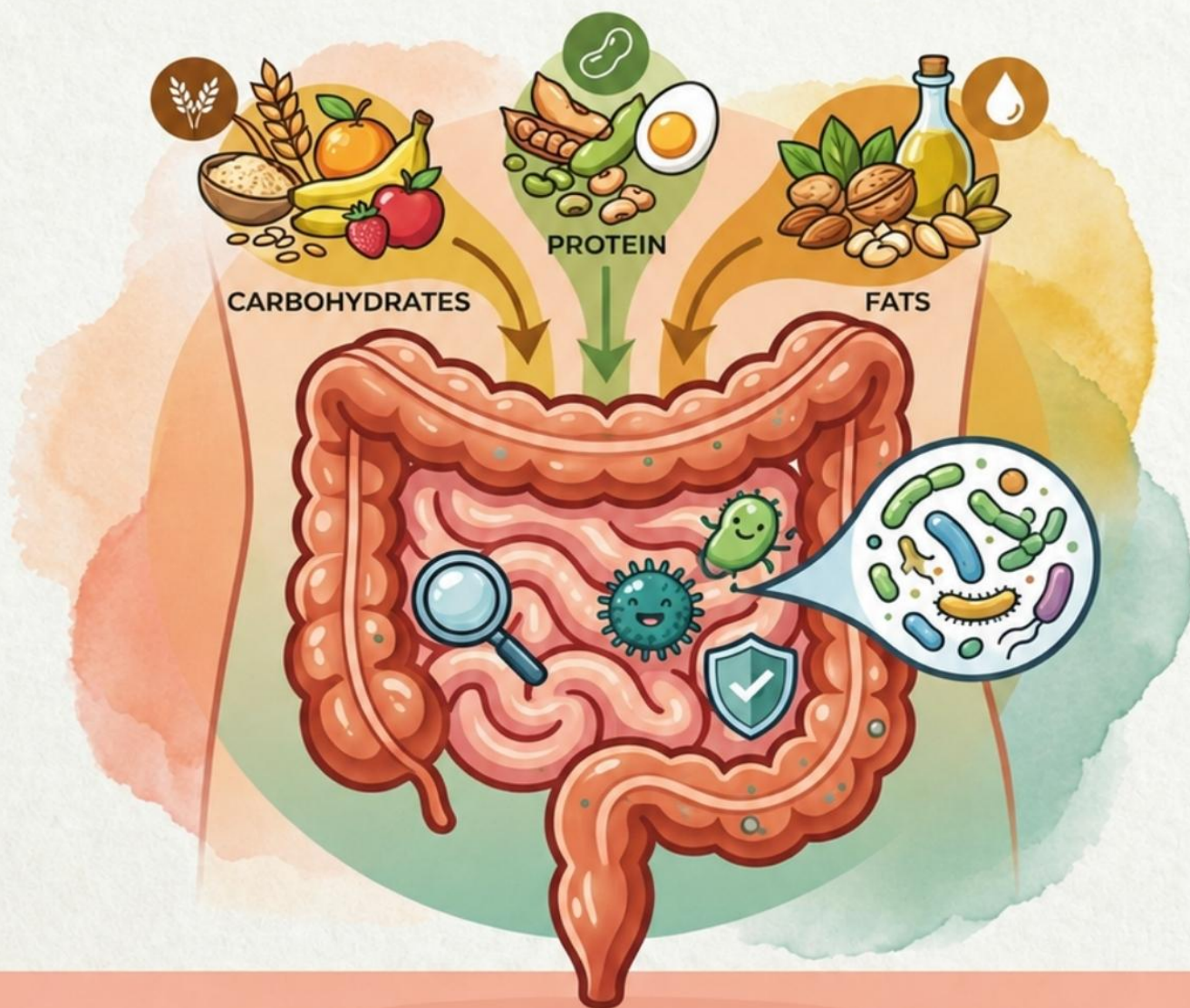


white paper on -

Gut Health in Modern Nutrition: Understanding the Role of Food Composition, Lifestyle & Preventive Nutrition



**"Gut Health in Modern Nutrition:
Understanding the Role of
Food Composition, Lifestyle &
Preventive Nutrition"**

Title: "Gut Health in Modern Nutrition: Understanding the Role of Food Composition, Lifestyle & Preventive Nutrition"

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Rationale of the whitepaper: This whitepaper will give an insight into the science demonstrating the impact of food composition, matrix and level of processing on gut microbiome. Also, will be highlighting the effects of different related factors, national/global recommendations on the topic, etc.

No of pages: 40

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Executive Summary:

The relationship between food and health has been recognized since ages. Recent scientific advances have understood this and brought renewed focus to one of the most dynamic mediators of this relationship, which is the gut microbiome. The trillions of microorganisms residing in the human gastrointestinal tract (GI tract) play a central role in digestion, metabolism, immune regulation, and a person's overall well-being. Increasing evidence suggests that the food we eat, their composition, and the degree to which they are processed can significantly influence the diversity and function of this microbial ecosystem.

This whitepaper, ***Gut Health in Modern Nutrition: Understanding the Role of Food Composition, Lifestyle & Preventive Nutrition***, has been developed to provide a science-based overview of how dietary macronutrients- carbohydrates, proteins, and fats, interact with the gut microbiota. It also helps one understand how food matrix, processing methods, meal patterns, and lifestyle factors contribute to gut microbial balance or imbalance/dysbiosis. By incorporating current evidence, the white paper aims to translate emerging microbiome science into practical relevance for nutrition professionals, researchers, food industry stakeholders, and health-conscious consumers.

Due to rising non-communicable diseases, the food and health sectors are moving towards more personalized and preventive nutrition models, and hence, understanding the gut microbiome has become increasingly important. Our white paper provides a comprehensive overview that focuses on both the opportunities and the challenges in leveraging food-based strategies to support gut health, while emphasizing the need for further research and responsible innovation.

The authors, with their diverse and wholesome expertise, brought together the critical elements of scientific literature, policy guidelines, and recommendations on macronutrients, including definitions, health benefits, factors influencing, etc. Furthermore, we hope this white paper serves as a valuable reference for informed decision-making and stimulates further conversation on the role of food composition in shaping a healthier future.

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1. Introduction: Food composition and gut microbiome

GUT MICROBIOTA

Gut microbiota describes the community of living microorganisms residing in the lower human gastrointestinal tract, comprising over 100 trillion microbes. It consists of six major phyla—*Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Proteobacteria*, *Fusobacteria*, and *Verrucomicrobia*—with *Firmicutes* and *Bacteroidetes* being the predominant groups (Hou et al., 2022). The gut microbiome refers to the collective genomes of all microorganisms in the gut environment, encompassing not only the microbial community but also their structural components, metabolites, and surrounding environmental conditions. It provides insights into the functional potential of the gut ecosystem and its impact on host health and disease (Berg et al., 2020).

Development of the gut microbiota

Gut microbiota development is a critical process that begins at birth—or possibly *in utero*—and is shaped by multiple factors. Delivery mode strongly influences initial colonization, with vaginally delivered infants showing greater microbial diversity than those born via caesarean section, and this composition continues to evolve over the first 1,000 days, heavily shaped by breastfeeding and complementary feeding practices, transitioning from *Bifidobacterium* dominance to *Firmicutes* and *Bacteroidetes* during weaning, and eventually maturing into an adult-like microbiota (Pantazi et al., 2023).

Gut microbiota concentration physiologically varies throughout the gastrointestinal tract and is shown in Table 1

Table 1: Human intestinal microbiota

Stomach and Duodenum	· Harbour low number of microorganisms: $< 10^3$ bacteria per gram of contents · Mainly <i>Lactobacilli</i> and <i>Streptococci</i> · Acid, bile and pancreatic secretions suppress most ingested microbes · Phasic propulsive motor activity impedes stable colonization of the lumen (also true for the small intestine)
Jejunum and Ileum	· Numbers progressively increase from 10^4 in the jejunum to 10^7 cells per gram of contents in the distal ileum
Large intestine	· Heavily populated by anaerobes: up to 10^{12} cells per gram of luminal contents

Reproduced from *Global Guidelines: Probiotics and Prebiotics*, by World Gastroenterology Organisation, 2023.

Role of gut microbiota in the body

The interaction between the host and gut microbiota is largely symbiotic, with a balanced microbial community being closely linked to overall human health and disease prevention. The gut microbiota influences numerous physiological processes, including immune regulation, metabolism, gut–brain communication, and protection against pathogens.

- a. **Digestion Function & Metabolism:** The microbiota primarily helps in the fermentation of Non-Digestible Carbohydrates, producing SCFAs, primarily acetate, propionate, and butyrate, which act as key energy sources for colonic cells, modulate immune responses, reduce inflammation, and possess anti-obesity and anticancer properties (Lin and Medeiros, 2023).
- b. **Antimicrobial activity:** The gut microbiota forms a crucial barrier and prevents colonization of pathogens in the gut. It also protects against pathogens through the production of various organic acids, bacteriocins and hydrogen peroxide, along with metabolic competition (Garcia-Gutierrez et al., 2019).
- c. **Immune System Modulation:** The gut microbiota exerts a profound immunomodulatory effect by interacting with intestinal immune cells and influencing the development, maturation, and regulation of both innate and adaptive immunity. Through microbial metabolites such as short-chain fatty acids and signalling via pattern recognition receptors, it helps maintain immune tolerance and suppresses excessive inflammation (Kim et al., 2025)
- d. **Synthesis of Nutrients:** the microbiota synthesises essential vitamins, including vitamin K and various B vitamins. Many strains are known to produce vitamin B12- a vitamin crucial for vegetarians and vegans (Oz et al., 2023).
- e. **Gut-Brain Axis Communication:** The gut microbiota plays a key role in gut–brain axis communication by producing neuroactive compounds, modulating vagus nerve signalling, and influencing immune and endocrine pathways that affect brain function and behaviour (Chakrabarti et al., 2022).

