Prospects for Prebiotic Intervention in Inflammatory Bowel Disease." Gut Microbes 8, no. 2 (2017): 95–101.

23. Liu, Huan, Liping Wang, and Yong Q. Chu. "Butyrate: A Double-Edged Sword for Health?" Advances in Nutrition 9, no. 1 (2018): 21–29.

24. Zhang, Yiqiang, et al. "Butyrate Inhibits Interleukin-17 and Generates Tregs to Ameliorate Colitis." Nature Communications 9 (2018): 1–13.

25. Kelly, Christopher J., et al. "Crosstalk between Microbiota-Derived Short-Chain Fatty Acids and Intestinal Epithelial HIF Augments Tissue Barrier Function." Cell Host & Microbe 17, no. 5 (2015): 662–671. 26. Parada Venegas, Daniela, et al. "Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases." Frontiers in Immunology 10 (2019): 277.

27. van der Beek, Christina M., et al. "Role of Short-Chain Fatty Acids in Colonic Inflammation, Carcinogenesis, and Mucosal Protection." Nutrition Reviews 75, no. 4 (2017): 286–305.

28. Koh, Aaron, et al. "From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites." Cell 165, no. 6 (2016): 1332– 1345.

29. Morrison, Douglas J., and Tom Preston. "Formation of Short Chain Fatty Acids by the Gut Microbiota and Their Impact on Human Metabolism." Gut Microbes 7, no. 3 (2016): 189–200.

30. Sun, Meng, et al. "Microbiota-Derived Short-Chain Fatty Acids Promote Th1 Cell IL-10 Production to Maintain Intestinal Homeostasis." Nature Communications 9, no. 1 (2018): 3555.

31. Corrêa-Oliveira, Rodrigo, Fernanda B. Fachi, Renata S. Vieira, AdrianoS. Vinolo. "Regulation of Immune Cell Function by Short-Chain FattyAcids." Clinical & Translational Immunology 5, no. 4 (2016): e73.

Avoid Recreational And Illicit Drugs



Recreational drugs are substances taken for pleasure rather than for medical reasons. They are used primarily to alter one's mood, perception, or consciousness. Recreational drugs have been found to alter the intestinal microbiome.¹⁻⁵

Illicit drugs are those with no currently accepted medical use and a high potential for abuse. They include heroin, LSD, ecstasy, methaqualone, and peyote.

REFERENCES:

¹Cuesta, S., P. Burdisso, A. Segev, S. Kourrich, and V. Sperandio. "Gut Colonization by Proteobacteria Alters Host Metabolism and Modulates Cocaine Neurobehavioral Responses." *Cell Host & Microbe* 30, no. 11 (2022): 1615–1629.e5. <u>https://doi.org/10.1016/j.chom.2022.09.014.</u> ² Yang, J., Y. Xiong, Y. Bai, et al. "The Association of Altered Gut Microbiota and Intestinal Mucosal Barrier Integrity in Mice with Heroin Dependence." *Frontiers in Nutrition* 8 (2021): Article 765414. <u>https://doi.org/10.3389/fnut.2021.765414.</u>

³ Baslam, A., A. Aitbaba, A. Lamrani Hanchi, et al. "Modulation of Gut Microbiome in Ecstasy/MDMA-Induced Behavioral and Biochemical Impairment in Rats and Potential of Post-Treatment with *Anacyclus Pyrethrum* L. Aqueous Extract to Mitigate Adverse Effects." *International Journal of Molecular Sciences* 24, no. 10 (2023): 9086. <u>https://doi.org/10.3390/ijms24109086.</u>

⁴ Li, Y., D. Kong, K. Bi, and H. Luo. "Related Effects of Methamphetamine on the Intestinal Barrier via Cytokines, and Potential Mechanisms by Which Methamphetamine May Occur on the Brain-Gut Axis." *Frontiers in Medicine* 9 (2022): Article 783121.

https://doi.org/10.3389/fmed.2022.783121.

⁵ Inserra, A., G. Giorgini, S. Lacroix, et al. "Effects of Repeated Lysergic Acid Diethylamide on the Mouse Brain Endocannabinoidome and Gut Microbiome." *British Journal of Pharmacology* 180, no. 6 (2023): 721–739. <u>https://doi.org/10.1111/bph.15977.</u>

MINIMIZE INHALATION OF AIR POLLUTANTS



Air Pollution and Digestive Health: A Growing Concern

Air pollution is a well-documented public health hazard, impacting respiratory and cardiovascular systems, but emerging evidence underscores its effects on digestive health. Pollutants such as particulate matter (PM), ozone (O₃), nitrogen dioxide (NO₂), and polycyclic aromatic hydrocarbons (PAHs) can enter the digestive tract via ingestion, inhalation, or bloodstream absorption.

1. The Digestive System as a Target of Pollutants

Airborne pollutants are not confined to the lungs; they can settle on food and water sources or be swallowed with mucus cleared from the respiratory tract. Once in the digestive system, these pollutants encounter a sensitive epithelial lining and a diverse gut microbiota. Both are susceptible to the toxic effects of pollutants. Research shows that particulate matter smaller than 2.5 micrometers (PM) can translocate across the intestinal barrier, triggering systemic inflammation and oxidative stress.¹

2. Impact on Gut Microbiota

The gut microbiota plays a crucial role in digestion, immune modulation, and nutrient metabolism. Air pollution, particularly PM and heavy metals, can disrupt microbial diversity and abundance, leading to dysbiosis.² Dysbiosis has been implicated in conditions such as irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), and obesity. A study in mice exposed to diesel exhaust particles revealed a significant reduction in beneficial bacteria, alongside increased populations of pro-inflammatory microbes.³

3. Gut Inflammation and Intestinal Permeability

Air pollutants can exacerbate gut inflammation through direct and indirect mechanisms. Direct exposure to pollutants such as ozone and PAHs can damage epithelial cells, while systemic inflammation from inhaled pollutants can disrupt gut homeostasis. Chronic exposure to these irritants has been linked to increased intestinal permeability, often referred to as "leaky gut," which allows harmful substances to enter the bloodstream and trigger widespread inflammation.⁴ This condition is a known risk factor for autoimmune disorders and metabolic syndrome.

<u>4. Contribution to Gastrointestinal Disorders</u>

Air pollution has been associated with a range of gastrointestinal conditions, including:

- Inflammatory Bowel Disease (IBD): Studies suggest that individuals living in areas with high air pollution levels are more likely to develop Crohn's disease and ulcerative colitis.⁵ Pollutants are thought to trigger immune dysregulation and chronic inflammation, hallmark features of IBD.
- Irritable Bowel Syndrome (IBS): While IBS is multifactorial, air pollution may exacerbate symptoms by

inducing oxidative stress and altering gut-brain communication pathways.⁶

 <u>Gastroesophageal Reflux Disease (GERD)</u>: Exposure to airborne irritants can worsen GERD symptoms, due to increased inflammation and heightened sensitivity of the esophageal lining.⁷

5. Increased Risk of Gastrointestinal Cancers

Long-term exposure to air pollution has been linked to an elevated risk of gastrointestinal cancers, particularly colorectal and gastric cancer.⁸ Pollutants such as PAHs and heavy metals can damage DNA, promote the formation of carcinogens, and impair immune surveillance, thereby facilitating tumor growth. A study involving over 500,000 participants found a significant association between PM exposure and colorectal cancer incidence.⁹

6. Mitigation Strategies

Given the pervasive nature of air pollution, mitigating its impact on digestive health requires both individual and systemic approaches:

 Air Purification: Two ways to reduce exposure to air pollution is to install a portable air filtration unit that contains a HEPA filter and an activated carbon filter in sleeping and recreational areas within the household using indoor air purifiers and incorporating air-filtering plants.

CONCLUSION:

The intersection of air pollution and digestive health is a critical but underexplored area of research. The evidence highlights how pollutants can disrupt gut microbiota, compromise intestinal barriers, and increase the risk of chronic diseases, including IBD and gastrointestinal cancers. As urbanization and industrialization continue to escalate, addressing air pollution's impact on digestive health should be a public health priority.

REFERENCES:

- Miller, M. R., C. A. Shaw, and J. P. Langrish. "From Particles to Patients: Oxidative Stress and the Cardiovascular Effects of Air Pollution." *Future Cardiology* 8, no. 4 (2012): 577–602.
- Li, J., J. Sun, H. Li, H. Deng, and X. Zhang. "Air Pollution and Gut Microbiota: A New Frontier in Health Research." *Gut Microbes* 10, no. 5 (2019): 665–676.
- ^{3.} Kish, L., A. Hotte, A. E. Kaplan, et al. "Diesel Exhaust Particles Disrupt Intestinal Microbiota and Mucosal Homeostasis." *Nature Communications* 11, no. 1 (2020): 276.
- ^{4.} Fukui, H., K. Xu, and E. Eda. "Leaky Gut and Air Pollution: The Overlooked Connection." *International Journal of Molecular Sciences* 21, no. 15 (2020): 5367.
- ^{5.} Kaplan, G. G., C. Tanyingoh, D. A. Dixon, et al. "Air Pollution and the Risk of Inflammatory Bowel Disease." *Alimentary Pharmacology & Therapeutics* 49, no. 2 (2019): 282–292.

- ^{6.} Chiu, Y. H., P. G. Kim, Y. J. Kim, et al. "Air Pollution and Functional Gastrointestinal Disorders: A Review." *Journal of Gastroenterology and Hepatology* 35, no. 1 (2020): 56–64.
- ^{7.} Zhou, J., Y. Lu, J. Ma, et al. "Airborne Pollutants and Gastroesophageal Reflux Disease Symptoms: A Cross-Sectional Study." *Environmental Research* 181 (2020): 108928.
- ^{8.} Turner, M. C., D. Krewski, M. Jerrett, et al. "Long-Term Exposure to Outdoor Air Pollution and Cancer Mortality: A Cohort Study." *The Lancet Oncology* 20, no. 9 (2019): 1270–1281.
- ^{9.} Weuve, J., J. L. James, D. Laden, et al. "Air Pollution and Colorectal Cancer Risk: Evidence from a Large Cohort Study." *Cancer Epidemiology, Biomarkers & Prevention* 30, no. 6 (2021): 1123–1130.





Restorative Sleep and the Microbiome: A Cornerstone of Digestive Well-Being

Sleep is a vital physiological process that occupies roughly onethird of human life.¹ It serves as a critical restorative period for nearly every organ system, particularly the brain, immune system, and gastrointestinal tract. Over recent decades, disruptions in sleep patterns have become increasingly prevalent due to lifestyle, environmental stressors, and technological exposure. Mounting evidence now links sleep disorders—such as insomnia, sleep fragmentation, and obstructive sleep apnea—not only to cardiometabolic conditions like obesity, diabetes, and hypertension, but also to significant alterations in gut microbial composition and function.

Sleep is not a homogenous state but rather a cycle of dynamic and predictable stages that alternate throughout the night.² These include non-rapid eye movement (NREM) stages (1 through 3, with stage 3 being slow-wave or deep sleep) and rapid eye movement (REM) sleep. NREM stage 3 is crucial for physical repair, immune modulation, and microbial regulation, while REM sleep supports neural plasticity, memory consolidation, and emotional regulation. Disruption of this cycle, especially fragmentation of slow-wave and REM sleep, has been shown to induce systemic inflammation and negatively impact the gut microbiota.

Emerging studies using both animal models and human cohorts have demonstrated that inadequate or fragmented sleep can reduce microbial diversity and skew the microbial profile toward pro-inflammatory organisms.³ Sleep deprivation appears to promote the overgrowth of taxa associated with dysbiosis, including pathobionts from the phyla Proteobacteria and Firmicutes, while reducing populations of beneficial organisms like *Faecalibacterium prausnitzii*, known for its butyrate production. This disruption in microbial equilibrium not only contributes to gut inflammation and increased intestinal permeability (commonly known as "leaky gut") but also affects the bidirectional gut-brain axis, exacerbating mood disorders, cognitive decline, and poor sleep quality—a self-reinforcing feedback loop.

Conversely, consistent and restorative sleep supports the flourishing of beneficial microbes, enhances the production of short-chain fatty acids (SCFAs) like butyrate, and promotes mucosal immunity.⁴ SCFAs have been shown to interact with Gprotein coupled receptors and influence enteroendocrine cell function, modulate circadian rhythms in gut epithelial cells, and even affect sleep-promoting pathways through the vagus nerve. This suggests that one cannot restore digestive well-being or rebalance the microbiome without addressing sleep hygiene as a core therapeutic intervention.

The gut microbiome itself appears to have a circadian rhythm, with fluctuations in microbial abundance and metabolite production tied to the host's light-dark and feeding cycles.⁵ Sleep disturbances may therefore desynchronize this natural rhythm, impairing digestion, nutrient absorption, and immune surveillance. Restoring this harmony may require multifaceted approaches, including dietary interventions rich in fermentable fiber, timed feeding schedules, stress reduction, and prioritizing sleep quality.

In summary, restorative sleep is not a passive state but an active process that governs the integrity of the digestive ecosystem.⁶ Through its regulation of microbial diversity, metabolic activity, mucosal barrier integrity, and neuroimmune communication, sleep should be regarded as an essential component of any comprehensive strategy to restore and maintain gut health. In the pursuit of digestive well-being, sleep must no longer be considered secondary—it is foundational.

REFERENCES:

- ^{1.} Benedict, Christian, and Jonathan Cedernaes. "Could a Good Night's Sleep Improve Your Microbiota?" *Nature Reviews Gastroenterology & Hepatology* 19, no. 1 (2022): 3–4.
- ^{2.} Irwin, Michael R. "Sleep and Inflammation: Partners in Sickness and in Health." *Nature Reviews Immunology* 19, no. 11 (2019): 702–715.
- ^{3.} Anderson, J. R., et al. "A Preliminary Examination of Gut Microbiota, Sleep, and Cognitive Flexibility in Healthy Older Adults." *Sleep Medicine* 38 (2017): 104–107.
- ^{4.} Poroyko, V. A., et al. "Chronic Sleep Disruption Alters Gut Microbiota, Induces Systemic and Adipose Tissue Inflammation and Insulin Resistance in Mice." *Scientific Reports* 6 (2016): 35405.
- ^{5.} Gonzalez, M. M., and E. S. Aston-Jones. "Circadian Regulation of Arousal: Role of the Locus Coeruleus Noradrenergic System." *Sleep* 29, no. 10 (2006): 1327–1336.

 ^{6.} Thaiss, Christoph A., et al. "Microbiota Diurnal Rhythmicity Programs Host Transcriptome Oscillations." *Cell* 167, no. 6 (2016): 1495– 1510.e12.

AVOID MEDICATING WITH MULTIPLE UNREGULATED DRUGS HYPER-POLYPHARMACY



DEFINITION:

The word "hyper-polypharmacy" is a portmanteau combining "hyper" meaning excessive and "polypharmacy" which refers to the use of multiple medications, usually ten or more. The term emphasizes that extreme numbers of medications present risks including adverse drug reactions, alteration of the gut microbe populations, medication errors and greater health costs.

Most Supplements Are Unregulated:

Many medications taken are sold as unregulated dietary supplements. The supplement industry operates under different regulatory conditions compared to prescription medications. This leads to significant challenges in ensuring the safety and efficacy of these products.

Unlike pharmaceuticals, which must undergo rigorous testing and approval processes by the U.S. Food and Drug Administration (FDA) before they can be marketed, over-the- counter supplements do not require pre-market approval from the FDA. This means that the responsibility for the safety and efficacy of dietary supplements lies primarily with the manufacturers and not with the regulatory agency.¹

Many dietary supplements are manufactured overseas, where regulations and manufacturing standards can vary widely. In some countries, the lack of stringent regulatory oversight and quality assurance measures can result in products that are of questionable quality and may even contain harmful contaminants or not contain the advertised ingredients at all.^{2, 3}

FDA Oversight Is Limited:

This situation is compounded by the fact that the FDA's authority over dietary supplements is limited to post-market regulation, which means the agency can only act against a supplement if it is proven to be unsafe after it has already been sold to consumers.⁴ The minimal oversight by the FDA in this area leads to a market flooded with products with claims related to health that are not always substantiated by scientific evidence. Rarely are these claims supported by robust scientific studies, and the results of those studies that are conducted are often not widely published or peer reviewed as those concerning prescription drugs.

This lack of transparency and accountability can put consumers at risk, who may believe they are consuming safe and effective products when this may not be the case.

Given these concerns, it is critical for consumers to remain skeptical of bold claims related to health made by dietary supplement manufacturers.

Adverse Drug Reactions (ADRs): One of the most significant risks associated with hyperpolypharmacy is the heightened potential for adverse drug reactions (ADRs). The interaction between multiple medications (drug-drug interactions) can lead to unpredictable side effects where one drug may inhibit or enhance the metabolism of another, reducing efficacy or increasing toxicity.

A healthcare professional should be consulted before using any new dietary supplement.

OTHER RISKS OF HYPER-POLYPHARMACY

Polypharmacy Cascade: The use of multiple medications (prescription and non-prescription) can trigger a polypharmacy

cascade, wherein the side effects of one drug are mistakenly interpreted as symptoms of another condition, leading to further medication prescriptions. This vicious cycle can exacerbate health issues and complicate treatment regimens.

Cognitive Impairment: The cognitive burden imposed by managing numerous medications can lead to medication errors, non-adherence, and cognitive impairment. This, in turn, increases the risk of adverse outcomes such as falls, hospitalizations, and diminished quality of life.

REFERENCES:

¹ U.S. Food and Drug Administration, Dietary Supplement Products & Ingredients.

² Aliyu, Abubakar Ahmad, et al. "A Review on Dietary Supplements: Health Benefits, Market Trends, and Challenges." *International Journal of Scientific Development and Research* 5, no. 11 (2020): 26–35.

³ U.S. Pharmacopeia. (2024). Regulatory reform is necessary to help ensure the quality of dietary supplements. USP Global Public Policy Position.

⁴ Office of Dietary Supplements - National Institutes of Health, "Regulations Governing Dietary Supplements."

Effect On The Microbiome: Many medications, including antibiotics, antacids, and psychotropic medications, can disrupt the gut microbe population, reducing beneficial bacteria and allowing pathogenic bacteria to thrive. <u>Alteration Of Microbe Metabolism</u>: Changes in gut microbes can affect the metabolism of medications, leading to unpredictable drug levels and potential toxicity or therapeutic failures.

AVOID DRINKING UNPASTEURIZED MILK OR INGESTING PRODUCTS MADE FROM UNPASTURIZED MILK



The following excerpt comes from the Food and Drug Administration letter to State, Local, and Tribal Health Partners... dated May 6, 2024.

