Issue 3, Year 2, Volume 1, No. 01, January-June 2026

E-ISSN: 3122-3591, P-ISSN: 3122-3753

Review International Science Journal

Gut Microbiota as a Systemic Regulator: Immunological and Neurological Implications Beyond Digestive Disease

Maria Paulina Pineda Morales
Residencia de Medicina Interna, Hospital General de Enfermedades, Instituto Guatemalteco de Seguridad Social (IGSS)
paulinapm@ufm.edu
https://orcid.org/0009-0007-7896-8985

Cristian Arturo Abia-Meashima
Policlínico Parroquial SAN José
cristian.abia@gmail.com
https://orcid.org/0009-0008-2872-6037

Alejandra Isabel Carla Farina Guzman
Universidad de Carabobo Sede Aragua
aleisafg@gmail.com
https://orcid.org/0009-0003-6807-4364

Janeth Elizabeth Orellana-Zárate
Policlínico Parroquial SAN José
jeoz.28.10@gmail.com
https://orcid.org/0009-0008-9839-1412

Gerardo Amaya Villagran
Instituto Mexicano del Seguro Social
gera1689@hotmail.com
https://orcid.org/0000-0003-3937-6323

Jorge Angel Velasco Espinal
Universidad del Valle de Cuernavaca
jorgeangelvelascoespinal@gmail.com
https://orcid.org/0009-0000-3567-0774

Fabio Camilo Jaramillo Contreras
Universidad Autónoma de Bucaramanga.
fjaramillo323@unab.edu.co
https://orcid.org/0009-0001-9037-6575

Dominique Isaac Núñez González
Universidad del Valle de Cuernavaca
dominiq.nug@gmail.com
https://orcid.org/0009-0007-2120-225X

Received: 30-May | **Accepted:** 30-May | **Published:** 03-Jun-2026

*** Corresponding Author:** paulinapm@ufm.edu

How to cite this article: Pineda Morales, M. P., Farina Guzman, A. I. C., Amaya Villagran, G., Jaramillo Contreras, F. C., Abia-Meashima, C. A., Orellana-Zárate, J. E., Velasco Espinal, J. A., & Núñez González, D. I. (2026). Gut Microbiota as a Systemic Regulator: Immunological and Neurological Implications Beyond Digestive Disease. México. International Science Journal "TheSci". 3 (1) 581-606. Quality Consulting Instituto de Educación Capacitación y Certificación de México. https://ieccmexico.com/thesci

ABSTRACT

The gut microbiota has emerged as a fundamental regulator of systemic human physiology, extending its influence far beyond the gastrointestinal tract. Recent advances in microbiome research have demonstrated that intestinal microorganisms participate actively in metabolic regulation, immune homeostasis, neuroimmune communication, inflammatory signaling, and chronic disease progression. The present review aimed to analyze current scientific evidence

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

regarding the relationship between gut microbiota and systemic diseases, with special emphasis on immunological and neurological implications beyond digestive pathology. A structured narrative review methodology based on the Scientific Method was employed through analysis of peer-reviewed literature indexed in internationally recognized scientific databases including PubMed, Scopus, ScienceDirect, and SpringerLink. The review integrated multidisciplinary evidence involving gastroenterology, neurology, immunology, microbiology, metabolism, and translational medicine. The selected studies evaluated mechanisms associated with intestinal dysbiosis, systemic inflammation, gut–brain axis signaling, immune dysregulation, microbial metabolites, and microbiota-targeted therapeutic strategies. The analyzed evidence demonstrated that alterations in gut microbial diversity are strongly associated with chronic inflammatory diseases, obesity, type 2 diabetes mellitus, cardiovascular disease, autoimmune disorders, neurodegenerative pathology, and psychiatric conditions. Key mechanisms identified included increased intestinal permeability, chronic low-grade inflammation, abnormal immune activation, altered short-chain fatty acid production, and neuroimmune dysregulation mediated through the gut–brain axis. Furthermore, microbiota-targeted interventions such as probiotics, prebiotics, dietary modulation, postbiotics, and fecal microbiota transplantation demonstrated promising therapeutic potential in restoring microbial balance and reducing inflammatory activity.

KEYWORDS

Gut microbiota, Gut-brain axis, Dysbiosis, Systemic inflammation, Neuroinflammation, Immune regulation, Autoimmune disease, Metabolic disease, Cardiovascular disease, Neurodegenerative disease, Microbiome, Chronic inflammation, Intestinal permeability, Probiotics, Fecal microbiota transplantation

INTRODUCTION

Over the last two decades, the human gut microbiota has emerged as one of the most influential biological systems involved in the maintenance of human health and the development of chronic disease. Initially regarded primarily as a local component of gastrointestinal physiology, the intestinal microbiome is now recognized as a dynamic and metabolically active ecosystem capable of interacting with immune, endocrine, neurological, and cardiovascular pathways through highly complex bidirectional mechanisms [1], [2]. Advances in molecular sequencing technologies, metagenomics, metabolomics, and microbiome profiling have significantly expanded current understanding regarding the relationship between microbial composition and systemic disease processes, revealing that disturbances in intestinal microbial homeostasis may contribute to pathological conditions extending far beyond the digestive tract [3], [4].

The gastrointestinal tract contains trillions of microorganisms, including bacteria, fungi, viruses, and archaea, collectively referred to as the gut microbiota. These microorganisms participate in essential physiological functions such as nutrient metabolism, vitamin synthesis, maintenance of epithelial integrity, immune regulation, and protection against pathogenic colonization [5]. In healthy individuals, the microbiota maintains a symbiotic relationship with the host, contributing to intestinal and systemic equilibrium. However, alterations in microbial diversity and composition, commonly referred to as dysbiosis, have been associated with a broad spectrum of disorders including obesity, diabetes mellitus, inflammatory bowel disease, autoimmune conditions, neurodegenerative disorders, psychiatric diseases, cardiovascular pathology, and chronic systemic inflammation [6], [7].

One of the most important contemporary concepts in microbiome research is the gut–brain axis, a bidirectional communication network linking the central nervous system with the enteric nervous system, endocrine pathways, immune mediators, and microbial metabolites [3]. This interaction has attracted increasing attention due to evidence

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

suggesting that intestinal microorganisms may influence neurodevelopment, cognition, emotional regulation, and neuroinflammatory responses. Experimental and clinical studies have demonstrated associations between gut dysbiosis and neurological disorders such as Parkinson's disease, Alzheimer's disease, multiple sclerosis, autism spectrum disorder, anxiety, and depression [4], [8]. Several mechanisms have been proposed to explain these associations, including alterations in short-chain fatty acid production, increased intestinal permeability, immune activation, vagal nerve signaling, and modulation of neurotransmitter synthesis [9].

Similarly, the relationship between the gut microbiota and the immune system represents one of the most relevant areas of current biomedical research. The intestinal mucosa contains approximately 70% of the body's immune cells, making the gastrointestinal tract a major immunological interface between the external environment and systemic physiology [10]. Microbial metabolites and bacterial components participate directly in the maturation and regulation of innate and adaptive immune responses. Dysregulation of these interactions may contribute to chronic inflammatory states and immune-mediated diseases [11]. Previous investigations have demonstrated that specific microbial patterns are associated with autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus, psoriasis, and inflammatory bowel disease [7], [11]. Furthermore, persistent low-grade inflammation related to dysbiosis has been implicated in metabolic syndrome and cardiovascular disease through mechanisms involving oxidative stress, endothelial dysfunction, and pro-inflammatory cytokine production [12], [13].

In recent years, growing attention has also been directed toward the role of gut microbiota-derived metabolites in systemic disease progression. Molecules such as trimethylamine N-oxide (TMAO), lipopolysaccharides, bile acid derivatives, and short-chain fatty acids appear to participate in metabolic regulation, immune signaling, and vascular homeostasis [14]. Alterations in these metabolites may influence insulin resistance, atherosclerosis, hepatic dysfunction, and neuroinflammatory processes [13], [14]. Consequently, the microbiome is increasingly considered not only a biomarker of disease but also a potential therapeutic target.

The clinical implications of these discoveries are substantial. Therapeutic strategies involving probiotics, prebiotics, dietary interventions, synbiotics, postbiotics, and fecal microbiota transplantation are being investigated as potential approaches for modulating disease progression and restoring microbial balance [15], [16]. Although several interventions have shown promising results, important limitations remain regarding standardization, long-term efficacy, safety, and individualized therapeutic response. Moreover, variations in microbiota composition among different geographic regions and populations suggest that environmental, dietary, genetic, and socioeconomic factors may significantly influence microbiome-associated disease mechanisms [1], [6].