Table 2: Definitions

Probiotics	Live microorganisms that, when administered in adequate amounts, confer a health benefit on the host
Prebiotic	A selectively fermented ingredient that results in specific changes in the composition and/or activity of the gastrointestinal microbiota, thus conferring benefit(s) upon host health
Synbiotics	A mixture comprising live microorganisms and substrate(s) selectively utilized by host microorganisms that confers a health benefit on the host. There are two types of synbiotics: complementary (mixtures of probiotics and prebiotics) and synergistic (mixtures of live microbes selected to utilize a co-administered substrate for a health effect)
Postbiotic	A preparation of inanimate microorganisms and/or their components that confers a health benefit on the host

Reproduced from *Global Guidelines: Probiotics and Prebiotics*, by World Gastroenterology Organisation, 2023.

From a comprehensive microbiome-support perspective, probiotics, prebiotics, and postbiotics each represent complementary and promising strategies for modulating gut microbiota function and mitigating dysbiosis-associated disease. Probiotics introduce beneficial live microorganisms that can help restore microbial balance and competitively inhibit pathobionts. Prebiotics selectively nourish commensal bacteria, promoting the growth and metabolic activity of health-associated microbial populations. Postbiotics, consisting of bioactive metabolites and microbial components, exert direct physiological effects—such as enhancing barrier integrity and modulating immune responses—without requiring microbial viability. Together, these approaches offer stable, targeted, and potentially synergistic interventions to support microbial homeostasis and long-term health.

POSTBIOTICS

Postbiotics are bioactive compounds, metabolic byproducts, or cellular components produced by probiotic microorganisms during fermentation or growth that confer health benefits to the host. Unlike probiotics, they are non-viable, meaning the microbial cells themselves are dead or inactivated, but their metabolites remain biologically active (Salminen et al., 2021).

Formally, they can include:

- Cell-free supernatants of bacterial cultures
- Metabolites like short-chain fatty acids (SCFAs), exopolysaccharides, peptides, and organic acids
- Cell wall components like lipoteichoic acids, peptidoglycans, and surface proteins

There is a delicate balance in microbiota populations in the gut, and disruption in this balance leads to dysbiosis and overgrowth of pathobionts, triggering pathologic immune responses and contributing to disease development. Research highlights that the gut microbiome is highly malleable to environmental factors—including diet, stress, medications, infections, and lifestyle—providing meaningful opportunities for targeted interventions.

2. Factors influencing gut microbiome variability among individuals

The gut microbiota is an intricate collection of bacteria inhabiting the intestinal tract. While the stomach hosts a considerably smaller bacterial population, the number of bacteria escalates as they move through the digestive tract, starting from the stomach and progressing through the duodenum, jejunum, and ileum, culminating in the colon, which harbours an estimated 10^9 to 10^{13} bacteria (Wen L. et al. 2017). The microbiota of the human gut, a complex of microorganisms that inhabit the gastrointestinal tract, has become a central modulator of metabolic health, with effects on physiological processes, energy, immune response, and neurobehavioral response via the gut-brain axis (Montagnani M. et al., 2023; Maquod F. et al., 2025). Human gut microbiota is influenced by multiple biological, environmental, physiological, intrinsic, extrinsic, and pathological factors. The change usually ranges from rapid to long-term, and the impact also varies with the intensity of the interaction of the gut and the factors influencing.

In this section, the factors like age, gender, body mass index (BMI), ethnicity, stress, sleep and food composition will be discussed in detail.

Non-Modifiable Factors:

1. Age:

Human gut health undergoes significant, dynamic changes throughout life, transitioning from initial colonization to a diverse adult state, and eventually to a less diverse, more personalized state in old age. These changes are driven by physiological, environmental, and diet-lifestyle influences. They are strongly linked to the maturation and aging of the immune system and overall gut health.

After birth, the initial colonization of gut microbiota starts and is significantly influenced by the mode of delivery. Vaginally delivered babies have higher early gut bacterial diversity, dominated by *Bifidobacterium* and *Lactobacillus*, as compared to C-section delivered newborns. Secondly, breastfeeding promotes *Bifidobacterium*, which matures the immune system. The transition to solid foods (weaning) causes a major shift in microbial composition, increasing diversity as the gut adjusts to a more varied diet (Rodriguez JM et al., 2015).

Adolescence A transitional phase with increased levels of *Bifidobacteria* and *Clostridia* compared to adults, with the microbiota maturing to support fiber digestion and pathogen resistance. (Schoultz I. et al., 2025)

In adulthood, the microbiome is characterized by high diversity and relative stability. Dominated by the phyla *Firmicutes* and *Bacteroidetes*, which are crucial for fiber digestion (Schoultz I. et al., 2025).

Aging is accompanied by substantial alterations in gut physiology, marked by reduced microbial diversity, heightened inflammatory activity, and compromised intestinal barrier structure.

A recent metagenomic investigation involving 6,653 healthy individuals across the lifespan (categorized by WHO guidelines into four groups: 0 - 4, 5-17, 18-64, and 65 +) found that species richness matures in early life and reaches stability during childhood and adolescence. Results demonstrated that aging is characterized by a ‘continuous rearrangement’ of existing taxa rather than a gain or loss of species (Mancabelli L. et al., 2024).

2. Gender

Emerging evidence suggests that both sex- and gender-based differences influence susceptibility to GI diseases, and these differences may be mediated, at least in part, by variations in gut microbiota composition. Additionally, the metabolism of sex hormones, such as estrogens and androgens, is closely linked to the gut microbiome. Because gut microorganisms participate in the metabolism, circulation, and excretion of sex hormones, the concept of the “**microgenderome**” has been proposed to describe the bidirectional interactions between sex hormones and gut microbial communities (Yoon K et al., 2021).

Notably, gut maturation and shifts in sex hormone levels occur simultaneously across the lifespan, highlighting critical windows during which microbiota–hormone interactions may shape long-term health outcomes. A large population-based study involving 1,135 individuals reported that females exhibited greater gut microbial diversity compared with males, with a higher abundance of *Akkermansia muciniphila* observed in females (Sinha T et al., 2019). In contrast, males demonstrated increased levels of *Prevotella* and *Escherichia*, microbial genera associated with heightened susceptibility to infections and inflammatory conditions (Ghaffer T. et al., 2025). Furthermore, dietary patterns, antibiotic exposure, and environmental factors have been shown to influence gut microbiota composition in a gender-dependent manner, further underscoring the complex interplay between biological sex, lifestyle factors, and microbial ecology (Valeri F., Endres K. 2021).

3. Ethnicity

Gut microbiome composition and diversity vary substantially across ethnic groups, largely influenced by differences in diet, lifestyle, geography, and environmental exposures rather than host genetics alone. Studies demonstrate that distinct ethnic populations harbour unique microbial profiles, with measurable differences emerging as early as three months of age. Reports suggest that individuals of Asian and African descent often show higher abundances of *Prevotella*, whereas those of European descent frequently show a predominance of *Bacteroides*. These variations often mirror social, cultural, and environmental determinants of health, underscoring the role of modifiable exposures in shaping the gut microbiota across the life course.

A recent multi ethnic population cohort study in Singapore reported that ethnic Indians showed enrichment of multiple *Bifidobacterium* species associated with greater intake of traditional grain-based staples such as Idli and Dosai; ethnic Malays exhibited higher abundance of *Ruminococcaceae* associated with coconut and rice-based dishes; and ethnic Chinese participants had greater levels of *Bacteroides* associated with seafood- and meat-rich diets (Zhou R. et al. 2026; Liang L. et al. 2026).

