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A SYSTEMATIC REVIEW ON THE ROLE OF GUT MICROBIOTA IN NUTRITION AND HEALTH

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ABSTRACT

The gut microbiota, a diverse community of trillions of microorganisms residing in the human gastrointestinal tract, plays a pivotal role in maintaining host nutrition, immunity, and metabolic function. Emerging research highlights its significant influence on the development and progression of various diseases, including obesity, type 2 diabetes, inflammatory bowel disease (IBD), and neuropsychiatric disorders. This narrative review aimed to synthesize recent findings (2020–2025) on the relationship between gut microbiota, diet, and health outcomes. A comprehensive search of databases such as PubMed, Scopus, and Google Scholar identified 110 peer-reviewed studies examining the functional roles of gut microbes, dietary interventions, and therapeutic strategies. The findings emphasize that microbial diversity and composition are influenced by factors such as diet, age, medication, birth mode, and lifestyle. High-Fiber diets, such as the Mediterranean diet, promote beneficial microbes like *Bifidobacterium* and *Lactobacillus*, while Western diets are associated with dysbiosis and chronic inflammation. Therapeutic approaches including probiotics, prebiotics, synbiotics, and faecal microbiota transplantation (FMT) demonstrated varying success in modulating gut flora to improve health. Dysbiosis was notably linked to metabolic disorders, cognitive decline, immune dysfunction, and gastrointestinal diseases. In conclusion, the gut microbiota acts as a key mediator between diet and health, influencing disease onset and therapeutic response. Personalized nutrition, combined with targeted microbial modulation, offers promising avenues for disease prevention and management. Future research should focus on standardized methods, long-term clinical trials, and multi-omics approaches to unlock the full therapeutic potential of the gut microbiome.

INTRODUCTION

1.1 Gut microbiota vs gut Microbiome

A lot of microorganisms (bacteria, viruses, fungi, and archaea) reside in the human body. They coexist with us, either on our tissues or inside some of them, usually in the digestive system, and have at least as many cells as humans. They are all referred to as "microbiota" or "microbiome" (Riccio, and Rossano, 2021). The total number of microorganisms themselves is known as microbiota, while the collected genomes of microorganisms in a specific environment are referred to as the microbiome (Valdes, *et* al., 2018).

Microbial communities are transferred to the infant's gut by breast milk before transition, which also helps to form the gut microbiota before and after delivery. After it is established, the gut microbiota's variety and abundance hold steady into adulthood. In people, at least 40 bacterial species are found for at least a year, making up 75% of the gut microbiota abundance. In addition, for five years, an average of 60% of the microbial species present in the adult gut are preserved. The human body is home to a variety of microbiota, but when compared to other locations like the skin and vagina, the gut has the most varied and prolific microbiota (Liu, *et al*., 2025).

Gut as a microbial ecosystem

The human gut is a diverse community of microbes known as the microbiota controls host immune systems and aids in ensuring general human health (Guo, *et al.,* 2021).The gut microorganism that resides within the gastrointestinal system, secrete bioactive chemicals, microorganism that colonized the gastrointestinal system, produce bioactive metabolites, and keep the host's homeostasis is known as the human gut flora (Hemmati, *et al.,* 2023).

The gastrointestinal (GI) tract of humans is one of the largest interfaces (250–400 m^2), inhabiting trillions of symbiotic microorganisms including both prokaryotes and eukaryotes (Srivastava, *et al.,* 2021). The human gastrointestinal tract receives about 60 tons of food during a period of an entire life, along with an abundance of environmental microbes which contribute significant threats to gut health (Thursby, *et al.,* 2017). About 150 times many genes are more present in the human gut microbiota as in the entire human genome (Afzaal, *et al.,* 2022).

Research has shown that the most prevalent bacteria in the human gut are Firmicutes (64%), followed by *Bacteriodetes* (23%). Proteobacteria and Actinobacteria are also present in different proportions. The stomach contains acidophilic taxa such *Helicobacter pylori, Streptococcus, Lactobacillus, Candida,* and *Peptostreptococcus* (Bajinka, *et al.,* 2020). Intestinal microorganism is an important bridge between diet and human health and plays a vital role in maintaining the homeostasis of the human body (Song, *et al.,* 2021).

Importance of gut microbiota in human physiology and health

Human health depends on healthy microbiota for a variety of physiological processes, including food digestion and energy production, pathogen defense, and host immune development (Srivastava, *et al.,* 2021).

The human microbiota is sometimes referred to as our "forgotten organ" because of its significant influence on both health and illness. Energy harvesting and storage, as well as several metabolic processes including digesting and absorbing undigested carbohydrates, are all facilitated by microbiota. IM provides bacterial fermentation to the host through its products. The organ's epithelial cells use butyric acid, the primary product, as its primary energy substrate. Both starch and non-starch polysaccharides the latter most referred to as dietary fiber are the IM's primary energy sources (chartios, *et al.,* 2025).

Perhaps more significantly, the gut microbiota communicates with the immune system by sending signals that encourage immune cell maturation and the proper development of immunological functions (Clemente, *et al.,* 2012). The intestinal microbiota supports both acquired immunity and the immune system's maturation at the level of gut-associated lymphoid tissue (GALT)(chartios, *et al.,* 2025).

Using the axes of microbe–microbe and microbe–host interactions, commensal bacteria often control the population and activity of the pathogenic bacteria directly or indirectly to preserve the typical, healthy gut microbial composition. By generating poisonous chemicals such bacteriocins, secondary bile acids, and proteinaceous toxins, commensals either kill the pathogens or inhibit their growth, hence mediating colonization resistance. This is the direct mechanism to prevent commensals from colonizing pathogens. However, in the indirect approach, the commensals in the gut microbiota primarily fight the pathogens by triggering the host immune system to fight them (Khan, *et al.,* 2021).

Increase in research interest

Research in the rapidly expanding field of microbiota-gut-brain (MGB) has major consequences for our understanding of human behavior and brain function. By modifying gut microorganisms, or "microbiota," scientists can uncover links between the microbiota and either pathological conditions (such anxiety, mood disorders, and neural developmental disorders like autism) or normal brain processes (including cognition, emotion, and memory). Regarding the causal links between human behavior and gut microbiota, numerous assertions are made. By identifying these connections, MGB research seeks to provide fresh perspectives on mental health and possible therapeutic approaches (Hooks Konsman, and Malley, 2018).

In recent years, gut microbiota has garnered a lot of attention from researchers. Given the importance of the gut microbiome to human health, it is critical to gain a better understanding of the factors influencing the makeup and activity of this microbial community (Duman and Karav, 2025). In the context of probiotics and dietary bioactive, this review paper explores how these substances affect gut health and general well-being, highlighting their functions in regulating inflammation, gut microbiota, and metabolic health. Probiotics are defined as live bacteria that improve the host's health, mostly by influencing the gut microbiota. The review seeks to clarify the ways in which probiotics can improve gut health and treat metabolic diseases when added to both conventional and contemporary dietary systems. It looks at the different kinds of probiotics found in different foods and how they work, including how they affect the immune system and metabolic health. by investigating the connections between probiotics and health outcomes like immunological support, mental health, and digestive health (Mafe *et al.,* 2025).

Culture based studies

The great majority of knowledge regarding the gut microbiome was derived via time-consuming in-vitro culture-based techniques (the development of affordable, next-generation sequencing methods has significantly advanced our current knowledge of the gut microbiota. The bacterial 16s ribosomal RNA's highly variable sections (V1–V9), which allow for easy species differentiation, are the primary focus of these high-throughput sequencing techniques. Furthermore, the great sensitivity and resolution of whole metagenomics approaches may provide a more trustworthy repertoire of the diversity and composition of gut microbes (Srivastava, *et al.,* 2021).

Investigation of the gut microbiome, metagenomics is a revolutionary tool that reveals functional roles, illness associations, and genetic profiles. It reveals various microorganisms, unique enterotypes, the mysterious gut Virom, the dynamics of antibiotic resistance, and the implications of disease-related dysbiosis. For a thorough understanding of gut microbiota gene expression and function, including its influence on health, metagenomics must be integrated with other omics techniques. The identification of tiny molecules and bacterial peptides that affect the host's physiology can be aided by multi-omics techniques (Mathuria, *et al.,* 2024). The aim of this study is to find the complex relationship between diet, the gut microbiota, and host health, with examples of how diet can support health, increase an individual's risk for disease, and be used as a therapy for specific diseases. Objectives of this review are to examine how many and what kinds of gut microbes are present in people with different eating patterns and to investigate how interactions between the microbiota and the host affect disease resistance, metabolic health, and inflammation.

1.2 GUT MICROBIOTA COMPOSITION AND DYNAMIC

Microbial landscape

The *Firmicutes phylum* is composed of more than 200 different genera such as *Lactobacillus, Bacillus, Clostridium, Enterococcus, and Ruminicoccus. Clostridium* genera represent 95% of the Firmicutes phyla (Rinninella, *et al.,* 2019). The *Bacteroidetes phylum* includes *Bacteroides, Prevotella, Parabacteroides* and *Alistipes*. Other bacterial phyla within the healthy colonic microbiota include *Actinobacteria* that include *Bifidobacterium spp, Proteobacteria including Escherichia coli, and Verrucomicrobia* including *Akkermansia muciniphila* (Flint, *et al.,* 2015).

Core microbiome vs individual variability

The core microbiome, also referred to as a "hidden organ," has fascinated scientists as a crucial component in comprehending the close connection between microbial ecosystems and human health (Zhao, *et al*., 2025).The term "core microbiome" broadly refers to any group of microbial taxa or the functional and genetic characteristics of those taxa that are unique to a host or environment of interest. Core microbiomes are typically defined as the microbial taxa that are present in two or more samples from a specific host or environment (Neu Allen and Ro, 2021).

Most of our knowledge regarding individual variations in the microbiome comes from human research that divides the bacterial composition into enterotypes, or unique profiles based on the proportion of microorganisms from various taxonomic groupings. Numerous studies have examined gastrointestinal diversity to identify the core microbial communities linked to internal (e.g., age, heredity) and external (e.g., pharmaceutical, dietary) factors. Humans have an extremely diverse microbiome that includes between 1000 and 1150 different bacterial species (Davidson, *et al*., 2018)

Influencing factor

Microbiota composition and function are affected by multiple reasons, including diet, age, environmental exposures, and medication, mode of delivery, infant feeding (Perler, Friedman, and Wu, 2023)

Diet

The infant's food (breast or formula milk) has the initial impact on the gut flora after delivery. The early gut microbiota is shaped by the milk's composition. Breast milk contains oligosaccharides that are easily broken down by Lactobacillus and Bifidobacterium, which dominate the gut microbiota in breastfed infants. This leads to an increase in short-chain fatty acids, which triggers the immune system to produce more immunoglobulin. Enterococcus, Enterobacteria, Bacteroides, Clostridium, and Streptococcus are the most common species in infant fed formula. The makeup of the primary microbiota during this time is crucial to protecting infants from illnesses because it may play a significant impact in the development of the infant's initial immunity (Hasan, and Yeng,2019).