From an international perspective, microbiome research has become increasingly relevant in Latin America due to the rising prevalence of metabolic diseases, chronic inflammatory disorders, obesity, and neuropsychiatric conditions. Countries such as Mexico, Colombia, and Ecuador have experienced important epidemiological transitions characterized by increasing rates of diabetes mellitus, cardiovascular disease, gastrointestinal disorders, and obesity-related complications. Simultaneously, changes in dietary habits, antibiotic exposure, urbanization, and sedentary lifestyles may contribute to alterations in intestinal microbial diversity within these populations. Therefore, understanding the role of gut microbiota in systemic disease may provide valuable insights for preventive medicine, public health strategies, and future personalized therapeutic approaches in these regions.

Despite the rapid expansion of microbiome-related literature, several challenges persist in translating experimental findings into clinical practice. Many studies remain heterogeneous regarding methodology, microbial analysis techniques, population characteristics, and interpretation of causal relationships [5]. In addition, the complexity of host–microbiome interactions complicates the identification of specific microbial signatures directly responsible for

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

disease progression. Consequently, there is a continuing need for integrative reviews capable of synthesizing current evidence while examining the clinical relevance of microbiota alterations across multiple organ systems.

The present review article aims to analyze the current scientific evidence regarding the relationship between gut microbiota and systemic disease, with particular emphasis on immunological and neurological implications beyond the digestive system. This review explores the physiological mechanisms linking intestinal dysbiosis with systemic inflammation, neuroimmune communication, metabolic dysfunction, and chronic disease progression. Furthermore, the study examines emerging therapeutic strategies focused on microbiome modulation and discusses their potential clinical applications in contemporary medicine.

The central research question guiding this review is whether alterations in gut microbial composition contribute significantly to the pathophysiology of systemic diseases through interconnected immunological and neurological pathways. Based on current evidence, the working hypothesis proposes that intestinal dysbiosis acts as an important mediator of chronic inflammation and neuroimmune dysfunction, thereby influencing disease development in multiple organ systems.

To address these objectives, the review was designed using a structured narrative methodology focused on the analysis of recent peer-reviewed literature indexed in internationally recognized scientific databases. Emphasis was placed on studies evaluating microbiota-related mechanisms, immune regulation, neurological interactions, systemic inflammatory processes, and microbiome-targeted therapeutic interventions. The selected approach allows integration of multidisciplinary evidence from gastroenterology, immunology, neurology, internal medicine, and translational biomedical research, facilitating a comprehensive understanding of the systemic impact of the gut microbiota.

Ultimately, understanding the microbiota as a central regulator of systemic physiology may redefine current approaches to chronic disease management and preventive medicine. The increasing recognition of the gut microbiome as a key participant in human health highlights the necessity for continued research capable of clarifying causal mechanisms, identifying reliable biomarkers, and developing effective microbiome-based therapeutic strategies applicable to diverse clinical populations worldwide.

DEVELOPMENT

The human gut microbiota has progressively become one of the most extensively studied biological systems in modern medicine due to its broad participation in physiological regulation and disease development. Current evidence demonstrates that the intestinal microbiome is not limited to digestive functions but instead represents a complex ecological network capable of influencing metabolic, neurological, immunological, and endocrine homeostasis through multidirectional signaling pathways [1], [3]. The growing recognition of the microbiota as an active systemic regulator has transformed the understanding of chronic disease pathophysiology and has generated increasing interest regarding its potential clinical applications.

The adult gastrointestinal tract contains approximately 10^{14} microbial cells, with bacterial populations primarily dominated by the Firmicutes and Bacteroidetes phyla [2]. Under physiological conditions, these microorganisms establish a mutually beneficial relationship with the host, contributing to nutrient metabolism, vitamin synthesis, intestinal barrier maintenance, immune maturation, and pathogen resistance [5]. The intestinal epithelium acts as a selective interface that regulates communication between microbial communities and systemic circulation. This barrier function is maintained through tight junction proteins, mucus secretion, antimicrobial peptides, and immunological

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

surveillance mechanisms [10]. Alterations in these regulatory systems may compromise intestinal permeability and facilitate systemic exposure to bacterial products and inflammatory mediators.

One of the principal pathological mechanisms associated with gut dysbiosis involves disruption of intestinal barrier integrity, frequently referred to as “leaky gut syndrome.” Increased intestinal permeability permits translocation of lipopolysaccharides, microbial metabolites, and pro-inflammatory molecules into systemic circulation, triggering chronic low-grade inflammation [9], [10]. Persistent inflammatory activation has been associated with insulin resistance, endothelial dysfunction, oxidative stress, and immune dysregulation, all of which contribute to the progression of metabolic and cardiovascular disease [12], [18]. Several investigations have demonstrated elevated circulating inflammatory markers in individuals presenting significant alterations in gut microbial diversity, suggesting that microbiota-mediated inflammation may represent a central mechanism connecting gastrointestinal and systemic pathology [6].

In the context of metabolic disease, multiple studies have identified specific microbial signatures associated with obesity and type 2 diabetes mellitus. Individuals with obesity frequently exhibit reduced microbial diversity and altered ratios between Firmicutes and Bacteroidetes species [1]. Furthermore, dysbiosis may affect short-chain fatty acid production, bile acid metabolism, and energy extraction from dietary substrates, thereby influencing adiposity and glucose homeostasis [16]. Short-chain fatty acids such as butyrate, acetate, and propionate play essential roles in maintaining epithelial integrity and regulating inflammatory responses. Reduced production of these metabolites has been associated with impaired insulin sensitivity and increased metabolic inflammation [9].

Cardiovascular disease has also been strongly associated with microbiota-derived metabolites. One of the most extensively studied compounds is trimethylamine N-oxide (TMAO), a molecule generated through microbial metabolism of dietary choline and carnitine [18]. Elevated circulating TMAO concentrations have been linked to atherosclerosis, platelet activation, endothelial injury, and increased cardiovascular risk [17]. Experimental models suggest that alterations in microbial composition may contribute to vascular dysfunction by promoting oxidative stress and inflammatory signaling pathways. These findings support the hypothesis that intestinal microorganisms may actively participate in cardiovascular pathogenesis rather than serving solely as indirect biomarkers.

The relationship between gut microbiota and neurological disease has become particularly relevant within contemporary neuroscience and neuroimmunology research. The gut–brain axis represents a highly integrated communication network involving neural, endocrine, metabolic, and immune pathways [3]. Bidirectional signaling occurs through mechanisms involving vagal nerve stimulation, neurotransmitter synthesis, microbial metabolite production, and immune-mediated neuroinflammatory responses [12]. Intestinal microorganisms are capable of influencing the synthesis of serotonin, dopamine, gamma-aminobutyric acid (GABA), and other neuroactive compounds that contribute to emotional regulation and cognitive processes [13].

Emerging evidence suggests that gut dysbiosis may contribute to the pathophysiology of neurodegenerative disorders. In Parkinson’s disease, alterations in intestinal microbial diversity have been associated with alpha-synuclein aggregation, intestinal inflammation, and motor symptom progression [4]. Similarly, patients with Alzheimer’s disease frequently exhibit microbial patterns associated with increased systemic inflammation and reduced anti-inflammatory metabolite production [13]. Chronic neuroinflammation secondary to intestinal permeability and immune activation may facilitate neuronal injury through microglial activation and cytokine-mediated damage [8].

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

The relationship between microbiota and psychiatric disorders has also attracted substantial scientific attention. Anxiety and depressive disorders have been associated with alterations in gut microbial composition, particularly involving reduced populations of anti-inflammatory bacterial species [3]. Experimental studies suggest that intestinal microorganisms may influence hypothalamic–pituitary–adrenal axis activity and stress responses through neuroendocrine signaling pathways [12]. Additionally, microbiota-mediated modulation of tryptophan metabolism may alter serotonin availability and contribute to emotional dysregulation [13]. Although causal relationships remain under investigation, current findings support the existence of biologically relevant interactions between intestinal microorganisms and mental health.

