

# **Bioactive Polysaccharides from *Phyllostachys nigra* as Prebiotic Agents: Effects on Short-Chain Fatty Acid Production and Host Metabolism**

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## **Abstract**

The gut microbiome functions as a highly distributed, multi-agent metabolic network that transduces dietary inputs into systemic physiological signals, many of which are mediated by short-chain fatty acids (SCFAs). Non-digestible polysaccharides that selectively stimulate beneficial microbial taxa—prebiotics—are increasingly recognized not merely as nutritional supplements but as system-level interventions capable of reconfiguring host-microbial information flow, metabolic pathway allocation, and endocrine feedback loops. This paper examines the prebiotic potential of bioactive polysaccharides derived from the black bamboo species *Phyllostachys nigra*. Drawing on emerging structural and functional evidence, the analysis explores how the unique monomeric composition, glycosidic linkage patterns, and molecular weight distribution of these polysaccharides shape their fermentation kinetics, SCFA profiles, and subsequent effects on host glycolipid metabolism. Moving beyond reductionist biochemical description, the paper adopts a socio-technical and infrastructural lens to assess the architecture of gut microbial ecosystems under polysaccharide perturbation, the robustness and resilience of SCFA-producing networks, and the fairness implications of prebiotic deployment strategies. Production scalability, bamboo feedstock sustainability, regulatory governance, and integration into public health infrastructures are critically evaluated. The system-level perspective reveals structural trade-offs between personalization and population-wide standardization, between rapid fermentability and distal colonic targeting, and between ecological diversity and therapeutic specificity. By reframing a traditional nutraceutical topic within the discourse of complex systems, governance, and policy, the paper identifies knowledge gaps and proposes a research agenda that foregrounds architectural design principles for microbiome-directed nutrition.

## Keywords

prebiotics, *Phyllostachys nigra* polysaccharides, short-chain fatty acids, gut microbiome, system-level architecture, metabolic regulation, dietary fiber governance.

## 1. Introduction

The human gastrointestinal tract houses a dense, dynamic microbial consortium whose collective genomic capacity vastly exceeds that of the host. This microbial organ operates as a decentralized processing architecture, converting dietary substrates into a repertoire of metabolites that interface with host epithelial, immune, and endocrine networks. Among these metabolites, short-chain fatty acids—principally acetate, propionate, and butyrate—act as both local energy substrates and long-range signaling molecules that regulate energy homeostasis, insulin sensitivity, and inflammatory tone. The recognition that certain non-digestible carbohydrates can selectively stimulate the growth or activity of SCFA-producing bacteria gave rise to the prebiotic concept, which has since evolved into a systems-oriented paradigm in which dietary fibers are viewed as inputs that reconfigure microbial community structure, metabolic flux distributions, and host physiological endpoints.

Bamboo shoots and leaves from the genus *Phyllostachys* have long been part of traditional pharmacopoeias in East Asia, yet their polysaccharide constituents have only recently attracted attention as potential prebiotic agents. *Phyllostachys nigra*, or black bamboo, is distinguished by its rapid growth, high biomass yield, and presence in managed agroforestry systems. The polysaccharides extracted from its culms, leaves, and shoots exhibit an array of bioactive properties, including antioxidant, immunomodulatory, and metabolic regulatory activities. A detailed understanding of how these macromolecules traverse the upper gastrointestinal tract, undergo microbial deconstruction in the colon, and ultimately influence host metabolism through SCFA-mediated pathways is essential for evaluating their translational potential.

This paper situates the analysis of *Phyllostachys nigra* polysaccharides within a broader system-level framework that extends beyond biochemical pathways to encompass production infrastructure, regulatory governance, ecological resilience, and distributive fairness. Microbial ecosystems, like engineered distributed systems, exhibit nonlinear dynamics, redundancy, and emergent behaviors that can be modulated through targeted inputs. The architecture of the gut microbial network—its modularity, keystone species dependencies, and functional degeneracy—shapes how a prebiotic intervention propagates from localized fermentation events to whole-body metabolic outcomes. Simultaneously, the deployment of a novel prebiotic agent raises questions about the scalability of raw material supply, the environmental sustainability of bamboo cultivation, the design of appropriate regulatory frameworks, and the equitable access to gut health-promoting technologies across different socioeconomic strata. By linking molecular-level insights to these macroscopic concerns, the paper provides an integrated perspective that is relevant to researchers, policy makers, and industry stakeholders.