The gut microbiota is greatly affected by dietary intake with different diets having a significant effect on the variety, stability, and functioning of the microbial community in the GI tract (Ross*, et al.,* 2024). Most of the items in the lifestyle diet today are highly processed, heavy in fats, simple sugars, and preservatives, and low in fiber and other nutrients. This bad diet may change the composition of the gut flora. Dysbiosis is being implicated in the etiology of several disorders, and these changes may make it worse. Human health is increasingly thought to depend on the relationship between food and gut bacteria (Salam, *et al.,* 2025).

Age

More than 50% of the changes of gut microbiota have been associated with dietary habits and major changes in diet during adulthood can alter the microbiota only a few days (Oriach, *et al.,*2016). Age-related disorders are caused by a decrease in the variety of gut microbiomes, which increases dangerous bacteria and decreases healthy ones. Increased vulnerability to infections, chronic inflammation, metabolic problems, and cognitive impairment have all been linked to these age-related changes. The gut, mouth, and skin microbiota of older persons showed significant variety and decreased stability over time, according to a longitudinal study. Knowing how food, gut microbiota, and good aging are related; research indicates that older people who maintain a diversified gut microbiota have better health outcomes (Golshany, *et al.,* 2025).

The development of the gut microbiome begins in infancy and continues to evolve over the course of the following three years, changing throughout life. From babies to adults, the gut microorganisms and the host are co-evolving and interacting, and it's critical to create an environment that is conducive to both. The gut microbiome's general makeup can remain consistent for years in healthy humans, although the relative quantity of each component varies greatly (Su, and liu, 2021).

Medication

The interaction between medication and gut microbe composition is essential for understanding drug pharmacological process and the beginning of various adverse effects of medication (Vila, *et al.,* 2020). One important factor influencing the composition of the gut microbiota is medication. Drugs such as osmotic laxatives, progesterone, TNF-α inhibitors, and rupatadine had the greatest explanatory power on microbiota composition 10% of community variation), according to a large Dutch Belgian population study. Higher prevalence of gastrointestinal infections in patients taking proton pump inhibitors may be explained by other research that has demonstrated significant effects of these medications on the microbial ecosystem.60 It is obvious that antibiotics affect gut microorganisms, and animals are frequently given low dosages of antibiotics to boost their weight and growth. A major share of antibiotic use in many countries is for agriculture, particularly intensive farming of chicken and beef (Valdes, *et al.,* 2018).

Antibiotics are the most obvious treatments that have an impact on gut microorganisms, lowering SCFAs and BAs and making people more vulnerable to Clostridium difficile infections, but non-antibiotic drugs also have direct impacts. According to vitro research, 24% of non-antibiotic substances inhibited the development of at least one bacterial strain; the most effective inhibitory effects were seen with proton pump inhibitors (PPIs) and antipsychotics. Even after stopping the medication, PPIs have been linked to negative health consequences due to their long-lasting effects on the gut microbiota. Furthermore, gut bacterial enzymes degrade medications such as gemcitabine, simvastatin, digoxin, and L-dopa, affecting their activation or inactivation. It's interesting to note that drug interactions can also be influenced by the gut microbiota (Pires, *et al.,* 2024).

Lifestyle

The way that exercise affects gut microbiota depends on the number of variables, including diet, training volume, and environment. Physical activity may have a positive impact on the intestinal microbial ecosystem's richness in both qualitative and quantitative dimensions, indicating that exercise has positive effects on mood, gastrointestinal function, and other brain functions. A number of interrelated factors and pathways, including (i) changes in the bile acid profile that may exert antimicrobial activity and/or select certain bacterial species; (ii) increased production of immunoglobulins A (IgA) linked to the resistance to colonization by specific microorganisms; (iii) increased production of SCFA; and (iv) decreased intestinal transit time, are likely responsible for these changes, though the exact mechanism of action is still unclear (Campaniello, *et al.,* 2022).

Mode of delivery

Compared to infants delivered vaginally, infants born via cesarean birth (C-section, CS) show greatly changed neonatal gut microbial characteristics (Mitchell*, et al.,* 2020*).* The difference in gut microbiota between C section (CS) and vaginally delivered (VD) infants over the first year of life. In VD infants, we find relation between fecal microbiota adding from mother to infant and a greater stability of microbiota development in early life as compared with CS infants (Reyman*, et al.,* 2019).

Bacteria from the mother's stomach may enter the amniotic fluid during pregnancy by crossing the placenta from the mother's bloodstream. The discovery of maternal gut microbes in mechanism and umbilical cord blood has demonstrated this. Full-term babies born vaginally would be exposed to the intestinal and vaginal germs of their mothers. However, the gut microbiota of neonates delivered via cesarean section is devoid of diversity and presence within the Bacteroidetes phylum. This could be because ambient bacteria, not gut microorganisms, have colonized the infant's gut. Because of their gut flora, newborns born via the caesarean section are more likely to develop obesity and asthma (Maa, and Lee, 2025).

Age-related changes

Newborns can colonize their digestive tracts either horizontally (from the environment to the kid) over an extended period or vertically (from mother to child) soon after delivery. A delivery method is a typical illustration of colonization influence. In contrast to meconium samples of children delivered vaginally, which are mostly colonized by the Dothideomycetes and Pezizomycotina, the genus Saccharomyces and the class Exobasidiomycetes are the early colonizers of infants born via C-section, according to research on European newborns. Drinking breast milk could be another way for colonization to occur. Its makeup changes when a more varied diet replaces breast milk (Belvoncikova, *et al.,* 2022).

Host organ function may also influence how the gut-microbial community structures are created. Since the intestine experiences major age-related changes in tissue integrity and function, including changes in peristalsis, mucus layer composition, epithelial barrier formation, and regenerative capacity, it is probable that changes in the mucosal niche play a role in dysbiotic states as we age. These subclinical alterations in intestinal integrity may encourage the emergence of chronic inflammatory illness, systemic low-grade inflammation, microbial extravasation to systemic locations, and early mortality. However, determining causal linkages in humans is still difficult, as will be covered later (Bosco, and Noti, 2021).

The intestine tissue and the microbiota and other luminal substances are physically separated by the intestinal epithelium, a single cell layer. Occludin and zona occludens-1 (ZO-1) are two examples of intercellular tight junction proteins that join intestinal epithelial cells (IECs) and control material migration between the cells. The host's health depends on the intestinal barrier's ability to remain intact. Another name for intestinal barrier breakdown is "leaky gut." Locally, metabolic diseases like obesity and diabetes, colorectal cancer, celiac disease, and inflammatory bowel disease (IBD) have all been connected to intestinal barrier damage (Walrath, *et al.,* 2021).

Dysbiosis

Dysbiosis of the gut referred to the changes in the composition of the gut microbiota that is associated with functional changes in the microbial transcriptome, proteome, or metabolome. The microorganisms of our intestines play an important role in gastrointestinal tissue permeability; they control the fermentation and utilization of dietary polysaccharides to generate short-chain fatty acids, which also explain their major role in monitoring fat buildup and the subsequent development of obesity-related diseases (Hamjane, *et al.,* 2024).

Dysbiosis is caused by several interrelated factors, such as dietary habits, environment, and heredity (Manzoor, *et al.,* 2022).Dysbiosis can be caused by factors such as genetic background, health status (infections, inflammation), and lifestyle habits or—more importantly—environmental factors such as diet (high sugar, low fiber), xenobiotics (antibiotics, drugs, food additives), and hygiene (Hrncir, *et al* 2022).

There are several factors that contribute to gut microbiota dysbiosis, such as immunological dysregulation, metabolic processes, proinflammatory processes, and microbiome imbalance. Numerous T cell-related illnesses, such as rheumatoid arthritis (RA), type 1 and type 2 diabetes, asthma, cardiovascular disease, inflammatory bowel disease (IBD), cancer, liver disease, and mental illnesses, are brought on by dysbiosis (Shim, *et al*., 2023).

Two methods of microbiome modulation are 1) direct (nutrients affect the microbiome's composition and metabolic activity) or 2) indirect (alterations in gut physiology alter the intestinal lumen's environment, which alters the microbiome) (Bedani, *et al.,* 2024).

1.3 FUNCTION OF THE GUT MICROBIOTA

Metabolic function

The three SCFAs that are most frequently found in feces are butyrate, propionate, and acetate; their molar ratios typically range from 3:1:1 to 10:2:1. The most significant SCFA for human health is probably butyrate. In addition to serving as the primary energy source for human colonocytes, it may have anti-cancer properties through its capacity to trigger the death of colon cancer cells and alter gene expression by blocking histone deacetylases. In addition to providing energy to the epithelial cells, propionate is also transported to the liver, where it contributes to gluconeogenesis. Its interaction with gut receptors has led to an emerging belief that it is a key chemical in satiety signaling. Being the most prevalent SCFA, acetate is a crucial co-factor and metabolite for the development of other microorganisms. The human body uses acetate for lipogenesis and cholesterol metabolism when it is delivered to the peripheral tissues (Rownald, *et al.,* 2018).

Among other metabolic processes, the microbiota breaks down complex, indigestible substances like dietary fibers and oligosaccharides to produce SCFA like butyrate, propionate, and acetate. These metabolites have anti-inflammatory and enterocyte-supplying properties.Symptoms including constipation, diarrhea, and stomach pain are caused by immunological modulation triggered by the microbiota and altered SCFA synthesis. Crohn's disease, ulcerative colitis, and other chronic inflammatory bowel illnesses (IBD) are noteworthy examples.

The mediterian diet (MD)may simultaneously decrease the number of microbial species linked to inflammation and metabolic dysfunction while encouraging the growth of beneficial bacteria that generate bioactive metabolites, including short-chain fatty acids (SCFA), according to new research. Key elements in the prevention of chronic illnesses include decreased intestinal permeability, enhanced gut barrier integrity, and decreased activation of systemic inflammatory pathways (Perrone, D'Angelo, 2025).

Dietary fibers are a diverse group of nutrients that are essential for preventing a few chronic illnesses. Since the gut microbiota ferments most dietary fibers, it may alter the ecology and metabolism of gut microbes, which could influence human health. Individual differences may exist in the impact of dietary fibers on the prevalence of bacterial taxa. There is disagreement regarding the impact of dietary fibers on microbial diversity. A precise evaluation of the microbiome is necessary to better understand the variable response to dietary fibers, according to many intervention studies involving dietary fibers in the setting of obesity and associated metabolic diseases. A high dietary fiber intake is strongly linked to a lower incidence of many types of cancer, according to epidemiological studies; however, the effects of intervention with dietary fibers on cancer risk, therapy efficacy and toxicity, and cancer cachexia need to be ascertained (Delzenne, *et al.,* 2025).

Bacterial lipids have long been researched because of their critical functions in preserving the membrane's structural integrity, promoting energy production via the electron transport chain, offering an appropriate environment for proteins in the outer membrane, and shielding the cell from external threats. Though most of what is known about gut bacterial lipid biosynthesis comes from research on one species, *Escherichia coli*, each bacterial species has its own lipid signature that reflects both the genetically encoded biosynthetic machinery and the lifestyle of the bacterium. Nine Remarkably, *E. Coli* has 10% lipids by dry weight; from the standpoint of biomass, lipids make up a large portion of the metabolic content of the microbiome (Brown, Clardey, and Xavier, 2023).