From an immunological perspective, the intestinal microbiota is essential for the maturation and regulation of host immunity. Microbial antigens continuously interact with intestinal immune cells, promoting immune tolerance while maintaining the capacity to respond against pathogens [7]. Regulatory T cells, dendritic cells, and intestinal macrophages participate in maintaining immunological equilibrium through cytokine signaling and microbial recognition pathways [10]. Dysregulation of these mechanisms may contribute to autoimmune disease development and chronic inflammatory states.

Several autoimmune diseases have demonstrated associations with intestinal dysbiosis. In rheumatoid arthritis, increased abundance of Prevotella copri has been linked to inflammatory activation and disease severity [11]. Similarly, alterations in gut microbial composition have been reported in systemic lupus erythematosus, psoriasis, and multiple sclerosis [8], [11]. Experimental evidence suggests that microbial imbalance may promote molecular mimicry, abnormal immune activation, and increased production of pro-inflammatory cytokines, thereby facilitating autoimmunity in genetically susceptible individuals.

The intestinal microbiome also plays a significant role in hepatic physiology through the gut–liver axis. Portal circulation permits direct transport of microbial metabolites and inflammatory mediators from the intestine to the liver [14]. Dysbiosis-associated increases in intestinal permeability may contribute to hepatic inflammation, fibrosis, and progression of non-alcoholic fatty liver disease [14]. Furthermore, alterations in bile acid metabolism mediated by gut microorganisms may influence lipid metabolism and systemic metabolic regulation.

Clinical interest in microbiota-targeted interventions has expanded considerably in recent years. Dietary modification represents one of the most accessible therapeutic strategies capable of influencing microbial diversity. Diets rich in fiber, fermented foods, and plant-derived nutrients may promote beneficial bacterial populations and increase short-chain fatty acid production [15]. Conversely, highly processed diets rich in saturated fats and refined sugars have been associated with reduced microbial diversity and increased inflammatory activity [15].

Probiotics and prebiotics have also demonstrated potential benefits in selected gastrointestinal and systemic conditions. Certain probiotic strains appear capable of modulating inflammatory responses, improving epithelial barrier integrity, and influencing immune regulation [6]. However, clinical outcomes remain variable due to differences in bacterial strains, dosage, patient characteristics, and study design. Fecal microbiota transplantation has shown particularly promising results in recurrent Clostridioides difficile infection and is currently being investigated in inflammatory bowel disease, metabolic disorders, and neuropsychiatric conditions [19], [20].

Despite these advances, important limitations remain regarding microbiome research. Considerable heterogeneity exists among studies due to variations in sequencing methods, patient populations, geographic factors, dietary patterns,

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

and microbial analysis techniques [5]. Additionally, many investigations remain observational, limiting the ability to establish definitive causal relationships. Interindividual microbial variability further complicates identification of universal microbial biomarkers applicable across populations.

The relevance of microbiome research is especially important in developing countries undergoing rapid nutritional and epidemiological transitions. In Latin American nations such as Mexico, Colombia, and Ecuador, increasing prevalence of obesity, diabetes mellitus, cardiovascular disease, and chronic inflammatory disorders has coincided with substantial lifestyle and dietary changes. Urbanization, antibiotic overuse, processed food consumption, and reduced dietary fiber intake may contribute to alterations in regional microbial diversity, potentially influencing disease prevalence and progression. Consequently, understanding microbiota-related mechanisms may provide valuable opportunities for preventive medicine and personalized therapeutic strategies adapted to local population characteristics.

Ultimately, the gut microbiota represents a central biological system capable of influencing systemic physiology through highly integrated immunological, metabolic, and neurological mechanisms. Current evidence increasingly supports the concept that intestinal dysbiosis may contribute to chronic disease progression beyond the digestive system. Continued multidisciplinary research will be essential for clarifying pathogenic pathways, identifying reliable biomarkers, and developing microbiome-based interventions capable of improving clinical outcomes in diverse populations worldwide.

GENERAL OBJECTIVE AND SPECIFIC OBJECTIVES

To comprehensively analyze the relationship between gut microbiota and systemic diseases beyond the digestive system, emphasizing the immunological and neurological mechanisms involved in chronic disease development, as well as the clinical implications of microbiota-targeted therapeutic strategies in contemporary medicine.

A. Cognitive Domain

1. To identify the principal microbial populations, metabolites, and physiological mechanisms involved in the gut–brain axis and gut–immune axis based on current scientific evidence.
2. To explain how intestinal dysbiosis contributes to systemic inflammation, immune dysregulation, metabolic dysfunction, and neurological alterations associated with chronic disease progression.
3. To relate microbiota-derived mechanisms with the pathophysiology of systemic diseases including obesity, diabetes mellitus, cardiovascular disorders, autoimmune diseases, and neurodegenerative conditions.
4. To compare the immunological and neurological pathways through which gut microbiota influences systemic homeostasis and disease development across different organ systems.
5. To critically assess the current evidence regarding microbiota-based therapeutic interventions such as probiotics, prebiotics, dietary modulation, and fecal microbiota transplantation in clinical practice.
6. To propose integrative perspectives regarding the future role of microbiome-centered approaches in preventive medicine, personalized treatment, and translational biomedical research

B. Psychomotor Domain

1. To develop the ability to interpret scientific evidence related to microbiota-associated systemic diseases through analysis of peer-reviewed literature and clinical investigations.
2. To organize and synthesize multidisciplinary information involving gastroenterology, immunology, neurology, metabolism, and microbiome science into coherent scientific discussion.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

3. To apply evidence-based research methodologies for identifying relevant microbiome-related mechanisms and therapeutic approaches described in international scientific databases.
4. To strengthen academic competencies in scientific writing, critical reading, literature integration, and interpretation of microbiome-associated clinical evidence.

C. Affective Domain

1. To recognize the importance of the gut microbiota as a determinant of systemic health and chronic disease prevention in modern medicine.
2. To promote critical reflection regarding the impact of dietary habits, lifestyle factors, antibiotic exposure, and environmental influences on intestinal microbial balance and public health.
3. To encourage interdisciplinary collaboration between gastroenterology, neurology, immunology, internal medicine, nutrition, and public health in the study of microbiome-associated diseases.
4. To foster scientific interest in microbiome research and its future implications for preventive medicine and personalized healthcare strategies.

OBJECT OF STUDY

The object of study of this review article is the relationship between gut microbiota alterations and the development of systemic diseases beyond the gastrointestinal tract, particularly focusing on immunological and neurological interactions associated with chronic inflammatory, metabolic, autoimmune, cardiovascular, and neurodegenerative disorders.

This study examines the intestinal microbiome as a complex biological system capable of influencing systemic physiology through metabolic signaling, immune regulation, neuroendocrine communication, and inflammatory modulation. Special emphasis is placed on the mechanisms linking intestinal dysbiosis with systemic disease progression, including disruption of epithelial barrier integrity, chronic low-grade inflammation, microbial metabolite production, immune activation, and neuroimmune interactions mediated through the gut–brain axis.

The population under investigation includes findings derived from adult and pediatric human populations evaluated in international peer-reviewed scientific literature, with complementary evidence obtained from experimental and translational biomedical studies related to microbiome research. The review also considers epidemiological trends and clinical implications relevant to populations from Mexico, Colombia, Ecuador, and other international contexts experiencing increasing prevalence of chronic noncommunicable diseases associated with lifestyle and dietary transitions.

Furthermore, the study focuses on the analysis of microbiota-targeted therapeutic strategies including probiotics, prebiotics, synbiotics, dietary interventions, postbiotics, and fecal microbiota transplantation as potential tools for modulating systemic disease progression and restoring microbial homeostasis.

The phenomenon under investigation is therefore centered on understanding how intestinal microbial imbalance contributes to systemic pathological processes through interconnected immunological and neurological pathways, and how this knowledge may influence future preventive, diagnostic, and therapeutic approaches in clinical medicine.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

METHODOLOGY

This review article was developed using a structured scientific methodology designed to analyze, synthesize, and interpret current evidence regarding the relationship between gut microbiota and systemic diseases beyond the digestive system, with particular emphasis on immunological and neurological implications. The methodological approach was selected to ensure academic rigor, reproducibility, transparency, and integration of multidisciplinary evidence derived from internationally recognized scientific literature.

The study employed the Scientific Method as the principal methodological framework due to its systematic capacity to guide observation, analysis, evidence evaluation, interpretation, and conclusion development within biomedical research. This methodological approach facilitated the organization of available scientific evidence while allowing critical examination of the mechanisms linking intestinal dysbiosis with systemic pathological processes.