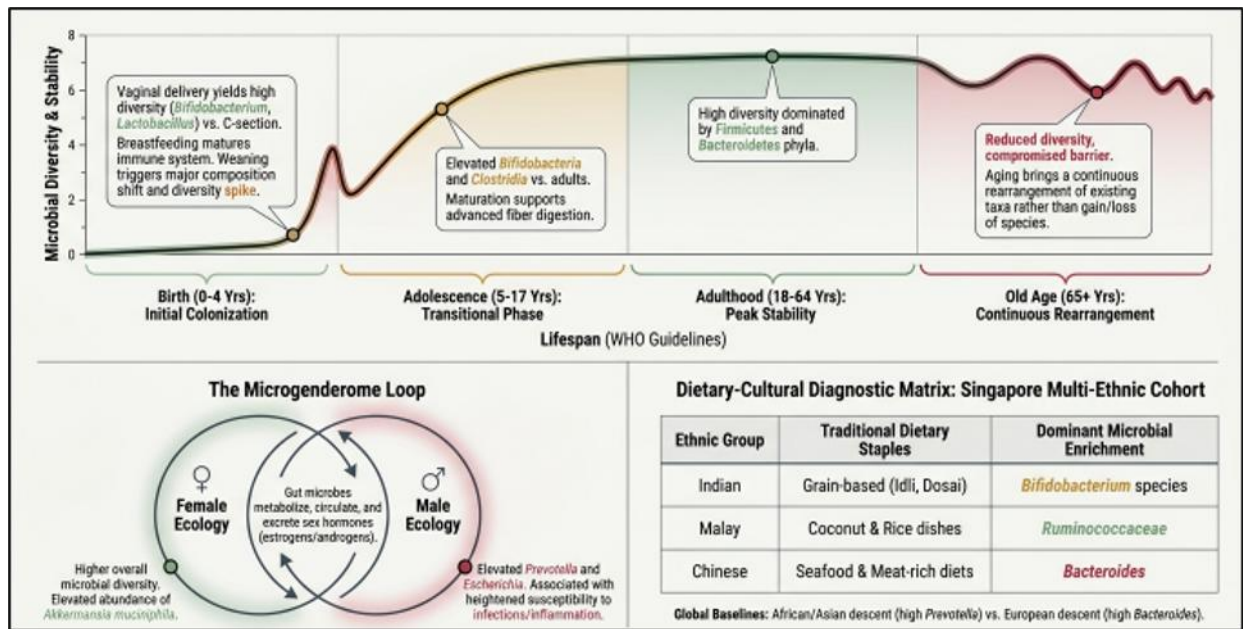


Figure 1: Non-modifiable factors influencing gut microbiome

Modifiable factors

4. BMI

The gut-brain-metabolic axis is a new conceptual framework of the two-way communication between the gut microbiota, central nervous system (CNS), and metabolic organs (Bhalla D. et al. 2024; Longo S. et al. 2023). Neural and endocrine mechanisms intermediate neuroactive products of gut microbes, including short-chain fatty acids (SCFAs), serotonin precursors, and gamma-aminobutyric acid (GABA), have an impact on appetite control, stress response, and energy expenditure (Han H. et al. 2021). A change in microbial diversity can thus interfere with neuroendocrine signaling, which is one of the causes of metabolic dysregulation and higher BMI, and how the biological sex of the host shapes its gut microbiota (Romaní-Pérez M. et al., 2025; Mitev K. et al., 2019). For example, dysbiosis can interfere with hypothalamic signaling of satiety, leading to the intake of more food and metabolic lipid problems. Additionally, the neuroimmune aspect of metabolic health is emphasized by the use of microbiota-derived metabolites to regulate systemic inflammation, a major causative connection between obesity and insulin resistance, and cardiovascular disease. (Goep NS. et al., 2025).

The bidirectional relation between BMI and gut microbiome has been reported in human trials with dietary interventions. Studies conducted among obese and lean populations reported that obese subjects had significantly fewer *Bacteroidetes* and more *Firmicutes* than lean control subjects at baseline. Also, after 1 year of weight loss intervention, the relative proportion of *Bacteroidetes* increased, while *Firmicutes* decreased, a finding well correlated with the percentage of weight loss (Ley RE et al. 2005; Kotzampassi K., 2013).

5. Stress

In today's fast life, stress is inevitable and thus resilience is crucial. The effect of stress exposure on alteration in the gut microbiota and their metabolites, affecting host physiology, has been reported by preclinical and clinical studies. Further, stress-induced shifts in the gut microbiota jeopardize tight junctions of the gut barrier, which can lead to translocation of bacteria and bacterial products from the gut to the bloodstream, lymph nodes, and other organs, thereby modifying systemic inflammatory responses. Increased circulating inflammation can be an etiological factor in stress-related psychiatric disorders, including some cases of depression. (Madison AA, Bailey MT. 2024). Triggering stress response also raises cortisol production, and chronic stress has been linked to gastrointestinal and cardiovascular illnesses and disrupts the immune response of the host (Ahmed F. et al., 2025). Further, chronic stress has also been linked to flared-up IBD, peptic ulcer, colitis, affects endocrine function, reduced gut motility and homeostasis. (Kounterek PC. et al. 2011; Zhang H. et al., 2023).

6. Sleep and circadian rhythm

The brain-gut-microbiome axis can affect health in many ways and is influenced by multiple environmental factors. It also shares a bidirectional relation with another crucial factor- sleep. Recent scientific focus on sleep quantity, quality and disturbance disorders uncovered a reciprocal relationship: while disrupted sleep patterns can disturb the gut microbiota, leading to dysbiosis and subsequent health implications, an imbalance in the microbiome can also exacerbate sleep issues, perpetuating a detrimental cycle. There is growing evidence indicating that sleep duration and quality have a direct impact on gut microbiome composition and diversity, and the effect might be seen in a short span. In humans, previous research has shown that partial sleep deprivation can alter the gut microbiome composition in as little as 48 hours (Benedict C. et al., 2016). Another recent study showed that high sleep quality was associated with a *Verrucomicrobia Lenti* gut microbiome containing a high proportion of bacteria and *sphaerae* phyla, and that this was associated with improved performance on cognitive tasks (Andersson JR et al., 2017). In spite of these findings, the mechanisms through which the gut microbiome can affect sleep remain unresolved, and in particular, the molecules that interface between sleep and the gut microbiome remain unidentified. A study on understanding the linkage between gut microbiome composition, sleep physiology and the immune system and cognition reported a positive association between microbiome diversity and sleep efficiency, total sleep time, and a negative association with wake

after sleep onset. Within phyla, richness of *Bacteroidetes* and *Firmicutes* was positively correlated with sleep efficiency, interleukin-6 concentrations and abstract thinking. (Smith RP. et al., 2019). A review suggests that specific gut bacteria, like *Lactobacillus* and *Bifidobacterium*, enhance sleep through serotonin and gamma-aminobutyric acid production, exemplifying direct microbiome influence (Lin Z. et al., 2024). Sleep fragmentation has also been reported to cause declines in genera such as *Prevotella*, *Sutterella*, *Parasutterella*, *Alloprevotella*, *Anaerobiospora*, and *Elusimicrobium*, alongside reduced levels of acetate, propionate, and butyrate. (Lin Z. et al., 2024).

Circadian disturbances are caused by factors including disturbed sleep, jet lag, and behavioural factors like irregular eating habits, which affect lipid metabolism, short-chain fatty acid (SCFA) synthesis, and gut microbial rhythms (Bajaj P. & Sharma M. 2025).

7. Meal timings

The gut microbiome is highly dynamic, exhibiting daily cyclical fluctuations in composition (Zarrinpar A. et al. 2014; Jennifer LK et al., 2017). Changes in tight junction proteins have been linked to irregular meal timing, which increases intestinal permeability and inflammation. Additionally, new research indicates a bidirectional relationship in which the gut bacteria might affect the central and peripheral circadian clocks. Thus, fixed meal timings and food composition, along with a balanced circadian rhythm, play a crucial role in gut microbiome stability and integrity. According to research, microbial diversity and function are enhanced by early-time-restricted feeding (eTRF), which synchronizes with circadian cycles. Cyclical changes in the gut microbiome from feeding/fasting rhythms contribute to the diversity of gut microflora and likely represent a mechanism by which the gut microbiome affects host metabolism. (Zarrinpar A. et al., 2014).

8. Diet

Diets rich in vegetables, fruits, and legumes boost bacterial richness, particularly aiding species that produce beneficial SCFAs like butyrate, which supports gut barrier integrity. Plant proteins are linked to increased beneficial bacteria, whereas high consumption of animal-based protein and saturated fats can decrease beneficial microbes and increase harmful, bile-tolerant bacteria. High intake of sugar, salt, and processed foods reduces microbial diversity and promotes dysbiosis (an imbalance in the microbiome). Different types of dairy (milk, yoghurt, cheese) influence different bacterial populations, and excessive saturated fat intake is associated with reduced diversity. Compounds found in nuts, seeds, and oils can enhance microbial diversity and act as prebiotics (Valdes AM et al. 2018; Rinninella E. et al. 2019; Aslam H. et al., 2021).

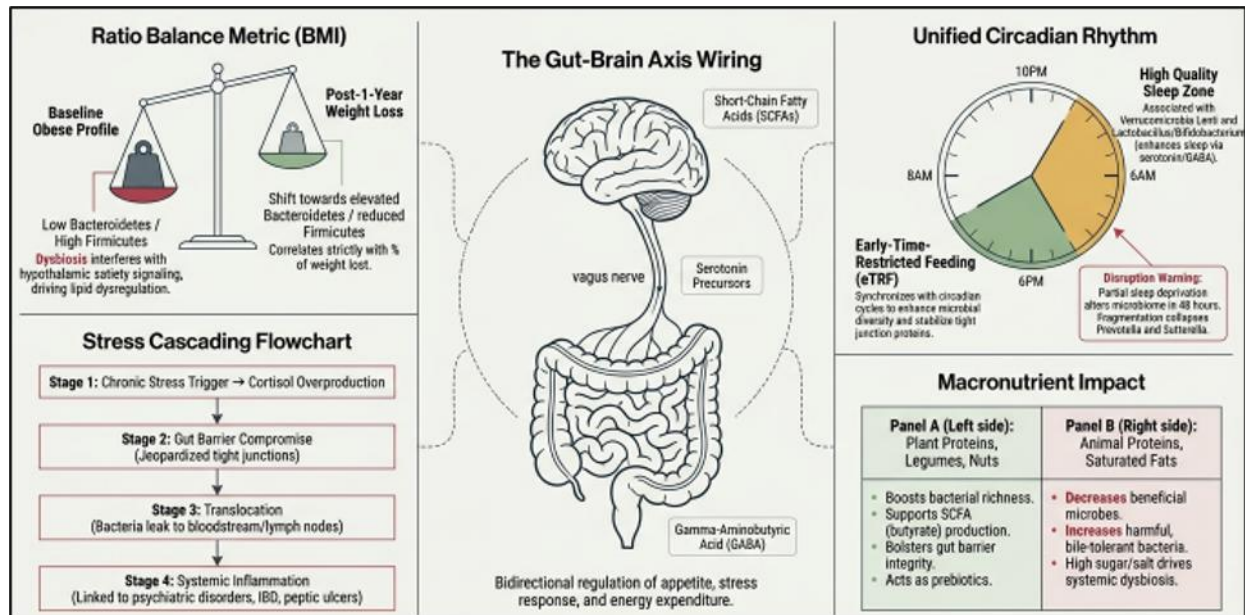


Figure 2: Modifiable factors influencing gut microbiome

3. Effect of Macronutrient Content and composition on gut microbiome

Diet is one of the key modulators of the volume and diversity of gut microbiota. In the past several decades, the transition from traditional to modern/western dietary patterns has become a growing health concern, as it is strongly associated with obesity and related metabolic diseases, inflammation, and both structural and behavioural changes in gut microbiota. Each dietary component, including macronutrients, micronutrients, dietary fiber and phytochemicals, prebiotics, and probiotics, has a crucial role in shaping and maintaining the gut microflora. Various studies have reported the contribution and efficacy of major dietary components to the gut microbiome (Figure-3).