## 2. Structural Characteristics and Bioactivity of Polysaccharides from *Phyllostachys nigra*

The prebiotic functionality of any polysaccharide is intimately coupled to its chemical architecture. Primary structural features—monosaccharide composition, sequence, glycosidic linkage types, branching degree, and molecular weight—determine the repertoire of carbohydrate-active enzymes required for depolymerization and thus dictate which members

of the gut consortium can initiate fermentation. *Phyllostachys nigra* polysaccharides have been characterized as heteropolysaccharides rich in xylose, arabinose, glucose, galactose, and uronic acids, with backbone structures often composed of beta-1,4-linked xylosyl residues and side chains containing arabinofuranosyl and galactopyranosyl units. The presence of acetyl groups and ferulic acid esters adds further complexity, influencing solubility, viscosity, and accessibility to microbial hydrolases.

Early investigations into bamboo-derived polysaccharides demonstrated that variations in extraction protocols—hot water, alkaline, or enzymatic—yield fractions with divergent molecular weight distributions and monomeric ratios, each displaying distinct antioxidant capacities *in vitro*. For instance, polysaccharides from *Phyllostachys pubescens* leaves exhibited dose-dependent radical scavenging activities that correlated with their uronic acid content and molecular weight range. Subsequent work extended these findings to other *Phyllostachys* species, uncovering immunomodulatory effects mediated through macrophage activation and complement system engagement. The genus has been reviewed comprehensively, mapping its phytochemical diversity including flavonoids, phenolic acids, and polysaccharides across multiple tissues and developmental stages [1]. While such studies established the bioactive credentials of bamboo polysaccharides, they largely omitted the microbial fermentation dimension that is central to prebiotic function.

Recent structural elucidation efforts have employed methylation analysis, Fourier-transform infrared spectroscopy, and nuclear magnetic resonance to resolve the fine structure of *Phyllostachys nigra* polysaccharides. The data reveal a complex arabinoxylan-type architecture interspersed with pectin-like rhamnogalacturonan domains. This composite structure is significant because arabinoxylans are well-established substrates for prominent SCFA-producing genera such as *Bacteroides*, *Roseburia*, and *Bifidobacterium*, while rhamnogalacturonan fragments can be fermented by specialized primary degraders including *Bacteroides thetaiotaomicron*. The molecular weight of the isolated polysaccharides typically ranges from tens to hundreds of kilodaltons, a parameter that influences colonic transit time, water-holding capacity, and the spatial distribution of fermentation along the proximal-to-distal axis of the colon. Higher molecular weight fractions tend to exhibit delayed fermentation, promoting SCFA production in the distal colon where butyrate is particularly critical for colonocyte health and where many chronic colonic diseases originate.

The relationship between structure and prebiotic selectivity has been illuminated through comparative studies with well-characterized prebiotics such as inulin and fructooligosaccharides. Unlike linear fructans that are rapidly fermented by a relatively narrow set of taxa, the heterogeneous, branched structure of *Phyllostachys nigra* polysaccharides may support a broader consortium of saccharolytic bacteria, potentially enhancing functional redundancy and network stability. This architectural property can be conceptualized as a form of diversity-oriented design, wherein the polysaccharide matrix provides multiple distinct metabolic niches that reduce competitive exclusion and foster cross-feeding interactions. The ecological consequence is a fermentation network that is more robust to perturbations, a theme that will be revisited in the context of system resilience.

### **3. Prebiotic Mechanisms and Short-Chain Fatty Acid Production**

The conversion of non-digestible polysaccharides into SCFAs proceeds through a multi-tiered metabolic cascade involving primary degraders, oligosaccharide scavengers, and cross-feeding specialists. Within this distributed processing architecture, *Phyllostachys nigra* polysaccharides first undergo extracellular hydrolysis by carbohydrate-active enzymes

secreted by specialized Bacteroides and Firmicutes members. The released oligosaccharides and monosaccharides are then internalized and metabolized via the Embden-Meyerhof-Parnas pathway, the pentose phosphate pathway, or the bifid shunt, depending on the taxonomic affiliation of the consumer. Acetate is produced by a broad range of enteric bacteria through acetyl-CoA hydrolysis, while propionate formation occurs via succinate, acrylate, or propanediol pathways that are phylogenetically more restricted. Butyrate is synthesized from two acetyl-CoA molecules by members of the Lachnospiraceae and Ruminococcaceae families, often utilizing acetate as a co-substrate in a process that exemplifies metabolic interdependence.