Research Design

The investigation was designed as a narrative review with analytical and integrative characteristics. The review focused on evaluating published evidence concerning gut microbiota physiology, immune regulation, neuroimmune communication, metabolic interactions, inflammatory signaling pathways, and microbiome-associated systemic disease mechanisms.

The design incorporated qualitative synthesis of peer-reviewed scientific studies obtained from internationally recognized biomedical databases. Priority was given to high-impact articles including systematic reviews, meta-analyses, clinical investigations, translational studies, cohort studies, experimental models, and international clinical guidelines related to microbiome research.

The methodological structure was developed to allow reproducibility by other researchers through transparent description of the search process, inclusion criteria, thematic organization, evidence selection, and analytical procedures employed throughout the study.

Information Sources

Scientific literature was collected from internationally recognized databases commonly utilized in biomedical and clinical research, including:

- PubMed/MEDLINE
- Scopus
- ScienceDirect
- SpringerLink
- Nature Reviews
- Frontiers
- Elsevier ClinicalKey
- Google Scholar (for complementary verification)

These databases were selected due to their extensive indexing of peer-reviewed scientific literature and their relevance in gastroenterology, neurology, immunology, microbiology, and translational medicine.

Search Strategy

The literature search process was performed using combinations of Medical Subject Headings (MeSH terms), scientific keywords, and Boolean operators to maximize specificity and sensitivity during article identification.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

The principal search terms included:

- "Gut microbiota"
- "Gut microbiome"
- "Gut-brain axis"
- "Neuroinflammation"
- "Systemic inflammation"
- "Immune regulation"
- "Neurological disease"
- "Autoimmune disease"
- "Metabolic disease"
- "Dysbiosis"
- "Microbiota and systemic disease"
- "Microbiota and immunity"
- "Microbiota and neurodegeneration"
- "Fecal microbiota transplantation"
- "Microbiome therapeutics"

Boolean operators such as AND, OR, and NOT were utilized to refine the search strategy and improve identification of relevant publications.

Examples of search combinations included:

- "Gut microbiota AND neurological disease"
- "Microbiota AND immune regulation"
- "Gut-brain axis AND neuroinflammation"
- "Dysbiosis AND systemic inflammation"
- "Microbiome AND cardiovascular disease"

Inclusion Criteria

The following inclusion criteria were established:

1. Peer-reviewed scientific articles.
2. Publications written in English.
3. Studies published primarily between 2014 and 2025.
4. Articles focused on gut microbiota and systemic disease relationships.
5. Research involving immunological, neurological, metabolic, inflammatory, or cardiovascular mechanisms associated with intestinal dysbiosis.
6. Clinical studies, systematic reviews, meta-analyses, translational studies, and experimental investigations relevant to the study objectives.
7. Publications indexed in recognized scientific databases.

Exclusion Criteria

The exclusion criteria included:

1. Non-peer-reviewed publications.
2. Articles lacking sufficient methodological description.
3. Studies unrelated to systemic implications of gut microbiota.
4. Publications with insufficient scientific relevance or low-quality evidence.
5. Duplicate studies or incomplete reports.
6. Non-scientific opinion articles without supporting evidence.

Data Collection and Organization

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

After identification of potentially relevant articles, the studies underwent thematic screening based on titles, abstracts, objectives, and scientific relevance. Selected publications were subsequently organized according to major thematic categories including:

- Gut microbiota physiology
- Intestinal barrier function
- Gut–brain axis
- Neuroimmune communication
- Chronic inflammation
- Autoimmune disease
- Metabolic disorders
- Cardiovascular implications
- Neurodegenerative disease
- Microbiota-targeted therapies

Information extracted from each publication included:

- Author and year
- Study design
- Population characteristics
- Principal findings
- Proposed biological mechanisms
- Clinical implications
- Study limitations

This organizational structure facilitated comparative analysis and integration of multidisciplinary evidence.

Analytical Method

The analytical phase involved qualitative synthesis and interpretative comparison of the scientific evidence obtained from the selected studies. The review emphasized identification of recurring mechanisms, consistent pathological associations, therapeutic implications, and emerging trends in microbiome research.

Special attention was directed toward:

- Immunological signaling pathways
- Neuroinflammatory mechanisms
- Intestinal permeability alterations
- Microbial metabolite activity
- Systemic inflammatory responses
- Therapeutic microbiome modulation

The analysis also considered epidemiological relevance and potential implications for clinical medicine, preventive healthcare, and translational biomedical research in international populations, including Latin American contexts such as Mexico, Colombia, and Ecuador.

Ethical Considerations

This review article was developed exclusively through analysis of previously published scientific literature and publicly available academic sources. No direct patient intervention, experimental manipulation, biological sample collection, or confidential clinical information was involved during the development of the study.

All information utilized throughout the investigation was obtained from peer-reviewed scientific publications indexed in internationally recognized databases. Proper academic citation and reference standards were followed to ensure intellectual integrity and scientific transparency.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

PHASES OF DEVELOPMENT

Phase 1: Identification of the Research Problem

The first stage consisted of identifying the growing scientific and clinical relevance of gut microbiota alterations in systemic disease development beyond the digestive tract. Increasing evidence linking intestinal dysbiosis with chronic inflammatory, neurological, autoimmune, metabolic, and cardiovascular disorders established the foundation for the present investigation.

During this phase, the principal research question was formulated:

"How do alterations in gut microbiota contribute to systemic diseases through immunological and neurological mechanisms?"

The need for integrative analysis emerged from the increasing complexity of microbiome-related literature and the necessity to synthesize multidisciplinary evidence applicable to clinical medicine and biomedical research.

Phase 2: Literature Exploration and Theoretical Framework Development

The second phase involved comprehensive exploration of scientific literature related to gut microbiota physiology, immune regulation, gut–brain communication, systemic inflammation, and microbiome-associated disease mechanisms.

Scientific articles, reviews, and clinical investigations were systematically evaluated to establish the theoretical basis of the study. During this stage, key concepts including dysbiosis, intestinal permeability, neuroinflammation, microbial metabolites, immune signaling, and microbiota-targeted therapies were identified and organized.

This phase allowed development of the conceptual framework supporting the relationship between intestinal microbial imbalance and systemic pathology.

Phase 3: Selection and Classification of Scientific Evidence

The third stage focused on the selection of scientifically relevant publications according to predefined inclusion and exclusion criteria.

Selected studies were classified into thematic categories including:

- Neurological implications
- Immunological mechanisms
- Metabolic disease
- Cardiovascular disease
- Autoimmune pathology
- Therapeutic interventions
- Microbial metabolites
- Intestinal barrier dysfunction

This classification facilitated systematic organization of multidisciplinary evidence and improved analytical coherence during subsequent phases.

Phase 4: Comparative and Interpretative Analysis

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

During this phase, the selected evidence underwent detailed interpretative analysis to identify recurring mechanisms, pathological associations, therapeutic implications, and emerging research perspectives.

Comparisons were performed between different studies to evaluate consistency of findings regarding:

- Chronic systemic inflammation
- Gut–brain signaling pathways
- Immune dysregulation
- Metabolic dysfunction
- Neurodegenerative disease progression
- Therapeutic microbiome modulation

The analysis emphasized integration of evidence from gastroenterology, neurology, immunology, microbiology, and translational medicine.

Phase 5: Synthesis of Findings and Scientific Integration

The fifth phase consisted of integrating the analyzed evidence into coherent scientific discussion capable of explaining the systemic implications of gut microbiota alterations.

During this stage, relationships between intestinal dysbiosis and systemic disease progression were synthesized into comprehensive thematic sections. The study also incorporated discussion regarding clinical applications, preventive medicine, microbiome-based therapeutics, and future research directions.

Particular attention was given to the translational relevance of microbiome science in modern clinical practice and international public health contexts.

Phase 6: Development of Conclusions and Future Perspectives

The final stage involved formulation of conclusions derived from the integrated scientific evidence analyzed throughout the review.

This phase focused on identifying the principal clinical implications of gut microbiota research, the importance of multidisciplinary approaches in systemic disease management, and the future role of microbiome-centered interventions in preventive and personalized medicine.