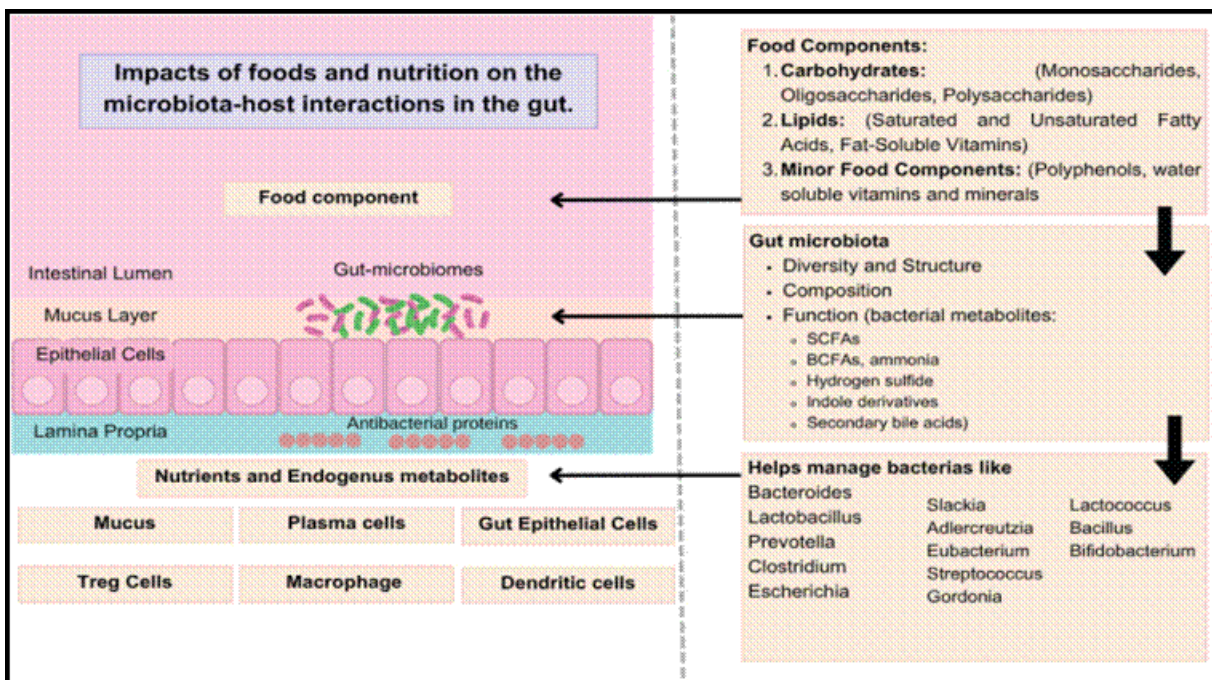


Figure 3: The impact of food components on the gut microbiota (Anyimadu et al., 2026).

The influence of macronutrients has been discussed below.

Carbohydrates

Dietary carbohydrates, derived from cereals, legumes, millets, fruits, and tubers, represent a major modifiable determinant of gut microbial ecology. Based on chemical structure and digestibility, carbohydrates are broadly categorized into simple (mono- and disaccharides) and complex (oligosaccharides and polysaccharides) forms.

Simple carbohydrates are rapidly digested and absorbed in the proximal small intestine, thereby limiting their availability to colonic microbiota. In contrast, non-digestible complex carbohydrates, including dietary fibre and resistant starch, escape host enzymatic digestion and reach the colon, where they undergo microbial saccharolytic fermentation, generating short-chain fatty acids (SCFAs), primarily acetate, propionate, and butyrate. SCFAs function not only as energy substrates for colonocytes and gut microbes but also as signalling molecules that regulate host metabolic pathways, inflammatory responses, gut barrier integrity, and immune homeostasis.

Thus, carbohydrate quality, rather than quantity alone, differentially shapes gut microbial composition and metabolic output. Diets rich in unrefined carbohydrates, particularly whole grains, are associated with increased abundance of butyrate-producing taxa such as *Roseburia*. Conversely, refined carbohydrate-rich diets have been reported to reduce the abundance of the other butyrate-producing genera such as *Anaerostipes* (Tyler Faits et al., 2020), suggesting species-specific microbial adaptations to substrate availability.

Dietary fibre and gut microbiome

Dietary fibers (DF) are bio-active non-starch polysaccharides and lignins available only from plants. These are non-digestible and absorbable in the human gut. Based on their solubility in water DF are classified as soluble (Pectins, gums and mucillages), and insoluble (cellulose, hemicellulose, and lignans) fibers ((**Figure 4**) (Mazhar M et al, 2023).

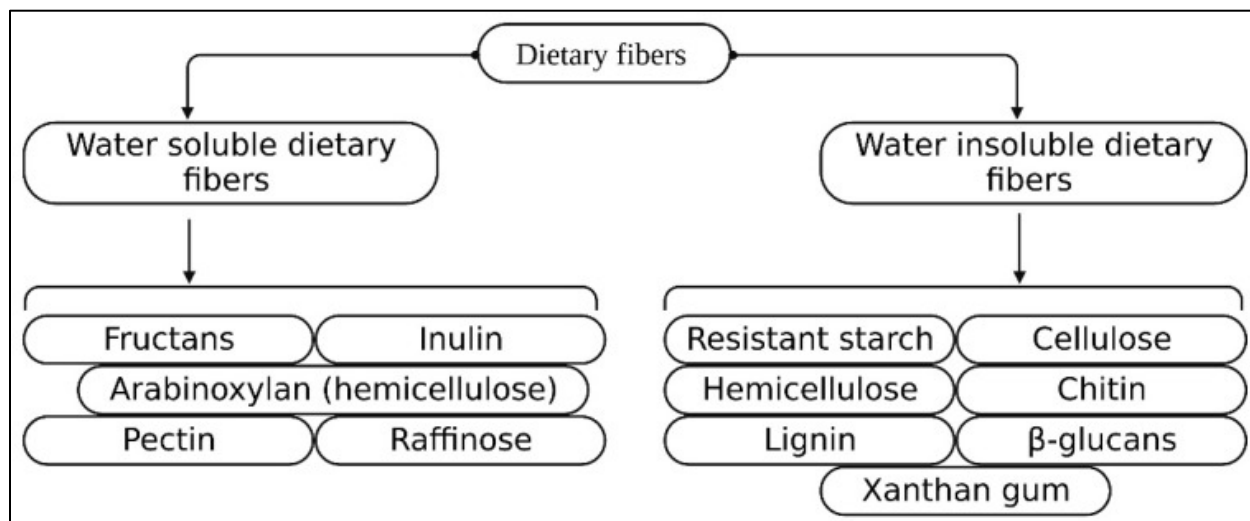


Figure 4: Dietary fiber classification based on water solubility/insolubility

In addition, based on the number of carbohydrate monomers, dietary fibers are also classified as Non Starch Polysaccharides (NPS) containing more than 10 units, (cellulose, hemicellulose, gums, pectin, mucilage, inulin, psyllium and Betaglucan, and resistant starch (RS), and resistant oligosaccharides contain 3-9 monomeric units (galacto-oligosaccharide and fructooligosaccharides (FOS) (**Figure 5**) (Fu J, Zheng Y, Gao Y, Xu W , 2022).