The fermentability of *Phyllostachys nigra* polysaccharides and the resulting SCFA profile have been investigated using in vitro batch culture systems inoculated with human fecal microbiota. These studies reveal a pronounced shift toward acetate and butyrate production, with a moderate increase in propionate. The acetate-to-propionate-to-butyrate molar ratio is a critical system property because it determines the partitioning of SCFAs between hepatic metabolism, peripheral tissue utilization, and colonic epithelial consumption. Acetate escapes hepatic first-pass clearance to a significant extent and reaches peripheral circulation, where it influences appetite regulation through central nervous system mechanisms. Propionate is largely extracted by the liver and serves as a gluconeogenic substrate, while also interacting with intestinal gluconeogenesis sensors that signal satiety via the gut-brain axis. Butyrate is primarily consumed by colonocytes as their preferred energy source and acts as a histone deacetylase inhibitor, modulating gene expression in a manner that reinforces barrier integrity and suppresses inflammation.

A recent investigation specifically examined the effects of polysaccharide extracted from *Phyllostachys nigra* on glycolipid metabolism and gut microbiome composition in a murine model [2]. That study demonstrated that dietary administration of the polysaccharide not only enriched butyrate-producing taxa but also significantly improved serum lipid profiles and glucose tolerance, findings that are directly relevant to the metabolic syndrome spectrum. The observed modulation of the Firmicutes-to-Bacteroidetes ratio and the expansion of *Akkermansia muciniphila* populations point to a remodeling of the gut ecosystem that extends beyond simple substrate-driven growth. The increase in *Akkermansia*, a mucin-degrading specialist, suggests a cascade effect wherein primary polysaccharide fermentation enhances mucosal turnover, thereby creating a secondary nutritional niche that further stabilizes the remodeled community.

The production of SCFAs is not solely a function of substrate chemistry; it is also shaped by the system-level properties of the microbial network, including thermodynamic constraints, pH feedback, and interspecies hydrogen transfer. Accumulation of acetate and butyrate lowers luminal pH, which can inhibit pH-sensitive pathogens while favoring acid-tolerant beneficial taxa. Hydrogen partial pressure, regulated by methanogens, sulfate-reducing bacteria, and acetogens, determines the thermodynamic feasibility of butyrate production from acetate. Thus, the prebiotic effect of *Phyllostachys nigra* polysaccharides is embedded within a complex adaptive system where multiple feedback loops stabilize SCFA output within a physiological range. Understanding these dynamics is essential for predicting inter-individual variability in response to prebiotic supplementation and for designing fiber blends that target specific SCFA profiles.

#### **4. Host Metabolism and Systemic Effects**

SCFAs derived from polysaccharide fermentation serve as molecular conduits that translate microbial activity into host metabolic regulation across multiple organ systems. The interplay between SCFAs and host metabolism has been dissected through a combination of stable isotope tracing, germ-free animal models, and G-protein-coupled receptor knockout studies. Acetate, propionate, and butyrate ligate free fatty acid receptors FFAR2 and FFAR3 on enteroendocrine L-cells, adipocytes, and immune cells, triggering the secretion of glucagon-like peptide-1 and peptide YY, which collectively enhance insulin secretion, slow gastric emptying, and promote satiety. This endocrine relay exemplifies how a dietary intervention operating at the microbial level can be transduced into systemic energy balance signals that operate on timescales ranging from minutes to hours.

The metabolic benefits of bamboo-derived polysaccharides extend to hepatic lipid handling. Propionate delivered via the portal vein reduces hepatic lipogenesis by downregulating sterol regulatory element-binding protein-1c and fatty acid synthase expression, while simultaneously serving as a gluconeogenic substrate that activates intestinal gluconeogenesis-sensing mechanisms. Butyrate, through its epigenetic modulation of colonic and hepatic gene expression, upregulates peroxisome proliferator-activated receptor gamma coactivator 1-alpha, fostering a shift from glycolytic to oxidative metabolic programs. The study cited in reference [2] corroborates these pathways by demonstrating that *Phyllostachys nigra* polysaccharide administration lowered hepatic triglyceride accumulation and improved insulin sensitivity in high-fat diet-fed mice. Such findings position the polysaccharide as a candidate for managing non-alcoholic fatty liver disease and type 2 diabetes, conditions that are increasingly viewed through the lens of gut-liver axis disruption.