"Based on the limited research and information available, we do not know at this time if the HPAI H5N1 virus can be transmitted to humans through consumption of raw milk and products made from raw milk from infected cows. However, exposures on affected farms are associated with three documented cases of H5N1 illness in dairy workers. While the introduction into interstate commerce of raw milk for human consumption is prohibited under the FDA's authority, we know that a number of states permit the intrastate sale of raw milk for human consumption, with varying structures and requirements to these state programs.

Because of our concerns related to HPAI H5N1 virus in raw milk, we are providing the following recommendations for states as we continue to work together to address this novel issue:

- 1. Distribute messaging to the public about the health risks of consuming raw milk and raw milk products. Health risks include illness, miscarriages, stillbirths, kidney failure and death. (source: Food Safety and Raw Milk/ FDA)
- 2. Monitor dairy cattle herds for signs of illness that would indicate infection with the HPAI H5N1 virus.
- 3. Producers should continue to discard milk, with suitable protocols, from symptomatic cows.
- 4. Any raw milk or raw milk products from exposed cattle that are fed to calves, or any other animals should be heattreated or pasteurized."

Based on FDA advice, the consumption of raw milk and products made from raw milk should be restricted.

ALL MILK AND MILK PRODUCTS SHOULD BE PASTEURIZED!



If raw milk products undergo pasteurization after the fermentation process, the product will no longer contain live organisms.

Since probiotics are live microorganisms that confer health benefits, the heating process during pasteurization will kill beneficial probiotic bacteria.

However, milk products may have live probiotic cultures added after the pasteurization process. In those cases, the milk product will still contain live organisms and can be considered a probiotic.

The label of such a product will contain a phrase like "contains live and active cultures" or will list specific probiotic strains in the ingredients.

GET 20-30 MINUTES OF MODERATE PHYSICAL ACTIVITY AT LEAST FIVE DAYS PER WEEK



The Multifaceted Health Benefits of Physical Activity and Risks of Sedentary Behavior

Introduction: The health benefits of physical activity are welldocumented in the scientific literature. Regular engagement in physical exercise is associated with reduced risks of chronic conditions, including cardiovascular disease, type II diabetes, and psychiatric disorders such as depression. Conversely, sedentary behavior—characterized by sitting or lying down with minimal energy expenditure—poses significant health risks, notably increasing the risk of type II diabetes and cardiovascular mortality. **Health Benefits of Physical Activity:** Multiple studies underscore the positive impact of physical activity on health outcomes. Regular exercise has been shown to lower the incidence of cardiovascular disease through mechanisms such as improved vascular health, enhanced metabolic profiles, and regulation of blood pressure and lipid levels¹. Additionally, research has consistently found that exercise reduces the risk of developing type II diabetes by improving insulin sensitivity and glycemic control². Physical activity has also been identified as a protective factor against depression, potentially due to its ability to enhance endorphin release and modulate neurotransmitter activity³.

<u>Risks of Sedentary Behavior</u>: In contrast, sedentary behavior is associated with adverse health effects. Defined as sitting or reclining activities that expend low amounts of energy, prolonged sedentary behavior correlates with an increased risk of metabolic syndrome, type II diabetes, and cardiovascular-related mortality⁴. Studies indicate that even individuals who meet recommended physical activity levels are at risk if their overall sedentary time is excessive⁵. This suggests that reducing sitting time is as important as engaging in regular physical exercise.

Physical Activity and the Gut Microbiome: Emerging research highlights the influence of physical activity on the gut microbiome, an integral part of human health. Regular exercise modulates the intestinal immune system, potentially reducing inflammation and enhancing gut barrier function⁶. Physical activity can also

accelerate intestinal transit time, which may prevent harmful microbial overgrowth⁷. Furthermore, increased blood flow induced by exercise supports mucosal health and nutrient absorption⁸. Physical activity has also been associated with changes in bile metabolism, which plays a role in microbial composition and digestive health⁹.

CONCLUSION:

The evidence overwhelmingly supports the benefits of regular physical activity and underscores the risks associated with a sedentary lifestyle. By incorporating consistent movement into daily life, individuals can mitigate the risk of chronic diseases, enhance mental health, and promote a balanced gut microbiome, reinforcing the interconnected nature of physical activity and overall well-being.

REFERENCES:

- ^{1.} Thompson, Paul D., Barry A. Franklin, Safdar S. Al-Zaiti, Beth A. Balady, Michael H. Bittner, Nehal N. Clark, Deborah R. Cohen, et al. "Exercise-Related Acute Cardiovascular Events and Potential Deleterious Adaptations Following Long-Term Exercise Training: Placing the Risks into Perspective—An Update: A Scientific Statement from the American Heart Association." *Circulation* 141, no. 13 (2020): e705– e736. <u>https://doi.org/10.1161/CIR.00000000000749</u>.
- ^{2.} Colberg, Sheri R., Ronald J. Sigal, Jane E. Yardley, Michael C. Riddell, David W. Dunstan, Paddy C. Dempsey, Delaine T. Horton, et al. "Physical Activity/Exercise and Diabetes: A Position Statement of the

American Diabetes Association." *Diabetes Care* 39, no. 11 (2016): 2065–2079. <u>https://doi.org/10.2337/dc16-1728</u>.

- ^{3.} Mikkelsen, Kim, Michael Stojanovska, Susan Polman, and Lily Stojanovska. "Exercise and Mental Health." *Maturitas* 106 (2017): 48– 56. <u>https://doi.org/10.1016/j.maturitas.2017.09.003</u>.
- ^{4.} Matthews, Charles E., Sarah M. George, Steven C. Moore, Heather R. Bowles, Aaron Blair, Yikyung Park, Albert Hollenbeck, and Arthur Schatzkin. "Amount of Time Spent in Sedentary Behaviors and Cause-Specific Mortality in US Adults." *American Journal of Clinical Nutrition* 95, no. 2 (2012): 437–445. <u>https://doi.org/10.3945/ajcn.111.019620</u>.
- ^{5.} Ekelund, Ulf, Jostein Steene-Johannessen, Wendy J. Brown, Mari H. Fagerland, Nils Petter Aspvik, Sigmund A. Anderssen, Peter T. Katzmarzyk, et al. "Does Physical Activity Attenuate, or Even Eliminate, the Detrimental Association of Sitting Time with Mortality? A Harmonised Meta-Analysis of Data from More Than 1 Million Men and Women." *The Lancet* 388, no. 10051 (2016): 1302–1310. <u>https://doi.org/10.1016/S0140-6736(16)30370-1.</u>
- ^{6.} Clarke, Siobhain F., Eileen F. Murphy, Orla O'Sullivan, Amanda J. Lucey, Mark Humphreys, Aoife Hogan, Paul Ross, et al. "Exercise and Associated Dietary Extremes Impact on Gut Microbial Diversity." *Gut* 63, no. 12 (2014): 1913–1920. <u>https://doi.org/10.1136/gutjnl-2013-</u> <u>306541.</u>
- ^{7.} O'Sullivan, Orla, Owen Cronin, Siobhain F. Clarke, Eileen F. Murphy, Paul W. O'Toole, Fergus Shanahan, and Paul D. Cotter. "Exercise and the Microbiota." *Gut Microbes* 6, no. 2 (2015): 131–136. <u>https://doi.org/10.1080/19490976.2015.1011875</u>.
- ^{8.} Batacan, Romeo B., Mitch J. Duncan, Vincent J. Dalbo, Patrick S. Tucker, and Andrew S. Fenning. "Effects of High-Intensity Interval Training on Cardiometabolic Health: A Systematic Review and Meta-

Analysis of Intervention Studies." *British Journal of Sports Medicine* 51, no. 6 (2017): 494–503. <u>https://doi.org/10.1136/bjsports-2015-095841</u>

^{9.} Allen, Jacob M., Laura J. Mailing, Gregory M. Niemiro, Robert Moore, Matthew D. Cook, Bryan A. White, Kelly S. Holscher, and Jeffrey A. Woods. "Exercise Alters Gut Microbiota Composition and Function in Lean and Obese Humans." *Medicine and Science in Sports and Exercise* 50, no. 4 (2018): 747–757.

https://doi.org/10.1249/MSS.00000000001495.

INCORPORATING "HEALTHY FATS" INTO A DIVERSE, MICROBIOME-

SUPPORTING DIET



A diet that supports both the host and the host's microbiome goes beyond simply ingesting a wide array of plant-based fibers, polyols, polyphenols, resistant starches, legumes, whole grains, nuts, and seeds.¹ While these components are essential for feeding the gut microbiome and generating beneficial microbial metabolites like short-chain fatty acids (SCFAs), equally important is the thoughtful inclusion of "healthy fats" — lipids that support cellular, metabolic, and cardiovascular health.

"Healthy fats", including monounsaturated fatty acids (MUFAs) and polyunsaturated fatty acids (PUFAs), play critical roles in maintaining membrane fluidity, supporting brain function, and modulating inflammation.² Sources like extra virgin olive oil, avocados, nuts (especially walnuts and almonds), fatty fish (such as salmon, sardines, and mackerel), and seeds (like flaxseeds and chia seeds) provide a rich array of these beneficial lipids.³ Omega-3 PUFAs, in particular, are well-known for their anti-inflammatory and cardioprotective effects, influencing triglyceride levels, blood pressure, and endothelial function.⁴

Importantly, the integration of "healthy fats" works synergistically with the microbiome-supporting components of the diet. For example, certain PUFAs can directly shape microbial composition, while the fat-soluble vitamins (A, D, E, and K) they carry are essential for immune regulation and mucosal integrity.⁵ Moreover, combining fats with fiber-rich or polyphenol-rich foods can enhance the bioavailability of critical phytonutrients and optimize nutrient absorption.⁶ Conversely, overconsumption of saturated fats (common in processed meats and industrial snacks) or trans fats has been linked to dysbiosis, increased intestinal permeability, and pro-inflammatory metabolic profiles.⁷ Thus, a healthy diet prioritizes minimally processed, unsaturated fat sources that align with microbiome and systemic health goals.

In summary, dietary health recognizes the importance of both microbial-accessible carbohydrates and high-quality lipids. Together, these elements foster a metabolic environment conducive to long-term health, supporting not only the host but also the symbiotic microbial communities within.

REFERENCES

¹ Stephen J. O'Keefe, "Diet, Microorganisms and Their Metabolites, and Colon Cancer," *Nature Reviews Gastroenterology & Hepatology* 13, no. 12 (2016): 691–706, <u>https://doi.org/10.1038/nrgastro.2016.165</u>.

² Dariush Mozaffarian and Jason H. Y. Wu, "Omega-3 Fatty Acids and Cardiovascular Disease: Effects on Risk Factors, Molecular Pathways, and Clinical Events," *Journal of the American College of Cardiology* 58, no. 20 (2011): 2047–67, <u>https://doi.org/10.1016/j.jacc.2011.06.063</u>.

³ Alice H. Lichtenstein et al., "Diet and Lifestyle Recommendations Revision 2006: A Scientific Statement from the American Heart Association Nutrition Committee," *Circulation* 114, no. 1 (2006): 82–96, <u>https://doi.org/10.1161/CIRCULATIONAHA.106.176158</u>

⁴ Philip Calder, "Omega-3 Fatty Acids and Inflammatory Processes: From Molecules to Man," *Biochemical Society Transactions* 45, no. 5 (2017): 1105–15, <u>https://doi.org/10.1042/BST20160474</u>.

⁵ Annemarie Boleij and Jos P. M. van Dissel, "The Role of Fat-Soluble Vitamins in the Regulation of Immunity," *Nutrients* 12, no. 1 (2020): 38, <u>https://doi.org/10.3390/nu12010038</u>.

⁶ Gunter G. C. Kuhnle et al., "Effect of Food Matrix on the Bioavailability of Isoflavones from Soy Foods," *Nutrition* 24, no. 3 (2008): 213–20, <u>https://doi.org/10.1016/j.nut.2007.11.001</u>.

⁷ Anthony F. Domenichiello and Richard P. Bazinet, "Saturated Fatty Acids and Dysbiosis: Mechanisms and Implications," *Biochimica et Biophysica Acta (BBA) - Molecular and Cell Biology of Lipids* 1864, no. 9 (2019): 1109–22, <u>https://doi.org/10.1016/j.bbalip.2019.07.001</u>.

<u>CONSIDER DRINKING</u> GREEN TEA



THE BENEFITS OF GREEN TEA

Green tea, derived from the leaves of *Camellia sinensis*, has been consumed for centuries as a staple of traditional medicine. It is a beverage that has been celebrated for its health-promoting properties.

Green tea is a versatile beverage with a rich history of health benefits, supported by modern science. Its unique composition of antioxidants, catechins, and polyphenols underpins its ability to combat oxidative stress, support cardiovascular and metabolic health, protect the brain, and possibly reduce cancer risk.

Green tea exemplifies the profound impact of dietary choices on overall health. By embracing green tea as part of a healthy lifestyle, individuals can harness its myriad benefits to enhance both physical and mental well-being.

Unlike black and oolong teas, green tea undergoes minimal oxidation during processing, preserving its unique bioactive compounds, including polyphenols, catechins, and flavonoids. Modern scientific research has extensively explored the myriad benefits of green tea, from its potent antioxidant effects to its role in preventing chronic diseases and promoting overall well-being. The following examines the key bioactive components of green tea and their impacts on immunity, metabolism, cardiovascular health, and neuroprotection.

Rich in Bioactive Compounds

Green tea generates bioactive molecules that contribute to its health benefits:

• <u>Catechins</u>: Green tea contains high concentrations of catechins, especially epigallocatechin gallate (EGCG), which is the most abundant and bioactive catechin. EGCG is a potent

antioxidant that combats oxidative stress, reduces inflammation, and neutralizes free radicals.

- **Flavonoids:** These polyphenols enhance vascular health and reduce oxidative damage.
- Caffeine and L-Theanine: The combination of caffeine, a mild stimulant, and L-theanine, an amino acid, stimulates an alert but calm mental state.

Antioxidant and Anti-Inflammatory Properties

The rich polyphenol content in green tea gives it potent antioxidant properties:

- <u>Reduction of Oxidative Stress</u>: EGCG protects cells and DNA from oxidative damage caused by free radicals, reducing the risk of chronic diseases.
- Anti-Inflammatory Effects: Green tea reduces inflammation by inhibiting pro-inflammatory cytokines like TNF-α and IL-6. These effects help manage inflammatory conditions such as arthritis and inflammatory bowel disease.

Cardiovascular Health

Green tea has been shown to improve various markers of cardiovascular health:

 <u>Cholesterol Regulation</u>: Studies show that green tea consumption lowers LDL cholesterol while increasing HDL cholesterol, reducing the risk of atherosclerosis.

- **Improved Vascular Function:** Flavonoids in green tea enhance the bioavailability of nitric oxide, improving endothelial function and promoting vasodilation.
- <u>Blood Pressure Control</u>: Regular green tea consumption is associated with modest reductions in blood pressure, contributing to lower risks of heart disease and stroke.

Metabolic and Weight Management Benefits

Green tea is often recognized for its role in supporting metabolism and weight management:

- <u>Thermogenesis and Fat Oxidation</u>: The combination of catechins and caffeine enhances metabolic rate and promotes fat oxidation, aiding in weight loss.
- <u>Blood Sugar Control:</u> Green tea has been shown to improve insulin sensitivity and lower fasting blood sugar levels, reducing the risk of type 2 diabetes.

Neuroprotection and Cognitive Health

Green tea's bioactive compounds benefit the brain by promoting cognitive health and reducing the risk of neurodegenerative diseases:

 <u>L-Theanine and Mental Clarity</u>: The synergistic effect of caffeine and L-theanine improves focus, attention, and alertness without causing jitteriness.

- <u>Neuroprotective Effects</u>: EGCG crosses the blood-brain barrier and protects neurons by reducing oxidative stress and inflammation, lowering the risk of Alzheimer's and Parkinson's diseases.
- Improved Mood: Regular green tea consumption is associated with reduced symptoms of anxiety and depression, likely due to its ability to modulate neurotransmitters.

Cancer Prevention

Emerging research suggests that green tea may help reduce cancer risk:

- <u>Anti-Cancer Properties</u>: EGCG induces apoptosis (cell death) in cancer cells while sparing normal cells, reducing the progression of certain cancers such as breast, prostate, and colorectal cancer.
- Inhibition of Carcinogenesis: Polyphenols inhibit the formation of harmful compounds like nitrosamines and neutralize carcinogenic free radicals.

Immune Support

Green tea strengthens the immune system through its antimicrobial and immunomodulatory effects:

 Antibacterial and Antiviral Properties: EGCG inhibits the growth of harmful bacteria like *Helicobacter pylori* and viruses like influenza, protecting against infections. Immune Modulation: Polyphenols enhance the activity of T cells and reduce excessive immune responses, contributing to immune balance.

Skin and Anti-Aging Benefits

The antioxidant and anti-inflammatory properties of green tea promote healthy skin:

- Protection Against UV Damage: Polyphenols in green tea reduce skin damage from UV radiation, decreasing the risk of photoaging and skin cancer.
- Anti-Aging Effects: The reduction of oxidative stress helps preserve skin elasticity and prevent wrinkle formation.

Limitations and Considerations

While green tea offers numerous health benefits, it should be consumed in moderation:

- **Excessive Caffeine:** High consumption can cause jitteriness, insomnia, and digestive discomfort.
- Iron Absorption: Polyphenols may inhibit iron absorption from non-heme sources, potentially leading to anemia in susceptible individuals.
- **Drug Interactions:** Green tea may interact with certain medications, including anticoagulants and beta-blockers, requiring caution.