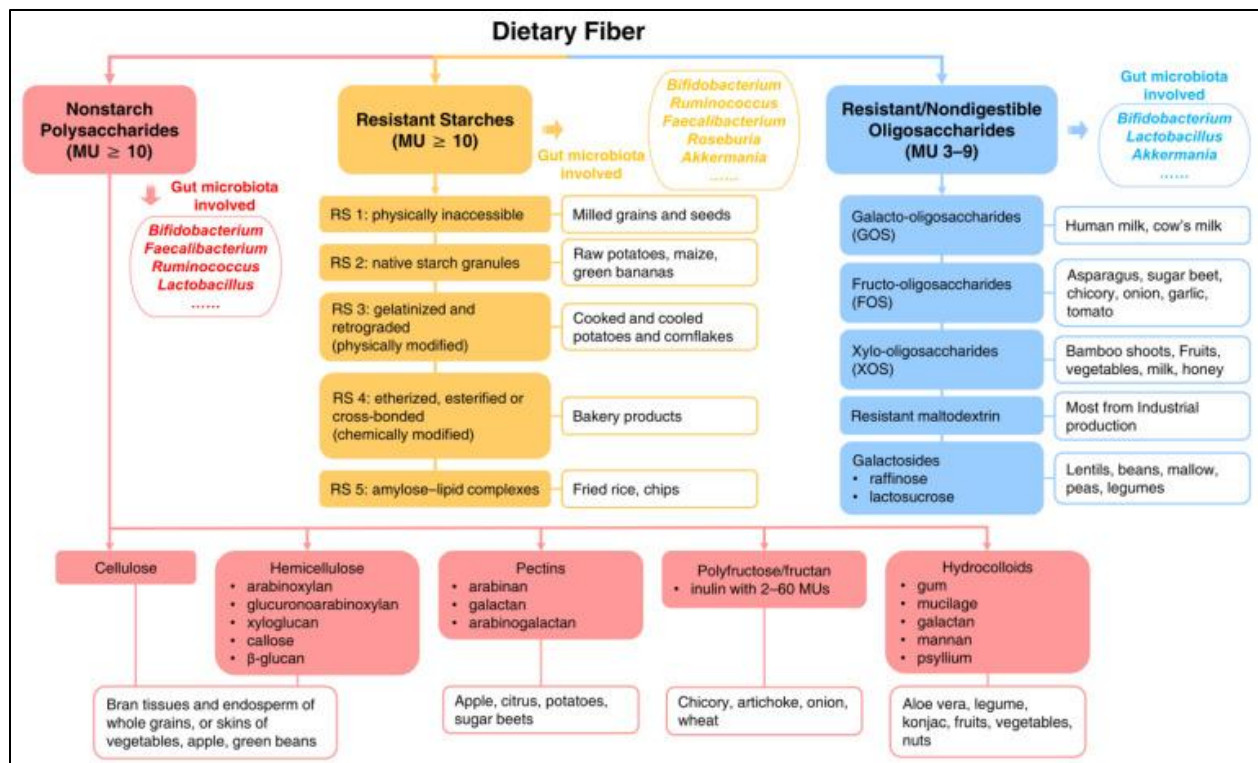


Figure 5: Classification of Dietary fiber based on chemical composition and food sources (Fu J, Zheng Y, Gao Y, Xu W, 2022)

Dietary fibres reach the colon intact, and are fermented by gut microbiota to produce short-chain fatty acids (butyrate, acetate, propionate) along with gases like methane and carbon dioxide. *Bacteroides* generally ferment fibre more efficiently than *Firmicutes*; however, microbial responses vary depending on the type of fibre and specific bacterial species (Mora-Flores et al., 2023). The insoluble dietary fibers form a platform on which microbes remain attached to carry out fermentation of soluble fiber and other constituents. The probiotic potential of dietary fiber is indicated by the SCFA production and changes in microbial diversity (both Alpha and Beta diversity). However, it is important to note that both the beneficial and pathogenic bacteria can produce SCFA from variety of food sources and hence cannot be regarded as a sole marker of probiotic potential of foods. (Rahat-Rosenbloom S, et al., 2014)

The fermentable dietary fibers, also known as microbiota-accessible carbohydrates (MACs), are largely present in whole grains, fruits and vegetables, and breast milk (Oligosaccharides). The MAC present in condiments such as garlic and onions is Inulin, and bananas and chicory root is Oligofructose (H.D. Holscher, 2017; Emanuele Rinninella et al, 2023).

The impact of dietary fibers on gut microbiota is complex, and is largely influenced by their type, source, and physiochemical properties (i.e. solubility, viscosity and fermentability/digestibility).

Also, the fiber fermentative capacity of gut microbes varies across the species (Cronin P et al, 2021).

Whole grain cereals are sources of a variety of dietary fibers such as glucofructans, cellulose, and hemicellulose along with other microbe-accessible substrates like lignin, protein fractions, phenolic compounds, waxes, saponins, phytates, or phytosterols (e.g. Ferulic acid) etc., all of which can cumulatively contribute to the prebiotic potential of these foods more than the extracted bran supplements (McClearyBV, 2010; Vitaglione P et al., 2015). The intestinal microbiota synthesizes essential enzymes necessary for the fermentation of diverse microbiota-accessible carbohydrates (MACs) found within whole food matrices, demonstrating a profound syntrophic relationship. Consequently, the consumption of unrefined whole foods facilitates both the generation of short-chain fatty acids (SCFAs) and the enhancement of gut microbial richness (Cronin P et al., 2021). It has been observed that communities maintaining a consistent intake of fermentable substrates rich in microbiota-accessible carbohydrates (MAC)—such as pectin, gums, and Beta-glucan—alongside insoluble fiber sources like whole wheat, corn, barley, and oats, exhibit significantly enhanced gut microbial alpha and beta diversity (Calatayud M et al., 2021).

Further, among the various types of resistant starch, RS4 favors the growth of *Actinobacteria* and *Bacteroidetes*, while negatively influencing the *Firmicutes*, but RS2 has no effect (Martínez I et al, 2010, Aoe S., et al., 2018). Inulin has been found to increase the abundance of *Faecalibacterium prausnitzii* in humans, and Arabinoxylan increases in the abundance of *Prevotella* and *Eubacterium rectale*.

In addition, the prebiotic benefits of dietary fiber have been tested in individuals who are at risk of or currently experiencing poor metabolic health. Prebiotic fiber supplementation has been found to regulate appetite and thereby blood sugar levels as reported by Kellow NJ, et al (2014). Evidence indicates that the Oat bran derived Beta glucan and Barley increased the volume of *Bacteroidetes* and reduced the abundance of *Firmicutes* in the overweight and obese persons with poor metabolic health. Connolly M.L. et al., (2016) reported a significant modulation ($p < 0.001$) of the volume of *Bifidobacteria*, *Lactobacilli*, and the total bacterial count ($p < 0.001$) in the cardiometabolic 'at risk' human participants with the daily administration of 45 grams of whole grain oats in breakfast. Nevertheless, the modulation of microbial profiles appears to be highly dependent upon the specific clinical state of the host. Consequently, it is imperative to identify the pivotal "keystone" taxa associated with various pathologies, facilitating the development of targeted, individualized nutritional interventions to optimize microbial homeostasis.

Given the surging consumer interest in gut health, there has been a significant trend toward fortifying diverse food products with processed fiber fractions. More recently, the food industry has begun incorporating Refined Dietary Fibers (RDF) into various convenience and ultra-processed food matrices. These may be (i) extracted fibers from food sources e.g. inulin, extracted

from chicory root, (ii) enzymatically modified - e.g. oligofructose, or (iii) semi-synthetic fibers - e.g. Methylcellulose (derived from chemically treated wood pulp). The impact of these processed fibers on gut health is under studied. Current scientific literature indicates that the disproportionate intake of products enriched with refined dietary fibers (RDF) may precipitate adverse gut health outcomes. Such consumption patterns are associated with microbial dysbiosis, heightened inflammatory responses, and the monopolization of specific taxa. Furthermore, an unregulated surge in short-chain fatty acid (SCFA) production under these conditions can compromise intestinal barrier integrity and induce significant gastrointestinal discomfort. (Kassem Makki, et al, 2018; Singh V, Vijay-Kumar M, 2020). To ensure microbial homeostasis and long-term health, it is imperative to exercise caution regarding the intake of products fortified with refined dietary fibers (RDF), such as ketogenic formulations, reduced-calorie ice creams, energy bars, and meat analogues etc.

Thus, dietary fibre has been extensively studied for its impact on gut microbiota. Regular consumption of dietary fiber in small quantities such as 5.7 g of wheat fiber/10 g barley fiber/ 7 g rye fiber provide significant measurable prebiotic effect within the first 3 weeks that lasts for almost a year (Freeland KR, Wilson C, Wolever TM.2010).

However, evidence on the role of functional carbohydrates extracted from various sources, individual sugars and carbohydrate-modified diets on the gut microbiome is slowly emerging ([Omar El-Kholy et al, 2025](#)).

Protein:

Protein provides nitrogen not only to the host but also to the gut microbiota. Existing evidence suggests a strong link between dietary protein and amino acids on the gut microbiota composition and functions. Gut microbes, especially proteolytic bacteria, ferment protein through complex metabolic pathways to produce a variety of end products, including ammonia, biogenic amines (BA), indoles, and short-chain fatty acids. Some of these products are absorbed and utilised by the colonocytes, and also have beneficial effects such as increasing the GLP-1 production. The main protein fermentative bacteria in the human gut are the species from the genera of

Clostridium, *Desulfovibrio*, *Peptostreptococcus*, *Acidaminococcus*, *Veillonella*, *Bacillus*, *Bacteroides*, *Propionibacterium*, and *Staphylococcus* (Dallas D.C et al, 2015).

The end products of microbial proteolytic fermentation vary with the source, composition, quantity and digestibility of dietary protein. Digestibility of a protein depends on the quality of the protein, the amino acid composition, and the food matrix through which the protein is consumed. Dietary fiber, protease inhibitors, tannins and phytates may decrease the digestibility of dietary protein. Though the SCFA are immunoregulatory products, excessive production of ammonia and BAs leads gut dysbiosis, inflammation, and impaired barrier integrity (Oliphant and Allen-Vercoe, 2019).

Microbial fermentation of branched-chain amino acids (leucine, isoleucine, and valine) results in the production of certain branched-chain fatty acids (isovalerate and isobutyrate) (Diether and Willing, 2019), which are reported to reduce insulin resistance in the liver. However, certain end products of protein fermentation in the colon, such as ammonia, phenol, and imidazole propionate, are detrimental to host health as proved in animal studies (Gilbert et al., 2018; Portune et al., 2016; Russell et al., 2011).