Beyond glycolipid metabolism, SCFAs reinforce the intestinal barrier by upregulating tight junction proteins such as occludin and claudin-1, thereby reducing systemic endotoxin exposure and low-grade inflammation that characterize metabolic syndrome. Butyrate, in particular, promotes the differentiation of regulatory T cells in the colonic lamina propria, enhancing immune tolerance and dampening inflammatory cascades that can propagate to adipose tissue and the liver. The immunomodulatory dimension of *Phyllostachys nigra* polysaccharides, although less explored than their metabolic effects, is likely to be significant given the structural similarity to immunostimulatory polysaccharides from other plant sources that engage pattern recognition receptors on dendritic cells and macrophages.

The systemic response to prebiotic intervention is not uniform across populations. Inter-individual variation in baseline microbiota composition, host genetic polymorphisms in SCFA receptors, and habitual dietary patterns all modulate the magnitude and direction of metabolic outcomes. This heterogeneity poses challenges for extrapolating results from controlled murine studies to diverse human cohorts. The observed efficacy of *Phyllostachys nigra* polysaccharides in normalizing glycolipid metabolism suggests that the substrate may act through robust, convergent pathways that are less susceptible to compositional variation, but this hypothesis requires validation in human trials that incorporate detailed microbiome phenotyping, metabolomic profiling, and anthropometric endpoints.

## **5. System-Level Perspectives: Production, Sustainability, and Policy Implications**

Framing *Phyllostachys nigra* polysaccharides as a prebiotic intervention compels an analysis that extends beyond the laboratory and clinic into the realms of agricultural production, industrial processing, environmental sustainability, and regulatory architecture. Bamboo, and *Phyllostachys nigra* in particular, is a perennial grass characterized by rapid biomass accumulation, a clonal propagation strategy that reduces the need for replanting, and

adaptability to marginal lands not suited for staple food crops. These traits confer significant sustainability advantages over terrestrial crops that are commonly used for prebiotic fiber production, such as chicory for inulin and sugarcane for fructooligosaccharides. The life cycle carbon footprint of bamboo cultivation is relatively low, and its extensive root system contributes to soil stabilization and carbon sequestration. However, scaling extraction to meet global demand requires careful management to avoid monoculture-induced biodiversity loss and to ensure that bamboo forestry does not compete with food production or displace indigenous land use practices.

The extraction and purification of polysaccharides from lignocellulosic bamboo biomass involves sequential unit operations including size reduction, delignification, aqueous or alkaline extraction, precipitation, and chromatographic polishing. The process architecture must balance yield, purity, and preservation of bioactive structural motifs against energy consumption, solvent toxicity, and waste generation. Green chemistry principles advocate for enzyme-assisted extraction, microwave or ultrasound pretreatment, and the use of recyclable solvent systems that reduce the environmental burden. The industrial deployment of such processes constitutes a socio-technical infrastructure, requiring not only chemical engineering expertise but also a skilled workforce, quality control systems, and supply chain logistics that can maintain the integrity of the polysaccharide product from field to consumer.

Regulatory governance of novel prebiotic agents is fragmented across jurisdictions. In the United States, *Phyllostachys nigra* polysaccharides would likely be classified as a dietary ingredient under the Dietary Supplement Health and Education Act, with structure-function claims permitted but disease prevention claims restricted without new dietary ingredient notification or generally recognized as safe affirmation. In the European Union, the product would fall under the Novel Food Regulation if a significant history of consumption cannot be demonstrated, triggering a comprehensive safety assessment by the European Food Safety Authority that includes compositional analysis, toxicological studies, and assessment of nutritional impact. These divergent regulatory architectures create a landscape in which the evidentiary requirements for market access vary widely, shaping the pharmaceutical versus nutraceutical identity of the product and influencing private sector investment in clinical trials. A harmonized, risk-based framework that recognizes the unique properties of microbiome-targeted interventions is needed to accelerate innovation while safeguarding public health.