REFERENCES:

- Bhagat, Arpan R., and Amélia Martins Delgado. "Review of the Role of Fluid Dairy in Delivery of Polyphenolic Compounds in the Diet: Chocolate Milk, Coffee Beverages, Matcha Green Tea, and Beyond." *Journal of AOAC International* 102, no. 5 (2019): 1365–1374. <u>https://doi.org/10.5740/jaoacint.19-0129</u>.
- Gunec, Cagri Baris. "A Mini Review on the Relationship Between Coffee and Tea Consumption and Iron Absorption in the Gut – Iron Deficiency Anemia." *Japan Journal of Clinical & Medical Research* 3, no. 1 (2023). <u>https://doi.org/10.47363/jjcmr/2023(3)145</u>.
- Chen, Wei, et al. "EGCG and Neuroprotection." *Molecular Nutrition & Food Research* 61, no. 6 (2017): 1600673. <u>https://doi.org/10.1002/mnfr.201600673.img1.wsimg.com</u>
- Di Sotto, Antonella, et al. "Efficacy and Safety of Oral Green Tea Preparations in Skin Ailments: A Systematic Review of Clinical Studies." *Nutrients* 14, no. 15 (2022): 3149. <u>https://doi.org/10.3390/nu14153149</u>.
- Dostal, Allison M., et al. "Green Tea Extract Does Not Impair Iron Absorption in Iron-Deficient Women." *The American Journal of Clinical Nutrition* 102, no. 4 (2015): 816–822. <u>https://doi.org/10.3945/ajcn.115.111336</u>.
- Dulloo, Abdul G., et al. "Green Tea and Metabolic Health: A Review." Obesity Reviews 12, no. 5 (2011): e621–e638. <u>https://doi.org/10.1111/j.1467-789X.2010.00758.x</u>.
- Fujiki, Hirota, et al. "Green Tea and Cancer Prevention." Proceedings of the Japan Academy, Series B 84, no. 2 (2008): 58–69. <u>https://doi.org/10.2183/pjab.84.58</u>.
- Joseph, Suja, and Deepak Nallaswamy. "A Glimpse Through the Origin, Composition, and Biomedical Applications of Green Tea and Its

Polyphenols: A Review." *Plant Science Today* 1, no. 1 (2024): 1–10. https://doi.org/10.14719/pst.3297.

- Kansal, Vinay, et al. "Regular Intake of Green Tea Polyphenols Suppresses the Development of Nonmelanoma Skin Cancer through miR-29-Mediated Epigenetic Modifications." *Journal of Clinical Medicine* 11, no. 2 (2022): 398. <u>https://doi.org/10.3390/jcm11020398</u>.
- Katiyar, Santosh K., et al. "Green Tea Polyphenols: Photoprotection and Skin Health." *The Journal of Investigative Dermatology* 123, no. 5 (2004): 982–986. <u>https://doi.org/10.1111/j.0022-202X.2004.23442.x</u>.
- Kim, Hae-Jeung, et al. "The Neuroprotective Effects of Green Tea Catechins: A Review." *Antioxidants* 10, no. 6 (2021): 854. <u>https://doi.org/10.3390/antiox10060854.img1.wsimg.com</u>
- Liang, Gaolin, et al. "Epigallocatechin Gallate (EGCG) Inhibits Tumorigenesis by Regulating Signal Transduction Pathways." *Experimental and Therapeutic Medicine* 2, no. 3 (2011): 483–487. <u>https://doi.org/10.3892/etm.2011.237</u>.
- Mancini, Elena, et al. "Green Tea and Weight Management." *Metabolites* 11, no. 6 (2021): 382. <u>https://doi.org/10.3390/metabo11060382</u>.
- Lazrak, Meryem, et al. "Tea Consumption Reduces Iron Bioavailability from NaFeEDTA in Nonanemic Women and Women with Iron Deficiency Anemia: Stable Iron Isotope Studies in Morocco." *The Journal of Nutrition* 151, no. 8 (2021): 2400–2407. <u>https://doi.org/10.1093/jn/nxab159</u>.
- Serafini, Mauro, et al. "Bioavailability of Polyphenols and Antioxidants in Functional Foods: A Case Study on Green Tea." *Food Science and Technology Research* 12, no. 4 (2006): 225–230. <u>https://doi.org/10.3136/fstr.12.225</u>

MATCHA GREEN TEA



Matcha, a finely ground powder of specially grown and processed green tea leaves, has gained widespread attention for its unique composition and remarkable health benefits. The cultivation and preparation of matcha sets it apart from other types of green tea, as it involves shading the tea plants several weeks before harvest to increase chlorophyll content, enhancing the concentration of bioactive compounds.

1. Antioxidant Properties

Matcha is known for its exceptionally high concentration of antioxidants, particularly catechins, a type of polyphenol. Among these, epigallocatechin gallate (EGCG) stands out for its potent ability to neutralize free radicals and reduce oxidative stress. Studies show that matcha contains up to 137 times more EGCG than regular green tea.

- Mechanism of Action: EGCG stabilizes free radicals, reducing cellular damage and slowing the aging process. Research suggests that this may help prevent chronic diseases associated with oxidative stress, such as cardiovascular diseases and neurodegenerative disorders.¹
 - **Evidence:** A study published in the *Journal of Chromatography A* (2019) demonstrated that matcha's antioxidant potential exceeds that of traditional green tea by several-fold, primarily due to its higher EGCG concentration.²

2. Metabolic Benefits

Matcha has been shown to enhance metabolic function, making it a valuable tool for weight management and improving overall metabolic health.

- <u>Thermogenesis and Fat Oxidation</u>: The catechins in matcha, combined with its caffeine content, have a synergistic effect on increasing thermogenesis (calorie burning) and fat oxidation. Studies indicate that regular consumption of matcha can boost the basal metabolic rate by 8-10%.³
- Blood Sugar Regulation: Matcha helps regulate glucose levels and improve insulin sensitivity, reducing the risk of type 2 diabetes. A 2020 study in *Nutrients* found that matcha intake significantly lowered fasting blood glucose in individuals with impaired glucose tolerance.⁴

3. Neuroprotective and Cognitive-Enhancing Effects

Matcha's unique combination of bioactive compounds supports brain health and enhances cognitive function.

- L-Theanine and Calm Focus: Matcha is rich in L-theanine, an amino acid that promotes relaxation without drowsiness. Ltheanine increases alpha brain wave activity, which is associated with a state of alert calmness, and works synergistically with caffeine to improve attention and focus.⁵
- Neurodegenerative Diseases: The antioxidants in matcha, particularly EGCG, protect neurons from oxidative damage and may reduce the risk of conditions like Alzheimer's and Parkinson's diseases. Animal studies have shown that EGCG can inhibit the aggregation of beta-amyloid plaques, a hallmark of Alzheimer's disease.⁶

4. Cancer Prevention

The chemopreventive potential of matcha is one of its most welldocumented medicinal properties.

- Mechanism of Action: EGCG and other catechins exert anticancer effects by inducing apoptosis (programmed cell death) in cancer cells, inhibiting angiogenesis (formation of new blood vessels in tumors), and reducing metastasis.
- **Evidence:** Research published in *Cancer Prevention Research* (2021) found that matcha extract significantly suppressed the

proliferation of breast and prostate cancer cells in vitro.⁷ Additionally, regular green tea consumption has been associated with a lower risk of various cancers, including lung, colorectal, and liver cancers.^{^8}

5. Immune Modulation

Matcha supports the immune system by enhancing the body's defense mechanisms.

- <u>Catechins and Antimicrobial Activity</u>: EGCG exhibits antimicrobial properties that help fight bacterial, viral, and fungal infections. For instance, it has been shown to inhibit the growth of *Staphylococcus aureus* and *Candida albicans*.
- Immune Cell Activation: Matcha also promotes the activity of regulatory T cells, which help maintain immune homeostasis and prevent autoimmune diseases.

6. Cardiovascular Benefits

Regular consumption of matcha has been linked to improved heart health.

- **<u>Cholesterol Reduction</u>**: Catechins in matcha lower LDL ("bad") cholesterol levels while increasing HDL ("good") cholesterol.
 - <u>Blood Pressure Control</u>: Matcha's vasodilatory effects, mediated by its antioxidants, contribute to reduced blood pressure and improved arterial function.

CONCLUSION:

The medicinal properties of matcha green tea are rooted in its unique combination of bioactive compounds, which work synergistically to promote overall health. From its unparalleled antioxidant capacity to its metabolic, neuroprotective, and cancerpreventive effects, matcha stands out as a powerful natural remedy supported by scientific evidence. Incorporating matcha into a balanced diet may provide numerous health benefits and contribute to disease prevention, making it an excellent addition to an integrated approach to well-being.⁹

REFERENCES:

- ^{1.} Suzuki, Y., T. Koyama, M. Nakamura, and H. Yamashita. "Antioxidant Activity of Catechins in Green Tea." *Journal of Chromatography A* 1601 (2019): 10–15.
- ^{2.} Tilles-Tirkkonen, T., K. Aittola, R. Männikkö, P. Absetz, M. Kolehmainen, U. Schwab, J. Lindström, T. Lakka, J. Pihlajamäki, and L. Karhunen. "Eating Competence Is Associated with Lower Prevalence of Obesity and Better Insulin Sensitivity in Finnish Adults with Increased Risk for Type 2 Diabetes: The StopDia Study." *Nutrients* 12, no. 1 (2020): 104. <u>https://doi.org/10.3390/nu12010104</u>.
- ^{3.} Kakuda, T. "Neuroprotective Effects of L-Theanine on Alzheimer's Disease Models." *Frontiers in Neuroscience* 14 (2020): 325.
- ^{4.} Singh, B. N., M. Shankar, and R. K. Srivastava. "Anticancer Properties of Green Tea Catechins: A Mechanistic Review." *Cancer Prevention Research* 14, no. 3 (2021): 233–245.

- ^{5.} Koyama, T., Y. Suzuki, and H. Yamashita. "Effects of Matcha on Glucose Tolerance and Cardiovascular Risk Factors." *Journal of Nutritional Biochemistry* 100 (2022): 108891.
- ^{6.} Lambert, J. D., and R. J. Elias. "The Antioxidant and Pro-Oxidant Activities of Green Tea Polyphenols: A Role in Cancer Prevention." *Archives of Biochemistry and Biophysics* 501, no. 1 (2010): 65–72. <u>https://doi.org/10.1016/j.abb.2010.06.013.</u>
- ^{7.} Reygaert, W. C. "The Antimicrobial Possibilities of Green Tea." *Frontiers in Microbiology* 5 (2014): 434. <u>https://doi.org/10.3389/fmicb.2014.00434.</u>
- ^{8.} Imai, K., K. Suga, and K. Nakachi. "Cancer-Preventive Effects of Drinking Green Tea Among a Japanese Population." *Preventive Medicine* 26, no. 6 (1997): 769–775. <u>https://doi.org/10.1006/pmed.1997.0242.</u>
- ^{9.} Cabrera, C., R. Artacho, and R. Giménez. "Beneficial Effects of Green Tea—A Review." *Journal of the American College of Nutrition* 25, no. 2 (2006): 79–99. <u>https://doi.org/10.1080/07315724.2006.10719518.</u>

SECTION TWENTY-NINE

INTRODUCTION TO THE

BIOTIC FAMILY

UNDERSTANDING PREBIOTICS, PROBIOTICS, POSTBIOTICS, AND SYNBIOTICS

While public interest in prebiotics, probiotics, postbiotics, and synbiotics has surged—spurred by claims of improved digestion, immunity, and even mental health—many of these terms are now used freely in consumer marketing, applied to everything from beverages to beauty products and even pet food. This popular enthusiasm has often outpaced the scientific evidence. In response, organizations such as the International Scientific Association for Probiotics and Prebiotics (ISAPP) and the American Gastroenterological Association (AGA) have issued evidence-based guidelines to clarify definitions, set minimum standards of efficacy, and promote responsible use of these bioactives in both clinical practice and consumer products.

Human health depends on a dynamic interaction between dietary inputs, microbial activity, and the metabolites produced from this interplay. This relationship can be simplified into a biochemical model: Prebiotics (A) + Probiotics (B) = Postbiotics (C).

$\mathbf{A} + \mathbf{B} = \mathbf{C}$

The Functional Equation of Gut Health

From Fuel to Function

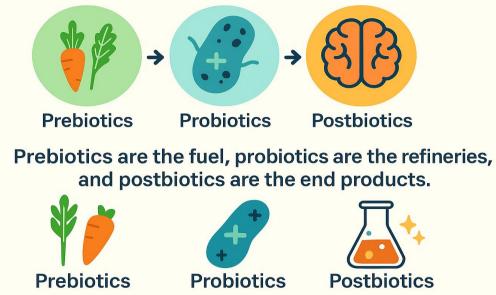


Figure 1: From Fuel to Function – An overview of how prebiotics, probiotics, and postbiotics interact to influence health.

In this framework, A represents prebiotics—the indigestible fibers, oligosaccharides, and polyphenols that nourish beneficial gut microbes. B stands for probiotics—the living microorganisms that consume these substrates and, through fermentation and metabolism, transform them into compounds that benefit the host. C refers to postbiotics—the end products of microbial action, including short-chain fatty acids, neurotransmitters, immune modulators, and vitamins that influence health outcomes throughout the body. Prebiotics (A) can be thought of as the raw fuel—nutrient-rich substrates like dietary fibers and oligosaccharides—that enter the digestive ecosystem and pass through the small intestines undigested. On their own, they have limited immediate value to the host.

Probiotics (B), in turn, are like biological refineries—specialized microbes capable of breaking down the unabsorged dietary fiber into bioactive compounds. The end products of this microbial metabolism are postbiotics (C), which include short-chain fatty acids (like butyrate), vitamins, neuroactive molecules, and immune modulators. Postbiotics are building blocks that power host physiology, mediate repair, and modulate systemic health.

In this way, prebiotics (A) + probiotics (B) = postbiotics (C) is not merely a mathematical formulation, but a metabolic equation of interdependence—fuel, processor, and end product.²

The health of the host depends not on a single intervention, but on the full sequence: proper substrates, metabolically competent microbes, and bioactive end products that can be absorbed and utilized. Therapeutic interventions that overlook any one element of this triad risk being incomplete or ineffective.

REFERENCES:

^{1.} Kennedy, E. A., et al. "Diet Outperforms Microbial Transplant to Drive Microbiome Recovery in Mice." *Nature* (April 30, 2025).

 ^{2.} Aguilar-Toalá, J. E., et al. "Postbiotics: An Evolving Term within the Functional Foods Field." *Trends in Food Science & Technology* 75 (2018): 105–114. <u>https://doi.org/10.1016/j.tifs.2018.03.009</u>

PREBIOTICS

Prebiotics are selectively fermented, non-digestible food components that confer a health benefit by modulating the composition or activity of the gut microbiota.¹ However, not all fibers are prebiotics—they must meet specific criteria for selective utilization by beneficial microbes.^{2,7,8,9}

While most recognized prebiotics are carbohydrates—such as inulin, fructooligosaccharides, and galactooligosaccharides—the field is expanding. Emerging research shows that certain noncarbohydrate compounds can also act as prebiotics, provided they are selectively metabolized by gut microbes and support host health. Examples include plant-derived polyphenols, specific amino acids, and even some peptides, all of which may influence microbial composition and metabolite output.

Prebiotics are often discussed in the broader context of MACs, or microbiota-accessible carbohydrates. MACs refer to any dietary carbohydrates that can be metabolized by gut microbes. However, not all MACs qualify as prebiotics. For a compound to be considered a true prebiotic, it must not only be fermentable by microbes, but also demonstrate selective utilization by beneficial organisms and confer a measurable health benefit to the host.

PROBIOTICS

Probiotics are live microorganisms which, when administered in adequate amounts, confer a health benefit on the host. The majority of probiotic microbes can carry out the chemical process of fermentation, particularly within the anaerobic (oxygen-free) environment of the colon. This fermentation of carbohydrates yields acids and metabolites that help acidify the gut, suppress pathogens, and promote mucosal health. However, a probiotic's ability to ferment is not a required characteristic. According to accepted definitions, a probiotic must simply demonstrate that its presence confers a measurable benefit to the host—regardless of its metabolic mechanism or oxygen tolerance. For example, *Saccharomyces boulardii*, a yeast-based probiotic, is capable of surviving in oxygen-rich environments and contributes to gut health through both fermentation and immune modulation, despite not being an obligate anaerobe.^{3,4}

Natural Sources of Probiotics

Kefir (Pasteurized)

A tangy, fermented milk drink made by inoculating milk with kefir grains—a symbiotic culture of bacteria and yeasts (SCOBY). Despite pasteurization post-fermentation reducing live content, some commercial kefirs may retain viable strains such as Lactobacillus kefiri and Saccharomyces unisporus, contributing to improved digestion and immune modulation.¹

<u>Kombucha</u>

A fizzy, tangy tea fermented by a SCOBY of acetic acid bacteria and yeast. Kombucha contains organic acids, antioxidants, and live microbes like *Gluconacetobacter xylinus* and *Zygosaccharomyces*, which may support gut barrier integrity and liver detoxification.²

Brined Pickles (Unpasteurized)

Cucumbers fermented in saltwater brine (not vinegar) can harbor Lactobacillus plantarum and other lactic acid bacteria. These strains aid in digestion and exhibit antimicrobial properties against foodborne pathogens.³

<u>Miso</u>

A fermented soybean paste used in Japanese cuisine. Fermentation with Aspergillus oryzae, along with lactic acid bacteria, creates a savory, umami-rich product with peptides that may lower blood pressure and support gut microbiota diversity.⁴

<u>Tempeh</u>

A firm, cake-like product made by fermenting cooked soybeans with the mold Rhizopus oligosporus. Though pasteurized for safety, tempeh retains prebiotic fibers and may contain residual live spores that support gut health and protein absorption.⁵

<u>Natto</u>

Fermented soybeans known for their strong flavor and sticky texture. Rich in Bacillus subtilis, natto produces nattokinase, an enzyme associated with cardiovascular benefits and clot prevention.⁶

<u>Kimchi</u>

A spicy Korean side dish of fermented cabbage and vegetables. Typically includes Lactobacillus brevis and Lactobacillus plantarum, along with beneficial metabolites like short-chain fatty acids (SCFAs) and vitamins.⁷

Yogurt (Pasteurized)

A dairy product fermented with Lactobacillus bulgaricus and Streptococcus thermophilus. Although pasteurization may reduce live content, many yogurts are supplemented with viable strains such as Lactobacillus acidophilus, offering benefits in lactose digestion and immune support.⁸

Apple Cider Vinegar with the "Mother"

Raw, unfiltered vinegar containing strands of proteins, enzymes, and beneficial bacteria like Acetobacter. The "mother" may aid digestion and regulate blood sugar levels.⁹

Kvass

A traditional Eastern European fermented beverage made from rye bread or beets. Contains lactic acid bacteria and yeast, offering mild probiotic effects and antioxidants.¹⁰

Coconut Kefir (Pasteurized)

A non-dairy version of kefir made from coconut water fermented with kefir grains. Often pasteurized post-fermentation, it may retain probiotic residues and offers electrolytes, organic acids, and a mild antimicrobial effect.¹¹

<u>Yakult</u>

A commercially available probiotic drink containing Lactobacillus casei Shirota. Extensively studied for its ability to reduce constipation, improve gut motility, and modulate immune function.¹²

REFERENCES:

¹ Bourrie, B. C. T., R. E. Willing, and G. Reid. "Kefir: A Probiotic Fermented Milk." Frontiers in Microbiology 7 (2016): 647.