Quantity of dietary protein and gut microbiome:

Several researchers reported a positive association between dietary protein intake and gut microbial diversity. However, the proteolytic fermentation depends on the amount of nitrogen that reaches the colon. Both the quantity of dietary protein and the presence of protein-digestibility-influencing factors in the diet interfere with the nitrogen availability in the colon, thereby influencing the composition and volume of the gut microbiome. It is observed that higher dietary protein intake leads to higher nitrogen accumulation in the colon. A protein intake of 1.2 to 1.6/KgBW is considered helpful in muscle building and repair, immunity, etc., but intake higher than >2.0g/KgBW was found to alter the gut microbial fermentation pathways leading to excessive production of harmful biogenic amines, facilitating growth of pathogenic bacteria, while decreasing beneficial bacterial numbers. The high biogenic amines thus synthesised impair intestinal barrier function, immune dysregulation, and elevate inflammatory responses (Omer, F et al, 2025). Moreover, protein intake above 30% of total dietary energy intake predominantly from animal sources leads to oxidative stress and inflammation in the gut. Interestingly, higher microbial diversity has been associated with high protein intake among athletes indicating the positive influence of exercise (Clarke, S.F. et al, 2014). However, a few researchers also reported nil impact of high protein intake (2RDA) on gut microbes in obese individuals (Mitchell, S.M. et al., 2020).

Protein supplements and gut microbiome:

Protein supplements are commonly used to enhance the quality of dietary protein intake and help individuals achieve higher protein consumption goals. Similar to proteins obtained from whole foods, the digestion products of protein supplements can reach the colon, where they influence the composition and activity of the gut microbiota. Protein supplements are derived from a variety of food sources, and their effects on the gut microbiota depend on factors such as the type, amount, and source of protein consumed, as well as the health status of the individual. Furthermore, different protein supplements affect specific microbial populations differently. For example, short term (10 weeks) supplementation of whey protein isolate and beef protein hydrolysate have been reported to promote the growth of *Bacteroides in endurance athletes*. The authors contraindicated on long term supplementation (Moreno-Pérez et al., 2018). Additionally, whey and pea protein supplements have been associated with increased abundance of beneficial commensal bacteria,

including *Bifidobacterium* and *Lactobacillus*, thereby contributing to improved gut health (Świątecka, D. et al, 2011).

Type and source of protein

Beyond quantity, the type and source of dietary protein significantly influence gut microbiota composition. Differences in amino acid profiles of proteins affect microbial fermentation differently, particularly amino acid-degrading enzyme activity and urease production. Increased protein fermentation may elevate deamination and ammonia generation, which is of concern in liver disease management. Gut microbes metabolize dietary choline and carnitine, nutrients abundant in red meat and other animal-based foods, to produce trimethylamine (TMA), a pro-inflammatory metabolite. TMA is subsequently oxidized in the liver to form trimethylamine N-oxide (TMAO), which has been strongly associated with several metabolic disorders, including cardiovascular disease (CVD), insulin resistance (IR), and type 2 diabetes mellitus (T2DM) (Randrianarisoa E, et al, 2016).

Animal studies report that purified egg white and brown rice proteins increase amino acid-degrading enzymes and mucus-degrading bacteria, potentially compromising gut barrier integrity. However, evidence in humans, particularly with proteins consumed as whole foods, requires further investigation (Blakeley-Ruiz, 2025).

Protein from vegetarian sources is not completely digestible to microbes due to the cell wall of these foods. Whereas animal protein is well digested and the remnants are fermented by gut microbiota. In spite of this fact, plant proteins are reported to favour gut microbiota. Soy protein was found to have a higher positive impact on the gut microbial diversity compared to milk, fish and egg proteins (Y. Xia et al., 2020). And even within the animal proteins the impact is different for different sources (Alexandria Bartlett, Manuel Kleiner, 2022). These observations indicate a strong need for further in-depth research in this area.

However, animal protein especially red meat negatively influences gut microbe diversity, and overall metabolic health through the proinflammatory compound-Trimethylamine (TMA) produced in the gut by microbes whereas vegetarian protein/protein from mediterranean diet exhibits positive influence. For example, pea protein increases *Bifidobacterium* and *Lactobacillus*, and decreases *Bacteroides fragilis* and *Clostridium perfringens* (D. Świątecka, 2011), and high-chicken-protein (HFHCH) or high-pork-protein (HFHP) diets induced dysbiosis through increased production of skatole and indole in the colon (Jie Shi et al, 2020) . Hence, selective inclusion of carbohydrate and protein sources is recommended to maintain a balance between the microbial saccharolytic and proteolytic fermentation products.

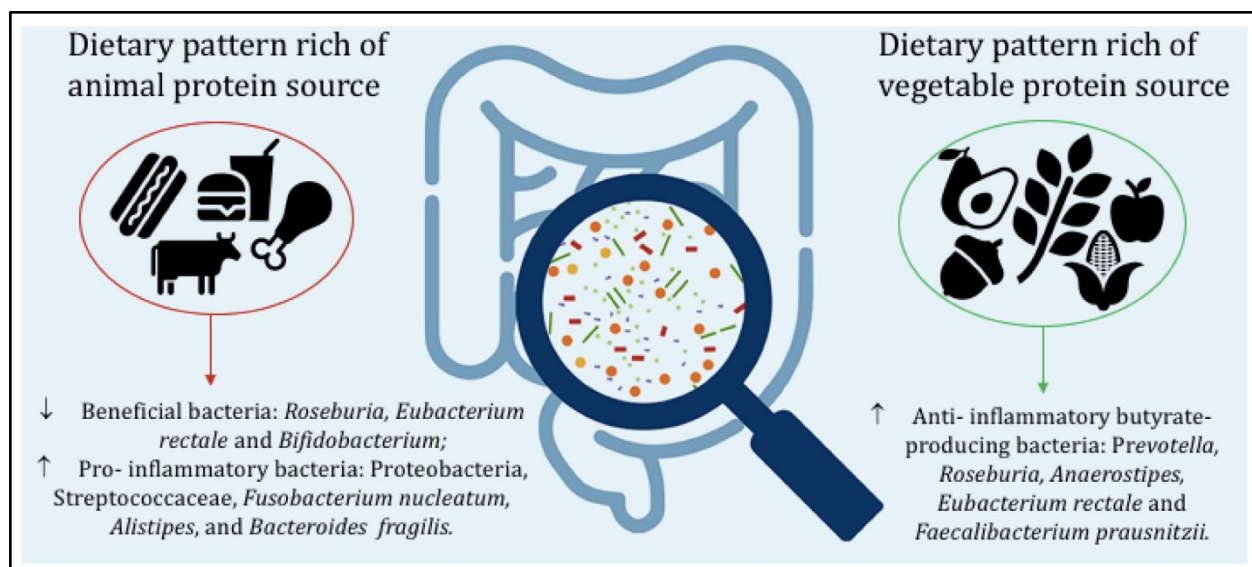


Figure 6: Effects of animal and vegetable protein on gut microbiota. (adapted from Di Rosa et al, 2023)

Based on the available evidence, it is advisable to consume high-quality protein sources as part of a balanced diet that includes adequate amounts of fermentable carbohydrates to support a healthy gut microbiota. While protein supplements can be beneficial for meeting increased protein requirements, long-term excessive consumption should be avoided due to the potential for unfavorable alterations in gut microbial composition and metabolism.

Furthermore, caution should be exercised when considering novel protein sources, such as algae- and fungi-derived proteins, as their long-term effects on gut microbiota and overall health remain insufficiently studied (Costantini, L., & Merendino, N., 2026).

Lipids:

Dietary recommendations for fat suggest consumption of 25-30% of total energy requirement with saturated fat intake limited to less than 10%, omega-6 polyunsaturated fatty acids (n-6 PUFA) and omega-3 polyunsaturated fatty acids (n-3 PUFA) to contribute to 2.5–9% (6.6 g/day) and 0.5–2% of total energy intake (2.2 g/day). Trans fat and dietary cholesterol intake need to be less than 1% and 250 mg/day (ICMR, 2020 and Liu, A.G. et al., 2017). Although the maximum amount of dietary fat is absorbed in the small intestine, a small portion of lipids remains undigested and reaches the colon. However, unhealthy dietary fat intake in terms of quantity and quality has been associated with increased *Firmicute-Bacteriodes* ratio, resulting in various metabolic diseases, including Obesity, T2DM, etc. (Indiani, C. et al., 2018; Crovesy, L. et al., 2020).

Properties of fatty acids, such as the carbon chain length, degree of saturation and location of the double bond in the structure, might influence the composition and diversity of the gut microbiota.

Effect of quantity of dietary fat intake on gut microbiome:

A high-fat (>40% TE) diet (HFD) has been well established as both pro-inflammatory and obesogenic. Beyond these effects, HFD induces gut dysbiosis, favouring the expansion of lipopolysaccharide (LPS)–producing bacteria. The combined influence of HFD and elevated LPS disrupts gut–brain satiety signalling by altering key hormonal and neuropeptide pathways. Specifically, it suppresses ghrelin and glucagon-like peptide-1 (GLP-1) secretion, promotes leptin dysregulation, and reduces the synthesis of anorexigenic neuropeptides in the central nervous system (Figure-2). These alterations collectively impair appetite regulation, leading to hyperphagia and, ultimately, the development of obesity. Moreover, a high-fat diet modulates the Gut-microbiota-Brain axis and triggers enteric as well as systemic inflammation by elevating the synthesis of several inflammatory chemicals (IL-6, Interferon), and pathways (TNF-gene and nitric oxide synthase (iNOS) expression) (Schéle et al., 2013; Rohr et al, 2020).