The policy implications extend to dietary guidelines and public health nutrition. Current fiber intake recommendations are couched in terms of total grams per day, without differentiation among fiber types or consideration of their differential effects on microbial ecology and SCFA production. Emerging evidence on the structure-specific prebiotic effects of bamboo polysaccharides supports a more granular approach to dietary guidance that specifies not only the quantity but also the quality and botanical source of fiber. Such a reorientation would require surveillance systems capable of monitoring population-level fiber intake with sufficient taxonomic resolution, as well as educational campaigns that translate complex matrix effects into actionable consumer messaging. The integration of *Phyllostachys nigra* polysaccharides into food matrices—such as functional beverages, bakery products, or medical foods—introduces additional layers of regulatory oversight related to food additives, labeling, and health claims substantiation, all of which must be navigated within the broader governance framework of food systems.

## **6. Robustness and Fairness in Microbiome-Targeted Interventions**

The resilience of the gut microbial ecosystem—its capacity to maintain functional SCFA production in the face of dietary, pharmaceutical, and pathogenic perturbations—is a system property of paramount importance. Prebiotic polysaccharides can be viewed as inputs that either reinforce or erode this robustness depending on their structural complexity and the diversity of metabolic pathways they recruit. Highly selective substrates that enrich a narrow clade of butyrate producers may increase functional efficiency but reduce ecological insurance, rendering the system vulnerable to collapse if that clade is decimated by antibiotics or bacteriophage predation. In contrast, the heterogeneous polysaccharide matrix of *Phyllostachys nigra*, with its arabinoxylan and rhamnogalacturonan domains, engages a broader metabolic guild and may promote functional redundancy that buffers against disturbance. This trade-off between specificity and robustness mirrors design principles well known in engineered distributed systems, where redundancy and modularity are key to fault tolerance.

Inter-individual variability in prebiotic response raises profound questions about fairness in the design of nutrition interventions. If a population is stratified into responders and non-responders based on baseline microbiota composition, a universal recommendation to consume bamboo-derived prebiotics may disproportionately benefit those with a permissive microbial configuration, potentially exacerbating health disparities. Personalized prebiotic strategies that employ microbiome sequencing to match substrates to individual community architecture hold promise but currently face cost, accessibility, and interpretive barriers that would favor affluent populations. A fairness-oriented policy must therefore invest in the development of low-cost, point-of-care microbiome assessment tools and consider the possibility of co-administering probiotic or synbiotic formulations that render more individuals permissive to the prebiotic effect. This approach transforms the prebiotic from a standalone product into a platform technology embedded in a broader ecosystem of diagnostics and companion biologics.

The global distribution of prebiotic interventions also intersects with food sovereignty and cultural acceptability. Bamboo has deep cultural roots in many Asian and African societies, where it is integrated into culinary traditions and local economies. The extraction of polysaccharides from *Phyllostachys nigra* for export to high-income markets could, if mismanaged, replicate extractive economic patterns that marginalize local communities. Conversely, cultivating local processing capacity and integrating bamboo prebiotics into regional food systems could generate economic value within producer communities and align public health goals with sustainable development objectives. Governance mechanisms that embed community benefit agreements, fair trade certification, and intellectual property provisions respecting traditional knowledge are essential to ensure that the deployment of this prebiotic technology is just and inclusive.

## **7. Governance, Infrastructure, and Public Health Deployment**

Translating the scientific evidence for *Phyllostachys nigra* polysaccharides into population-level health benefits requires an integration of technical, regulatory, and logistical infrastructures that spans agriculture, food manufacturing, clinical medicine, and public health surveillance. The governance architecture must be capable of addressing multiple objectives simultaneously: ensuring product safety and efficacy, incentivizing industrial innovation, protecting consumer autonomy, and reducing health inequities. Multi-stakeholder platforms that bring together researchers, industry representatives, regulators, and civil society organizations can co-design standards for prebiotic characterization and labeling, develop

post-market surveillance systems for adverse events, and establish transparent mechanisms for adjudicating health claims.

From an infrastructure perspective, the supply chain for bamboo polysaccharides must be resilient to climate variability, pest outbreaks, and geopolitical disruptions. Geographic diversification of cultivation zones, combined with the development of extraction facilities that can process multiple bamboo species, would reduce systemic risk. Cold chain requirements for intermediate products, shelf-life stability of final formulations, and compatibility with existing food distribution networks are practical considerations that influence deployment feasibility. Lessons from the fortification of staple foods with micronutrients suggest that the integration of a prebiotic into widely consumed vehicles—such as wheat flour, cooking oil, or salt—can achieve broad coverage, but only if the polysaccharide is chemically stable under cooking and storage conditions and does not alter organoleptic properties in unacceptable ways.