Both host- and bacterial-derived proteases and peptidases convert dietary proteins into peptides and amino acids. Both the host and intestinal microbes can use the released peptides and amino acids in other ways. Nonetheless, some transporters are probably needed for the metabolism of extracellular amino acids by bacteria (Duncan, Lyer, and Russell, 2020).

The metabolic activity and taxonomic profile of the gut microbiota are known to be significantly influenced by dietary intake of protein and carbohydrates. The dominant members of the colonic microbiota are specialized degraders of complex polysaccharides. The gut's microbial members use and compete for dietary and endogenous (non-dietary) proteins. These nitrogenous substrates can be used for biosynthesis (i.e., microbial synthesis of amino acids and proteins) or energy production (i.e., through fermentative pathways). The fermentation of amino acids is primarily carried out by specialized proteolytic bacteria in the distal colon, where carbohydrates are depleted. Amino acid fermentation as an energy source leads to the accumulation of various harmful end-products that negatively impact host epithelial cell physiology and are linked to the onset of diseases (Peled, and Liveny,2021).

Vitamins that work as cofactors in energy production may help bacteria with their energy metabolism and may even excite certain microbes, increase their frequency or improve their biologic capabilities (Bedani, *et al*., 2024). Vitamins other than vitamin D cannot be synthesized by humans. Therefore, external sources of additional vitamins must be found in food or the gut bacteria. In the human body, commensal bacteria like Lactobacillus and Bifidobacterium, which are prevalent in the gut, may produce vitamins from scratch. Most of the water-soluble B vitamins, including B12, B9, B6, B2, and B1, as well as vitamin K, can be produced by gut microbiota members. Most B vitamins are synthesized by the microbiota, and each has a unique synthesis method (Wibawo, and Pramadhani, 2024).

It has been demonstrated that vitamin K2 (VK2) may help to improve intestinal integrity. In addition to its fundamental function in blood coagulation, VK is linked to a few biological processes, including inflammation, atherogenesis, oxidative processes, bone metabolism, and cancer prevention. Through the inhibition of pro-inflammatory cytokine production, particularly interleukin-6 (IL-6) and TNF-α, VK can suppress the inflammatory process. The composition of the gut microbial community can be changed by dietary VK insufficiency, according to a recent study, even if the microbiota can produce VK2 on its own (Wang, *et al*., 2024).

Some B-group vitamins, such as B-1, B-6, B-9, and B-12, may be produced by intestinal tract microbes in humans. They are a class of eight water-soluble vitamins that are cofactors that are essential for the metabolism of fats and carbohydrates as well as the creation of DNA. Bacteroides species, Bifidobacterium species, and Enterococcus species are among the bacterial genera found in the distal intestine that are generally known to produce vitamins (Bedani, *et al*., 2024).

Protective and immunological function

The term "gut barrier" describes a physiological barrier system that occurs in the intestines and is mainly made up of the intestinal mucosa epithelial cells mucus layer, and intestinal defense system. The gut barrier's primary function is to maintain intestinal homeostasis, which can prevent immune system dysregulation and protect the body from infections. When the gut barrier fails, it can result in autoimmune diseases, intestinal inflammation, and other health problems (Zhuang, Zhang, and Cai, 2024).

Mucin, a type of glycoprotein, is the fundamental building block of mucus in both humans and animals. Mucus's main constituents are referred to as mucin. The biological gel that covers all the body's mucosal epithelia is called mucus. Protecting the epithelium from physical, chemical, and biological harm, it forms a physical barrier between the lumen and epithelial cells. Mucins are responsible for the viscoelastic and watery nature of mucus. Mucins are divided into two categories: Both transmembrane and gel-forming mucins are present (Yamaguchi, and Yamamtao, 2023).

While the latter have hydrophobic transmembrane regions and are affixed to the cell membrane, the former secretory mucins are released into the lumen by epithelial cells. The primary roles of transmembrane mucins are cell protection and host-microbe interaction; they do not aid in the creation of mucus gels (Pelaseyed, and Hansson, 2020). The interaction between microorganisms and the gastrointestinal tract's epithelial surfaces is significantly influenced by mucins. Carbohydrates make up 50% to 80% of their weight, and they have a high percentage of O-glycosylation changes (Hansson, 2020).

GALT sustains homeostasis by producing immunological effector cells that spread across the whole gastrointestinal tract. The special characteristics of GALT and its interactions with microbiota that promote the production of unique antibody specificities are discussed here, as well as how the same niche can support the development of subsets of systemic B cells in certain species, such as mediators of rapid systemic immunity to T-independent (TI) antigens in humans (Bemarker, *et al*., 2024).

The gut microbiota communicates with T cells through Toll-like receptors and Nod-like receptors, or by antigen-specific recognition. By mediating cell induction and function, these signals help the human immune system maintain homeostasis. It has been demonstrated that some microbiota species are linked to the development of T cells, including regulatory T (Treg), helper T (Th) 1, Th2, and Th17. Additionally, T cell activation and differentiation are regulated by short-chain fatty acids (SCFAs), which are metabolites of the gut microbiota.

According to a new study, the microbiome functions as an antigen for T cells, and certain microorganisms, such segmented filamentous bacteria (SFB), help the thymus create T cells that are specific to microbiota. Divided into CD4+ and CD8+ T cells, T cells primarily control adaptive immune responses. Cytotoxic CD8+ T cell activity and cell polarization are induced by a particular commensal microbiome. Furthermore, non-traditional T cells, such as mucosal-associated invariant T (MAIT) cells, natural killer T (NKT), and γδ T, identify groups of microorganisms by their metabolites generated from microbes (Shim, *et al*., 2023).

Most significantly, the gut microbiota plays a role in the maturation and development of the central nervous system (CNS), as well as the development and regulation of the immune response, among many other bodily activities. The microbiota-gut-brain axis is how it interacts with the brain and is a basic component of the gut-brain network.

By modulating the immune system, the hypothalamic-pituitary-adrenal (HPA) axis, tryptophan metabolism, and the production of metabolites like short-chain fatty acids (SCFAs), microorganisms can affect CNS processes in both directions through the vagus nerve. These SCFAs are involved in the interaction between the stomach, brain, and microbiota. There is increasing evidence that SCFAs have important physiological effects on the brain in addition to the colon's well-established roles in energy supply, trophic factors, and the control of T regulatory (Treg) cell colonies. After passing across the blood-brain and gut-blood barriers, SCFAs enter the central nervous system and build up inside cells (Barrio, Sanchez, and Monzon, 2022).

1.4 ASSOCIATION WITH SPECIFIC HEALTH CONDITION

Microbial imbalance known as intestinal dysbiosis is brought on by an overabundance of "bad" bacteria in the gut and can have detrimental effects such producing toxic metabolites or important metabolites incorrectly. To maintain the required immunological and metabolic processes, a balanced environment between the host and microorganisms is known to be crucial, even if the exact makeup of a "healthy microbiota" has not yet been determined. Multiple sclerosis, amyotrophic lateral sclerosis, cancer, autoimmune diseases, depression, anxiety, Parkinson's disease, obesity, diabetes, chronic fatigue syndrome, intestinal bowel syndrome, and other neuropsychiatric disorders have all been linked to dysbiosis in recent years (Varesi, *et al*., 2022).

Metabolic diseases

Obesity

An excessive buildup of body fat is the hallmark of obesity, a complex and diverse illness that can result in several metabolic conditions such as insulin resistance, type-2 diabetes (T2D), cardiovascular disease, and non-alcoholic fatty liver disease (NAFLD). (Piche, Techernof, and Despres 2020).

Multiple genetic and nongenetic variables, including environmental influences, contribute to obesity, a complicated metabolic condition. A body mass index (BMI) of 30 or more is considered obese by the World Health Organization, while national definitions differ. For instance, obesity is defined as having a BMI of 28 or above in China. A thorough examination reveals that around 10% of people worldwide are obese, and roughly one-third are overweight. Globally, there will be 1.12 billion obese people by 2030, according to predictions (Liu, *et al*., 2021). The role of the gut microbiome in regulating obesity and associated metabolic diseases has rapidly increased. Many studies have aimed to uncover the role of gut microbiota imbalance in these hormonal modification (Geng, *et al.,* 2022).

The role of the gut microbiota in the development of obesity and its complications has attracted increasing interest. Dysbiosis of the gut referred to the changes in the composition of the gut microbiota that is associated with functional changes in the microbial transcriptome, proteome, or metabolome. The microorganisms of our intestines play an important role in gastrointestinal tissue permeability; they control the fermentation and utilization of dietary polysaccharides to generate short-chain fatty acids, which also explain their major role in monitoring fat buildup and the subsequent development of obesity-related diseases (Hamjane, *et al.,* 2024).

Obesity is now a serious global public health concern, with its incidence reaching epidemic levels. Conventional approaches, like pharmacological therapies and lifestyle changes, frequently lead to modest weight reduction and are linked to high rates of weight gain. With significant weight loss and improvements in comorbidities, bariatric surgery has become the most successful long-term treatment for extreme obesity (Mohammadzadeh, *et al*., 2025).

Although there is ample evidence of the mechanical and physiological changes brought about by bariatric surgery, such as decreased stomach volume and nutrient absorption, there is also mounting evidence that the metabolic improvements seen in postoperative patients are also significantly influenced by changes in the gut microbiota (Faccioli, poitou, and clemente 2023).

T2D

A class of metabolic disorders known as diabetes are defined by hyperglycemia brought on by an insulin shortage, either direct or indirect. In type 1 diabetes (T1D), an autoimmune illness, antibodies are generated against different components of pancreatic β-cells; the insulin-producing islets degrade and eventually die, which results in insufficient insulin. Type 2 diabetes (T2D) is brought on by insulin resistance (IR), which raises the need for insulin in peripheral tissues and, consequently, results in β-cell dysfunction (Bielka, Przezak, and Pawlik 2022).

The connection between diabetes and gut microbiota has attracted a lot of attention, and new findings indicate that changes in the composition of the microbiota may both cause and exacerbate insulin resistance. Interestingly, dysbiosis in type 2 diabetes is linked to reduced microbial diversity, increased pro-inflammatory bacteria, and decreased beneficial species. Additionally, Gram-negative bacteria's outer membrane contains big chemicals called lipopolysaccharides (LPS). As the intestinal barrier is breached, as occurs in "leaky gut," LPS can enter the bloodstream and cause systemic inflammation. Inflammation and insulin resistance are tightly related. In Type 2 Diabetes (T2DM), endotoxemia—a disorder characterized by high LPS levels—is a result of bacterial translocation, in which bacteria and their constituents, including LPS, migrate from the stomach to the bloodstream (Murugesan, *et al*., 2025).

NAFLD

Lipid buildup in over 5% of hepatocytes is a hallmark of non-alcoholic fatty liver disease (NAFLD). Non-alcoholic fatty liver (simple steatosis), non-alcoholic steatohepatitis (NASH), and NAFLD-related hepatocellular carcinoma (NAFLD-HCC) are the three stages of the illness continuum. With 15–40% of the general population affected, NAFLD has emerged as the leading cause of chronic liver disease globally. The incidence of NAFLD in obese people might possibly be as high as 90% (Song, and Zhang, 2022).