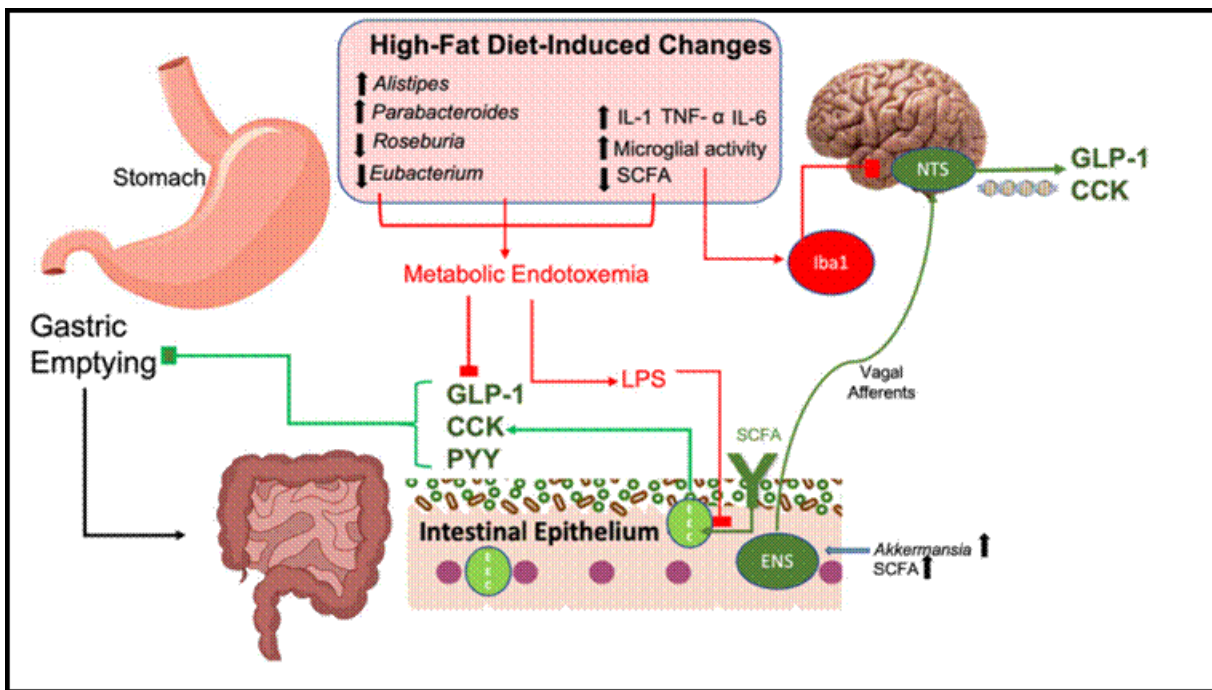


Figure 7: Effect of high-fat diet on gut microbiota, satiety signals and inflammation
(Hamamah, S. et al., 2023)

Evidence from human intervention trials supports the benefits of long-term low-fat intake on the diversity and counts of beneficial bacteria. Whereas high fat consumption >40% TE increased the *Bacteroides*, production of harmful inflammatory lipid metabolites such as indole and indoleacetic acid and p-cresol, and decreased concentration of SCFA (butyric acid and valeric acid) and decreased microbial diversity (Zeng, H, 2018).

Effect of quality of dietary fat on gut microbiome:

In addition to the quantity, the quality/source of dietary fat also influences gut microbiota. Both animal and human studies confirmed that saturated fat-rich lipids reduce the beneficial gut microbes, causing dysbiosis, decreasing the beneficial bacteria- *Bifidobacterium* and *Faecalibacterium* ratio (Yang, Q. et al, 2020). Conversely, unsaturated fats foster gut health by enhancing beneficial bacteria and reducing harmful ones.

Among various types of SFA, Long Chain SFA (Butter/Ghee, Lard and palm oil) contribute to the production of inflammatory metabolites by gut microbes, short chain SFA (acetate and Butyrate) positively modulate gut microbe diversity. Diets low in SFA sustain high alpha diversity of gut microbes that can easily ferment

Omega-3FA-rich fish oil diet was found to promote healthy gut microbiome composition with lower counts of *E. coli*, *Bacteroides* spp., and *Clostridium*, and higher numbers of *Lactobacillales* spp. (Li, Q.,2011). Among vegetable oils, Omega-6 PUFA rich oils such as soyabean oil decreased beneficial bacteria, and Omega 3 PUFA rich oil such as flax seed oil, oil blends with a healthy fatty acid ratio (PUFA:MUFA:SFA) closer to the recommendation (1:1.5:1) such as corn/safflower oil (69% linoleic acid) or a blend of flax/safflower oil (38% linoleic acid and 32% alpha-linolenic acid) and MUFA rich oils such as olive oil increased beneficial bacteria in the gut (Rudkowska,, 2025). Trans fatty acids, commonly found in baked foods, fried foods, and snack foods, negatively influence gut microbiota if consumed in excess (>1% TE) (Ge, Y et al., 2019).

Dietary patterns and gut microbiome

Modification of diet influences the gut microbial diversity. Changes in carbohydrate and fat ratios are one of the crucial methods for weight reduction, maintenance of healthy body composition and prevention/management of non-communicable diseases. Such modified diets have a profound influence on gut microbial volume and diversity. For example, low-carbohydrate (<30 energy%) diets decrease the relative abundance of several health-promoting bacteria, including *Bifidobacterium*, as well as a reduction in short-chain fatty acid (SCFA) levels in faeces. Whereas, highly refined/simple carbohydrate diets induce dysbiosis (Schoonakker, M. P et al, 2025). In contrast, low-fat diets (<30 energy%) increased alpha diversity, faecal SCFA levels and abundance of some beneficial bacteria, including *Faecalibacterium prausnitzii*.

The gut microbiota, particularly the *Firmicutes-to-Bacteroidetes* (F/B) ratio, has been widely investigated as a potential biomarker in the management and understanding of inflammatory and metabolic diseases. An elevated F/B ratio has often been associated with obesity and other metabolic disorders. However, the interpretation of this association remains controversial. Both phyla contribute significantly to the production of beneficial short-chain fatty acids (SCFAs), albeit through different metabolic pathways. *Firmicutes* are generally recognized as major producers of butyrate, whereas *Bacteroidetes* predominantly produce acetate and propionate.

Given the important physiological roles of these SCFAs in maintaining gut health, regulating immune function, and influencing energy metabolism, a high F/B ratio should not be interpreted as inherently detrimental in individuals with obesity. Current evidence suggests that the relationship between the F/B ratio and obesity is more complex than initially proposed. Therefore, further research employing robust study designs and high methodological rigor is needed to clarify the significance of the F/B ratio and establish its reliability as a biomarker in obesity and related metabolic conditions. (Magne F, et al., 2020).

High sugar and high-fat diets, which have been implicated in the occurrence of various non-communicable diseases, were found to induce dysbiotic effects towards a high F/B ratio, the effect being independent of dietary fat. Whereas, high-fat starch-based diets also induce dysbiosis but more towards a low F/B ratio, thus indicating the possibility of different microbial metabolic pathways for sugars and starch. More alarmingly, sucrose-induced dysbiosis was found to lead to dyslipidaemia and non-alcoholic fatty liver disease in animals. However, the influence of high-fat sucrose or fructose-based diets varies at the bacterial family and genus levels, producing species-specific contradictory results (Sun et al. 2021). The beneficial and detrimental effects of various types of diets on gut microbiome are presented in Figure 8, adapted from Debora Rondinella et al., (2025).

Beneficial Diets			
Mediterranean diet	High-fiber diets	Plant-based diets	High-fermented-food diet
 Taxonomic Shifts: ↑ <i>Faecalibacterium prausnitzii</i>, <i>Roseburia</i> spp., <i>Bifidobacterium</i> spp., <i>Prevotella</i> spp., beneficial <i>Clostridia</i>; ↓ <i>Ruminococcus</i> <i>gnavus</i>, <i>Proteobacteria</i>. Immune Impact: Reinforcement of mucosal barrier; enhanced immune tolerance; ↓ systemic inflammation Metabolic Impact: ↑ SCFAs (butyrate, acetate, propionate), supporting mucosal healing and epithelial repair.	 Taxonomic Shifts: ↑ <i>Faecalibacterium prausnitzii</i>, <i>Roseburia</i> spp., <i>Bifidobacterium</i> spp., <i>Prevotella</i> spp., beneficial <i>Clostridia</i>; ↓ <i>Ruminococcus</i> <i>gnavus</i>, <i>Proteobacteria</i>. Immune Impact: Reinforcement of mucosal barrier; enhanced immune tolerance; ↓ systemic inflammation and serum amyloid A. Metabolic Impact: ↑ SCFAs (butyrate, acetate, propionate), supporting mucosal healing and epithelial repair	 Taxonomic Shifts: ↑ <i>Faecalibacterium prausnitzii</i>, <i>Roseburia</i> spp., <i>Eubacterium</i> <i>rectale</i>, <i>Prevotella</i> spp., <i>Bifidobacterium</i> spp.; ↓ <i>Bilophila</i> <i>wadsworthia</i>, <i>Ruminococcus</i> <i>gnavus</i>, <i>Proteobacteria</i>. Immune Impact: Promotion of Treg activity; reduction of NF-κB signaling; attenuation of systemic and mucosal inflammation. Metabolic Impact: ↑ Butyrate and phytochemical- derived metabolites; ↓ TMAO levels; improved SCFA- associated pathways.	 Taxonomic Shifts: ↑ <i>Lactobacillus</i> spp., <i>Bifidobacterium</i> spp., <i>Streptococcus</i> <i>thermophilus</i>; ↑ microbial diversity; enrichment of butyrate producers. Immune Impact: ↓ circulating pro- inflammatory cytokines (IL-6, TNF-α); improved systemic immune regulation. Metabolic Impact: ↑ SCFA availability; strengthened gut barrier; ↓ CRP and gut permeability markers.