² Villarreal-Soto, S. A., et al. "Understanding Kombucha Tea Fermentation: A Review." Journal of Food Science 83, no. 3 (2018): 580–88.

³ Di Cagno, R., et al. "Fermented Vegetables: Microbial Changes and Health Benefits." Current Opinion in Biotechnology 49 (2018): 97–104.

⁴ Shurtleff, W., and A. Aoyagi. Miso and Soy Sauce: A Japanese Viewpoint. Soyinfo Center, 2012. ⁵ Steinkraus, K. H. "Fermentations in World Food Processing."
Comprehensive Reviews in Food Science and Food Safety 1, no. 1 (2002):
23–32.

⁶ Fujita, M., et al. "Nattokinase: A Potent and Safe Fibrinolytic Enzyme." Nutrition Reviews 63, no. 4 (2005): 111–21.

⁷ Lee, M.-E., et al. "The Effects of Kimchi Consumption on Gut Microbiota." Journal of Microbiology and Biotechnology 27, no. 6 (2017): 1125–32.

⁸ Marco, M. L., et al. "Health Benefits of Fermented Foods: Microbiota and Beyond." Current Opinion in Biotechnology 44 (2017): 94–102.

⁹ Johnston, C. S., et al. "Vinegar Ingestion at Bedtime Moderates Waking Glucose Concentrations in Adults with Well-Controlled Type 2 Diabetes." Diabetes Care 30, no. 11 (2007): 2814–15.

¹⁰ Četojević-Simin, D. D., et al. "Bioactive Components and Antioxidant Activity of Kvass Beverages." Food & Function 6, no. 1 (2015): 226–32.

¹¹ Rosa, D. D., et al. "Milk and Dairy Products and Their Impact on the Gut Microbiota and Health." Frontiers in Microbiology 10 (2019): 1046.

¹² Tuohy, K. M., et al. "The Probiotic Strain Lactobacillus casei Shirota Enhances Natural Killer Cell Activity in Humans." European Journal of Clinical Nutrition 57, no. 12 (2003): 1362–69.

Postbiotics

Postbiotics are the bioactive metabolites produced when probiotics ferment prebiotic substrates. These include short-chain fatty acids like butyrate, acetate, and propionate, as well as bacteriocins, enzymes, and peptidoglycans. They modulate inflammation, support gut barrier function, and influence systemic processes through gut-brain and gut-liver signaling pathways.⁵

SYNBIOTICS

Synbiotics are formulations that combine prebiotics and probiotics to enhance the viability and effectiveness of beneficial microbes. They may be complementary (independent effects) or synergistic (designed to support each other directly). Synbiotics are used in clinical and dietary applications to restore balance in the gut microbiome.⁶

EXAMPLES OF SYNBIOTIC COMBINATIONS

This table summarizes both natural and commercial synbiotic combinations—pairings of probiotics and prebiotics that work together to promote gut health. Natural sources rely on whole food combinations, while commercial products often use clinically tested strains and prebiotic compounds.

Cumbiatia	Drahiatia	Drahiatia	Turne	Notes /
Synbiotic	Probiotic	Prebiotic	Туре	Notes /
Source	Microbe(s)	Component		Citation
Yogurt +	L. acidophilus,	Inulin, FOS	Natural	Roberfroid
Banana	B. lactis	(banana)		2007 ¹
Kimchi + Leeks	L. plantarum	Inulin (leeks)	Natural	Marco et al. 2021 ²
Kefir +	Lactococcus,	Polyphenols,	Natural	Śliżewska et al.
Blueberries	Lactobacillus spp.	pectin		2022 ³
Tempeh +	Bacillus	Resistant	Natural	Gibson et al.
Barley	subtilis	starch, β-		2017 ⁴
		glucans		
VSL#3 +	Multiple	Psyllium husk	Commercial	Maurer et al.
Psyllium	strains	fiber		2020 ⁵
Seed DS-01	24 strains	Pomegranate	Commercial	Seed Health
	(e.g. <i>, L.</i>	polyphenol		White Paper
	fermentum)	blend		·
Pendulum	A. muciniphila,	Inulin (chicory	Commercial	Martens et al.
Glucose	C. butyricum	root)		2023 ⁶
Control				
Florastor®	S. boulardii	Soluble fiber	Commercial	McFarland
Synbiotic		blends		2015 ⁷
				-

REFERENCES:

¹ Roberfroid, Marcel. "Prebiotics: The Concept Revisited." *The Journal of Nutrition* 137, no. 3 Suppl 2 (2007): 830S–837S. https://doi.org/10.1093/jn/137.3.830S.

² Marco, Maria L., et al. "Health Benefits of Fermented Foods: Microbiota and Beyond." *Current Opinion in Biotechnology* 70 (2021): 135–141. <u>https://doi.org/10.1016/j.copbio.2021.04.004</u>.

³ Śliżewska, Katarzyna, et al. "Synergistic Effects of Kefir and Polyphenol-Rich Berries on Gut Microbiota." *Nutrients* 14, no. 3 (2022): 672. <u>https://doi.org/10.3390/nu14030672</u>. ⁴Gibson, Glenn R., et al. "The Concept of Synbiotics and Their Role in Gut Health." *Nutrition Research Reviews* 30, no. 2 (2017): 105–118. <u>https://doi.org/10.1017/S0954422417000079</u>.

⁵ Maurer, J. M., et al. "Synergistic Synbiotics: A Review of Mechanistic Interactions Between Prebiotics and Probiotics." *Food Research International* 137 (2020): 109682.

https://doi.org/10.1016/j.foodres.2020.109682.

Seed Health. "Seed DS-01[™] Daily Synbiotic White Paper." Accessed May 2025. https://seed.com/ds-01-white-paper

⁶ Martens, Eric C., et al. "Harnessing *Akkermansia muciniphila* in Synbiotic Combinations to Improve Metabolic Health." *Nature Metabolism* 5 (2023): 198–211. <u>https://doi.org/10.1038/s42255-023-00799-4</u>.

⁷ McFarland, Lynne V. "Systematic Review and Meta-Analysis of Saccharomyces boulardii in Adult Patients." World Journal of Gastroenterology 21, no. 20 (2015): 7459–7473. https://doi.org/10.3748/wjg.v21.i20.7459.

FOOD FIRST: TRUSTING NATURE'S DESIGN

While scientific understanding of prebiotics, probiotics, and postbiotics has led to a booming market of supplements, powders, and fortified products, the most effective and time-tested sources remain whole foods. Nature packages these bioactives within plant and fermented matrices—often combining fibers, polyphenols, organic acids, and live microbes—in ways that are chemically stable and biologically functional.

Fermented foods like yogurt, kefir, kimchi, and sauerkraut offer naturally occurring probiotics alongside metabolically active byproducts. Similarly, legumes, bananas, oats, and asparagus deliver fermentable fibers and oligosaccharides that fuel the microbiome.

By contrast, many commercial supplements deliver isolated strains or purified compounds divorced from their natural context sometimes at doses or in formats that bypass microbial ecology altogether. Nature knows best how to combine, balance, and release these compounds through digestion and microbial transformation.

Rather than seeking "silver bullets" in pill form, a food-first approach to gut health honors the complexity of our evolutionary relationship with diet and microbes. Indeed, recent findings show that dietary intervention outperforms even microbial transplantation in restoring microbiome function—highlighting the foundational role of food over laboratory manipulation.¹⁰

That said, there are times when manufactured forms of prebiotics, probiotics, postbiotics, and synbiotics may be helpful or necessary. This can include situations where whole-food sources are unavailable, unaffordable, unpalatable, or culturally restricted. Clinical conditions, dietary limitations, or accessibility challenges may also warrant supplementation. Still, when natural options are available and tolerated, food-based sources remain the preferred and most integrative approach to nurturing the microbiome.

FERMENTATION

The chemical engine driving the A + B = C relationship is fermentation. Prebiotics must be fermentable substrates resistant to digestion but accessible to microbial enzymes. The colon, an anaerobic chamber, serves as the body's primary fermentation bioreactor where probiotics convert prebiotics into postbiotics.

Understanding this continuum—prebiotic inputs, probiotic agents, and postbiotic outputs—offers a systems-level perspective on how diet influences health. Synbiotics optimize this cycle for preventive and therapeutic purposes in gastrointestinal and systemic health.

REFERENCES:

^{1.} Gibson, Glenn R., and Marcel B. Roberfroid. "Dietary Modulation of the Human Colonic Microbiota: Introducing the Concept of Prebiotics." *The Journal of Nutrition* 125, no. 6 (1995): 1401–12. <u>https://doi.org/10.1093/jn/125.6.1401</u>.

^{2.} Bindels, Laure B., Joël Walter, and Patrice D. Cani. "Towards a More Comprehensive Concept for Prebiotics." *Nature Reviews Gastroenterology & Hepatology* 12, no. 5 (2015): 303–10. <u>https://doi.org/10.1038/nrgastro.2015.47</u>.

^{3.} Hill, Colin, et al. "Expert Consensus Document: The International Scientific Association for Probiotics and Prebiotics Consensus Statement on the Scope and Appropriate Use of the Term Probiotic." *Nature Reviews Gastroenterology & Hepatology* 11, no. 8 (2014): 506–14. <u>https://doi.org/10.1038/nrgastro.2014.66</u>.

^{4.} Sonnenborn, U., and J. Schulze. "The Non-Pathogenic Escherichia coli Strain Nissle 1917 – Features of a Versatile Probiotic." *Microbial Ecology* *in Health and Disease* 21, no. 3–4 (2009): 122–158. <u>https://doi.org/10.3109/08910600903444267</u>.

^{5.} Salminen, Seppo, et al. "The International Scientific Association for Probiotics and Prebiotics (ISAPP) Consensus Statement on the Definition and Scope of Postbiotics." *Nature Reviews Gastroenterology & Hepatology* 18, no. 9 (2021): 649–667. <u>https://doi.org/10.1038/s41575-</u> <u>021-00440-6</u>.

^{6.} Swanson, Kelly S., et al. "The International Scientific Association for Probiotics and Prebiotics (ISAPP) Consensus Statement on the Definition and Scope of Synbiotics." *Nature Reviews Gastroenterology & Hepatology* 17, no. 11 (2020): 687–701. https://doi.org/10.1038/s41575-020-0344-2.

^{7.} Sonnenburg, J.L., and Sonnenburg, E.D. "Starving our Microbial Self: The Deleterious Consequences of a Diet Deficient in Microbiota-Accessible Carbohydrates." *Cell Metabolism* 20, no. 5 (2014): 779–786. https://doi.org/10.1016/j.cmet.2014.07.003.

^{8.} Cardona, F., et al. "Benefits of Polyphenols on Gut Microbiota and Implications in Human Health." *Journal of Nutritional Biochemistry* 24, no.
8 (2013): 1415–1422. <u>https://doi.org/10.1016/j.jnutbio.2013.05.001</u>.

^{9.} Ma, N., et al. "Amino Acid–Microbiome Interaction: A Promising Target for Improving Gut Health and Function." *Amino Acids* 53, no. 2 (2021): 513–528. <u>https://doi.org/10.1007/s00726-021-02945-7</u>.

^{10.} Kennedy, Elizabeth A., Johanna L. Lampe, Christopher J. Stewart, et al. "Diet Outperforms Microbial Transplant to Drive Microbiome Recovery in Mice." *Nature* 628, no. 8027 (April 30, 2025): 341–347. <u>https://doi.org/10.1038/s41586-025-07831-2</u>.

FECAL MICROBIAL TRANSPLANTS: A REVOLUTIONARY APPROACH TO RESTORING GUT ECOSYSTEM MICROBIOTA

Fecal Microbiota Transplantation



Fecal Microbial Transplants: The Superpowered Probiotic?

Disruptions of the microbial ecosystems, known as dysbiosis, have been implicated in numerous conditions, including *Clostridium difficile* infection (CDI), inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), metabolic, and neurological disorders. Fecal microbial transplants (FMT) have emerged as a novel therapeutic strategy to restore a healthy gut microbiota by delivering a complex consortium of microorganisms derived from the stool of a healthy donor or self-banked stool.¹ In contrast to conventional probiotics, fecal microbiota transplantation (FMT) delivers a far more diverse and concentrated microbial payload—trillions of live organisms—often with dramatic therapeutic effects in conditions like *Clostridioides difficile* colitis. In cases resistant to standard therapy, FMT has demonstrated superior outcomes, often with near-complete symptom resolution in short periods of time.

Ironically, even after FMT, long-term studies show that the specific microbial strains from the donor often do not stably engraft in the recipient's gut. This finding reinforces the concept that probiotics may act more as stimulants for recovery of the host's own microbial ecosystem than as permanent residents.

The Concept Behind the Use of Fecal Microbial Transplants

FMT involves the transfer of stool—containing hundreds of billions of microorganisms across multiple kingdoms of life—from a donor to a recipient's gastrointestinal tract.² Unlike manufactured probiotics or dietary interventions that typically introduce limited microbial strains, FMT delivers a highly diverse microbial community, encompassing bacteria, viruses, fungi, protozoa, and archaea. This holistic transfer of microbiota is unparalleled in its ability to re-establish a balanced and functional gut ecosystem.

The therapeutic potential of FMT was first recognized in treating recurrent CDI, achieving cure rates exceeding 85% in clinical trials.³ Beyond CDI, FMT is being explored for other conditions like

inflammatory bowel disease, fatty liver disease, and neuropsychiatric disorders through its modulation of the gut-brain axis.⁴

Auto-Fecal Microbial Transplants: Banking of Microbiota

Auto-fecal microbial transplants (auto-FMT) involve the storage of an individual's stool during a time of health for future use. This approach eliminates the risks associated with donor-derived FMT, such as the transmission of pathogens or mismatched microbiota.⁵ Self-banking stool is particularly relevant for individuals undergoing treatments like chemotherapy or antibiotics that may disrupt their microbiota, as it provides a personalized method to restore their gut health post-treatment.⁶ Emerging studies suggest that auto-FMT could be a preventative measure against dysbiosisrelated diseases and may have applications in personalized medicine. However, the feasibility of large-scale implementation depends on advancements in stool banking technologies and regulatory frameworks.⁷

The Role of Oral Capsules in FMT Delivery

Oral encapsulated FMT, exemplified by Vowst[®]—a recently FDAapproved treatment—has revolutionized the administration of FMT. This non-invasive method eliminates the discomfort and risks associated with colonoscopic or nasogastric delivery methods.⁸ Capsules are freeze-dried, ensuring the viability of microbes while improving safety and convenience. Clinical trials have demonstrated the efficacy of oral FMT capsules in preventing recurrent CDI, with comparable success rates to traditional methods.⁹

Potential Hazards and Ethical Considerations

Despite its promise, FMT is not without risks. The use of biologic materials from another human being raises concerns about pathogen transmission, including multidrug-resistant organisms, and the possibility of transferring undesirable traits, such as metabolic profiles linked to obesity. Rigorous donor screening protocols are essential to mitigate these risks. Ethical considerations also arise regarding informed consent, especially in vulnerable populations, and the standardization of FMT procedures to ensure consistent outcomes.¹⁰

The Unparalleled Complexity of FMT

FMT's unmatched ability to deliver an entire microbial ecosystem cannot be replicated by probiotics, prebiotics, or diet alone. The constructive interaction among thousands of microbial species and subspecies in FMT facilitates the re-establishment of homeostasis in the gut. This complex interaction between microbiota and host underscores the therapeutic superiority of FMT in treating dysbiosis-related conditions.

CONCLUSION:

Fecal microbial transplants represent a groundbreaking approach to restoring gut health, offering a multifaceted solution to conditions linked to dysbiosis. While challenges such as safety, standardization, and ethical concerns remain, innovations like auto-FMT and oral capsules are paving the way for safer and more accessible treatments. As research continues to uncover the vast potential of the human microbiome, FMT stands at the forefront of transformative therapies that redefine our approach to gut health.

REFERENCES:

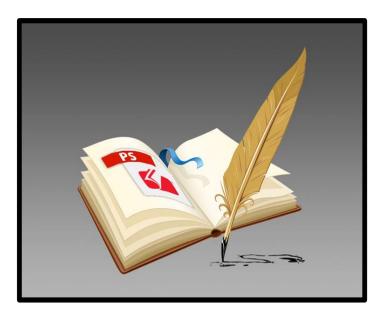
- ^{1.} Borody, T. J., and Alexander Khoruts. "Fecal Microbiota Transplantation and Emerging Applications." *Nature Reviews Gastroenterology & Hepatology* 9, no. 2 (2012): 88–96.
- ^{2.} Cryan, J. F., and T. G. Dinan. "Mind-Altering Microorganisms: The Impact of the Gut Microbiota on Brain and Behavior." *Nature Reviews Neuroscience* 13, no. 10 (2012): 701–712.
- ^{3.} Woodworth, M. H., M. D. Carpentieri, S. M. Sitchenko, and A. P. Kraft. "Auto-Fecal Microbiota Transplantations in Medical Treatments." *Journal of Translational Medicine* 17 (2019): 329.
- ^{4.} Ott, S. J., M. F. Waetzig, B. Rehman, C. G. Moltzau-Anderson, T. Bharti, and M. Scholz. "Efficacy of Auto-FMT in Gut Flora Restoration." *Gut Microbes* 4, no. 4 (2008): 293–306.
- ^{5.} Smith, M. B., S. Khoruts, and M. J. Foster. "Advances in Stool Banking Technologies." *Clinical Microbiology and Infection* 20, no. 11 (2014): 1117–1122.

- ^{6.} Khanna, S., and D. S. Pardi. "The Role of FMT Capsules in CDI Treatment." *Therapeutic Advances in Gastroenterology* 9, no. 1 (2016): 5–15.
- ^{7.} Kao, D., C. Roach, B. Silva, J. Beck, C. Rioux, T. C. Lee, and M. Louie.
 "Capsules for Fecal Transplantation in Recurrent Clostridium Difficile Infection." *Journal of the American Medical Association* 318, no. 20.
- ^{8.} Allegretti, J. R., C. Fischer, D. J. Sagi, and E. C. Smith. "Fecal Microbiota Transplantation: Risks and Safety." *Current Infectious Disease Reports* 20, no. 2 (2018): 8.
- ^{9.} Costello, S. P., L. K. Hughes, A. Waters, and M. D. Conlon. "Donor Screening in Fecal Microbiota Transplantation." *Journal of Gastroenterology and Hepatology* 30, no. 9 (2015): 1403–1409.
- ^{10.} de Groot, P. F., L. A. Frissen, M. I. de Clercq, and C. Nieuwdorp. "Ethical Considerations in Fecal Microbiota Transplantation." *Bioethics* 31, no. 9 (2017): 713–721.