Human gut microbiota has been found to be vital, and pre-clinical NAFLD/NASH models and NASH patients have validated its vital roles. The gut-liver axis is typically how gut microbes, and their metabolites cause inflammation and fat buildup in the liver. It is unclear, therefore, what pathophysiology underlies steatohepatitis caused by the gut microbiota. Recent research has linked gut microbial signatures, particularly Proteobacteria-enriched bacteria and the decline in *Rikenellaceae* and *Ruminococcaceae* abundance in NAFLD patients' guts, to the development of human NAFLD (Liu, *et al*., 2023).

Gastrointestinal diseases

IBS

A common gastrointestinal bowel illness, irritable bowel syndrome (IBS) is characterized by frequent abdominal pain and discomfort or changes in bowel habits. It's interesting to note that women are 1.67 times more likely than males to experience IBS (Xiao, *et al.*, 2021).

The chronic gastrointestinal condition known as irritable bowel syndrome (IBS), which has an unclear cause, is typified by irregular bowel movements and frequent stomach pain. IBS can be further classified into four subgroups based on symptoms: constipation-predominant IBS (IBS-C), mixed IBS (IBS-M), diarrhea-predominant IBS (IBS-D), and unclassified IBS. It has been reported that IBS-M accounts for 44% of all occurrences of IBS in the United States, whereas IBS-D and IBS-C are diagnosed in about 26% and 28% of patients, respectively (Shrestha, *et al.*, 2022).

Changes in the gut microbiota and its functions may be due to physiological changes in the gut brought on by IBS. On the other hand, gut dysbiosis might be the primary cause of the pathophysiological alterations in IBS. According to available data, these disorders might coexist. In any event, the gut microbiota's impact on mucosal immunity, gut barrier dysfunction, food metabolism, and the brain-gut-microbiome (BGM) axis is essential to comprehending why it is so important for the development and maintenance of IBS (Cheng *et al.*, 2024).

IBD

The chronic recurrent inflammatory condition known as inflammatory bowel disease (IBD) usually has two subtypes: Crohn's disease (CD) and ulcerative colitis (UC). (Zheng, et al., 2023). IBD is an idiopathic inflammatory gastrointestinal disease that affects 0.3% to 0.5% of the world's population. It is caused by a variety of factors, such as immune factors, genetic susceptibility, and gut microbiota. Numerous studies have shown that the gut microbiota composition of IBD patients differs significantly from that of healthy people (Qiu, *et al.*, 2022).

Antibiotic use also causes the gut microbiota's structure and function to change, which in turn causes IBD to develop. Maintaining the host's immune system's functionality depends heavily on the interaction between the gut microbiota and the host. Alterations in the environment, like overuse of antibiotics and dietary changes, can exacerbate autoimmune and inflammatory diseases by altering the composition of the gut microbiota and causing dysbiosis. The microbial populations in the human gut have a connection to IBD. The precise process by which gut microbiota dysfunction contributes to IBD is yet unknown, even though IBD is frequently linked to changed interactions between gut bacteria and the intestinal immune system. Patients with IBD frequently have an imbalance that manifests as an irritated gastrointestinal tract (Haneishi, et al., 2023).

Cardiovascular diseases

Atherosclerosis

Atherosclerosis is a degenerative vascular disease that is typified by the buildup of plaque made of complex carbohydrates and lipids found in blood. One major cause of death and a major risk to human life and health is atherosclerosis, a prevalent cardiovascular disease1. Disorders of lipid metabolism, a local or systemic inflammatory response, oxidative stress, and vascular endothelial dysfunction are among the many mechanisms and risk factors that contribute to the onset and progression of atherosclerosis. Conventional factors include diabetes, hypertension, obesity, and smoking (Mao, *et al.,* 2024).

An imbalance in the gut's microbial populations, commonly linked to changes in the microbial composition or the breakdown of the mucosal barrier, is referred to as gut dysbiosis. Many things, such as eating a lot of fat, having certain illnesses, and using antibiotics excessively, might cause this imbalance. These modifications to the composition of the gut microbiota impair gut permeability, which permits the entry of bacterial DNA, metabolites, and endotoxins into the blood and other organs (Majumder, Sen, and karanjai, 2025).

The gut normally maintains a robust barrier system that includes two layers of mucus and single-layered intestinal epithelial cells connected by tight junction proteins to prevent dangerous substances from entering the bloodstream (Magne, *et al.*, 2020).

Neuropsychiatric disorder

Alzheimer's diseases

Alzheimer's disease, or AD, is a progressive neurodegenerative condition that differs from normal aging in that it causes a variety of cognitive deficits that impact many parts of everyday living. Memory, reasoning, decision-making, communication, problem-solving, personality, and movement are all impacted by these disorders (Dissanayaka, *et al.*, 2024).

Many neuro-chemical pathways are regulated by gut microbes through the intricately linked gut-brain axis. Bidirectional communication between the gut and the brain is facilitated by the intestinal microbiota, according to recently discovered research. Because of this, the researchers have proposed that the microbiota in the human gut might potentially function as the "second brain" and be the cause of neurological diseases like Alzheimer's (Goyal, Ali, and Singh 2021).

Numerous studies have demonstrated that changes in the gut microbiota have a direct impact on cognitive impairment and actively contribute to the etiology and course of AD. Similar to what has been seen in human aging, AD patients typically have a reduced diversity of gut microbes and a notable shift toward pro-inflammatory taxa at the expense of the more advantageous anti-inflammatory ones (Varesi, *et al.*, 2022).

Parkinson's diseases

Recent research on Parkinson's disease (PD), a progressive neurodegenerative illness, indicates that the gut microbiota plays a major role in the pathophysiology and progression of the condition via the gut-brain axis. This study examines the molecular mechanisms underlying the gut-brain axis's function in Parkinson's disease (PD) using 16S rRNA sequencing, high-throughput transcriptome sequencing, and animal model tests. It focuses on short-chain fatty acids (SCFAs), which are mediated by the SCFA receptors FFAR2 and FFAR3 (Ni, *et al.*, 2024).

People with Parkinson's disease have a very different gut flora than healthy individuals. Important discoveries include a rise in potentially hazardous bacteria like *Verrucomicrobiaceae* and *Akkermansia* and a decline in beneficial bacteria like *Prevotellaceae*, *Lachnospiraceae*, and bacteria that produce short-chain fatty acids (SCFAs). The development of the disease and the intensity of its symptoms have been connected to these microbial alterations. Through a few ways, it is thought that alterations in the microbial makeup contribute to the pathophysiology of Parkinson's disease. These methods include influencing neuroinflammation and neurodegeneration, causing intestinal and systemic inflammation, increasing alpha-synuclein aggregation, and rupturing the integrity of the gut barrier. Furthermore, the finding that gastrointestinal symptoms frequently appear years before motor symptoms point to a possible early function for the gut microbiota in the development of Parkinson's disease (Suresh, *et al.*, 2024).

Cancer

Colorectal cancer

Colorectal cancer (CRC) is one of the most common cancer types worldwide. It holds the third rank in cancer incidence and is the second leading cause of cancer death. The risk factors of CRC include genetic and environmental factors related to the development of CRC, such as high-fat diets, animal-based foods consumption, obesity, sedentary lifestyle, etc. Besides these factors, the gut microbiome, which comes from food and probiotic supplements, determines the host's health and has become an influencing factor of CRC (Masheghati, *et al.*, 2024).

The role of microbiomes in the development of CRC has been increasingly emphasized. It is well known that the gut microbiome has an important role in the carcinogenesis of CRC, causing initial inflammation and modulating different signalling pathways. Because bacterial biomarkers have the potential to detect CRC and predict clinical outcomes, they have prognostic value. During the development of cancer, a complex interaction is established among the gut microbiome, tumor microbiome and immune system (Rebersek, *et al.*, 2021).

Certain bacteria are found to be greater in number in CRC patients, while others are found to lessen. Bacteria such as *Alistipes, Akkermansia spp. Fusobacteria, Porphyromonadaceae, Coriobacteridae,* and *Methanobacteriales* were found to be increasing in number in the colon microbiota of a CRC patient (Siddiqui, et al., 2022).

1.4. DIETARY MODULATION AND THERPEUTIC STRATIGIES

Probiotics

Probiotics, which are defined as beneficial bacteria that provide health benefits to the host when given in sufficient quantities, have attracted a lot of interest in food systems because of their substantial effects on gut health and general wellbeing. Beyond the conventional nutritional advantages, they play a significant role in intricate relationships with the immune system, metabolism, and gut microbiota (Mafe *et al.*, 2025).

As possible modulators of the gut microbiota, probiotics which the World Health Organization defines as "live microorganisms which, when administered in adequate amounts, confer a health benefit on the host"—have gained popularity (Oudat, okour,2025).

Probiotics encompass a wide variety of bacteria; the primary probiotics in this study are Lactobacillus, Bacillus, Saccharomycetes, and Bifidobacterium, among others. Probiotics' impacts on health have also emerged as a research hotspot at the same time. Probiotics have now been shown to help treat lactose intolerance, lower blood cholesterol, alleviate constipation and diarrhea, prevent pathogen infection, preserve the natural structure of gut flora, and support the development of the immune system. Three main parts make up probiotics' method of action: (1) strengthening the host's defenses, (2) combating microbes directly, and (3) metabolites serving a crucial role (Shen, *et al.*, 2024).

Probiotics can help restore microbial balance by introducing helpful bacteria or yeasts into the gut through dietary systems. To prevent dysbiosis, these probiotics work with the natural gut microbiota to maintain a balanced microbial composition. Moreover, probiotics have been demonstrated to generate short-chain fatty acids (SCFAs), which enhance intestinal barrier performance and lessen low-grade inflammation, a major cause of metabolic syndrome. (Mafe, *et al.*,2025).

Traditional examples of foods that naturally include probiotic bacteria and yeasts include yogurt, kefir, kimchi, sauerkraut, and kombucha (Dimidi, *et al.*, 2019). The integration of probiotic strains, such as Lactobacillus and Bifidobacterium, into a wider variety of goods is becoming more and more important in the context of contemporary food systems (Jikah, and Edo 2023).

Prebiotics

Prebiotics are indigestible dietary components that specifically promote the growth or activity of one or a small number of bacteria in the colon, enhancing the host's health in the process (Yoo, *et al.*,2024). Four new criteria were added to prebiotics in 2004: (1) resistance to gastrointestinal absorption, gastric acidity, and hydrolysis by mammalian enzymes; (2) they should only be fermented by GM; (3) they create luminal or systemic effects that are advantageous to host health; and (4) they specifically promote the growth and activity of GM linked to health and well-being (Megur, et *al.*, 2022).

Prebiotics provides a variety of health advantages, such as immune modulation via higher intestinal-specific immunoglobulins and immune-regulatory interleukins; decrease in pro-inflammatory interleukins and the synthesis of short-chain fatty acids

(SCFAs) like butyrate, propionate, and acetate (Pluta, *et al*., 2020). CFAs are known to enhance gut health by preserving intestinal barrier integrity, producing mucus, preventing inflammation, and lowering the risk of colorectal cancer and obesity. They are also a significant indicator of bacterial fermentation in the colon (Megur *et al*., 2022). Prebiotic supplements including fructooligosaccharides (FOS) and galactooligosaccharides (GOS) have been demonstrated in clinical trials to lower body fat and treat disorders linked to obesity. Furthermore, it has been noted that prebiotics improve postmenopausal women's calcium retention (Chu *et al*., 2025). Pharmaceuticals and treatments for diabetics are widely known for using prebiotics as a natural sweetener (Hanau, *et al*.,2020). Numerous studies on prebiotics have concentrated on substances linked to two main chemical groups: fructo-oligosaccharides and galacto-oligosaccharides (Swanson, *et al*., 2020). Prebiotics can be obtained and/or extracted from foods including seeds, whole grains, legumes, chicory roots, Jerusalem artichokes, onions, garlic, and some vegetables. However, a recent study discovered that prebiotics are also present in some aquatic plants, such as seaweed and microalgae (Megur *et al*., 2022).