Detrimental Diets		
Western diet	Low-carb / High-protein / Ketogenic diets	Gluten-free diet (in non-celiac IMDs)
 Taxonomic Shifts: ↑ <i>Bacteroides</i> spp., <i>Ruminococcus gnavus</i>, <i>Escherichia coli</i>, <i>Bifidobacterium</i> spp.; expansion of <i>Proteobacteria</i>; ↓ <i>Faecalibacterium prausnitzii</i>, <i>Akkermansia muciniphila</i>, <i>Bifidobacterium</i> spp., <i>Roseburia</i> spp. Immune Impact: Th17 skewing, reduced Treg activity; impaired mucosal tolerance ↑ increased systemic inflammation. Metabolic Impact: ↓ SCFA production; disruption of barrier integrity; ↑ intestinal permeability and LPS translocation → endotoxemia.	 Taxonomic Shifts: ↑ <i>Akkermansia</i> spp., <i>Parabacteroides</i>, <i>Desulfovibrio</i> spp.; ↓ <i>Bifidobacterium</i> spp. Immune Impact: Attenuation of Th17-driven inflammation (notably in multiple sclerosis); but expansion of mucolytic and sulfate-reducing taxa may exacerbate gut inflammation. Metabolic Impact: Altered amino acid metabolism; possible ↑ secondary bile acids; dual effect—neuroprotective in MS but potentially harmful for gut homeostasis.	 Taxonomic Shifts: ↑ <i>Enterobacteriaceae</i> (e.g., <i>Escherichia coli</i>), opportunistic taxa (<i>Vectivallaceae</i>, <i>Coriobacteriaceae</i>); ↓ <i>Bifidobacterium</i> spp., <i>Faecalibacterium prausnitzii</i>, <i>Roseburia</i> spp. Immune Impact: Loss of anti-inflammatory tone, impaired immune regulation in non-celiac individuals. Metabolic Impact: ↓ SCFA synthesis; loss of beneficial metabolic functions; possible worsening of barrier permeability.

Figure 8: Beneficial and harmful effects of various types of diets on gut microbiota (Debora Rondinella et al, 2025).

Processing of foods and gut microbiome:

Whole grain consumption is associated with healthy SCFA production by gut microbiota. The non-digestible carbohydrate from whole grains nourishes beneficial bacteria, whereas refined grains are digested and absorbed in the upper gastrointestinal tract, thus reducing the substrate for microbial survival. Thus, the processing of food influences the carbohydrate availability for microbial digestion. Moreover, processing of grains also influences protein content in grains (sorghum and corn). Cooking food increases the digestibility of starch in the gut. Whereas cooking followed by immediate cooling converts the digestible starch to non-digestible resistant starch, reducing its digestibility. Further, heat treatments increase extractability and bioaccessibility of phenolic compounds thereby facilitating the growth of gut microbes. Phenolic compounds enhance the growth of gut protective (*Lactobacillus* and *Bifidobacterium* species) and anti-inflammatory microbiota (*Faecalibacterium prausnitzii* and *Akkermansia muciniphila*). Nissen et al, (2022) demonstrated that frying at high temperature had a better impact on the growth of *Bifidobacteriaceae* *Lactobacillales* than grilling in dark purple eggplant.

However, the Maillard reactions induced by heating of food generate advanced glycation end products (AGEs), which would contribute to the sensory characteristics of food, but are detrimental to beneficial gut microbiota. Jiang et al., (2020) concluded that high heat cooking methods-frying and baking increased the production of AGEs in Oysters and stimulated the growth of harmful gut microbes such as *Clostridiales*, *Desulfovibrio*, and *Helicobacter*, whereas steaming increased the fermentability of Oyster protein, thereby increasing SCFA production. Also increased the growth of *Bifidobacterium*, *Faecalibaculum*, and *Roseburia*, and SCFA production.



Figure 9: Impact of food processing on gut microbiome

Various other food processing methods, such as Fermentation, germination, boiling, extrusion, etc., modify the availability of fermentable carbohydrate to the gut microbes by influencing the digestibility of foods. Fermentation promotes beneficial microbial growth, whereas germination

improves the digestibility and the amino acid profiles of foods, especially in millets and legumes, while reducing antinutritional factors (Anyimadu, C. F et al., 2026; Budhwar, S et al., 2020). Consumption of fermented foods (dairy, Kimchi, soy, and non-alcoholic beer, etc.) has been associated with improved gut microbiome.

In contrast, extrusion increases the non-digestible carbohydrate content. Boiling and sourdough breadmaking procedures decrease the same. Surprisingly, in spite of lower usable total carbohydrate content, boiled foods increase the counts of butyrate-producing bacteria. *Ruminococcaceae* and *Lachnospiraceae* (Smith, C., 2022).

The prebiotic potential of foods is enhanced by certain thermal processing techniques such as steaming, baking, and microwave treatment, and have been shown to support the growth of *Lactobacillus* spp. Advanced processing methods that increase the fermentability of dietary fibre, such as radiofrequency heating combined with enzymatic hydrolysis that uses rapid, volumetric heating to restructure food components, increase their porosity and surface area, enhance fibre fermentability and short-chain fatty acid production, thereby favour the gut microbiome balance. Overall, optimizing the food processing is essential to maximize nutritional and gut health benefits while minimizing nutrient losses due to over-processing.

High consumption of processed foods rich in saturated fats and synthetic additives, including emulsifiers and preservatives, has been linked to a range of adverse health outcomes, such as metabolic syndrome, gastrointestinal and hepatic disorders, cognitive impairment, and certain cancers. These dietary patterns are also associated with decreased gut microbial diversity and abundance, alongside an increased volume of pro-inflammatory microbial species. Consequently, adopting a diet based on minimally processed and whole foods may support a healthier gut microbiome and improve overall gut health (Rondinella, D et al., 2025).

4. Recommendations

Given the vast heterogeneity of gut microbial species, establishing standardized dosage guidelines for probiotics remains challenging. Most probiotic supplements typically provide between 1 and 10 billion CFU per dose; however, evidence suggests that efficacy is highly strain-specific. For instance, *Bifidobacterium longum* subsp. *longum* 35624 has been shown to alleviate symptoms of irritable bowel syndrome (IBS) at a dose of 100 million CFU per day, whereas other probiotic formulations may require substantially higher doses—ranging from 300 to 450 billion CFU administered three times daily (World Gastroenterology Organisation, 2023).

Moreover, the gut microbiome species were ranked for their association with cardiometabolic risk factors, including diet, anthropometry and biochemical markers by Asnicar, F. et al (2025), which is referred to as ‘ZOE Microbiome Health Ranking 2025’, indicating the possibility of modulating gut microbiome towards metabolic health.

The gut-friendly dietary recommendations include a plant-based Mediterranean diet and a diet rich in soy products, seafood, tubers, vegetables (including pickles), seaweed, mushrooms, and green tea, which favours the growth of *Bacteriodes*, resulting in a low *Firmicutes* to *Bacteriodes* ratio (Asano et al. 2020). Secondly, PUFA-rich diets, including a blend of corn/safflower oil (69% linoleic acid) or a blend of flax/safflower oil (38% linoleic acid and 32% alpha-linolenic acid) were also suggested (Ye, Z. et al, 2020). However, mindful consumption of processed foods and UPF consumption are necessary to facilitate survival and diversity of the gut microbiome.

5. Conclusion

This white paper collates current evidence on the development, composition, diversity, and functional significance of the gut microbiome, along with the emerging role of postbiotics and the key determinants of microbial ecology, including age, sex, ethnicity, body composition, and diet.

The composition and functional capacity of the gut microbiota are highly dynamic and are shaped by a complex interplay of host and environmental factors. Early-life microbial colonization is influenced by mode of delivery, followed by continuous modulation across the lifespan. Notably, sex-based differences in microbial diversity have been reported, with females often demonstrating greater microbial richness. Ethnicity-specific patterns further suggest that habitual dietary practices, particularly those rich in prebiotic and synbiotic components, may contribute to more favourable microbial profiles in certain populations.

The gut microbiome is now recognized as a critical determinant of human health, exerting extensive immunological and non-immunological effects both within and beyond the gastrointestinal tract. Its role in modulating metabolic pathways and mental health outcomes is well established. Dysbiosis, characterized by disruption in the balance and diversity of gut microbial communities, has been consistently associated with a wide spectrum of clinical conditions. In addition, emerging evidence indicates that stress and sleep disturbances can alter gut microbial composition, supporting a bidirectional relationship between the gut microbiome, mental health, and sleep regulation.

Dietary patterns remain among the most influential and modifiable determinants of gut microbiota composition. Regular meal timing, combined with adherence to a dietary pattern rich in dietary fibre, phytochemicals, and polyunsaturated fatty acids, appears to support microbial diversity and functional resilience. Plant proteins such as soya protein and pea protein and novel protein sources, such as algae- and fungi-derived proteins have also been reported to support gut health positively.

Collectively, these findings underscore the importance of integrated, lifestyle-based approaches to maintaining gut microbial homeostasis. Future research should prioritize mechanistic insights, longitudinal human studies, and the development of personalized nutrition and therapeutic strategies aimed at optimizing microbiome-mediated health outcomes.

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