POSTSCRIPT

WHAT HAPPENED TO CAROLINE?



Caroline's case was evaluated through the lens of a dysfunctional intestinal ecosystem. Her early life experiences were critical to understanding her health challenges. Born prematurely via Cesarean section and bottle-fed, she was at substantial risk for a compromised immune system.

During her first three years, Caroline had experienced multiple infections, requiring repeated courses of antibiotics that severely diminished the density and diversity of her intestinal microbiota, impairing her immune development. Throughout childhood, recurrent infections necessitated additional antibiotic treatments, further disrupting her microbial ecosystems.

In adolescence, she developed acne, leading to prolonged antibiotic use, which again reduced microbial diversity and may have eradicated species that could never be fully restored.

As a young adult, Caroline followed a diet deficient in dietary fiber, essential for sustaining a healthy microbiome. With an already compromised microbial population from early life, her lack of microbial nourishment weakened her immune defenses. This contributed to reduced protective mucus production and increased intestinal permeability, allowing toxins, microbes, and antigens to enter her system.

This persistent breach of her gut barrier triggered chronic inflammation, fueling both local intestinal symptoms and systemic health issues. Additionally, her poor oral hygiene led to periodontitis, creating another ongoing source of infection and inflammation. This oral microbial imbalance not only seeded her digestive tract with harmful bacteria but also contributed to systemic inflammatory burden.

Restoring Caroline's Microbiome

Addressing Caroline's dysbiosis was paramount. Although challenging, her recovery required a multifaceted approach, including:

- Meticulous oral hygiene and regular periodontal care
- Judicious antibiotic use to prevent further microbial disruption
- A diverse diet rich in fruits, vegetables, nuts, seeds, legumes, beans, whole grains, human milk oligosaccharides, resistant starches, polyols, and polyphenols
- The ingestion of "healthy fats"
- Lifestyle modifications: prioritizing sleep, exercise, and hydration, particularly with drinking distilled water
- Avoidance of alcohol, tobacco, and recreational drugs
- Incorporation of natural probiotics and prebiotics, prioritizing food sources rather than supplements
- Attention to air quality for reducing environmental microbial stressors
- Up-to-date immunizations to bolster immune resilience
- Reduction of unnecessary supplements to avoid potential microbiome disturbances

Implementing these strategies offered Caroline *and her microbiome* a path to improved digestive health.

Progress and Outcome

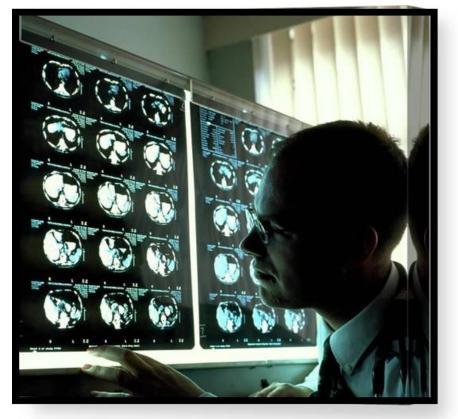
After months of commitment to these interventions, Caroline has experienced significant improvements. While not perfect, she felt markedly better. Her symptoms diminished, her energy levels increased, and her sleep became more restful. She regained mental clarity, and her body aches and pains subsided. Gastrointestinal symptoms—including burping, bloating, flatulence, and distention—decreased. Foods she had long avoided were gradually reintroduced without triggering discomfort.

Though she still experiences occasional bowel irregularity, with brief episodes of diarrhea or constipation, these occurrences are infrequent and typically linked to insufficient intake of dietary fiber or antibiotic use.

Caroline now takes greater care in her dietary choices and dental hygiene. With renewed confidence in her health, she envisions a more hopeful and sustainable future.



SECTION THIRTY-ONE A LOOK AT THE PAST AND A VIEW OF THE FUTURE



The Crossroads: Restoration or Ruin



The Human-Microbe Pact

"From the moment humans emerged as a distinct species, they forged an intimate and indispensable pact with their microbial counterparts. This synbiotic relationship was not simply a matter of coexistence but a deeply intertwined partnership. Microbes undertook vast responsibilities, performing functions humans were incapable of, yet essential for survival. These roles included aiding digestion, bolstering immunity, and offering protection. In return, humans provided their beneficial microorganisms with a safe habitat and a reliable supply of nutrients.

As humans progressed technologically and industrially, however, the commitment to this ancient pact has weakened, potentially charting a dangerous course that threatens human health and longevity.

The Microbial Pact: Foundations of Human Health

As highlighted repeatedly in this Digestive Health Guide and in the scientific literature, microbes have been pivotal in performing functions that humans cannot accomplish independently. They play a critical role in breaking down complex dietary fibers into short-chain fatty acids, which nourish human cells and regulate immune responses, among other vital processes. Without these microbial allies, human bodies would struggle to access certain nutrients or maintain a balanced immune system.

The Betrayal: Modern Lifestyle and Diet

With the advent of industrialization and changes in agricultural and food processing practices, the balance between microbes and humans has been severely disrupted. Modern diets, rich in sugars, refined carbohydrates, and processed foods, have impacted the viability of microbial populations. These foods often lack necessary fibers and are laden with substances harmful to intestinal microbes, including antimicrobials, pesticides, herbicides, and synthetic additives.

As a result, essential nutrients that support beneficial microbes remain locked away or absent from the human diet. The widespread use of antibiotics—though lifesaving—has indiscriminately decimated beneficial bacterial populations, further disrupting this delicate balance.

These disruptions have led to a marked decline in microbial diversity, density, and functionality, impairing their ability to carry out the critical functions that once sustained human health."

Consequences of Neglect: A Health Crisis

Scientists now suspect that neglecting and damaging beneficial microbes may be a major factor contributing to the rising prevalence of chronic diseases. With weakened microbial populations, the human body has become more vulnerable to deficiencies and systemic dysfunctions. The intestinal barrier, once fortified by a robust microbiome, has become more permeable, allowing toxins and pathogens to enter the bloodstream—a condition often referred to as "leaky gut."

This increased permeability is thought to drive chronic inflammation and has been linked to a range of modern ailments, including autoimmune diseases, allergies, and metabolic disorders such as obesity and diabetes. The long-term effects of this microbial neglect may well be contributing to a public health crisis that continues to unfold in the modern world.

The pivotal question facing humanity is whether we can restore our synbiotic relationship with our microbial partners.

The task is daunting but not insurmountable. The Digestive Health Guide outlines several strategies to rejuvenate the microbiome, many of which hinge on dietary shifts toward fiber-rich nutrients, avoiding toxins and drugs that disrupt microbial populations, minimizing the consumption of ultra-processed foods, seeking clean air and water, reducing antibiotic overuse, improving oral hygiene, and introducing into the diet naturally occurring probiotics and prebiotics that have been proven to support microbial health.

Understanding the complex interplay between human lifestyles, the environment, and microbial communities is critical, a point emphasized throughout this Digestive Health Guide.

A CALL TO ACTION CHARTING OUR FUTURE: RENEWING THE HUMAN-MICROBE PACT



The path we tread is fraught with the peril of continued neglect and disruption of our microbial allies. Yet, it is also illuminated by the possibility of renewal and restoration.

Recommitting to the ancient pact we share with our microbial partners is not only a matter of preserving human health but may also be crucial to ensuring the survival of our species.

<u>LIST 1</u>

FOODS CONTAINING FERMENTABLE FIBER THAT FUNCTION AS

NATURALLY OCCURRING PREBIOTICS

FRUITS

- Apples
- Apricots
- Bananas
- Blackberries
- Blueberries
- Cherries
- Coconut
- Dates
- Figs
- Kiwifruit
- Nectarines
- Oranges
- Peaches
- Pears
- Plums
- Pomegranates
- Prunes
- Raisins
- Raspberries
- Strawberries



VEGETABLES

- Acorn squash
- Artichokes
- Arugula
- Asparagus
- Avocados
- Beets
- Broccoli
- Brussels sprouts
- Cabbage
- Carrots
- Celery
- Collard greens
- Corn (sweet, boiled)
- Cauliflower
- Eggplant
- Green beans
- Green peas
- Edamame
- Kale
- Okra
- Olives
- Onions
- Parsnips
- Peppers
- Potato (baked, with skin)
- Pumpkin
- Radishes
- Rutabaga



- Shallots
- Snap peas
- Snow peas
- Spinach
- Squash
- Sweet potatoes
- Tomatoes
- Turnips
- White mushrooms
- Zucchini

<u>Nuts</u>

- Almonds
- Brazil nuts
- Cashews
- Chestnuts
- Granola
- Hazelnuts
- Macadamia nuts
- Pine nuts
- Peanuts
- Pecans
- Sunflower kernels
- Walnuts



SEEDS AND GRAINS

- Chia
- Flax
- Hemp
- Pistachios
- Pumpkin
- Quinoa
- Sesame
- Sunflower



BEANS AND LENTILS

- Wheat bran
- Baked beans
- Black beans
- Black-eyed peas
- Garbanzo beans
- Kidney beans
- Lentils
- Lima beans
- Mung beans
- Northern beans
- Navy beans
- Pinto beans
- Split peas
- Soybeans
- Soy yogurt
- Tempe
- Tofu



<u>LIST 2</u>

CHEMISTRY, DIETARY SOURCES AND COMMERCIAL AVAILABILITY OF COMMON PREBIOTICS

The following oligosaccharides are integral components of various foods and are utilized in the food and supplement industries for their beneficial effects on gut health, primarily through promoting the growth of beneficial gut bacteria. Obtaining these prebiotics through dietary sources is generally preferred over commercially prepared supplements.

1. Arabinooligosaccharides (AOS)

- <u>Chemistry</u>: Arabinooligosaccharides (AOS) are oligosaccharides composed of arabinose units. They are classified as non-digestible oligosaccharides and serve as prebiotic fibers. AOS promote the growth of beneficial gut bacteria such as *Bifidobacteria* and *Lactobacilli*.
- Dietary Sources: AOS are naturally found in various plant materials, particularly in the hemicellulose of cereals, legumes, and fruits like apples and pears.
- <u>Commercial Production</u>: Commercially, AOS are produced by hydrolyzing arabinans or arabinoxylans derived from plant sources such as beet pulp, cereal bran, or other agricultural by-

products. They are available in powder or liquid form for use in food products, dietary supplements, and functional foods.

2. Fructans

- <u>Chemistry</u>: Fructans are polysaccharides composed of fructose molecules linked together. They include inulin and other fructose polymers. Fructans are not digested by human enzymes but are fermented by gut microorganisms to produce short-chain fatty acids, contributing to gut health.
- Dietary Sources: Fructans occur naturally in foods such as chicory root, Jerusalem artichokes, garlic, onions, leeks, and asparagus.
- <u>Commercial Production</u>: Commercially, fructans like inulin are extracted from chicory root or Jerusalem artichokes. They are available as powders or syrups and are used as ingredients in various functional foods and dietary supplements.

3. Galactooligosaccharides (GOS)

- <u>Chemistry</u>: GOS consist of short chains of galactose molecules, typically with a degree of polymerization ranging from 2 to 8 sugar units. They are naturally found in human breast milk and selectively stimulate the growth and activity of beneficial gut bacteria, such as *Bifidobacteria* and *Lactobacilli*.
- **Dietary Sources:** GOS are found in smaller amounts in dairy products such as milk, yogurt, and cheese.

 <u>Commercial Production</u>: GOS is typically produced through the enzymatic treatment of lactose, where galactose residues are polymerized. It is widely used in infant formula, functional foods, and supplements.

4. Isomaltooligosaccharides (IMO)

- Chemistry: Isomaltooligosaccharides (IMO) are oligosaccharides composed of glucose units linked by α-(1→6) glycosidic bonds. They have prebiotic effects and are partially digestible.
- **Dietary Sources:** IMOs are found in lesser amounts in fermented foods like soy sauce and miso.
- <u>Commercial Production</u>: Commercial IMOs are produced through enzymatic conversion of starch, specifically from sources like corn or tapioca. They are available as sweeteners and dietary fibers in foods and supplements.

5. Mannooligosaccharides (MOS)

- <u>Chemistry</u>: Mannooligosaccharides (MOS) are oligosaccharides composed of mannose units. They are known for their ability to modulate gut microbiota and improve gut health.
- Dietary Sources: MOS can be found naturally in yeast cell walls, some legumes, and certain plant fibers.

<u>Commercial Production</u>: MOS is typically extracted from the cell walls of yeast (*Saccharomyces cerevisiae*) or produced through enzymatic hydrolysis of mannan-rich plant materials. They are used in animal feed, functional foods, and supplements.

6. Pectin-Derived Oligosaccharides (POS)

- Chemistry: Pectin-Derived Oligosaccharides (POS) are oligosaccharides derived from pectin, a complex polysaccharide found in the cell walls of plants. POS have prebiotic and anti-inflammatory properties.
- Dietary Sources: Pectin is naturally found in considerable amounts in apples, citrus fruits (oranges and lemons), and berries (strawberries, raspberries, and grapes).
- <u>Commercial Production</u>: POS are produced by the partial enzymatic or acid hydrolysis of pectin, extracted primarily from citrus peels or apple pomace. They are used in food products, supplements, and as functional ingredients.

7. Raffinose Family Oligosaccharides (RFOs)

• <u>Chemistry</u>: Raffinose Family Oligosaccharides (RFOs) include raffinose, stachyose, and verbascose. They are composed of galactose units attached to sucrose and are non-digestible by humans, acting as prebiotic fibers.

- Dietary Sources: RFOs are naturally found in legumes (such as beans, lentils, and peas), cruciferous vegetables, and whole grains.
- <u>Commercial Production</u>: RFOs are extracted from plant sources, particularly legumes, or synthesized through enzymatic processes. They are used in functional foods and as dietary supplements to promote gut health.

8. Xylooligosaccharides (XOS)

- <u>Chemistry</u>: Xylooligosaccharides (XOS) are short-chain oligosaccharides composed of xylose units linked by β-(1→4) glycosidic bonds. They are recognized for their prebiotic effects, particularly in promoting the growth of beneficial bacteria like *Bifidobacteria* and *Lactobacilli*.
- Dietary Sources: XOS are naturally present in various plantbased foods, including fruits, vegetables, and grains. Notable sources encompass bamboo shoots, carrots, onions, garlic, asparagus, and chicory root.
- <u>Commercial Production</u>: Commercially, XOS are produced through the hydrolysis of xylan-rich lignocellulosic biomass, such as corn cobs, wheat straw, and sugarcane bagasse. This process typically involves enzymatic or chemical methods to break down xylan into XOS.

9. Fructooligosaccharides (FOS) and Inulin

Chemistry: Fructooligosaccharides (FOS) and inulin are fructans, comprising fructose units linked by β-(2→1) glycosidic bonds, typically terminating with a glucose unit. They are non-digestible by human enzymes and serve as prebiotic fibers, promoting the growth of beneficial gut bacteria such as *Bifidobacteria* and *Lactobacilli*.

Agave and chicory inulin differ in their degree of polymerization (DP), referring to the number of fructose units in their chains. Agave inulin generally has a lower DP, meaning its chains are shorter compared to chicory inulin. This structural difference affects fermentation rates in the colon; agave inulin is typically fermented more rapidly than chicory inulin.

Due to its rapid fermentation, agave inulin may quickly stimulate the growth of beneficial bacteria but can also lead to faster gas production, potentially causing bloating in sensitive individuals. In contrast, chicory inulin, with its longer chains, tends to have a more sustained prebiotic effect, promoting intestinal motility and providing a consistent source of short-chain fatty acids.

 Dietary Sources: Inulin and FOS are naturally found in foods such as chicory root, Jerusalem artichokes, garlic, onions, leeks, and asparagus. **Commercial Production:** Commercially, inulin is extracted from chicory root or Jerusalem artichokes, while FOS can be synthesized from sucrose using enzymatic processes. They are available in powder or syrup forms and are used in functional foods, dietary supplements, and as fat replacers in various food products.

10. Lactulose

- <u>Chemistry</u>: Lactulose is a synthetic disaccharide composed of galactose and fructose. It is not absorbed in the small intestine and acts as a prebiotic fiber and laxative.
- Dietary Sources: Lactulose is not found naturally in foods; it is a synthetic product.
- <u>Commercial Production</u>: Lactulose is synthesized from lactose by isomerizing the glucose unit to fructose. It is used in medical settings as a laxative and in treating hepatic encephalopathy, as well as a prebiotic in functional foods and supplements.

<u>11. Maltodextrin</u>

- Chemistry: Maltodextrin is a polysaccharide composed of glucose units linked by α-(1→4) glycosidic bonds. It is partially digestible and used as a source of energy and as a thickening agent.
- Dietary Sources: Maltodextrin is not found naturally; it is produced from starch.

 <u>Commercial Production</u>: Maltodextrin is produced by the enzymatic hydrolysis of starch, typically derived from corn, rice, or potatoes. It is widely used as a food additive, energy supplement, and in sports drinks

12. Soy Oligosaccharides

- <u>Chemistry</u>: Soy oligosaccharides are a group of oligosaccharides found in soybeans, primarily consisting of raffinose and stachyose. They have prebiotic properties and contribute to the health benefits associated with soy consumption.
- Dietary Sources: Soy oligosaccharides are naturally found in soybeans and other legumes.
- Commercial Production: These oligosaccharides are extracted from soybeans during the production of soy protein or soy milk. They are available in powder or supplement form and are used in functional foods.

13. Wheat Dextrin

 <u>Chemistry</u>: Wheat dextrin is a soluble fiber derived from the partial hydrolysis of wheat starch. It is commonly used to promote regular bowel movements. A common brand of wheat dextrin is Benefiber[®].

Since wheat dextrin is derived from wheat, it may contain gluten. Individuals with celiac disease or severe gluten

sensitivity should consult a healthcare provider before using wheat dextrin.

- Dietary Sources: Wheat dextrin is not found naturally in foods; it is a processed product.
- <u>Commercial Production</u>: Wheat dextrin is produced by the enzymatic or acid hydrolysis of wheat starch. It is available as a powder or in tablet form and is used in fiber supplements, functional foods, and as a thickening agent.

REFERENCES

Arabinooligosaccharides (AOS):

Mikš, Miroslav H., et al. "Arabinooligosaccharides: A Novel Class of Prebiotics." *Journal of Nutritional Science* 3 (2014): e26.