Public health deployment strategies must also contend with the communication challenge of explaining microbiome science to lay audiences. The concept of feeding one's gut bacteria with bamboo-derived fiber to produce metabolites that improve metabolism is not intuitively grasped, and simplistic messaging risks overselling benefits or ignoring uncertainties. Health literacy initiatives, co-developed with community health workers and social media influencers, can translate the systems logic into relatable narratives that emphasize dietary diversity, whole foods, and the interconnection of human and microbial health. The framing of prebiotic supplementation as a complement to, rather than a substitute for, a fiber-rich diet is critical to avoid undermining established dietary guidelines.

Finally, the integration of prebiotic interventions into clinical practice pathways for metabolic disease will require alignment with reimbursement models and health technology assessment frameworks. Demonstrating cost-effectiveness through reduced incidence of type 2 diabetes or non-alcoholic steatohepatitis in at-risk populations will necessitate long-term randomized controlled trials with hard endpoints, as well as real-world evidence generated from electronic health records and wearable metabolic monitors. The design of such trials must account for the ecological nature of the intervention—where the endpoint is not simply a change in a single biomarker but a reconfiguration of a complex host-microbial system—and accordingly adopt composite outcomes, adaptive trial designs, and systems-level statistical modeling.

## **8. Conclusion**

Bioactive polysaccharides extracted from *Phyllostachys nigra* represent a promising addition to the prebiotic armamentarium, distinguished by a structural complexity that engages diverse microbial guilds, promotes robust SCFA production, and modulates host glycolipid metabolism through multi-organ signaling cascades. The evidence reviewed in this paper establishes a plausible mechanistic chain from polysaccharide architecture to fermentation kinetics, SCFA profiles, and systemic metabolic benefits, with particular support from the recent demonstration of improved glucose tolerance and lipid homeostasis in a murine model. However, the translational pathway from these findings to a marketed prebiotic product and, ultimately, to improved public health is laden with system-level considerations that extend far beyond the biochemical domain. The sustainability of bamboo feedstock, the architectural resilience of the gut microbial network, the fairness of personalized and population-level deployment, and the coherence of regulatory and health system infrastructures collectively determine the real-world impact of the technology.

A systems lens reveals structural trade-offs that must be navigated deliberately. The same chemical heterogeneity that confers ecological robustness and cross-feeding stability also complicates standardization and quality control. The regional abundance of bamboo offers sustainability advantages but introduces risks of monoculture and inequitable value chains. The promise of personalized prebiotic regimens challenges the one-size-fits-all paradigm of dietary guidelines but risks exacerbating health disparities if access to diagnostic and tailored products is unevenly distributed. Addressing these trade-offs requires interdisciplinary research that couples structural carbohydrate chemistry with microbial ecology, metabolic physiology, industrial process engineering, health economics, and political science. Only through such integrative inquiry can the potential of *Phyllostachys nigra* polysaccharides as prebiotic agents be realized in a manner that is scientifically sound, ecologically sustainable, and socially just.

## References

1. He, X., Wang, X., Fang, J., Chang, Y., Ning, N., Guo, H., Huang, L., Huang, X., & Li, H. (2017). The genus *Phyllostachys*: A review on its phytochemistry and pharmacology. *Journal of Ethnopharmacology*, 206, 290–320.
2. Gibson, G. R., & Roberfroid, M. B. (1995). Dietary modulation of the human colonic microbiota: Introducing the concept of prebiotics. *The Journal of Nutrition*, 125(6), 1401–1412.
3. Gill, S. R., Pop, M., DeBoy, R. T., Eckburg, P. B., Turnbaugh, P. J., Samuel, B. S., Gordon, J. I., Relman, D. A., Fraser-Liggett, C. M., & Nelson, K. E. (2006). Metagenomic analysis of the human distal gut microbiome. *Science*, 312(5778), 1355–1359.
4. Flint, H. J., Scott, K. P., Louis, P., & Duncan, S. H. (2012). The role of the gut microbiota in nutrition and health. *Nature Reviews Gastroenterology & Hepatology*, 9(10), 577–589.
5. Cummings, J. H., Pomare, E. W., Branch, W. J., Naylor, C. P., & Macfarlane, G. T. (1987). Short chain fatty acids in human large intestine, portal, hepatic and venous blood. *Gut*, 28(10), 1221–1227.
6. den Besten, G., van Eunen, K., Groen, A. K., Venema, K., Reijngoud, D. J., & Bakker, B. M. (2013). The role of short-chain fatty acids in the interplay between diet, gut microbiota, and host energy metabolism. *Journal of Lipid Research*, 54(9), 2325–2340.
7. Koh, A., De Vadder, F., Kovatcheva-Datchary, P., & Bäckhed, F. (2016). From dietary fiber to host physiology: Short-chain fatty acids as key bacterial metabolites. *Cell*, 165(6), 1332–1345.
8. Sonnenburg, E. D., & Sonnenburg, J. L. (2014). Starving our microbial self: The deleterious consequences of a diet deficient in microbiota-accessible carbohydrates. *Cell Metabolism*, 20(5), 779–786.
9. Holscher, H. D. (2017). Dietary fiber and prebiotics and the gastrointestinal microbiota. *Gut Microbes*, 8(2), 172–184.
10. Lu, X., Chen, Z., Gu, Z., & Han, Y. (2017). Isolation and characterization of polysaccharides from bamboo (*Phyllostachys pubescens*) leaves and their antioxidant activities. *International Journal of Biological Macromolecules*, 98, 516–523.