Synbiotics

A synbiotic is a combination of probiotics and prebiotics, a word invented in 1995 by Glenn R. Gibson and Marcel Roberfroid. It described how live microbial dietary supplements can survive and colonize the gastrointestinal tract and benefit the host by selectively promoting the growth or activating the metabolism of one or a small number of beneficial and health-promoting bacteria, thereby improving the host's overall health (Yoo, *et al*.,2024).

Synbiotics are a type of dietary supplement that works in concert with probiotics and prebiotics to increase their positive effects. When two dietary components or supplements are taken together, the beneficial benefits often fall into one of three categories: additive effects, synergy, or potentiation (Hamasalim., *et al* 2016).

This combination's main goal is to increase the probiotic microorganisms' ability to survive in the digestive system. Synbiotics were developed to get around the problems that probiotics might have in the gastrointestinal system. They have both prebiotic and probiotic qualities. Probiotics have a positive impact on intestinal homeostasis and create a barrier that protects the digestive system. When probiotics and prebiotics are combined in a single product, the result can be better than when either component is used alone since prebiotics give probiotic microorganisms energy and nutrients (Markowiah, and Slizewska 20218). The ability of synbiotic foods containing arabinose, lactulose, and Lactobacillus plantarum to successfully control blood sugar, blood fat, and body weight in individuals with Type 2 Diabetes Mellitus (T2DM) has drawn attention. Making a banana smoothie with kefir or yogurt is another way to prepare this tasty and nourishing beverage that optimizes the advantages for gut flora. When you stir-fry tempeh, asparagus, garlic, and leeks, you can promote healthy gut flora (Kumar, *et al*., 2025).

With increased research on the topic, a variety of synbiotic products have become available to the public. Atopic dermatitis, gastrointestinal disorders, hepatic encephalopathy, irritable bowel syndrome, metabolic disorders, and type 2 diabetes can all be effectively treated with different synbiotic combinations. As a new generation of products that follow probiotics and prebiotics, Synbiotics share their benefits and work together to produce a better therapeutic effect (Jiang, *et al*., 2022).

Fecal microbiota transplant

Fecal microbiota transplantation (FMT), also known as "feces transplantation," "human intestinal microbiota transfer," or "fecal bacteriotherapy," is a therapeutic procedure in which fecal samples from healthy volunteers are mixed, blended, and filtered before being endoscoped or administered as capsules to another person's digestive tract. Restoring the damaged or unbalanced gut microbiota, encouraging the diversity and balance of intestinal bacteria, and ultimately improving some gut-related illnesses are the goals (Hou, *et al*., 2025).

The main reason for the early adoption of FMT is that doctors are looking for alternative treatment to treat a potentially fatal illness that affected their patients. Because FMT entails the transfer of live microorganisms found in fecal material from donor to recipient, regulators were naturally worried about the possibility of causing microbiome-mediated diseases like metabolic syndrome in recipients or transferring harmful microbiota like infectious pathogens or multidrug-resistant organisms along with beneficial microbes (Hoffmann, et al., 2025).

Because of its demonstrated efficacy and safety, FMT has been authorized by the FDA to treat recurrent *Clostridium difficile* infections (rCDI). FMT has demonstrated promise in the treatment of neurological illnesses, cancer, metabolic diseases, chronic infections, and IBD in addition to rCDI. Remission was only attained by 45 percent of individuals receiving treatment for IBD (22 percent of patients with ulcerative colitis (UC) and 60.5% of patients with Crohn's disease). Following FMT, 61.29 percent of patients with active UC experienced remission, according to another research investigation. Research indicates that donor microbiota stability may influence the efficacy of FMT, particularly about the survival of important taxa such as bile acid converters and short-chain fatty acid (SCFA) makers. Therefore, maintaining the survivability of beneficial microbial strains depends on maintaining the stability of the donor microbiota (Fan, *et al*., 2025).

Procedure

A thorough FMT protocol is provided, specifically for the treatment of CDI. It entails combining 200–300 mL of a diluent with 50–60 g of stool until a liquid suspension is formed. The mixture is filtered through gauze after being allowed to settle for five minutes. The resultant liquid can be frozen for up to 30 days at -20°C, refrigerated for up to 24 hours at 2–8°C, or utilized right away. The fecal material can be kept at -80 °C without losing its efficacy if glycerin is added. FMT can be administered in a few ways, such as orally (via the upper gastrointestinal tract), nasally, or rectoally (by colonoscopy) (Gulati, *et al*., 2020). However, the large concentrations of harmful bacteria in the upper digestive and respiratory tracts may cause problems when FMT is administered by a nasogastric or nasoduodenal tube, possibly resulting in gastrointestinal or pulmonary problems (Perez, *et al*., 2016).

Apart from its function in preventing recurrent CDI, FMT has demonstrated potential in the field of oncology, particularly in reducing the adverse effects of malignant radiation (Ding, *et al*., 2024). The FMT triggers a significant reaction that reduces the inflammatory response, especially involving regulatory T cells, iNKT cells, and antigen-presenting cells (among others). This has been demonstrated in patients with other illnesses in addition to those infected with Clostridium difficile. Since many pancreatic disorders are caused by inflammation, lowering the activity of the inflammatory system may have major benefits (Boicean, *et al*., 2024).

Dietary Patterns

In current society, numerous dietary patterns have been created to enhance people's health and quality of life. The amount and diversity of foods consumed, together with the frequency of ingestion of edibles, are all components of dietary patterns. Diets that are rich in calories (like the Western diet), mixed-balanced (like the Mediterranean diet), plant-based (like the vegetarian diet), or low in carbohydrates (like the ketogenic diet) are some of the primary dietary variations. While the impact of these diets on physiological wellbeing varies, some of them have characteristics in common (Borrego, and Borrego 2024).

However, following a specific diet ultimately depends on self-perception and physical fitness, health maintenance, psychological well-being, and awareness of geography, culture, ethics, and the environment (Hargreaves, *et al*., 2023). One of the most significant factors affecting health is dietary patterns, which have an impact via a variety of pathways, including inflammation, oxidative stress, tryptophan metabolism, epigenetics, CNS and HPA functions, mitochondria, and gut microbiota (Marx, *et al*., 2021).

Mediterranean Diet

The Mediterranean diet is a well-balanced diet that includes a variety of food groups that are high in nuts, fruits, vegetables, and olive oils. It also includes moderate amounts of wine, fish, and chicken, as well as less red and processed meat (Estruch, *et al*., 2018).

Dietary fiber content is high in several of the ingredients. Due to its accessibility, health benefits, and variety of dietary categories, it is still becoming more and more popular with medical and nonmedical staff. Low-density lipoprotein (LDL) and plasma cholesterol have been shown to decrease, cardiovascular disease (CVD) and all-cause mortality have been shown to decrease, insulin sensitivity has improved, and the Mediterranean diet has been shown to have anti-inflammatory and antioxidant effects. A Mediterranean diet has been shown to have a variety of effects on the gut flora in human studies. Bifidobacterium has been found to be more abundant in several investigations. One of these investigations also showed an increase in *Bacteroides, Enterococcus,* and *Prevotella.* Another study discovered that while *Ruthenibacterium lactatiformans, Flavonifractor plautii, Parabacteroides merdae, Ruminococcus torques,* and *Ruminococcus gnavus* decreased in abundance, *Faecalibacterium prausnitzii, Roseburia,* and *Lachnospiraceae* increased. *Firmicutes and Lactobacillus* have increased, according to other studies. Individual elements of the Mediterranean diet have been shown to change the composition of the gut flora. For instance, ingestion of walnuts was linked to higher relative abundances of *Lachnospiraceae, Leuconostocaceae, Roseburia,* and *Eubacterium eligens* group (Perler, Friedmen, and Wu, 2023). According to numerous studies, following the MD is linked to improved memory and cognition, a decreased risk of cognitive impairment, a postponement of cognitive decline, and a decreased risk of neurodegenerative illnesses. This diet's anti-inflammatory properties and increased SCFA content are the causes of these positive effects (Borrego, and Borrego 2024).

Western diet

The WD is characterized by the high frequent consumption of animal proteins, processed foods, refined carbohydrates, and saturated fats. It is primarily adopted by people in Western developed countries, although its use is also growing in developing. Obesity and metabolic diseases result from long-term consumption of a WD, which has a significant impact on gut flora compared to a Mediterranean diet. Several investigations revealed significant compositional alterations and a decline in gut microbial diversity.

The genus *Prevotella* is more underrepresented in fecal samples from patients after WD than in those who consume a high-vegetable, high-fiber diet. *Alistipes* species, *Bilophila species, Proteobacteria, Firmicutes,* and *Enterobacteriaceae* (*Escherichia, Klebsiella, Shigella*) may also become more abundant because of WD. When it comes to illnesses and dysbiosis, certain bacterial species and families are extremely important. *Lactobacillus species, Roseburia species, E. Rectale, Bacillus Bifidus,* and *Enterococcus* are among the beneficial bacteria whose numbers may be reduced by WD (Ranielle, *et al*., 2023).

Obesity and WD are risk factors for psychotically and neuropsychiatric conditions such depression, dementia, and moderate cognitive impairment. Certain brain regions may experience neurochemical changes because of WD components; specifically, hippocampal dysfunction impairs cognitive function by interfering with normal intake control and memory functions (Borego, and Borego, 2024). Chronic exposure to WD may cause compulsive eating by causing the mesocorticolimbic system to release dopamine (Stevenson, *et al.*, 2020). Corticosterone's secretion causes the HPA axis to become dysregulated, which leads to long-term stress, anxiety, and depression (Taboada, Pardo, and Conejo, 2020).

Ketogenic Diet

Ketogenic diets are intended to cause a change in metabolism, usually by consuming a lot of fat and very few carbohydrates. This causes ketone bodies to rise in the blood and changes the demands on energy. This diet is a very good way to treat children with drug-resistant epilepsy. In a tiny human pilot research, a ketogenic diet led to a slight increase in energy expenditure but no increase in body fat loss. More recently, ketogenic diets have been investigated for their potential to cure obesity (Perler,Friedmen,and Wu 2023).