Fructans:

Salazar, Nuria, et al. "Inulin-Type Fructans Modulate Intestinal Bifidobacterium Species Populations and Decrease Fecal Short-Chain Fatty Acids in Obese Women." *Clinical Nutrition* 34, no. 3 (2015): 501–507. <u>https://doi.org/10.1016/j.clnu.2014.06.001</u>.

Galactooligosaccharides (GOS):

Singh, Dhananjay P., et al. "Galactooligosaccharides (GOS) as Prebiotics: Recent Advances in Their Synthesis, Prebiotic Applications, and Health Benefits." *Food Bioscience* 22 (2018): 10– 19. <u>https://doi.org/10.1016/j.fbio.2017.12.003</u>.

Isomaltooligosaccharides (IMO):

Goffin, D., et al. "Will Isomalto-Oligosaccharides, a Well-Established Functional Food in Asia, Break through the European and American Market?" *Food Science and Technology* 22, no. 2 (2011): 129–134. https://doi.org/10.1016/j.tifs.2010.09.013.

Mannooligosaccharides (MOS):

Ganan, Monica, et al. "Prebiotic Potential of Mannooligosaccharides Derived from Saccharomyces cerevisiae Cell Walls: Effect on the Adhesion of Pathogens to Caco-2 Cells." *Journal of Functional Foods* 17 (2015): 356–365. <u>https://doi.org/10.1016/j.jff.2015.05.001</u>

Pectin-Derived Oligosaccharides (POS):

Chung, Wing S. F., et al. "Prebiotic Potential of Pectins and Pectic Oligosaccharides." *Journal of Functional Foods* 27 (2016): 549–561. <u>https://doi.org/10.1016/j.jff.2016.10.012</u>

Raffinose Family Oligosaccharides (RFOs):

Martínez-Villaluenga, Cristina, et al. "Raffinose Family Oligosaccharides and Sucrose Contents in 13 Spanish Lupin Cultivars." *Food Chemistry* 91, no. 4 (2005): 645–649. <u>https://doi.org/10.1016/j.foodchem.2004.06.031</u>

Xylooligosaccharides (XOS):

Haque, Md. Anamul, et al. "Xylooligosaccharides (XOS) as an Emerging Prebiotic: Their Production from Biomass Waste and Application in Health Care." *Biotechnology and Applied Biochemistry* 68, no. 5 (2021): 1081–1094. <u>https://doi.org/10.1002/bab.2080</u>

Fructooligosaccharides (FOS) and Inulin:

Kolida, Sofia, and Glenn R. Gibson. "Prebiotic Capacity of Inulin-Type Fructans." *Journal of Nutrition* 137, no. 11 (2007): 2503S– 2506S. <u>https://doi.org/10.1093/jn/137.11.2503S</u>.

Lactulose:

Vandeputte, D., et al. "Prebiotic Inulin-Type Fructans Induce Specific Changes in the Human Gut Microbiota." *Gut* 64, no. 11 (2015): 1968–1974. <u>https://doi.org/10.1136/gutjnl-2014-309126.</u>

Maltodextrin:

Wolf, B. W., et al. "Gastrointestinal Tolerance and Absorption of Isomaltooligosaccharides in Healthy Male Volunteers." *Food Additives & Contaminants* 16, no. 5 (1999): 203–209. <u>https://doi.org/10.1080/026520399283957.</u>

Soy Oligosaccharides:

Karr-Lilienthal, Lisa K., et al. "Chemical Composition and Protein Quality Comparisons of Soybeans and Soybean Meals from Five Leading Soybean-Producing Countries." *Journal of Agricultural and Food Chemistry* 52, no. 20 (2004): 6195–6200. <u>https://doi.org/10.1021/jf049795+.</u>

Wheat Dextrin:

 Gamage, Hasinika K. A. H., et al. "Fiber Supplements Derived from Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different in Vitro Effects on the Human Gut Microbiota." *Frontiers in Microbiology* 9 (2018): 1246.

https://doi.org/10.3389/fmicb.2018.01246.



FOOD ITEMS THAT CONTAIN RESISTANT STARCHES

Cooked and cooled poatoes¹

- Cooked and then cooled white potatoes
- Cooked and then cooled sweet potatoes

Green bananas²

Underripe or green bananas

<u>Plantains³</u>

Green or underripe plantains

Cooked and cooled rice⁴

- Cooked and then cooled white rice
- Cooked and then cooled brown rice

Cooked and cooled legumes⁵

- Lentils
- Chickpeas
- Black beans
- Kidney beans

Cooked and cooled pasta⁶

Cooked and then cooled pasta

Oats⁷

- Rolled oats
- Steel-cut oats

Barley⁸

- Pearl barley
- Hulled barley

<u>Cornmeal</u>

Cornmeal

Cooked and cooled millet

Cooked and then cooled millet

Cooked and cooled quinoa

Cooked and then cooled quinoa

REFERENCES:

- Bello-Pérez, L. A., L. E. Contreras-Ramos, and J. M. Méndez-Montealvo. "Isolation and Characterization of Resistant Starch from Unripe Banana Flour." *International Journal of Biological Macromolecules* 99 (2017): 59–65. <u>https://doi.org/10.1016/j.ijbiomac.2016.04.064</u>.
- ^{2.} Bhattacharya, K. R., and M. Zakiuddin Ali. "Resistant Starch and Its Measurement in Food and Feeds: A Review." *Journal of Agricultural and Food Chemistry* 33, no. 5 (1985): 1185–1190. <u>https://doi.org/10.1021/jf00065a001</u>.
- ^{3.} Topping, D. L., and P. M. Clifton. "Short-Chain Fatty Acids and Human Colonic Function: Roles of Resistant Starch and Non-Starch Polysaccharides." *Physiological Reviews* 81, no. 3 (2001): 1031–1064. <u>https://doi.org/10.1152/physrev.2001.81.3.1031</u>.
- ^{4.} Birt, D. F., T. Boylston, S. Hendrich, J. L. Jane, J. Hollis, L. Li, J. McClelland, et al. "Resistant Starch: Promise for Improving Human Health." *Advances in Nutrition* 4, no. 6 (2013): 587–601. <u>https://doi.org/10.3945/an.113.004325</u>.
- ^{5.} Keenan, M. J., J. Zhou, S. Hegsted, R. Pelkman, M. Durham, R. C. Coulon, M. C. Martin, R. Raggio, and G. L. Tulley. "Role of Resistant Starch in Improving Digestive Tract Health, Adiposity, and Insulin

Resistance." *Advances in Nutrition* 6, no. 2 (2015): 198–205. https://doi.org/10.3945/an.114.007419.

- ^{6.} Ha, V., A. Jayalath, L. Cozma, A. L. Mirrahimi, R. E. de Souza, A. Chiavaroli, J. L. Wang, M. W. Beyene, and J. L. Sievenpiper. "Effect of Fructose on Blood Pressure: A Systematic Review and Meta-Analysis of Controlled Feeding Trials." *Hypertension* 68, no. 4 (2016): 832–839. <u>https://doi.org/10.1161/HYPERTENSIONAHA.116.07872</u>.
- ^{7.} Bhatty, R. S., and J. I. Christison. "Functional Properties of Oat Fractions in Non-Food Applications." *Cereal Chemistry* 76, no. 4 (1999): 575–578. <u>https://doi.org/10.1094/CCHEM.1999.76.4.575</u>.
- ^{8.} Sanz-Penella, J. M., E. Laparra, and E. Haros. "Impact of Legume Processing on Their Nutritional Quality and Implications on Human Health." *Critical Reviews in Food Science and Nutrition* 52, no. 10 (2012): 105–122. <u>https://doi.org/10.1080/10408398.2010.500528</u>.

LIST 4

WATER CONTENT OF COMMON FOODS AND BEVERAGES

(Source: U.S. Department of Agriculture (USDA), FoodData Central)

Coffee	99% water
Теа	99% water
Cucumber	96% water
Lettuce (Iceberg)	
Celery	95% water
Beer	

Tomato Zucchini	
Watermelon	
Strawberries	91% water
Spinach	91% water
Broccoli	90% water
Cantaloupe	
Peach	89% water
Carrots	88% water
Grapefruit	88% water
Milk (whole)	87% water
Orange	86% water
Apple	
Pineapple	
Yogurt	85% water

<u>List 5</u>

FACTORS THAT INFLUENCE THE MICROBIOME

ACTIVITY-EXERCISE	DIET	ALCOHOL
AGE	GENDER	ETHNICITY
ANTIBIOTICS USAGE	IMMUNITY	DEPRESSION

BILE SALTS-TYPE AND AMOUNT	GRAVITY	GENES
BODY TEMPERATURE	CHEMO-RADIATION	VITAMIN DEFICIENCIES
DIAGNOSTIC RADIATION	STARVATION	STRESS
FASTING	IMMUNIZATIONS	GEOGRAPHIC LOCALE
DIGESTIVE TRACT ENZYMES	SLEEP DEPRIVATION	CIRCADIAN RHYTHMS
HORMONES	AIR POLLUTANTS	PETS
INHALED GASES	AMBIENT TEMPERATURE	SEA LEVEL ALTITUDE
MENOPAUSE	EDUCATION LEVEL	SIBLINGS
MENSTRUATION	CULTURAL/RELIGIOUS PRACTICES	MATURITY AT BIRTH PREMATURITY
MODE OF BIRTH NATURAL vs C- SECT	INFECTIONS	TOXINS

OCCUPATIONAL EXPOSURES	NUTRACEUTICALS	DIGESTIVE TRACT MOTILITY
PHARMACEUTICALS	BODY TRAUMA	AMBIENT RADIATION
SURGERIES	RECREATIONAL DRUGS	FOOD ADDITIVES
TOBACCO	HYDRATION	ORAL-DENTAL PATHOLOGY
WATER CONTAMINANTS	DIGESTIVE TRACT- BRAIN AXIS	BILE ACIDS
ARTIFICIAL SWEETENERS	BOTTLE vs BREAST FED INFANTS	ULTRA- PROCESSED FOOD

LIST 6 EXAMPLES OF GRAMS OF FIBER IN SELECTED NUTRIENTS*

<u>*Harvard Health Publishing</u>

<u>Grams fiber</u>
9.2
8.8
8.3
8.2

Lentils, cooked, 1/2 cup	7.8
Pinto beans, cooked, 1/2 cup	7.7
Black beans, cooked, 1/2 cup	7.5
Chickpeas/garbanzo beans, cooked, 1/2 cup	6.3
Great northern beans, cooked, 1/2 cup	6.2
Kidney beans, cooked, 1/2 cup	5.7
White beans, cooked, 1/2 cup	5.7
Soybeans, cooked, 1/2 cup	5.2
Snow peas, cooked, 1 cup	4.5
Edamame, cooked, 1/2 cup	4.1
Snap green beans, cooked, 1 cup	4.0

<u>Fruit</u>	<u>Grams fiber</u>
Guava, 1 cup	8.9
Raspberries, 1 cup	8.0
Blackberries, 1 cup	7.6
Boysenberries, 1 cup	7.0
Passion fruit, 1/4 cup	6.1
Pear, 1 medium (Bartlett, Bosc, Anjou)	5.5

Kiwi, 1 cup	5.4	
Grapefruit, 1 fruit	5.0	
Apple, medium size, with skin	4.8	
Orange, 1 medium	3.7	
Figs, dried, 1/4 cup	3.7	
Blueberries, 1 cup	3.6	
Mandarin orange or tangerine, 1 cup	3.5	
Pomegranate seeds, 1 cup	3.5	
Pears, dried, 1/4 cup	3.4	
Peaches, dried, 1/4 cup	3.3	
Banana, medium size	3.2	
Apricots, 1 cup	3.1	
Prunes, 1 cup	3.1	
Strawberries, 1 cup	3.0	
Dates, 1/4 cup	3.0	
Cherries, 1 cup	2.9	

Vegetables	<u>Grams fiber</u>
Artichoke, cooked, 1 cup	9.6
Pumpkin, canned, 1 cup	7.1
Brussels sprouts, cooked, 1 cup	6.4
Sweet potato, cooked, 1 cup	6.3
Broccoli, cooked, 1 cup	5.2
Avocado, 1/2 cup	5.0
Cauliflower, cooked, 1 cup	4.9
Carrots, cooked, 1 cup	4.8
Kale, cooked, 1 cup	4.7
Spinach, cooked, 1 cup	4.3
Escarole, cooked, 1 cup	4.2
Cabbage, red, cooked, 1 cup	4.1
Okra, cooked, 1 cup	4.0
Corn, cooked, 1 cup	4.0

Potato, baked, with skin, 1 medium	3.9
Carrots, raw, 1 cup	3.6
Mushrooms, cooked, 1 cup	3.4
Red bell pepper, raw, 1 cup	3.1
Plantains, cooked, 1 cup	3.1
Asparagus, cooked, 1 cup	2.9
Onions, cooked, 1 cup	2.9
Beets, cooked, 1 cup	2.8

Whole grains	<u>Grams fiber</u>
Cereal, high fiber, unsweetened, 1/2 cup	14.0
Cereal, whole grain kernels, 1/2 cup	7.5
Cereal, shredded wheat, 1 cup	6.2
Popcorn, 3 cups	5.8
Cereal, bran flakes, 3/4 cup	5.5
Bulgur, cooked, 1/2 cup	4.1

Spelt, cooked, 1/2 cup	3.8	
Barley, pearled, cooked, 1/2 cup	3.8	
Brown rice, cooked, long grain	3.5	
Cereal, toasted oat	3.0	
Multigrain bread, 1 large slice	3.0	
Oat bran, 1/2 cup	2.9	
Whole wheat crackers, 1 oz.	2.9	
Whole wheat tortillas, 1 oz.	2.8	

Nuts and seeds	<u>Grams fiber</u>
Pumpkin seeds, 1 ounce	5.2
Coconut, 1 ounce	4.6
Chia seeds, 1 tablespoon	4.1
Almonds, 1 ounce	3.5
Chestnut, 1 ounce	3.3
Sunflower seeds, 1 ounce	3.1

Pine nuts, 1 ounce	3.0
Pistachio nuts, 1 ounce	2.9
Flax seeds, 1 tablespoon	2.8
Hazelnuts, 1 ounce	2.8

<u>List 7</u>

FACTORS MAKING UP THE EXPOSOME

1. Physical Environment

• Air Quality

- Outdoor pollutants (e.g., particulate matter, nitrogen dioxide, sulfur dioxide)
- Indoor pollutants (e.g., tobacco smoke, radon, volatile organic compounds from furniture and cleaning products)
- Natural allergens (e.g., pollen, mold spores)

• Water Quality

- Drinking water contaminants (e.g., lead, arsenic, chromium, volatile organic compounds, microplastics)
- Recreational water exposure (e.g., chlorine, pathogens in pools or lakes)
- Soil and Land Use

- Pesticides and herbicides in agricultural areas
- Heavy metals in soil (e.g., mercury, cadmium)

<u>Climate and Weather</u>

- UV radiation (sun exposure)
- Extreme weather events (e.g., heatwaves, floods, wildfires)
- Seasonal temperature variations

• Noise Pollution

- Urban noise (e.g., traffic, industrial noise)
- Low-frequency vibrations

• Electromagnetic Radiation

- Natural sources (e.g., solar radiation)
- Artificial sources (e.g., wireless devices, power lines)

2. Chemical Exposures

- Dietary Chemicals
 - Pesticide residues in food
 - Preservatives (e.g., flavorings, colorants, shelf life extenders, texture enhancers, artificial sweeteners)
 - Contaminants (e.g., BPA, microplastics, heavy metals)
 - Cooking byproducts (e.g., acrylamide, polycyclic aromatic hydrocarbons)
- Industrial and Household Chemicals

- Cleaning agents and disinfectants
- Personal care products (e.g., parabens, phthalates in cosmetics)
- Flame retardants in furniture and electronics

Tobacco and Nicotine Products

- Active smoking or vaping
- Secondhand and thirdhand smoke exposure

Alcohol and Other Substances

- Ethanol (drinking alcohol)
- Recreational drugs (e.g., cannabis, opioids)
- Illicit drugs

Pharmaceuticals and Supplements

- Antibiotics and their role in microbiome disturbance
- Over-the-counter medications
- Nutraceuticals, vitamins, and herbal supplements

3. Biological Exposures

• Microbial Ecosystems

- Pathogens (e.g., bacteria, viruses, fungi, parasites)
- Dysbiosis in the gut microbiome
- Exposure to beneficial microbes (e.g., probiotics, fermented foods)

Infectious Diseases

- Viral infections (e.g., influenza, SARS-CoV-2, HIV, Respiratory Syncytial virus)
- Parasitic infections (e.g., Giardia, malaria)
- Fungal infections (e.g., Candida)

• Allergens and Biotoxins

- Animal dander and dust mites
- Mycotoxins from mold
- Plant-based allergens (e.g., poison ivy, ragweed)

4. Social and Behavioral Exposures

Dietary Patterns

- High-fat, high-sugar diets
- Fiber-deficient versis plant-based diets

Physical Activity

- Sedentary lifestyles versus active routines
- Occupational or recreational exposure to physical exertion

<u>Substance Use and Abuse</u>

- Tobacco, alcohol, and recreational drug use
- Social Stressors
 - Socioeconomic status and inequality

- Workplace stress, unemployment, and job insecurity
- Social isolation versus community support

• **Psychological Stressors**

- Adverse childhood experiences (ACEs)
- Chronic stress, anxiety, and depression

5. Lifestyle Exposures

- <u>Sleep Patterns</u>
 - Chronic sleep deprivation
 - Night-shift work and circadian rhythm disruptions

• Hygiene and Sanitation

- Excessive hygiene practices ("hygiene hypothesis")
- Poor sanitation or access to clean water

• Travel and Migration

- Exposure to new pathogens and microbiomes
- Changes in diet and environment due to relocation

6. Occupational Exposures

<u>Chemical Hazards</u>

- Solvents, asbestos, and heavy metals
- Pesticides and industrial chemicals
- Physical Hazards

- Radiation exposure (e.g., diagnostic and therapeutic Xray, gamma radiation)
- Repetitive strain or ergonomic challenges

Biological Hazards

- Zoonotic diseases from animal handling
- Hospital-acquired infections

7. Developmental and Early-Life Exposures

• Prenatal Exposures

- Maternal diet and toxin exposure
- Hormonal disruptions and medications during pregnancy

Birth and Early-Life Events

- Mode of delivery (C-section versus vaginal birth)
- Breastfeeding versus formula feeding
- Early exposure to antibiotics
- <u>Childhood Environment</u>
 - Passive smoking exposure
 - Microbiome imprinting by home environment and diet

8. Genetic and Epigenetic Interactions

- Inherited Susceptibilities
 - Genetic predispositions to diseases

9. Exposure Timing and Lifespan Factors

• Cumulative Exposures

- Lifetime accumulation of toxins
- Long-term impacts of early-life insults

• Critical Windows of Susceptibility

- In utero development
- Puberty and hormonal changes
- Aging and immunosenescence

REFERENCES:

- Andrew J. Macpherson and Nicola L. Harris, "Interactions Between Commensal Intestinal Bacteria and the Immune System," *Nature Reviews Immunology* 4, no. 6 (2004): 478–485, <u>https://doi.org/10.1038/nri1373</u>.
- Andrew P. Feinberg, "The Key Role of Epigenetics in Human Disease Prevention and Treatment," *New England Journal of Medicine* 378, no. 14 (2018): 1323–1334, <u>https://doi.org/10.1056/NEJMra112518</u>.
- Anna J. Jasinska and Li Yu, "Stress, Brain, and Behavior: Role of Glucocorticoids," *Nature Reviews Neuroscience* 16, no. 7 (2015): 435–446, <u>https://doi.org/10.1038/nrn3953</u>.
- Annette Prüss-Ustün, Jamie Bartram, Thomas Clasen, John M. Colford Jr., Oliver Cumming, Valerie Curtis, Sandy Cairncross, et al., "Burden of Disease from Inadequate Water, Sanitation, and Hygiene in Low- and Middle-Income Settings: A Retrospective Analysis of Data from 145 Countries," *Tropical Medicine & International Health* 19, no. 8 (2014): 894–905, <u>https://doi.org/10.1111/tmi.12329</u>.