11. Luo, X., Wang, Q., Zheng, B., Lin, L., Chen, B., Zheng, Y., & Xiao, J. (2016). Hydration properties and binding capacities of dietary fibers from bamboo shoot shell and its micronized products. *Food & Function*, 7(8), 3494–3502.
12. Sun, L., Wang, L., & Zhou, Y. (2012). Immunomodulation and antitumor activities of different-molecular-weight polysaccharides from *Porphyridium cruentum*. *Carbohydrate Polymers*, 87(2), 1206–1210.
13. Chen, G., Xie, M., Wan, P., Chen, D., Dai, Z., Ye, H., Liu, R., & Liu, Y. (2018). Structural characterization and immunomodulatory activity of a water-soluble polysaccharide from the fruiting bodies of *Pleurotus eryngii*. *Food & Function*, 9(5), 2944–2954.
14. Zhang, Y., Xu, X., & Zhang, L. (2012). Structure and bioactivities of polysaccharides from bamboo shoots (*Phyllostachys praecox*). *Food Chemistry*, 135(3), 1970–1976.
15. Cani, P. D., & Delzenne, N. M. (2009). The role of the gut microbiota in energy metabolism and metabolic disease. *Current Pharmaceutical Design*, 15(13), 1546–1558.
16. Sonnenburg, J. L., & Bäckhed, F. (2016). Diet-microbiota interactions as moderators of human metabolism. *Nature*, 535(7610), 56–64.
17. Zhao, K., Wu, X., Han, G., Sun, L., Zheng, C., Hou, H., ... & Shi, Z. (2024). *Phyllostachys nigra* (Lodd. ex Lindl.) derived polysaccharide with enhanced glycolipid metabolism regulation and mice gut microbiome. *International journal of biological macromolecules*, 257, 128588.
18. 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.
19. Ríos-Covián, D., Ruas-Madiedo, P., Margolles, A., Gueimonde, M., de los Reyes-Gavilán, C. G., & Salazar, N. (2016). Intestinal short chain fatty acids and their link with diet and human health. *Frontiers in Microbiology*, 7, 185.
20. Morrison, D. J., & Preston, T. (2016). Formation of short chain fatty acids by the gut microbiota and their impact on human metabolism. *Gut Microbes*, 7(3), 189–200.
21. Canfora, E. E., Jocken, J. W., & Blaak, E. E. (2015). Short-chain fatty acids in control of body weight and insulin sensitivity. *Nature Reviews Endocrinology*, 11(10), 577–591.
22. Fan, Y., & Pedersen, O. (2021). Gut microbiota in human metabolic health and disease. *Nature Reviews Microbiology*, 19(1), 55–71.
23. Marchesi, J. R., Adams, D. H., Fava, F., Hermes, G. D., Hirschfield, G. M., Hold, G., Quraishi, M. N., Kinross, J., Smidt, H., Tuohy, K. M., Thomas, L. V., Zoetendal, E. G., & Hart, A. (2016). The gut microbiota and host health: A new clinical frontier. *Gut*, 65(2), 330–339.
24. Thursby, E., & Juge, N. (2017). Introduction to the human gut microbiota. *Biochemical Journal*, 474(11), 1823–1836.
25. Roberfroid, M. (2007). Prebiotics: The concept revisited. *The Journal of Nutrition*, 137(3), 830S–837S.