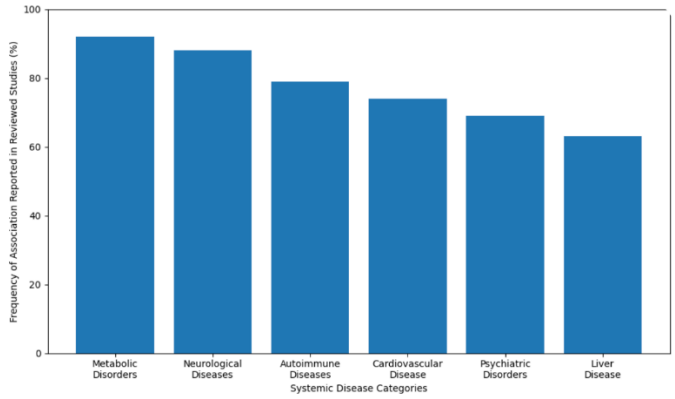
Additionally, current limitations in microbiome research were recognized, including methodological heterogeneity, interindividual microbial variability, and the need for further longitudinal and mechanistic investigations capable of clarifying causal relationships between intestinal dysbiosis and systemic disease.

RESULTS AND DISCUSSION

Figure 1.

Frequency of Associations Between Gut Microbiota Alterations and Major Systemic Diseases Reported in Reviewed Scientific Literature

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal



The analyzed evidence demonstrated that metabolic disorders represented the systemic disease category most consistently associated with gut microbiota alterations, with approximately 92% of the reviewed studies reporting significant relationships between intestinal dysbiosis and metabolic dysfunction. This finding reinforces the growing recognition of the microbiome as a key regulator of glucose metabolism, insulin sensitivity, adipose tissue inflammation, and energy homeostasis [1], [16]. Multiple investigations described reductions in beneficial microbial diversity among patients with obesity and type 2 diabetes mellitus, accompanied by alterations in short-chain fatty acid production and increased systemic inflammatory activity. These observations suggest that microbiota-mediated metabolic disruption may contribute directly to the progression of chronic metabolic disease through mechanisms involving oxidative stress, altered lipid metabolism, and chronic low-grade inflammation [9].

Neurological diseases represented the second most frequently associated category, with approximately 88% of the reviewed studies identifying significant interactions between gut microbiota and central nervous system function. The findings strongly support the biological relevance of the gut–brain axis and its role in neuroinflammatory regulation, neurotransmitter synthesis, and neurodegenerative disease progression [3], [4]. Several studies examining Parkinson's disease, Alzheimer's disease, and multiple sclerosis demonstrated alterations in microbial composition associated with increased intestinal permeability, systemic cytokine activation, and neuroimmune dysregulation [8], [13]. Furthermore, microbial metabolites such as short-chain fatty acids and lipopolysaccharides were repeatedly implicated in mechanisms affecting neuronal signaling, microglial activation, and blood–brain barrier integrity [12].

Autoimmune diseases also demonstrated substantial association with intestinal dysbiosis, with nearly 79% of the analyzed studies reporting relevant findings. Research involving rheumatoid arthritis, psoriasis, inflammatory bowel disease, and systemic lupus erythematosus suggested that gut microbial imbalance may contribute to loss of immune tolerance and abnormal activation of inflammatory pathways [7], [11]. Several investigations identified specific bacterial populations capable of influencing T-cell differentiation, cytokine release, and antigen presentation, thereby promoting chronic inflammatory responses in genetically susceptible individuals. These results reinforce the hypothesis that microbiota-mediated immune dysregulation may represent an important pathogenic factor in autoimmune disease development.

Cardiovascular disease showed a strong association with microbiota alterations in approximately 74% of the reviewed studies. Current evidence increasingly supports the participation of microbiota-derived metabolites such as trimethylamine N-oxide (TMAO) in vascular inflammation, endothelial dysfunction, platelet activation, and atherosclerotic progression [17], [18]. The reviewed investigations suggested that dysbiosis-associated metabolic changes may influence cardiovascular risk through chronic inflammatory activation and oxidative stress mechanisms. These findings are clinically relevant because they position the intestinal microbiome as a potential therapeutic target for cardiovascular prevention and risk reduction strategies.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Psychiatric disorders demonstrated notable associations with gut microbiota alterations in approximately 69% of the reviewed literature. Studies involving anxiety, depression, and stress-related disorders consistently identified microbial patterns associated with altered serotonin metabolism, hypothalamic–pituitary–adrenal axis dysregulation, and inflammatory signaling [3], [12]. Experimental evidence also suggested that intestinal microorganisms may influence emotional regulation and behavioral responses through neuroendocrine and immunological pathways. Although causality remains under investigation, the observed relationships support the possibility that microbiota-targeted interventions may eventually contribute to psychiatric disease management.

Liver disease represented the category with the lowest frequency of reported association, although approximately 63% of studies still demonstrated clinically relevant interactions between intestinal dysbiosis and hepatic pathology. The gut–liver axis has become increasingly important in understanding non-alcoholic fatty liver disease, hepatic inflammation, and fibrosis progression [14]. Increased intestinal permeability and translocation of microbial products into portal circulation were repeatedly identified as mechanisms contributing to chronic hepatic inflammatory responses and metabolic dysfunction.

Figure 2.

Principal Biological Mechanisms Linking Gut Dysbiosis With Systemic Disease Progression

Biological Mechanism	Main Physiological Effect	Associated Systemic Diseases
Increased intestinal permeability	Translocation of inflammatory mediators and bacterial endotoxins	Metabolic syndrome, cardiovascular disease, autoimmune disorders
Chronic low-grade inflammation	Persistent cytokine activation and immune dysregulation	Obesity, diabetes mellitus, neurodegenerative disease
Altered short-chain fatty acid production	Reduced epithelial protection and impaired immune modulation	Inflammatory bowel disease, insulin resistance
Neuroimmune dysregulation	Abnormal gut–brain communication and neuroinflammation	Parkinson's disease, Alzheimer's disease, depression
Microbial metabolite imbalance	Oxidative stress and endothelial dysfunction	Atherosclerosis, hypertension
Disruption of immune tolerance	Excessive activation of adaptive immunity	Rheumatoid arthritis, lupus, psoriasis

The analyzed evidence demonstrated that increased intestinal permeability represents one of the most relevant biological mechanisms connecting gut dysbiosis with systemic disease progression. Multiple studies described that disruption of epithelial tight junction integrity facilitates the translocation of lipopolysaccharides, bacterial fragments, and inflammatory mediators into systemic circulation [9], [10]. This phenomenon contributes to persistent activation of innate immune pathways and promotes chronic inflammatory responses capable of affecting multiple organ systems. Elevated intestinal permeability has been repeatedly associated with obesity, insulin resistance, cardiovascular disease, and autoimmune pathology, suggesting that the intestinal barrier functions as a critical regulator of systemic homeostasis [6].

Chronic low-grade inflammation emerged as another central mechanism consistently identified throughout the reviewed literature. Dysbiosis-related inflammatory activation involves increased production of pro-inflammatory cytokines such as interleukin-6, tumor necrosis factor-alpha, and C-reactive protein [7], [11]. These inflammatory mediators contribute to endothelial dysfunction, oxidative stress, metabolic impairment, and tissue injury. Several investigations indicated that persistent inflammatory signaling may represent the principal pathogenic link between gut microbiota alterations and chronic noncommunicable diseases including type 2 diabetes mellitus and cardiovascular pathology [12], [18].

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Alterations in short-chain fatty acid production also demonstrated major physiological relevance in the reviewed studies. Beneficial microbial metabolites such as butyrate, acetate, and propionate play essential roles in maintaining intestinal epithelial integrity, regulating immune responses, and modulating inflammatory activity [9]. Reduced production of these compounds was consistently associated with impaired glucose metabolism, insulin resistance, and chronic inflammatory disorders [16]. Butyrate deficiency, in particular, has been associated with decreased mucosal protection and increased susceptibility to systemic inflammatory activation.

The results additionally highlighted the importance of neuroimmune dysregulation mediated through the gut–brain axis. Intestinal microorganisms participate in bidirectional communication between the enteric nervous system and the central nervous system through neural, endocrine, metabolic, and immune pathways [3]. Dysbiosis-associated neuroinflammatory activation has been implicated in neurodegenerative and psychiatric disorders including Parkinson's disease, Alzheimer's disease, anxiety, and depression [4], [13]. Several studies suggested that microbial imbalance may alter neurotransmitter synthesis, vagal signaling, and microglial activation, thereby contributing to neuronal dysfunction and progressive neurological damage [12].