- Berthold Koletzko et al., "Long-Chain Polyunsaturated Fatty Acids and Neonatal Development," *Pediatrics* 108, no. 3 (2001): 816–821, <u>https://doi.org/10.1542/peds.108.3.816</u>.
- Bryan S. Samuel and Jeffrey I. Gordon, "A Humanized Gnotobiotic Mouse Model of Host-Archaeal-Bacterial Mutualism," *Proceedings of the National Academy of Sciences* 103, no. 26 (2006): 10011–10016, <u>https://doi.org/10.1073/pnas.0602187103</u>.
- J. Hernandez and M. J. Blaser, "Dysbiosis in the Gut Microbiome and Its Role in Disease," *Nature Reviews Microbiology* 15, no. 5 (2017): 286–290, <u>https://doi.org/10.1038/nrmicro.2017.16</u>.
- Dong Wang and Li Wang, "Hygiene Hypothesis and Its Application in the Development of Immune-Related Diseases," *Clinical Reviews in Allergy & Immunology* 59, no. 3 (2020): 243–257, <u>https://doi.org/10.1007/s12016-019-08700-4</u>.
- Emily Oken and Matthew W. Gillman, "Fetal Origins of Obesity," *Obesity Research* 11, no. 4 (2003): 496–506, <u>https://doi.org/10.1038/oby.2003.69</u>.
- Francesco P. Cappuccio, Lanfranco D'Elia, Pasquale Strazzullo, and Michelle A. Miller, "Sleep Duration Predicts Cardiovascular Outcomes: A Systematic Review and Meta-Analysis of Prospective Studies," *European Heart Journal* 32, no. 12 (2011): 1484–1492, <u>https://doi.org/10.1093/eurheartj/ehr007</u>.
- Frank W. Booth, Christopher K. Roberts, and Matthew J. Laye, "Lack of Exercise Is a Major Cause of Chronic Diseases," *Comprehensive Physiology* 2, no. 2 (2012): 1143–1211, <u>https://doi.org/10.1002/cphy.c110025</u>.
- Fredrik Bäckhed, Ruth E. Ley, Justin L. Sonnenburg, Daniel A. Peterson, and Jeffrey I. Gordon, "Host-Bacterial Mutualism in the Human Intestine,"

Science 307, no. 5717 (2005): 1915–1920, https://doi.org/10.1126/science.1104816.

- Gary L. Ginsberg, "The Impact of Lead Exposure on Health: Epidemiological Trends and Biological Mechanisms," *Environmental Toxicology and Pharmacology* 34, no. 3 (2012): 745–758, <u>https://doi.org/10.1016/j.etap.2012.09.003</u>.
- George P. Chrousos, "Stress and Disorders of the Stress System," Nature Reviews Endocrinology 5, no. 7 (2009): 374–381, <u>https://doi.org/10.1038/nrendo.2009.106</u>.
- Günter Weiss and Lawrence T. Goodnough, "Anemia of Chronic Disease," New England Journal of Medicine 352, no. 10 (2005): 1011–1023, <u>https://doi.org/10.1056/NEJMra041809</u>.
- H. Vally and P. J. Thompson, "Allergic and Respiratory Effects of Fungal Bioaerosols: A Review of the Epidemiological Evidence," *International Journal of Environmental Research and Public Health* 15, no. 7 (2018): 1406, <u>https://doi.org/10.3390/ijerph15071406</u>.
- Hiroshi Okada, Charles Kuhn, Hervé Feillet, and Jean-François Bach, "The Hygiene Hypothesis for Autoimmune and Allergic Diseases: An Update," *Clinical and Experimental Immunology* 160, no. 1 (2010): 1–9, <u>https://doi.org/10.1111/j.1365-2249.2010.04139.x</u>.
- Inês Cho and Martin J. Blaser, "The Human Microbiome: At the Interface of Health and Disease," *Nature Reviews Genetics* 13, no. 4 (2012): 260– 270, <u>https://doi.org/10.1038/nrg3182</u>.
- James Hope, "A Review of the Mechanism of Injury and Treatment Approaches for Mycotoxin-Induced Neurotoxicity," *Toxicology Research* 2, no. 2 (2013): 126–132, <u>https://doi.org/10.1039/c2tx20020b</u>.

- Jelle Vlaanderen, Roel Vermeulen, Dick Heederik, and Hans Kromhout, "Occupational Exposure to Pesticides and Risk of Chronic Diseases," *Annals of Occupational Hygiene* 58, no. 3 (2014): 320–337, <u>https://doi.org/10.1093/annhyg/meu017</u>.
- Jo Leonardi-Bee, John Britton, and Amanda Venn, "Environmental Tobacco Smoke and Respiratory Health: Systematic Review and Meta-Analysis," *The BMJ* 342 (2011): d442, <u>https://doi.org/10.1136/bmj.d442</u>.
- John E. McGowan Jr., "Resistance in Nonfermenting Gram-Negative Bacteria: Multidrug Resistance to the Maximum," *American Journal of Medicine* 119, no. 6 Suppl 1 (2006): S29–S36, <u>https://doi.org/10.1016/j.amjmed.2006.03.012</u>.
- John N. Mandl, Christina Schneider, David S. Schneider, and Michelle L. Baker, "Viral Infections: Mechanisms and Consequences for Human Health," *Current Topics in Microbiology and Immunology* 429 (2020): 117– 133, <u>https://doi.org/10.1007/82_2019_192</u>.
- John R. Kelly et al., "Transferring the Blues: Depression-Associated Gut Microbiota Induces Neurobehavioural Changes in the Rat," *Journal of Psychiatric Research* 82 (2016): 109–118, <u>https://doi.org/10.1016/j.jpsychires.2016.07.019</u>.
- John R. Wingard, "Importance of Candida Species Other Than Candida Albicans as Pathogens in Oncology Patients," *Clinical Infectious Diseases* 20, no. 1 (1995): 115–125, <u>https://doi.org/10.1093/clinids/20.1.115</u>.
- Julianne Holt-Lunstad, Timothy B. Smith, and J. Bradley Layton, "Social Relationships and Mortality Risk: A Meta-Analytic Review," *PLOS Medicine* 7, no. 7 (2010): e1000316, https://doi.org/10.1371/journal.pmed.1000316.

- Justin L. Sonnenburg, Largus T. Angenent, and Jeffrey I. Gordon, "Getting a Grip on Things: How Do Communities of Bacterial Symbionts Become Established in Our Intestine?" *Nature Immunology* 5, no. 6 (2004): 569– 573, <u>https://doi.org/10.1038/ni1079</u>.
- Keith A. Hruska, Sanjay Mathew, Richard Lund, Ping Qiu, and Robert Pratt, "Hyperphosphatemia of Chronic Kidney Disease," *Kidney International* 74, no. 2 (2008): 148–157, <u>https://doi.org/10.1038/ki.2008.130</u>.
- Li Lu and Wei Wang, "Addiction to Electronic Cigarettes and Smoking Cessation Outcomes: A Systematic Review," *Addiction* 114, no. 5 (2019): 782–795, <u>https://doi.org/10.1111/add.14528</u>.
- Majid Ezzati et al., "Selected Major Risk Factors and Global and Regional Burden of Disease," *The Lancet* 360, no. 9343 (2002): 1347–1360, <u>https://doi.org/10.1016/S0140-6736(02)11403-6</u>.
- Maria R. Pereira and Fatima Martel, "Iron Supplements During Pregnancy: Impact on Maternal and Fetal Outcomes," *Clinical Nutrition* 23, no. 6 (2004): 1374–1380, <u>https://doi.org/10.1016/j.clnu.2004.04.012</u>.
- Marianna Virtanen, Stephen A. Stansfeld, Rachel Fuhrer, Jane E. Ferrie, and Mika Kivimäki, "Overtime Work as a Predictor of Major Depressive Episode: A 5-Year Follow-Up of the Whitehall II Study," *PLoS ONE* 7, no. 1 (2012): e30719, <u>https://doi.org/10.1371/journal.pone.0030719</u>.
- Mark J. Mendell, Andrew G. Mirer, Kyung-Hee Cheung, My Tong, and Jeroen Douwes, "Respiratory and Allergic Health Effects of Dampness, Mold, and Dampness-Related Agents: A Review of the Epidemiologic Evidence," *Environmental Health Perspectives* 119, no. 6 (2011): 748–756, <u>https://doi.org/10.1289/ehp.1002410</u>.

- Michael A. Kaliner, "Plant Allergens: Mechanisms of Allergic Reaction," *Current Opinion in Allergy and Clinical Immunology* 9, no. 5 (2009): 382– 386, <u>https://doi.org/10.1097/ACI.0b013e32832f4f05</u>.
- Michael J. Postma and Jan C. Jager, "Drinking Water Quality and Gastrointestinal Health: Emerging Evidence from Systematic Reviews," *The Lancet Gastroenterology & Hepatology* 1, no. 3 (2016): 174–184, <u>https://doi.org/10.1016/S2468-1253(16)30005-6</u>.
- Michael T. Bailey, Susannah E. Dowd, Jason D. Galley, Amanda R. Hufnagle, Robert G. Allen, and Mark Lyte, "Exposure to a Social Stressor Alters the Structure of the Intestinal Microbiota: Implications for Stressor-Induced Immunomodulation," *Brain, Behavior, and Immunity* 25, no. 3 (2011): 397–407, <u>https://doi.org/10.1016/j.bbi.2010.10.023</u>.
- Paul D. Thompson et al., "Exercise and Physical Activity in the Prevention and Treatment of Atherosclerotic Cardiovascular Disease," *Circulation* 107, no. 24 (2003): 3109–3116, https://doi.org/10.1161/01.CIR.0000075572.40158.77.
- Paula Braveman, Susan Egerter, and David R. Williams, "The Social Determinants of Health: It's Time to Consider the Causes of the Causes," *Public Health Reports* 129, Suppl 2 (2014): 19–31, <u>https://doi.org/10.1177/00333549141291S206</u>.
- Peter J. Hotez, "Parasitic Diseases and the Global Burden of Disease," New England Journal of Medicine 374, no. 17 (2016): 1662–1668, <u>https://doi.org/10.1056/NEJMra1515243</u>.
- R. D. Heijtz et al., "Normal Gut Microbiota Modulates Brain Development and Behavior," *Proceedings of the National Academy of Sciences* 108, no. 7 (2011): 3047–3052, <u>https://doi.org/10.1073/pnas.1010529108</u>.

- Renata Micha et al., "Association Between Dietary Factors and Mortality from Heart Disease, Stroke, and Type 2 Diabetes in the United States," JAMA 317, no. 9 (2017): 912–924, <u>https://doi.org/10.1001/jama.2017.0947</u>.
- Rhythms and Sleep Quality: A Systematic Review," Chronobiology International 38, no. 6 (2021): 773–784, <u>https://doi.org/10.1080/07420528.2021.1884375</u>.
- Robert A. White et al., "Gut Microbiota Development in Early Life: The Impact of Delivery Mode, Diet, and Antibiotics," *Science Translational Medicine* 12, no. 556 (2020): eaaz5861, <u>https://doi.org/10.1126/scitranslmed.aaz5861</u>.
- Robert D. Brook et al., "Particulate Matter Air Pollution and Cardiovascular Disease: An Update to the Scientific Statement from the American Heart Association," *Circulation* 121, no. 21 (2010): 2331–2378, <u>https://doi.org/10.1161/CIR.0b013e3181dbece1</u>.
- Robert West and Jamie Brown, "Tobacco Use, Addiction, and Cessation," Annual Review of Clinical Psychology 16 (2020): 105–136, <u>https://doi.org/10.1146/annurev-clinpsy-082719-102654</u>.
- S. K. Gill, "The Use of Maternal Medications During Pregnancy and Their Effect on Fetal Development," *Canadian Family Physician* 55, no. 9 (2009): 845–847, <u>https://doi.org/10.46747/cfp.5509845</u>.
- Sandra Macfarlane and George T. Macfarlane, "Fermentation in the Human Large Intestine: Its Physiologic Consequences and the Potential Contribution of Prebiotics," *Journal of Clinical Gastroenterology* 45, Suppl 3 (2011): S120–S127, <u>https://doi.org/10.1097/MCG.0b013e31822fecfe</u>.

- Sarah Smith and Li-Fang Wang, "Global Burden of Zoonotic Diseases and Insights into Their Control," *The Lancet Infectious Diseases* 18, no. 10 (2018): e285–e295, <u>https://doi.org/10.1016/S1473-3099(18)30315-6</u>.
- Sheldon Cohen, "Psychological Stress and Disease Susceptibility," *Psychological Bulletin* 133, no. 1 (2007): 1–23, <u>https://doi.org/10.1037/0033-2909.133.1.1</u>.
- Siew C. Ng and Arthur L. Hart, "Mechanisms of Action of Probiotics: Recent Advances," *Inflammatory Bowel Diseases* 15, no. 2 (2009): 300– 310, <u>https://doi.org/10.1002/ibd.20625</u>.
- Stephen S. Lim et al., "A Comparative Risk Assessment of Burden of Disease and Injury Attributable to 67 Risk Factors and Risk Factor Clusters in 21 Regions, 1990–2010: A Systematic Analysis for the Global Burden of Disease Study 2010," *The Lancet* 380, no. 9859 (2012): 2224–2260, <u>https://doi.org/10.1016/S0140-6736(12)61766-8</u>.
- Sydney M. Finegold, "Normal Indigenous Intestinal Flora," American Journal of Clinical Nutrition 36, no. 5 (1983): 1015–1027, <u>https://doi.org/10.1093/ajcn/36.5.1015</u>.
- Tessa Strain and Paul Kelly, "The Forgotten Benefits of Physical Activity: Evidence for the Workplace," *American Journal of Preventive Medicine* 59, no. 1 (2020): 26–36, <u>https://doi.org/10.1016/j.amepre.2020.01.004</u>.
- Theodora Turner and Theodora Scarato, "Electromagnetic Radiation from Wireless Devices: Health Impacts and Public Perceptions," *Journal of Public Health Policy* 42, no. 3 (2021): 123–136, <u>https://doi.org/10.1057/s41271-021-00287-7</u>.

- Thomas A. E. Platts-Mills and Scott P. Commins, "Allergens and Their Role in Allergic Disease," *Journal of Allergy and Clinical Immunology* 137, no. 1 (2016): 3–13, <u>https://doi.org/10.1016/j.jaci.2015.11.050</u>.
- Timothy F. O'Callaghan and Douwe van Sinderen, "The Gut Microbiome as a Virtual Endocrine Organ with Implications for Maternal and Infant Health," *Journal of Animal Science and Biotechnology* 7 (2016): 28, <u>https://doi.org/10.1186/s40104-</u>
- Ulrich E. Schaible and Stefan H. E. Kaufmann, "Malnutrition and Infection: Complex Mechanisms and Global Impacts," *PLoS Medicine* 4, no. 5 (2007): e115, <u>https://doi.org/10.1371/journal.pmed.0040115</u>.
- Vincent J. Felitti et al., "Relationship of Childhood Abuse and Household Dysfunction to Many of the Leading Causes of Death in Adults: The Adverse Childhood Experiences (ACE) Study," *American Journal of Preventive Medicine* 14, no. 4 (1998): 245–258, <u>https://doi.org/10.1016/S0749-3797(98)00017-8</u>.
- W. C. Winkler and R. R. Breaker, "Genetic Control by Metabolite-Binding Riboswitches," *ChemBioChem* 4, no. 10 (2003): 1024–1032, <u>https://doi.org/10.1002/cbic.200300685</u>.
- Wolfgang R. Streit and Ruth A. Schmitz, "Metagenomics—The Key to the Uncultured Microbes," *Current Opinion in Microbiology* 7, no. 5 (2004): 492–498, <u>https://doi.org/10.1016/j.mib.2004.08.002</u>.

<u>LIST 8</u>

Sources of Healthy Fats

This table lists key sources of healthy fats, including both natural dietary items and processed or refined oils. These sources provide monounsaturated fats (MUFAs), polyunsaturated fats (PUFAs), and omega-3 fatty acids, which are known to support cardiovascular, metabolic, and immune health.

<u>Category</u>	<u>Examples</u>	<u>Main Healthy Fat</u> <u>Components</u>
Plant Oils	Extra virgin olive oil, canola oil, avocado oil	Primarily MUFAs; some PUFAs
Nuts	Almonds, walnuts, hazelnuts, macadamia nuts	MUFA; walnuts also rich in omega-3 PUFAs
Seeds	Flaxseeds, chia seeds, hemp seeds, sunflower seeds	PUFAs, including omega-3 (ALA) and omega-6
Fatty Fish	Salmon, mackerel, sardines, trout, anchovies	Long-chain omega-3 PUFAs (EPA, DHA)
Avocados	Fresh avocado	High in MUFAs; small amounts of PUFAs
Soy Products	Tofu, soybeans, soybean oil	PUFAs, including omega-6; some MUFAs
Synthetic or Refined Oils	Refined canola oil, safflower oil, sunflower oil, corn oil	PUFAs, mainly omega-6; variable MUFA content

MATCHA TEA



Preparing matcha tea requires careful ingredient selection and precise steps to achieve the desired taste and nutritional benefits. This guide outlines a method for making matcha tea enriched with inulin prebiotics, human milk oligosaccharide (HMO) extracts, and polyols to support digestive and immune health.