Indeed, a recent study that involved human individuals consuming diets at will for two weeks revealed that a plant-based low-fat diet dramatically reduced energy intake when compared to an animal-based ketogenic low-carbohydrate diet (Hall, *et al.*, 2021). This dietary plan provides ketone bodies for energy instead of glucose, meeting the body's nutritional needs. Acetone (Ac), beta-hydroxybutyrate (β-HB), and acetoacetate (AcAc) are examples of ketones, which are intermediates in the oxidative degradation of fatty acids. While encouraging quick and long-lasting weight loss, KD satisfies nutritional needs by severely restricting carbohydrate intake and permitting a substantial intake of lipids, especially saturated fats. Furthermore, it has been linked to favorable biomarker outcomes, including lower blood hemoglobin A1c levels in individuals with type 2 diabetes. Ketone therapy has also been demonstrated to improve mitochondrial respiration, promote long-term neural potentiation, and raise the expression of brain-derived neurotrophic factor (BDNF), all of which lower inflammation and oxidative stress (Jiang, *et al.*,2025).

Vegetarian Diet

A vegetarian diet is one that completely or partially avoids foods derived from animals. The seven varieties of vegetarianism, *veganism, lacto-ovo vegetarianism, ovo-vegetarianism, lacto-vegetarianism, semi-vegetarianism, raw veganism,* and *pescetarianism*, are further separated based on whether seafood, eggs, or dairy are also omitted (Xiao, *et al.*, 2022).

By substituting plant-based foods for animal-based ones, the consumption of resistant starch (cereals, legumes, and nuts) and insoluble fiber is significantly increased. Vegetarian and vegan diets may be linked to lower levels of *Bilophila wadsworthia*, higher ratios of Bacteroides/Prevotella, and higher abundances of *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme, Klebsiella pneumoniae,* and *Faecalibacterium prausnitzii* when compared to an omnivore diet (Rinninela, *et al.*, 2023). On the other hand, omnivore and vegan/vegetarian diets did not significantly differ in fecal SCFA and methane levels, according to several studies (Eetemadi, et al., 2021). According to other research, compared to an omnivorous diet, a vegan diet could significantly lower the abundances of potentially hazardous metabolites such lithocholic acid, BCAAs, and aromatic compounds while increasing the formation of SCFAs and their derivatives (Prochazkova, *et al.*,2021).

A vegetarian diet or a brief 3-month dietary intervention with an MD does not significantly alter gut microbiota within the family. The abundance of *Enterorhabdus, Lachnoclostridium,* and *Parabacteroides* may be considerably altered at the genus level by MD, whereas the number of *Anaerostipes, Streptococcus,* and

Odoribacter may increase with a vegetarian diet. (Pagliai, et al., 2020)

CONCLUSIONS

The increasing amount of data emphasizes how crucial gut microbiota is in determining human immunity, metabolism, nutrition, and general health. Through the gut-brain axis, this complex microbial ecosystem affects host immunological responses, inflammatory processes, and even neurological function in addition to aiding nutrient absorption and energy control. Fiber-rich, plant-based, and fermented meals support microbial diversity and metabolic resilience, making diet a key regulator of microbial composition.

An imbalance in gut microbial populations, known as dysbiosis, has been repeatedly linked to several non-communicable diseases, such as type 2 diabetes, obesity, inflammatory bowel disease, and some mental health conditions. These correlations show how effective microbiota-targeted approaches may be in both therapeutic and preventative settings. Even said, a lot of these connections are still correlative, and science needs to deal with serious issues including inter-individual variability, causal inference, and the intricacy of host-microbe interactions. To fully exploit the potential of gut microbiota in improving human health, rigorously planned longitudinal studies, standardized procedures, and tailored therapies are needed in future study. Public health nutrition and clinical practice can undergo a radical change toward more personalized and preventative healthcare models by incorporating microbiome knowledge. In summary, the gut microbiota represents a frontier in nutrition and health science, providing opportunities for novel dietary and therapeutic approaches as well as insight into human physiology. To convert microbiome research into practical health benefits, ongoing interdisciplinary initiatives will be crucial.

RECOMENDATIONS

More long-term, high-quality human research is required to determine the causal links between microbial populations and health outcomes like mental health, diabetes, obesity, and cardiovascular disease. Precision nutrition strategies that modify dietary treatments according to each person's unique gut microbiota composition may provide better alternatives for both disease prevention and treatment. Policymakers and health authorities should think about integrating microbiome research into nutritional guidelines. To increase reproducibility and comparability across research, standardized procedures for sample collection, sequencing, and data interpretation are required. Inform people on the importance of the gut microbiota for general health, emphasizing how lifestyle, antibiotic use, and diet affect microbial balance.

More study should examine the processes by which the gut microbiota influences the brain and behavior considering growing data that links it to neurological and mental health. Examine the therapeutic potential and long-term implications of treatments including postbiotics, Synbiotics, and fecal microbiota transplant.

REFERENCE:

. Afzaal, M., Saeed, F., Shah, Y. A., Hussain, M., Rabail, R., Socol, C. T., ... & Aadil, R. M. (2022). Humans gut microbiota in health and disease: Unveiling the relationship. *Frontiers in microbiology*, *13*, 999001.

. Bajinka, O., Darboe, A., Tan, Y., Abdelhalim, K. A., & Cham, L. B. (2020). Gut microbiota and the human gut physiological changes. *Annals of microbiology*, *70*, 1-9.

. Barrio, C., Arias-Sánchez, S., & Martín-Monzón, I. (2022). The gut microbiota-brain axis, psychobiotics and its influence on brain and behaviour: A systematic review. *Psychoneuroendocrinology*, *137*, 105640.

. Bedani, R., Cucick, A. C. C., de Albuquerque, M. A. C., LeBlanc, J. G., & Saad, S. M. I. (2024). B-group vitamins as potential prebiotic candidates: their effects on the human gut microbiome. *The Journal of Nutrition*, *154*(2), 341-353.

5. Bedani, R., Cucick, A. C. C., de Albuquerque, M. A. C., LeBlanc, J. G., & Saad, S. M. I. (2024). B-group vitamins as potential prebiotic candidates: their effects on the human gut microbiome. *The Journal of Nutrition*, *154*(2), 341-353.

6. Bedani, R., Cucick, A. C. C., de Albuquerque, M. A. C., LeBlanc, J. G., & Saad, S. M. I. (2024). B-group vitamins as potential prebiotic candidates: their effects on the human gut microbiome. *The Journal of Nutrition*, *154*(2), 341-353.

7. Belvoncikova, P., Splichalova, P., Videnska, P., & Gardlik, R. (2022). The human mycobiome: colonization, composition and the role in health and disease. *Journal of Fungi*, *8*(10), 1046.

8. Bemark, M., Pitcher, M. J., Dionisi, C., & Spencer, J. (2024). Gut-associated lymphoid tissue: a microbiota-driven hub of B cell immunity. *Trends in Immunology*, *45*(3), 211-223.

9. Bielka, W., Przezak, A., & Pawlik, A. (2022). The role of the gut microbiota in the pathogenesis of diabetes. *International journal of molecular sciences*, *23*(1), 480.

10. Boicean, A., Ichim, C., Todor, S. B., Anderco, P., & Popa, M. L. (2024). The importance of microbiota and fecal microbiota transplantation in pancreatic disorders. *Diagnostics*, *14*(9), 861.

11. Borrego-Ruiz, A., & Borrego, J. J. (2025). Human gut microbiome, diet, and mental disorders. *International Microbiology*, *28*(1), 1-15.

12. Borrego-Ruiz, A., & Borrego, J. J. (2025). Human gut microbiome, diet, and mental disorders. *International Microbiology*, *28*(1), 1-15.

13. Borrego-Ruiz, A., & Borrego, J. J. (2025). Human gut microbiome, diet, and mental disorders. *International Microbiology*, *28*(1), 1-15.

14. Bosco, N., & Noti, M. (2021). The aging gut microbiome and its impact on host immunity. *Genes & Immunity*, *22*(5), 289-303.

15. Brown, E. M., Clardy, J., & Xavier, R. J. (2023). Gut microbiome lipid metabolism and its impact on host physiology. *Cell host & microbe*, *31*(2), 173-186.

16. Campaniello, D., Corbo, M. R., Sinigaglia, M., Speranza, B., Racioppo, A., Altieri, C., & Bevilacqua, A. (2022). How diet and physical activity modulate gut microbiota: evidence, and perspectives. *Nutrients*, *14*(12), 2456.

17. Charitos, I. A., Scacco, S., Cotoia, A., Castellaneta, F., Castellana, G., Pasqualotto, F., ... & Carone, M. (2025). Intestinal Microbiota Dysbiosis Role and Bacterial Translocation as a Factor for Septic Risk. *International Journal of Molecular Sciences*, *26*(5), 2028.

8. Charitos, I. A., Scacco, S., Cotoia, A., Castellaneta, F., Castellana, G., Pasqualotto, F., ... & Carone, M. (2025). Intestinal Microbiota Dysbiosis Role and Bacterial Translocation as a Factor for Septic Risk. *International Journal of Molecular Sciences*, *26*(5), 2028.

9. Chen, Z., Liang, N., Zhang, H., Li, H., Guo, J., Zhang, Y., ... & Shi, N. (2024). Resistant starch and the gut

0. Cheng, X., Ren, C., Mei, X., Jiang, Y., & Zhou, Y. (2024). Gut microbiota and irritable bowel syndrome: Status and prospect. *Frontiers in Medicine*, *11*, 1429133.

1. Chu, X., Xing, H., Chao, M., Xie, P., & Jiang, L. (2025). Gut Microbiota Modulation in Osteoporosis: Probiotics, Prebiotics, and Natural Compounds. *Metabolites*, *15*(5), 301.

2. Clemente, J. C., Ursell, L. K., Parfrey, L. W., & Knight, R. (2012). The impact of the gut microbiota on human health: an integrative view. *Cell*, *148*(6), 1258-1270.

3. Davidson, G. L., Cooke, A. C., Johnson, C. N., & Quinn, J. L. (2018). The gut microbiome as a driver of individual variation in cognition and functional behaviour. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *373*(1756), 20170286.

24. Delzenne, N. M., Bindels, L. B., Neyrinck, A. M., & Walter, J. (2024). The gut microbiome and dietary fibres: implications in obesity, cardiometabolic diseases and cancer. *Nature Reviews Microbiology*, 1-14.

25. Dimidi, E., Cox, S. R., Rossi, M., & Whelan, K. (2019). Fermented foods: definitions and characteristics, impact on the gut microbiota and effects on gastrointestinal health and disease. *Nutrients*, *11*(8), 1806.

26. Ding, X., Li, Q., Li, P., Chen, X., Xiang, L., Bi, L., ... & Zhang, F. (2020). Fecal microbiota transplantation: A promising treatment for radiation enteritis? *Radiotherapy and Oncology*, *143*, 12-18.

27. Dissanayaka, D. S., Jayasena, V., Rainey-Smith, S. R., Martins, R. N., & Fernando, W. B. (2024). The role of diet and gut microbiota in Alzheimer's disease. *Nutrients*, *16*(3), 412.

28. Duman, H., & Karav, S. (2025). Fiber and the gut microbiome and its impact on inflammation. In *Nutrition in the Control of Inflammation* (pp. 51-76). Academic Press.

29. Duncan, S. H., Iyer, A., & Russell, W. R. (2021). Impact of protein on the composition and metabolism of the human gut microbiota and health. *Proceedings of the Nutrition Society*, *80*(2), 173-185.

30. Eetemadi, A., & Tagkopoulos, I. (2021). Methane and fatty acid metabolism pathways are predictive of Low-FODMAP diet efficacy for patients with irritable bowel syndrome. *Clinical Nutrition*, *40*(6), 4414-4421.