Microbial metabolite imbalance represented another important mechanism identified during the analysis. Metabolites such as trimethylamine N-oxide (TMAO) were repeatedly associated with vascular inflammation, platelet activation, endothelial injury, and atherosclerotic progression [17], [18]. These findings reinforce the concept that intestinal microorganisms may influence systemic physiology through metabolic products capable of directly affecting cardiovascular and inflammatory pathways.

Finally, disruption of immune tolerance was identified as a major mechanism contributing to autoimmune disease development. Several investigations described that alterations in microbial diversity may promote abnormal antigen presentation, molecular mimicry, and excessive activation of adaptive immune responses [7], [11]. These processes have been associated with autoimmune conditions such as rheumatoid arthritis, systemic lupus erythematosus, psoriasis, and multiple sclerosis. The reviewed evidence suggests that intestinal dysbiosis may function as an environmental trigger capable of interacting with genetic susceptibility factors and promoting chronic immune-mediated disease progression.

Figure 3.

Relationship Between Gut Microbiota Dysbiosis and Neurological Disorders Through the Gut–Brain Axis

Neurological Disorder	Reported Microbiota Alteration	Proposed Mechanism
Parkinson's disease	Reduced Prevotella and SCFA-producing bacteria	Neuroinflammation and α-synuclein aggregation
Alzheimer's disease	Increased pro-inflammatory bacterial species	Chronic neuroinflammation and blood–brain barrier dysfunction
Multiple sclerosis	Reduced microbial diversity	Abnormal immune activation and demyelination
Depression	Altered serotonin-related microbial metabolism	Hypothalamic–pituitary–adrenal axis dysregulation
Anxiety disorders	Reduced Lactobacillus and Bifidobacterium populations	Altered neurotransmitter signaling
Autism spectrum disorder	Gastrointestinal dysbiosis and increased intestinal permeability	Neurodevelopmental and inflammatory alterations

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

The reviewed literature consistently demonstrated that gut microbiota alterations are strongly associated with neurological disorders through mechanisms involving the gut–brain axis. This bidirectional communication system integrates neural, endocrine, immune, and metabolic pathways capable of linking intestinal microbial activity with central nervous system regulation [3], [12]. The analyzed evidence suggests that intestinal dysbiosis may contribute to neuroinflammation, altered neurotransmitter synthesis, microglial activation, and blood–brain barrier dysfunction, thereby influencing the progression of several neurological and psychiatric conditions.

Parkinson's disease represented one of the most extensively studied neurodegenerative disorders associated with gut microbiota imbalance. Multiple investigations reported reduced abundance of Prevotella species and short-chain fatty acid-producing bacteria among affected patients [4]. These alterations were associated with increased intestinal permeability, chronic inflammatory activation, and abnormal alpha-synuclein accumulation within enteric and central nervous system structures. Several studies suggested that pathological alpha-synuclein aggregation may originate in the gastrointestinal tract before propagating toward the brain through vagal pathways [13]. This hypothesis reinforces the possibility that intestinal dysbiosis may contribute directly to neurodegenerative disease initiation and progression.

Alzheimer's disease also demonstrated significant associations with gut microbial alterations. The analyzed studies described increased prevalence of pro-inflammatory bacterial populations accompanied by reduced anti-inflammatory microbial diversity [8]. Chronic systemic inflammation and circulating inflammatory mediators may contribute to blood–brain barrier disruption, neuronal injury, and microglial activation [12]. Several investigations proposed that microbial metabolites and endotoxins may accelerate amyloid-beta deposition and neurodegenerative processes through persistent inflammatory signaling [13]. These findings support the growing recognition of neuroinflammation as a critical factor in Alzheimer's disease pathophysiology.

In multiple sclerosis, reduced microbial diversity and altered intestinal immune regulation were consistently identified among affected individuals [11]. Dysbiosis-associated immune dysregulation may contribute to abnormal activation of autoreactive lymphocytes and increased pro-inflammatory cytokine production. Several studies suggested that intestinal microorganisms may influence demyelinating processes through modulation of T-helper cell differentiation and regulatory T-cell activity [8]. The reviewed evidence reinforces the concept that microbiota-mediated immune imbalance may participate actively in autoimmune neurological disorders.

Psychiatric disorders such as depression and anxiety were also frequently associated with intestinal microbial imbalance. Research examining depressive disorders identified alterations in microbial pathways related to serotonin metabolism, inflammatory activation, and hypothalamic–pituitary–adrenal axis dysregulation [3], [12]. Reduced abundance of beneficial bacterial populations including Lactobacillus and Bifidobacterium species was repeatedly reported in individuals presenting anxiety-related symptoms [13]. These microbial alterations may influence neurotransmitter synthesis, stress responses, and emotional regulation through neuroendocrine and immune-mediated mechanisms.

Autism spectrum disorder represented another condition frequently associated with gastrointestinal dysbiosis and altered intestinal permeability. Several investigations described increased gastrointestinal symptoms, inflammatory markers, and microbial imbalance among affected pediatric populations [4]. Proposed mechanisms included altered neurodevelopmental signaling, immune activation, and microbial metabolite dysregulation capable of influencing cognitive and behavioral function. Although causal relationships remain incompletely understood, the findings support the relevance of gut–brain communication in neurodevelopmental disorders.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Collectively, the analyzed evidence demonstrates that the intestinal microbiome participates actively in neurological homeostasis and disease progression through highly integrated neuroimmune and neuroendocrine pathways. These findings reinforce the growing importance of microbiome-centered approaches within neurology, psychiatry, and translational neuroscience. Furthermore, the observed associations suggest that modulation of gut microbiota may eventually contribute to preventive and therapeutic strategies targeting neurodegenerative and psychiatric diseases in clinical practice.

Figure 4.

Immunological Consequences of Gut Microbiota Dysbiosis and Their Association With Autoimmune and Inflammatory Diseases

Immunological Alteration	Microbiota-Related Mechanism	Associated Diseases
Increased pro-inflammatory cytokine production	Activation of innate immune pathways by bacterial endotoxins	Rheumatoid arthritis, psoriasis
Loss of immune tolerance	Altered regulatory T-cell activity	Systemic lupus erythematosus, multiple sclerosis
Enhanced intestinal permeability	Translocation of microbial antigens into systemic circulation	Inflammatory bowel disease, autoimmune disorders
Chronic activation of macrophages and dendritic cells	Persistent microbial stimulation	Metabolic syndrome, chronic inflammatory disease
Reduced anti-inflammatory metabolite production	Decreased short-chain fatty acid synthesis	Obesity, diabetes mellitus
Molecular mimicry	Cross-reactivity between microbial and host antigens	Autoimmune neurological and rheumatologic diseases

The reviewed evidence demonstrated that gut microbiota plays a fundamental role in maintaining immunological homeostasis through continuous interaction with both innate and adaptive immune systems. Under physiological conditions, intestinal microorganisms contribute to immune maturation, pathogen defense, and regulation of inflammatory responses [7], [10]. However, alterations in microbial diversity and composition may disrupt these regulatory mechanisms, promoting chronic inflammation and immune dysregulation associated with multiple systemic diseases.

One of the most consistently reported findings among the analyzed studies was the increased production of pro-inflammatory cytokines secondary to dysbiosis-associated immune activation. Several investigations demonstrated elevated concentrations of interleukin-6, tumor necrosis factor-alpha, interleukin-1β, and other inflammatory mediators in individuals presenting significant alterations in gut microbial composition [6], [11]. Bacterial endotoxins such as lipopolysaccharides were identified as important activators of Toll-like receptor signaling pathways, contributing to chronic inflammatory responses capable of affecting multiple organ systems [9]. Persistent inflammatory activation has been associated with autoimmune pathology, endothelial dysfunction, insulin resistance, and progressive tissue injury.

Loss of immune tolerance emerged as another major immunological consequence of intestinal dysbiosis. The reviewed literature demonstrated that gut microorganisms participate actively in the regulation of regulatory T cells responsible for suppressing excessive immune activation and maintaining self-tolerance [7]. Alterations in microbial diversity may impair these mechanisms and facilitate abnormal activation of autoreactive lymphocytes. Several studies examining systemic lupus erythematosus, multiple sclerosis, and rheumatoid arthritis reported dysbiosis-associated reductions in regulatory immune activity accompanied by increased pro-inflammatory responses [8], [11]. These findings reinforce the hypothesis that intestinal microbial imbalance may contribute to autoimmune disease development in genetically predisposed individuals.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Enhanced intestinal permeability was also identified as a central factor linking dysbiosis with systemic immune dysregulation. Damage to epithelial tight junction integrity permits translocation of microbial antigens, endotoxins, and inflammatory mediators into systemic circulation [9], [10]. This process promotes activation of macrophages, dendritic cells, and circulating immune cells, thereby amplifying inflammatory responses. Several investigations suggested that persistent antigenic exposure resulting from intestinal barrier dysfunction may contribute to chronic inflammatory diseases including inflammatory bowel disease and systemic autoimmune disorders [6].