Ingredients & Their Benefits

<u>1. Matcha Tea</u>

- Choose ceremonial-grade matcha for the best flavor and quality. Matcha is available as a loose powder or in preportioned packets.
- Rich in antioxidants, particularly catechins, matcha helps support immune function, reduce inflammation, and boost metabolism.

2. Distilled Water

• Using distilled water ensures purity by eliminating minerals, toxins, and impurities that could alter the taste.

3. Inulin Powder

 Add ½ teaspoon each of Jarrow Formulas Inulin-FOS[®] and Bare Organics Agave Inulin[®] to introduce prebiotic fiber, which promotes beneficial gut bacteria and supports digestion.

4. Prebiotic Enhancers

Mix in ½ teaspoon of Bifido-Boost[®] and ½ teaspoon of Layer
 Origin Pure HMO[®] to further nourish gut-friendly microbes.

5. Manuka Honey (optional)

 Stir in one heaping teaspoon of manuka honey with an MGO (Methylglyoxal) rating above 500 or a UMF (Unique Manuka Factor) rating above 15 for antimicrobial and medicinal benefits.

UMF-to-MGO Conversion Guide:

- UMF 5+ ≈ MGO 83
- UMF 10+ ≈ MGO 263
- UMF 15+ ≈ MGO 514
- UMF 20+ ≈ MGO 829

6. Flavor Enhancers (optional)

For additional aroma and sweetness, consider:

- A cinnamon stick (e.g., McCormick[®]) for a spiced flavor.
- Stevia in the Raw[®] or a preferred coffee creamer for sweetness and smooth texture.

Preparation Steps

<u>1. Heat the Water</u>

- Pour 14 ounces of distilled water into a 16-ounce Pyrex[®] cup.
- Heat in the microwave until the temperature reaches 170°F but does not boil. This preserves matcha's delicate flavor and nutrients.

2. Mix the Matcha

- Remove the heated water and add matcha powder.
- Stir vigorously until it is smooth and free of lumps. Matcha's fine texture requires thorough mixing for the best consistency.

3. Add Prebiotics

 Gradually mix in Bifido-Boost[®] and Pure HMO Prebiotic Powder[®] until fully dissolved.

4. Incorporate Honey & Flavoring for taste

- Stir in manuka honey until completely blended (optional).
- Add a cinnamon stick, if desired, for aroma and flavor (optional).

5. Sweeten to Taste

 Adjust sweetness using Stevia in the Raw[®] or a coffee creamer of your choice.

This proposed method creates a matcha tea with added prebiotics and health-boosting properties.

MICROBIOME STUDY GLOSSARY

UNRAVELING THE MYSTERIES OF MICROBIAL FUNCTION AND THEIR INTERACTIONS WITH THE BODY AND THE ENVIRONMENT

The study of the microbiome has burgeoned in recent years, driven by advances in various scientific fields such as metabolomics, genomics, and proteomics. These disciplines provide unique insights into the functioning of our microbial inhabitants and their interactions with the host and the environment. The following terms are explained to help navigate the new world of microbe exploration.

Metabolomics: Metabolomics is the study of small molecules known as metabolites. It provides a snapshot of the metabolic state of a microbiome.

Metabolites are the end products of cellular processes, and their analysis can reveal how microbes process nutrients, respond to environmental changes, and interact with their host. By profiling the metabolome, researchers can identify metabolic pathways that are active in microbial communities, shedding light on their functional capabilities. For instance, metabolomics has revealed how gut bacteria produce short-chain fatty acids from dietary fibers, which are critical for colon health and energy metabolism.

Genomics: Genomics involves the study of the complete DNA sequence of organisms, including those in the microbiome. By sequencing microbial genomes, scientists can identify the genes present in a community and predict the potential functions these genes encode. This approach has that enable microbes to thrive in specific environments. Genomic studies have also shown how horizontal gene transfer among microbes can spread antibiotic resistance, emphasizing the need for prudent antibiotic use.

Transcriptomics: While genomics provides a blueprint of the genetic potential of microbial communities, transcriptomics reveals which genes are actively being expressed at any given time. By analyzing RNA transcripts, researchers can determine how microbial gene expression responds to environmental stimuli, dietary changes, or disease states. This dynamic view of gene activity helps in understanding the functional roles of microbes and their adaptive strategies.

For example, transcriptomic studies have shown how gut bacteria alter their gene expression in response to different diets, influencing nutrient absorption and metabolism. **Proteomics:** Proteomics is the large-scale study of proteins. This study complements genomics and transcriptomics by identifying and quantifying the proteins produced by microbial communities. Proteins are the workhorses of the cell, conducting essential functions such as catalysis, transport, and signaling. By mapping the protein landscape of the microbiome, researchers can gain insights into the biochemical activities of samples. This approach has revolutionized microbiome research by allowing the study of entire microbial communities in their natural habitats.

Metagenomic analyses provide a comprehensive view of the genetic composition and functional potential of microbial ecosystems. Metagenomic studies have highlighted the ecological roles of microbes in nutrient cycling, pollutant degradation, and synbiotic relationships.

Proteomic analyses have identified microbial enzymes involved in metabolizing complex carbohydrates, revealing how microbes contribute to the host's digestive processes.

Metagenomics: Metagenomics bypasses the need for culturing microbes by directly sequencing DNA from the environment.

Systems Biology Perspective: Understanding the complexity of the microbiome and its interactions with the host and the environment requires integrative approaches that combine data from multiple disciplines. Systems biology uses computational models to integrate genomic, transcriptomic, proteomic, and

metabolomic data, providing a holistic view of microbial function and interaction.

This approach helps in identifying key regulatory networks and metabolic pathways, offering insights into how microbial communities maintain stability and respond to perturbations.

CONCLUSION:

The scientific exploration of the microbiome through metabolomics, genomics, transcriptomics, proteomics, and other disciplines has unraveled many mysteries of microbial function and interaction. These studies have highlighted the intricate relationships between microbes, the host, and the environment that make up the intestinal ecosystems, emphasizing the importance of balanced interactions to maintain intestinal wellbeing.

As research progresses, integrative approaches and systems biology will provide deeper insights, paving the way for personalized therapies and interventions.

COMMON POLYPHENOLS

Polyphenols: A Vast Spectrum of Bioactive Compounds for Dietary Enrichment

Polyphenols, a diverse group of plant-derived compounds, represent one of the most abundant categories of micronutrients in the human diet. With estimates suggesting that over 9,000 distinct polyphenolic compounds have been identified, these bioactive molecules are integral to the health-promoting properties of fruits, vegetables, grains, teas, and spices. While the biochemical diversity among polyphenols is immense, their common feature lies in the presence of multiple phenol structural units, which confer antioxidant, anti-inflammatory, antimicrobial, and cardioprotective activities.

For the health-conscious consumer, the vast array of dietary polyphenols can be both an opportunity and a challenge. Which compounds should one prioritize? What food sources provide the richest and most diverse polyphenolic profiles? The following introduces readers to a broad selection of commonly available polyphenols, presented in a structured table to serve as both a reference and a practical guide for dietary incorporation.

Table 1 : Commonly Available Polyphenols and Their Food Sources¹

Polyphenol Class	Example Compounds	Food Sources
Flavonoids	Quercetin, Kaempferol, Catechins	Onions, apples, berries, green tea, citrus fruits
Flavonols	Myricetin, Fisetin	Spinach, kale, berries, tea
Flavan-3-ols	Epicatechin, Procyanidins	Cocoa, dark chocolate, grapes, apples

Flavones	Apigenin, Luteolin	Parsley, celery, chamomile, artichoke
Isoflavones	Genistein, Daidzein	Soybeans, soy products, legumes
Anthocyanins	Cyanidin, Malvidin	Blueberries, blackberries, red cabbage, cherries
Phenolic Acids	Caffeic acid, Ferulic acid	Coffee, whole grains, spinach, eggplant
Stilbenes	Resveratrol, Piceatannol	Grapes, peanuts, cocoa
Lignans	Secoisolariciresinol, Matairesinol	Flaxseeds, sesame seeds, whole grains, berries

This table offers just a glimpse of the chemical diversity available to the everyday eater. Incorporating a variety of these compounds through a colorful, plant-rich diet ensures not only sensory delight but also potential health benefits through multiple biological pathways.

¹ Table adapted from Scalbert, Augustin, Ian T. Johnson, and Mike Saltmarsh. "Polyphenols: Antioxidants and Beyond." *American Journal of Clinical Nutrition* 81, no. 1 Suppl (2005): 2155–217S. https://doi.org/10.1093/ajcn/81.1.215S.

READING REFERENCES



- Blaser, Martin J., M. D. *Missing Microbes: How the Overuse of Antibiotics Is Fueling Our Modern Plagues.* First edition, Henry Holt and Company, LLC, 2014.
- Bulsiewicz, Will, M.D.: *Fiber Fueled*, First edition, Penguin Random House, 2020
- Dettmer, Philip. Immune: A Journey into The Mysterious System That Keeps You Alive, First edition, Random House, 2021.
- Fasano, Alessio /Flaherty, Susie: Digestive Tract Feelings: The Microbiota and Our Health, First edition, MIT Press, 2012
- Lustig, Robert. Metabolical: The Lure and the Lies of Processed Food, Nutrition, and Modern Medicine, First

edition, Harper Collins, 2021.

- Nayal, A., Hack Your Health—The Secrets of Your Digestive Tract, Netflix Documentary, 2024.
- Wulsin, Lawson, M.D., *Toxic Stress: How Stress Is Making Us III and What We Can Do About It.* Cambridge University Press, 2024.
- Yong, Ed. I Contain Multitudes: The Microbes Within Us and a Grander View of Life. First US edition, Bodley Head, 2016.
- Kinross, James, M.D., *Dark Matter*. First edition, Penquin, Random House, UK, 2023.

APPENDIX

GLOSSARY

Activated Charcoal Filtration: A filtration method that uses a porous form of carbon to trap impurities, toxins, and chemicals from air or water. In medical contexts, activated charcoal is used for detoxification by adsorbing substances onto its surface rather than absorbing them internally.

Anthocyanins: Natural pigments found in red, purple, and blue fruits and vegetables. These compounds have strong antioxidant properties and may help reduce inflammation, support cardiovascular health, and protect against oxidative damage.

Blood-Brain Barrier: A tightly regulated barrier composed of endothelial cells that separates circulating blood from the brain's extracellular fluid. It protects the brain by blocking the entry of harmful substances while allowing essential nutrients and gases to pass through.

<u>Carotenoids</u>: Plant pigments responsible for yellow, orange, and red colors in foods such as carrots and tomatoes. They serve as antioxidants and include beta-carotene, which the body converts into vitamin A. Carotenoids play a role in vision, immune function, and skin health.

Cytokines: Small protein messengers secreted by immune cells that regulate inflammation, immunity, and cellular communication. Pro-inflammatory cytokines (like TNF-alpha and IL-6) can trigger fever and immune activation, while anti-inflammatory cytokines (like IL-10) help resolve immune responses.

Eco-biologic Systems: A conceptual framework that views human health as deeply interwoven with the environment, including microbes, food webs, and ecological exposures. This systems-based approach considers how disruptions to microbial ecosystems, biodiversity, or natural cycles can influence disease and resilience.

Epigenetics: The study of how gene expression is regulated without altering the DNA sequence itself. Environmental factors, diet, stress, and microbial metabolites can all modify epigenetic markers, which in turn affect how genes are turned on or off across the lifespan.

Fatty Acid Oxidation: A metabolic process that breaks down fatty acids in the mitochondria to generate energy. This process is essential for maintaining energy homeostasis, especially during fasting or prolonged exercise.

FxR Receptor: Short for Farnesoid X Receptor, a nuclear receptor activated by bile acids. It plays a critical role in regulating bile acid synthesis, lipid metabolism, and inflammation, especially within the gut-liver axis.

Genome: The complete set of genetic material in an organism, including all of its genes and non-coding sequences. In humans, the genome provides the blueprint for development, function, and inheritance.

Immunity: The body's defense system that identifies and eliminates pathogens such as bacteria, viruses, and toxins. Immunity can be innate (present at birth) or adaptive (developed through exposure), and is influenced by microbial health, diet, age, and environment.

<u>**IL-1</u></u>: Short for Interleukin-1, a pro-inflammatory cytokine that is released early during immune responses. It plays a key role in fever induction, inflammation, and the activation of immune cells.</u>**

IL-6: Interleukin-6 is a multifunctional cytokine involved in inflammation, immune regulation, and metabolic control. It is elevated in many chronic diseases and can serve both protective and harmful roles depending on context.

IL-10: A cytokine with anti-inflammatory properties that helps limit immune responses and prevent damage to host tissues. It plays a crucial role in maintaining immune tolerance and homeostasis.

Immunosenescence: The gradual deterioration of the immune system associated with aging. It includes reduced responsiveness to infections and vaccines, and a higher risk of inflammatory diseases.

Inflammatory Bowel Disease (IBD): A group of chronic conditions, including Crohn's disease and ulcerative colitis, characterized by persistent inflammation of the gastrointestinal tract. IBD is linked to immune dysregulation, microbiome alterations, and genetic susceptibility.

Irritable Bowel Syndrome (IBS): A functional gastrointestinal disorder marked by abdominal pain, bloating, and altered bowel habits. IBS is often linked to gut-brain axis dysfunction, microbial imbalances, and visceral hypersensitivity.

Leaky Gut: A non-medical term referring to increased intestinal permeability, where the tight junctions between gut lining cells become compromised. This can allow toxins, microbes, and undigested food particles to enter the bloodstream, potentially triggering immune and inflammatory responses.

MACs (Microbiota-Accessible Carbohydrates): Dietary fibers and resistant starches that are not digested by human enzymes but are fermented by gut microbes. These carbohydrates support the growth of beneficial bacteria and are essential for short-chain fatty acid production.

Microglia: Specialized immune cells located in the central nervous system that act as the brain's first line of defense. Microglia respond to injury, remove debris, and regulate neuroinflammation. They are increasingly implicated in neurodegenerative diseases.

<u>Mitochondrial DNA</u>: Genetic material located in the mitochondria, distinct from nuclear DNA. It is inherited maternally and codes for proteins essential to energy metabolism. Damage to mitochondrial DNA is associated with aging and chronic disease.

MUFA (Monounsaturated Fatty Acids): A type of healthy fat found in olive oil, avocados, and certain nuts. MUFAs can improve cholesterol levels, reduce inflammation, and support metabolic health.

Oxidative Stress: A state where the production of reactive oxygen species (ROS) exceeds the body's ability to neutralize them. This imbalance can damage DNA, proteins, and lipids, contributing to aging and chronic disease.

<u>рН</u>

A scale that measures the acidity or alkalinity of a substance, ranging from 0 (very: acidic) to 14 (very alkaline), with 7 being neutral. pH regulation is vital for enzymatic activity, microbial balance, and physiological stability.

Polyol: A sugar alcohol used as a low-calorie sweetener. Polyols are poorly absorbed in the gut and can cause bloating or gas in sensitive individuals. Some, like xylitol, have beneficial effects on dental health.

Polyphenols: A diverse group of plant compounds with antioxidant and anti-inflammatory properties. Found in tea, berries, and spices, polyphenols can influence the gut microbiota and support immune and metabolic health.

Postbiotics: The beneficial byproducts produced when probiotics ferment prebiotics in the gut. These include short-chain fatty acids and other metabolites that support gut barrier function, reduce inflammation, and modulate immunity.

<u>Prebiotics</u>: Non-digestible food components, typically fibers or plantbased compounds, that selectively nourish beneficial gut microbes. Prebiotics support the growth of probiotic bacteria and contribute to shortchain fatty acid production.

Probiotics: Live microorganisms that, when consumed in adequate amounts, confer health benefits to the host. Common probiotic strains include species of Lactobacillus and Bifidobacterium, often found in fermented foods or supplements.

Preeclampsia: A pregnancy-related condition characterized by high blood pressure, protein in the urine, and potential damage to organs such as the liver or kidneys. It involves inflammation, oxidative stress, and endothelial dysfunction.

<u>REM Sleep</u>: Short for Rapid Eye Movement sleep, a unique phase of sleep characterized by vivid dreaming, muscle atonia, and increased brain activity. REM sleep supports cognitive function, emotional processing, and memory consolidation.

<u>Resistant Starches</u>: Types of starch that resist digestion in the small intestine and reach the colon intact, where they are fermented by gut microbes. This fermentation produces short-chain fatty acids and supports metabolic and digestive health.

Shotgun Metagenomics: An advanced sequencing technique that analyzes all genetic material present in a sample, allowing researchers to identify

and quantify entire microbial communities and their functional genes without needing to isolate individual organisms.

Saturated Fats: Fats in which all carbon atoms are bonded with hydrogen atoms, making them solid at room temperature. Found in butter, cheese, and red meat, excessive intake of saturated fats has been associated with cardiovascular risk.

Symbiotics: Combinations of probiotics and prebiotics that work synergistically to promote a healthy gut microbiome. Symbiotics enhance microbial colonization, diversity, and metabolic activity in the gastrointestinal tract.

TgR5 Receptor: Also known as TGR5 or GPBAR1, this is a bile acid receptor located on various cell types including intestinal and immune cells. Activation of TgR5 can reduce inflammation and regulate energy expenditure.

TNF-alpha: Tumor Necrosis Factor-alpha is a potent pro-inflammatory cytokine involved in immune regulation and inflammation. Elevated TNF-alpha is linked to autoimmune disorders, sepsis, and chronic inflammatory conditions.

Treg Cell: Short for regulatory T cell, a type of immune cell that helps maintain tolerance to self-antigens and prevents autoimmune disease. Treg cells suppress excessive immune responses and promote immune balance.

Unsaturated Fats: Fats that have one or more double bonds in their carbon chains, making them liquid at room temperature. They are typically found in plant oils, nuts, seeds, and fish, and are considered heart-healthy.

Volatile Organic Compounds: Carbon-based compounds that easily evaporate into the air. In the context of health, VOCs can be emitted by

building materials, cleaning agents, or even gut microbes, and may contribute to indoor air pollution or microbial communication.

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