31. El-Salam, A., Mohamed, H., El-Shibiny, S., Assem, F. M., El-Sayyad, G. S., Hasanien, Y. A., ... & Soliman, T. N. (2025). Impact of Fermented Milk on Gut Microbiota and Human Health: A Comprehensive Review. *Current Microbiology*, *82*(3), 1-18.

32. Estruch, R., Ros, E., Salas-Salvadó, J., Covas, M. I., Corella, D., Arós, F., ... & Martínez-González, M. A. (2018). Primary prevention of cardiovascular disease with a Mediterranean diet supplemented with extra-virgin olive oil or nuts. *New England journal of medicine*, *378*(25), e34.

33. Faccioli, N., Poitou, C., Clément, K., & Dubern, B. (2023). Current treatments for patients with genetic obesity. *Journal of clinical research in pediatric endocrinology*, *15*(2), 108.

34. Fan, J., Wu, Y., Wang, X., Ullah, H., Ling, Z., Liu, P., ... & Li, X. (2025). The probiotic enhances donor microbiota stability and improves the efficacy of fecal microbiota transplantation for treating colitis. *Journal of Advanced Research*.

35. Flint, H. J., Duncan, S. H., Scott, K. P., & Louis, P. (2015). Links between diet, gut microbiota composition and gut metabolism. *Proceedings of the Nutrition Society*, *74*(1), 13-22.

6. Geng, J., Ni, Q., Sun, W., Li, L., & Feng, X. (2022). The links between gut microbiota and obesity and obesity related diseases. *Biomedicine & Pharmacotherapy*, *147*, 112678.

7. Golshany, H., Helmy, S. A., Morsy, N. F. S., Kamal, A., Yu, Q., & Fan, L. (2025). The gut microbiome across the lifespan: How diet modulates our microbial ecosystem from infancy to the elderly. *International Journal of Food Sciences and Nutrition*, *76*(2), 95-121.

8. Goyal, D., Ali, S. A., & Singh, R. K. (2021). Emerging role of gut microbiota in modulation of neuroinflammation and neurodegeneration with emphasis on Alzheimer's disease. *Progress in Neuro-Psychopharmacology and Biological Psychiatry*, *106*, 110112.

9. Gulati, M., Singh, S. K., Corrie, L., Kaur, I. P., & Chandwani, L. (2020). Delivery routes for faecal microbiota transplants: Available, anticipated and aspired. *Pharmacological Research*, *159*, 104954.

0. Guo, X., Jiao, Y., Song, J., & Wang, F. S. (2021). Gut microbiota alteration in hepatobiliary diseases: cause-and-effect relationship. *Hepatology International*, *15*, 1305-1308.

1. Hall, K. D., Guo, J., Courville, A. B., Boring, J., Brychta, R., Chen, K. Y., ... & Chung, S. T. (2021). Effect of a plant-based, low-fat diet versus an animal-based,

ketogenic diet on ad libitum energy intake. *Nature medicine*, *27*(2), 344-353.

42. Hamasalim, H. J. (2016). Synbiotic as feed additives relating to animal health and performance. *Advances in Microbiology*, *6*(04), 288.

43. Hamjane, N., Mechita, M. B., Nourouti, N. G., & Barakat, A. (2024). Gut microbiota dysbiosis-associated obesity and its involvement in cardiovascular diseases and type 2 diabetes. A systematic review. *Microvascular Research*, *151*, 104601.

44. Hamjane, N., Mechita, M. B., Nourouti, N. G., & Barakat, A. (2024). Gut microbiota dysbiosis-associated obesity and its involvement in cardiovascular diseases and type 2 diabetes. A systematic review. *Microvascular Research*, *151*, 104601.

45. Hanau, S., Almugadam, S. H., Sapienza, E., Cacciari, B., Manfrinato, M. C., Trentini, A., & Kennedy, J. F. (2020). Schematic overview of oligosaccharides, with survey on their major physiological effects and a focus on milk ones. *Carbohydrate Polymer Technologies and Applications*, *1*, 100013.

46. Haneishi, Y., Furuya, Y., Hasegawa, M., Picarelli, A., Rossi, M., & Miyamoto, J. (2023). Inflammatory bowel diseases and gut microbiota. *International journal of molecular sciences*, *24*(4), 3817.

47. Hansson, G. C. (2020). Mucins and the microbiome. *Annual review of biochemistry*, *89*(1), 769-793.

48. Hargreaves, S. M., Rosenfeld, D. L., Moreira, A. V. B., & Zandonadi, R. P. (2023). Plant-based and vegetarian diets: an overview and definition of these dietary patterns. *European journal of nutrition*, *62*(3), 1109-1121.

49. Hasan, N., & Yang, H. (2019). Factors affecting the composition of the gut microbiota, and its modulation. *PeerJ*, *7*, e7502.

50. Hemmati, M., Kashanipoor, S., Mazaheri, P., Alibabaei, F., Babaeizad, A., Asli, S., ... & Eslami, M. (2023). Importance of gut microbiota metabolites in the development of cardiovascular diseases (CVD). *Life Sciences*, 121947.

51. Hoffmann, D. E., Javitt, G. H., Kelly, C. R., Keller, J. J., Baunwall, S. M. D., & Hvas, C. L. (2025). Fecal microbiota transplantation: a tale of two regulatory pathways. *Gut Microbes*, *17*(1), 2493901.

52. Hooks, K. B., Konsman, J. P., & O'Malley, M. A. (2019). Microbiota-gut-brain research: a critical analysis. *Behavioral and Brain Sciences*, *42*, e60.

3. Hou, S., Yu, J., Li, Y., Zhao, D., & Zhang, Z. (2025). Advances in Fecal Microbiota Transplantation for Gut Dysbiosis-Related Diseases. *Advanced Science*, *12*(13), 2413197.

4. Hrncir, T. (2022). Gut microbiota dysbiosis: triggers, consequences, diagnostic and therapeutic options. *Microorganisms*, *10*(3), 578.

5. Jiang, H., Cai, M., Shen, B., Wang, Q., Zhang, T., & Zhou, X. (2022). Synbiotics and gut microbiota: new perspectives in the treatment of type 2 diabetes mellitus. *Foods*, *11*(16), 2438.

6. Jiang, Y., Chen, Y., Chen, Y., Gong, X., Chen, Z., & Zhang, X. (2025). Ketogenic Diet and Gut Microbiota: Exploring New Perspectives on Cognition and Mood. *Foods*, *14*(7), 1215.

7. Jikah, A. N., & Edo, G. I. (2023). Mechanisms of action by sulphur compounds in Allium sativum. A review. *Pharmacological Research-Modern Chinese Medicine*, *9*, 100323.

8. Khan, I., Bai, Y., Zha, L., Ullah, N., Ullah, H., Shah, S. R. H., ... & Zhang, C. (2021). Mechanism of the gut microbiota colonization resistance and enteric pathogen infection. *Frontiers in Cellular and Infection Microbiology*, *11*, 716299.

9. Kumar, S., Mukherjee, R., Gaur, P., Leal, É., Lyu, X., Ahmad, S., ... & Pandey, R. P. (2025). Unveiling roles of beneficial gut bacteria and optimal diets for health. *Frontiers in Microbiology*, *16*, 1527755.

0. Liu, B. N., Liu, X. T., Liang, Z. H., & Wang, J. H. (2021). Gut microbiota in obesity. *World journal of gastroenterology*, *27*(25), 3837.

1. Liu, J., Sun, J., Yu, J., Chen, H., Zhang, D., Zhang, T., ... & Yu, X. (2023). Gut

microbiome determines therapeutic effects of OCA on NAFLD by modulating bile acid metabolism. *npj Biofilms and Microbiomes*, *9*(1), 29.

62. Liu, S., Tao, Z., Qiao, M., & Shi, L. (2025). The Functions of Major Gut Microbiota in Obesity and Type 2 Diabetes. *Metabolites*, *15*(3), 167.

63. López-Taboada, I., González-Pardo, H., & Conejo, N. M. (2020). *Western diet: implications for brain function and behavior. Front Psychol 11: 564413*.

64. Ma, Z. F., & Lee, Y. Y. (2025). The Role of the Gut Microbiota in Health, Diet, and Disease with a Focus on Obesity. *Foods*, *14*(3), 492.

65. Mafe, A. N., Iruoghene Edo, G., Akpoghelie, P. O., Gaaz, T. S., Yousif, E., Zainulabdeen, K., ... & Umar, H. (2025). Probiotics and Food Bioactives: Unraveling Their Impact on Gut Microbiome, Inflammation, and Metabolic Health. *Probiotics and Antimicrobial Proteins*, 1-42.

66. Magne, F., Gotteland, M., Gauthier, L., Zazueta, A., Pesoa, S., Navarrete, P., & Balamurugan, R. (2020). The firmicutes/bacteroidetes ratio: a relevant marker of gut dysbiosis in obese patients? *Nutrients*, *12*(5), 1474.

67. Manzoor, R., Ahmed, W., Afify, N., Memon, M., Yasin, M., Memon, H., ... & Alhajri, N. (2022). Trust your gut: the association of gut microbiota and liver disease. *Microorganisms*, *10*(5), 1045.

68. Mao, Y., Kong, C., Zang, T., You, L., Wang, L. S., Shen, L., & Ge, J. B. (2024). Impact of the gut microbiome on atherosclerosis. *Mlife*, *3*(2), 167-175.

69. Markowiak, P., & Śliżewska, K. (2018). The role of probiotics, prebiotics and synbiotics in animal nutrition. *Gut pathogens*, *10*, 1-20.

70. Marx, W., Lane, M., Hockey, M., Aslam, H., Berk, M., Walder, K., ... & Jacka, F. N. (2021). Diet and depression: exploring the biological mechanisms of action. *Molecular psychiatry*, *26*(1), 134-150.

71. Masheghati, F., Asgharzadeh, M. R., Jafari, A., Masoudi, N., & Maleki-Kakelar, H. (2024). The role of gut microbiota and probiotics in preventing, treating, and boosting the immune system in colorectal cancer. *Life Sciences*, 122529.

72. Mathuria, A., Chaudhary, A., Sharma, H., & Mani, I. (2024). Multi-omics in Gut Microbiome. In *Multi-Omics Analysis of the Human Microbiome: From Technology to Clinical Applications* (pp. 181-213). Singapore: Springer Nature Singapore.

3. Megur, A., Daliri, E. B. M., Baltriukienė, D., & Burokas, A. (2022). Prebiotics as a tool for the prevention and treatment of obesity and diabetes: classification and ability to modulate the gut microbiota. *International journal of molecular sciences*, *23*(11), 6097.

4. microbiome: Exploring beneficial interactions and dietary impacts. *Food Chemistry: X*, *21*, 101118.

5. Mitchell, C. M., Mazzoni, C., Hogstrom, L., Bryant, A., Bergerat, A., Cher, A., ... & Yassour, M. (2020). Delivery mode affects stability of early infant gut microbiota. *Cell Reports Medicine*, *1*(9).

6. Mohammadzadeh, N., Razavi, S., Shahriari, M., & Ebrahimipour, G. (2025). Impact of bariatric surgery on gut microbiota in obese patients: A systematic review. *Indian Journal of Gastroenterology*, 1-21.