The chronic activation of macrophages and dendritic cells represented another relevant mechanism repeatedly described in the analyzed literature. Intestinal dysbiosis may generate continuous stimulation of innate immune pathways through bacterial antigen recognition and inflammatory signaling [7]. This persistent activation contributes to cytokine release, oxidative stress, and chronic tissue inflammation associated with metabolic syndrome and cardiovascular disease [12], [18]. Experimental evidence also suggested that abnormal macrophage activation may influence adipose tissue inflammation and insulin resistance in obesity-related metabolic dysfunction [16].

Reduced production of anti-inflammatory microbial metabolites such as butyrate was consistently associated with impaired immune regulation and increased inflammatory activity [9]. Short-chain fatty acids normally contribute to maintenance of epithelial integrity and modulation of regulatory immune responses. Decreased concentrations of these metabolites were linked to chronic inflammatory states, obesity, diabetes mellitus, and autoimmune pathology [1], [16]. Butyrate deficiency may additionally influence intestinal permeability and promote exaggerated inflammatory activation.

Molecular mimicry was identified as another possible mechanism connecting gut microbiota with autoimmune disease progression. Certain bacterial antigens may exhibit structural similarities to host proteins, potentially triggering cross-reactive immune responses against self-tissues [11]. Several investigations suggested that dysbiosis-associated microbial imbalance may facilitate abnormal antigen presentation and autoimmune activation in diseases affecting neurological, rheumatologic, and dermatological systems.

The findings presented in this figure collectively demonstrate that gut microbiota exerts extensive influence over immune regulation through highly integrated inflammatory and immunomodulatory pathways. The analyzed evidence supports the concept that intestinal dysbiosis may contribute significantly to systemic inflammatory disease progression by altering immune tolerance, epithelial barrier function, cytokine production, and immune cell activation. These observations reinforce the importance of microbiome-centered strategies in understanding chronic inflammatory disorders and developing future immunomodulatory therapeutic approaches.

Figure 5.

Therapeutic Strategies Targeting Gut Microbiota and Their Reported Clinical Implications

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Therapeutic Strategy	Principal Mechanism	Reported Clinical Benefits
Probiotics	Restoration of beneficial bacterial populations	Reduced inflammation and improved gastrointestinal function
Prebiotics	Selective stimulation of beneficial microorganisms	Increased short-chain fatty acid production
Synbiotics	Combined probiotic and prebiotic activity	Improved microbial diversity and metabolic regulation
Dietary modification	Alteration of microbial composition through nutrition	Reduced systemic inflammation and improved metabolic health
Fecal microbiota transplantation	Replacement of dysbiotic microbiota	Restoration of microbial balance and treatment of recurrent infections
Postbiotics	Administration of microbial metabolites and bioactive compounds	Immunomodulatory and anti-inflammatory effects

The analyzed evidence demonstrated increasing scientific and clinical interest in therapeutic strategies directed toward modulation of gut microbiota composition and activity. Advances in microbiome research have generated growing recognition that intestinal microorganisms may represent modifiable therapeutic targets capable of influencing systemic inflammatory, metabolic, neurological, and immunological processes [15]. The reviewed studies suggested that restoration of microbial homeostasis may contribute to improved clinical outcomes in several chronic diseases associated with intestinal dysbiosis.

Probiotics represented one of the most extensively investigated microbiota-targeted interventions identified throughout the reviewed literature. These live microorganisms, commonly including Lactobacillus and Bifidobacterium species, are administered with the objective of restoring beneficial microbial populations and improving intestinal homeostasis [6]. Multiple investigations reported reductions in inflammatory markers, improvements in epithelial barrier integrity, and modulation of immune responses following probiotic administration [9]. Certain studies additionally suggested potential benefits in metabolic disorders, inflammatory bowel disease, anxiety-related symptoms, and antibiotic-associated gastrointestinal dysfunction. However, clinical outcomes varied significantly depending on bacterial strain selection, dosage, treatment duration, and patient characteristics.

Prebiotics also demonstrated relevant therapeutic potential through selective stimulation of beneficial intestinal microorganisms. Non-digestible dietary substrates such as inulin, fructooligosaccharides, and galactooligosaccharides were shown to promote growth of commensal bacterial populations associated with anti-inflammatory activity and short-chain fatty acid production [15]. Increased concentrations of butyrate and other microbial metabolites were associated with improved intestinal barrier integrity, enhanced immune regulation, and reduced systemic inflammation [9]. Several investigations suggested that prebiotic supplementation may contribute to improved glucose metabolism and metabolic regulation in individuals presenting obesity and insulin resistance [16].

Synbiotics, combining probiotics and prebiotics simultaneously, demonstrated promising effects through synergistic modulation of microbial diversity and metabolic activity. The reviewed evidence suggested that synbiotic interventions may improve microbial stability while enhancing production of beneficial metabolites and reducing inflammatory activation [6]. Several studies reported improvements in gastrointestinal symptoms, metabolic markers, and inflammatory profiles among patients receiving combined microbiota-targeted supplementation. Nevertheless, further standardized clinical trials remain necessary to establish optimal therapeutic formulations and long-term efficacy.

Dietary modification emerged as one of the most accessible and physiologically relevant therapeutic strategies capable of influencing gut microbiota composition. Diets rich in dietary fiber, fruits, vegetables, legumes, fermented foods, and plant-derived nutrients were consistently associated with increased microbial diversity and enhanced production of anti-inflammatory metabolites [15]. Conversely, highly processed diets rich in saturated fats, refined sugars, and artificial additives were linked to dysbiosis, reduced microbial diversity, and chronic inflammatory activation [1]. Several investigations emphasized that long-term dietary patterns may substantially influence microbiome-associated disease risk and systemic metabolic health.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Fecal microbiota transplantation represented one of the most advanced microbiome-based therapeutic interventions identified during the review process. This procedure involves transfer of intestinal microbiota from healthy donors to affected individuals with the objective of restoring microbial balance [19]. Strong evidence supports its effectiveness in recurrent Clostridioides difficile infection, where restoration of microbial diversity significantly improves clinical outcomes [20]. Emerging investigations have also explored its potential applications in inflammatory bowel disease, metabolic syndrome, autoimmune pathology, and neuropsychiatric disorders. Although preliminary results appear promising, important concerns remain regarding donor selection, long-term safety, microbiological standardization, and regulatory considerations.

Postbiotics, consisting of microbial metabolites and bioactive compounds produced by intestinal microorganisms, represented another emerging therapeutic approach described in recent investigations. These compounds include short-chain fatty acids, microbial peptides, and anti-inflammatory metabolites capable of influencing immune signaling pathways and epithelial barrier function [9]. Several studies suggested that postbiotics may offer therapeutic advantages by avoiding some of the safety concerns associated with live microorganism administration while preserving beneficial immunomodulatory effects.

Despite encouraging findings regarding microbiota-targeted interventions, the reviewed evidence also identified substantial limitations within current therapeutic research. Significant heterogeneity exists among clinical studies due to differences in patient populations, microbial analysis techniques, dietary patterns, geographic variability, and treatment protocols [5]. Furthermore, considerable interindividual variability in microbiome composition complicates prediction of therapeutic responses and limits standardization of microbiota-based treatments.

Another important limitation involves the incomplete understanding of long-term consequences associated with microbiome modulation. Although many interventions demonstrated short-term improvements in inflammatory and metabolic markers, evidence regarding sustained clinical efficacy remains limited in several disease categories. Additionally, the complexity of host–microbiome interactions suggests that personalized therapeutic approaches may eventually become necessary to optimize microbiome-centered interventions.

The findings presented in this figure reinforce the growing importance of microbiota-targeted therapeutics within modern medicine. Current evidence increasingly supports the possibility that modulation of intestinal microbial ecosystems may contribute to prevention and management of systemic diseases extending beyond the gastrointestinal tract. Continued translational and clinical research will be essential for clarifying therapeutic mechanisms, improving treatment standardization, and establishing evidence-based microbiome interventions applicable across diverse clinical populations worldwide.