7. Murugesan, R., Kumar, J., Leela, K. V., Meenakshi, S., Srivijayan, A., Thiruselvam, S., ... & Chaithanya, V. (2025). The Role of Gut Microbiota and Bacterial Translocation in the Pathogenesis and Management of Type 2 Diabetes Mellitus: Mechanisms, Impacts, and Dietary Therapeutic Strategies. *Physiology & Behavior*, 114838.

8. Neu, A. T., Allen, E. E., & Roy, K. (2021). Defining and quantifying the core microbiome: challenges and prospects. *Proceedings of the National Academy of Sciences*, *118*(51), e2104429118.

9. Ni, Y., Tong, Q., Xu, M., Gu, J., & Ye, H. (2025). Gut microbiota-induced modulation of the central nervous system function in Parkinson's disease through the gut-brain Axis and short-chain fatty acids. *Molecular neurobiology*, *62*(2), 2480-2492.

0. Oriach, C. S., Robertson, R. C., Stanton, C., Cryan, J. F., & Dinan, T. G. (2016). Food

for thought: The role of nutrition in the microbiota-gut–brain axis. *Clinical Nutrition Experimental*, *6*, 25-38.

81. Oudat, Q., & Okour, A. (2025). The Role of Probiotics in Modulating Gut Microbiota and Metabolic Health for Weight Management: A Mini Review. *Acta Microbiologica Hellenica*, *70*(1), 5.

82. Pagliai, G., Russo, E., Niccolai, E., Dinu, M., Di Pilato, V., Magrini, A., ... & Amedei, A. (2020). Influence of a 3-month low-calorie Mediterranean diet compared to the vegetarian diet on human gut microbiota and SCFA: The CARDIVEG Study. *European Journal of Nutrition*, *59*, 2011-2024.

83. Pelaseyed, T., & Hansson, G. C. (2020). Membrane mucins of the intestine at a glance. *Journal of cell science*, *133*(5), jcs240929.

84. Peled, S., & Livney, Y. D. (2021). The role of dietary proteins and carbohydrates in gut microbiome composition and activity: A review. *Food Hydrocolloids*, *120*, 106911.

85. Perez, E., Lee, C. H., & Petrof, E. O. (2016). A practical method for preparation of fecal microbiota transplantation. *Clostridium difficile: Methods and Protocols*, 259-267.

86. Perler, B. K., Friedman, E. S., & Wu, G. D. (2023). The role of the gut microbiota in the relationship between diet and human health. *Annual review of physiology*, *85*(1), 449-468.

87. Perrone, P., & D’Angelo, S. (2025). Gut Microbiota Modulation Through Mediterranean Diet Foods: Implications for Human Health. *Nutrients*, *17*(6), 948.

88. Piché, M. E., Tchernof, A., & Després, J. P. (2020). Obesity phenotypes, diabetes, and cardiovascular diseases. *Circulation research*, *126*(11), 1477-1500.

89. Pires, L., González-Paramás, A. M., Heleno, S. A., & Calhelha, R. C. (2024). The role of gut microbiota in the etiopathogenesis of multiple chronic diseases. *Antibiotics*, *13*(5), 392.

90. Pluta, R., Ułamek-Kozioł, M., Januszewski, S., & Czuczwar, S. J. (2020). Gut microbiota and pro/prebiotics in Alzheimer’s disease. *Aging (albany NY)*, *12*(6), 5539.

91. Prochazkova, M., Budinska, E., Kuzma, M., Pelantova, H., Hradecky, J., Heczkova, M., ... & Cahova, M. (2022). Vegan diet is associated with favorable effects on the metabolic performance of intestinal microbiota: a cross-sectional multi-omics study. *Frontiers in nutrition*, *8*, 783302.

2. Rebersek, M. (2021). Gut microbiome and its role in colorectal cancer. *BMC cancer*, *21*(1), 1325.
3. Reyman, M., van Houten, M. A., van Baarle, D., Bosch, A. A., Man, W. H., Chu, M. L. J., ... & Bogaert, D. (2019). Impact of delivery mode-associated gut microbiota dynamics on health in the first year of life. *Nature communications*, *10*(1), 4997.
4. Riccio, P., & Rossano, R. (2020). The human gut microbiota is neither an organ nor a commensal. *FEBS letters*, *594*(20), 3262-3271.
5. Rinninella, E., Raoul, P., Cintoni, M., Franceschi, F., Miggiano, G. A. D., Gasbarrini, A., & Mele, M. C. (2019). What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms*, *7*(1), 14.
6. Rinninella, E., Tohumcu, E., Raoul, P., Fiorani, M., Cintoni, M., Mele, M. C., ... & Ianiro, G. (2023). The role of diet in shaping human gut microbiota. *Best Practice & Research Clinical Gastroenterology*, *62*, 101828.
7. Ross, F. C., Patangia, D., Grimaud, G., Lavelle, A., Dempsey, E. M., Ross, R. P., & Stanton, C. (2024). The interplay between diet and the gut microbiome: implications for health and disease. *Nature Reviews Microbiology*, 1-16.
8. Rowland, I., Gibson, G., Heinken, A., Scott, K., Swann, J., Thiele, I., & Tuohy, K. (2018). Gut microbiota functions: metabolism of nutrients and other food components. *European journal of nutrition*, *57*, 1-24.

99. Shen, X., Xie, A., Li, Z., Jiang, C., Wu, J., Li, M., & Yue, X. (2024). Research progress for probiotics regulating intestinal flora to improve functional dyspepsia: a review. *Foods*, *13*(1), 151.

100. Shim, J. A., Ryu, J. H., Jo, Y., & Hong, C. (2023). The role of gut microbiota in T cell immunity and immune mediated disorders. *International journal of biological sciences*, *19*(4), 1178.

101. Shrestha, B., Patel, D., Shah, H., Hanna, K. S., Kaur, H., Alazzeh, M. S., ... & Venugopal, S. (2022). The role of gut-microbiota in the pathophysiology and therapy of irritable bowel syndrome: a systematic review. *Cureus*, *14*(8).

102. Siddiqui, R., Boghossian, A., Alharbi, A. M., Alfahemi, H., & Khan, N. A. (2022). The pivotal role of the gut microbiome in colorectal cancer. *Biology*, *11*(11), 1642.

103. Song, Q., & Zhang, X. (2022). The role of gut–liver axis in gut microbiome dysbiosis associated NAFLD and NAFLD-HCC. *Biomedicines*, *10*(3), 524.

104. Song, Q., Wang, Y., Huang, L., Shen, M., Yu, Y., Yu, Q., ... & Xie, J. (2021). Review of the relationships among polysaccharides, gut microbiota, and human health. *Food Research International*, *140*, 109858.

105. Srivastava, A., Prabhakar, M. R., Mohanty, A., & Meena, S. S. (2022). Influence of gut microbiome on the human physiology. *Systems Microbiology and Biomanufacturing*, 1-15.

106. Stevenson, R. J., Francis, H. M., Attuquayefio, T., Gupta, D., Yeomans, M. R., Oaten, M. J., & Davidson, T. (2020). Hippocampal-dependent appetitive control is impaired by experimental exposure to a Western-style diet. *Royal Society open science*, *7*(2), 191338.

107. Su, Q., & Liu, Q. (2021). Factors affecting gut microbiome in daily diet. *Frontiers in nutrition*, *8*, 644138.

108. Suresh, S. B., Malireddi, A., Abera, M., Noor, K., Ansar, M., Boddeti, S., & Nath, T. S. (2024). Gut Microbiome and Its Role in Parkinson's Disease. *Cureus*, *16*(11).

109. Swanson, K. S., De Vos, W. M., Martens, E. C., Gilbert, J. A., Menon, R. S., Soto-Vaca, A., ... & Slavin, J. L. (2020). Effect of fructans, prebiotics and fibres on the human gut microbiome assessed by 16S rRNA-based approaches: a review. *Beneficial microbes*, *11*(2), 101-130.

110. Thursby, E., & Juge, N. (2017). Introduction to the human gut microbiota. *Biochemical journal*, *474*(11), 1823-1836.

111. Valdes, A. M., Walter, J., Segal, E., & Spector, T. D. (2018). Role of the gut microbiota in nutrition and health. *Bmj*, *361*.

112. Varesi, A., Pierella, E., Romeo, M., Piccini, G. B., Alfano, C., Bjørklund, G., ... & Pascale, A. (2022). The potential role of gut microbiota in Alzheimer’s disease: from diagnosis to treatment. *Nutrients*, *14*(3), 668.

113. Vich Vila, A., Collij, V., Sanna, S., Sinha, T., Imhann, F., Bourgonje, A. R., ... & Weersma, R. K. (2020). Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. *Nature communications*, *11*(1), 362.

114. Walrath, T., Dyamenahalli, K. U., Hulsebus, H. J., McCullough, R. L., Idrovo, J. P., Boe, D. M., ... & Kovacs, E. J. (2021). Age-related changes in intestinal immunity and the microbiome. *Journal of Leucocyte Biology*, *109*(6), 1045-1061.

115. Wang, H., Liu, Z., Zhan, K., Ma, Q., Xu, L., Li, Y., & Liu, Y. (2024). Vitamin K2 alleviates dextran sulfate sodium-induced colitis via inflammatory responses, gut barrier integrity, and the gut microbiota in mice. *International Journal of Biological Macromolecules*, *280*, 136091.

116. Wibowo, S., & Pramadhani, A. (2024). Vitamin B, role of gut microbiota

and gut health. *Vitamin B and Vitamin E-Pleiotropic and Nutritional Benefits*.

117. Xiao, L., Liu, Q., Luo, M., & Xiong, L. (2021). Gut microbiota-derived metabolites in irritable bowel syndrome. *Frontiers in Cellular and Infection Microbiology*, *11*, 729346.

118. Xiao, W., Zhang, Q., Yu, L., Tian, F., Chen, W., & Zhai, Q. (2022). Effects of vegetarian diet-associated nutrients on gut microbiota and intestinal physiology. *Food Science and Human Wellness*, *11*(2), 208-217.

119. Yamaguchi, M., & Yamamoto, K. (2023). Mucin glycans and their degradation by gut microbiota. *Glycoconjugate Journal*, *40*(4), 493-512.

120. Yoo, S., Jung, S. C., Kwak, K., & Kim, J. S. (2024). The role of prebiotics in modulating gut microbiota: implications for human health. *International Journal of Molecular Sciences*, *25*(9), 4834.

121. Yoo, S., Jung, S. C., Kwak, K., & Kim, J. S. (2024). The role of prebiotics in modulating gut microbiota: implications for human health. *International Journal of Molecular Sciences*, *25*(9), 4834.

122. Zhao, L. (2025). Relational Stability: A New Strategy for Defining the Human Core Microbiome. *Phenomics*, 1-4.

123. Zheng, J., Sun, Q., Zhang, J., & Ng, S. C. (2022). The role of gut microbiome in inflammatory bowel disease diagnosis and prognosis. *United European Gastroenterology Journal*, *10*(10), 1091-1102.

124. Zhuang, M., Zhang, X., & Cai, J. (2024). Microbiota–gut–brain axis: interplay between microbiota, barrier function and lymphatic system. *Gut microbes*, *16*(1), 2387800.