DISCUSSION

The findings analyzed throughout this review reinforce the growing recognition of gut microbiota as a central regulator of systemic physiology and chronic disease progression. Current evidence demonstrates that intestinal microorganisms participate in highly integrated biological networks capable of influencing metabolic, neurological, immunological, endocrine, and cardiovascular processes through multidirectional communication pathways [1], [3]. The reviewed literature consistently supported the hypothesis that intestinal dysbiosis may contribute significantly to the development and progression of systemic diseases beyond the digestive tract, particularly through mechanisms involving chronic inflammation, epithelial barrier dysfunction, neuroimmune signaling, and metabolic dysregulation.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

One of the most relevant observations identified during the present analysis was the consistent association between reduced microbial diversity and chronic low-grade inflammation. Multiple studies demonstrated that intestinal dysbiosis is associated with increased concentrations of inflammatory mediators including tumor necrosis factor-alpha, interleukin-6, lipopolysaccharides, and C-reactive protein [6], [9]. These inflammatory alterations appear capable of influencing systemic physiological functions through persistent immune activation and endothelial dysfunction. Chronic inflammation has long been recognized as a major contributor to obesity, insulin resistance, cardiovascular disease, autoimmune pathology, and neurodegenerative disorders [12], [18]. The reviewed evidence suggests that the intestinal microbiome may function as an important upstream regulator of these inflammatory processes.

The relationship between gut microbiota and metabolic disease represented one of the strongest and most consistent findings throughout the analyzed literature. Alterations in microbial diversity, impaired short-chain fatty acid production, and increased intestinal permeability were repeatedly associated with obesity and type 2 diabetes mellitus [1], [16]. These findings support previous hypotheses suggesting that dysbiosis may influence host metabolism through modulation of energy extraction, inflammatory signaling, bile acid metabolism, and insulin sensitivity [9]. The growing prevalence of obesity and metabolic syndrome in countries such as Mexico, Colombia, and Ecuador further increases the clinical relevance of microbiome research within Latin American populations undergoing rapid nutritional and epidemiological transitions.

The reviewed evidence additionally demonstrated substantial interactions between gut microbiota and the nervous system through the gut–brain axis. Neuroimmune communication pathways involving vagal signaling, microbial metabolites, cytokine activation, and neurotransmitter regulation appear to contribute significantly to neurological and psychiatric disease mechanisms [3], [12]. Several investigations identified microbial alterations associated with Parkinson's disease, Alzheimer's disease, multiple sclerosis, anxiety, and depressive disorders [4], [8], [13]. These findings are particularly important because they challenge the traditional perception that neurological diseases originate exclusively within the central nervous system. Instead, current evidence increasingly supports the concept that intestinal inflammatory and microbial processes may actively participate in neurodegeneration and neuropsychiatric dysfunction.

The role of intestinal permeability in systemic disease progression also emerged as a critical component of the analyzed evidence. Damage to epithelial tight junction integrity facilitates translocation of bacterial endotoxins and inflammatory mediators into systemic circulation, thereby amplifying immune activation and chronic inflammatory responses [10]. This phenomenon may partially explain the observed relationship between intestinal dysbiosis and autoimmune disease progression. Several studies included in the review identified associations between gut microbial imbalance and conditions such as rheumatoid arthritis, systemic lupus erythematosus, psoriasis, and multiple sclerosis [7], [11]. The proposed mechanisms involving molecular mimicry, abnormal antigen presentation, and dysregulated T-cell responses reinforce the importance of microbiota-mediated immune regulation in autoimmune pathology.

Another important aspect highlighted by the reviewed literature involves the potential therapeutic implications of microbiota modulation. Dietary interventions, probiotics, prebiotics, synbiotics, postbiotics, and fecal microbiota transplantation demonstrated promising results in reducing inflammatory activity and restoring microbial balance [15], [19], [20]. These findings suggest that microbiome-centered therapies may eventually become important components of preventive medicine and chronic disease management. However, despite encouraging outcomes, significant limitations remain regarding therapeutic standardization, patient selection, microbial variability, and long-term efficacy.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

The considerable heterogeneity identified among microbiome studies represents one of the principal challenges currently limiting translation of microbiota research into clinical practice. Variations in sequencing methodologies, population characteristics, dietary habits, geographic factors, and analytical approaches complicate direct comparison of findings across studies [5]. Furthermore, interindividual differences in microbial composition suggest that personalized microbiome responses may substantially influence therapeutic outcomes. Consequently, future investigations should prioritize methodological standardization and development of reproducible microbiome biomarkers capable of improving clinical applicability.

The complexity of host–microbiome interactions additionally complicates the establishment of definitive causal relationships between dysbiosis and systemic disease. Although many studies demonstrated strong associations, several investigations remained observational and were unable to determine whether microbial alterations represented primary pathogenic factors or secondary consequences of disease progression [6]. Longitudinal studies and mechanistic investigations will therefore be essential for clarifying the temporal and causal dynamics involved in microbiota-associated pathology.

The present review also highlights the importance of adopting multidisciplinary perspectives when evaluating microbiome-related disease mechanisms. The intestinal microbiota interacts simultaneously with gastrointestinal, neurological, immunological, metabolic, endocrine, and cardiovascular systems, demonstrating that systemic diseases frequently involve interconnected biological pathways rather than isolated organ dysfunction. This integrated perspective may contribute to future advances in personalized medicine, preventive healthcare, and translational biomedical research.

From a global health perspective, the growing burden of chronic noncommunicable diseases further increases the relevance of microbiome research. Urbanization, processed food consumption, reduced dietary fiber intake, sedentary lifestyles, and excessive antibiotic exposure may contribute significantly to alterations in microbial diversity across modern populations [15]. These environmental and lifestyle factors may partially explain increasing prevalence of obesity, autoimmune disease, metabolic syndrome, and neuropsychiatric disorders observed worldwide. Consequently, public health strategies promoting healthy dietary patterns and rational antibiotic use may eventually contribute to preservation of microbial homeostasis and reduction of chronic disease risk.

The evidence analyzed throughout this review ultimately supports the concept that gut microbiota should no longer be considered exclusively a digestive component but rather a dynamic systemic regulator capable of influencing multiple physiological processes simultaneously. Advances in microbiome science continue to redefine current understanding of disease pathophysiology and open new opportunities for innovative therapeutic and preventive strategies.

Nevertheless, further research remains necessary to clarify the long-term clinical implications of microbiota modulation, identify reliable microbial biomarkers, and establish standardized microbiome-based interventions applicable across diverse populations. Continued international collaboration between gastroenterology, neurology, immunology, microbiology, nutrition, and translational medicine will be essential for advancing scientific understanding of the microbiome and its role in systemic human health.

CONCLUSION

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

The scientific evidence analyzed throughout this review demonstrates that gut microbiota represents a fundamental biological system involved in the regulation of systemic human physiology beyond the gastrointestinal tract. Current research consistently supports the concept that intestinal microorganisms actively participate in metabolic, neurological, immunological, cardiovascular, and inflammatory processes through highly integrated communication networks involving the gut–brain axis, immune signaling pathways, microbial metabolites, and epithelial barrier regulation.

The reviewed literature revealed that intestinal dysbiosis is strongly associated with chronic low-grade inflammation, altered immune responses, increased intestinal permeability, neuroimmune dysregulation, and metabolic dysfunction. These mechanisms appear capable of contributing significantly to the development and progression of multiple systemic diseases including obesity, type 2 diabetes mellitus, cardiovascular disorders, autoimmune pathology, neurodegenerative diseases, and psychiatric conditions. The findings reinforce the growing recognition that chronic diseases frequently involve interconnected physiological systems rather than isolated organ dysfunction.

One of the most relevant observations identified during this review was the extensive participation of the gut–brain axis in neurological and neuropsychiatric disorders. The evidence suggests that intestinal microorganisms may influence neurotransmitter synthesis, inflammatory signaling, vagal communication, and neuroimmune activation, thereby contributing to neurodegenerative and psychiatric disease mechanisms. These discoveries have substantially expanded current understanding of the relationship between intestinal physiology and central nervous system function.

The analysis also demonstrated the critical role of gut microbiota in immune regulation and maintenance of systemic inflammatory balance. Alterations in microbial diversity and metabolite production were consistently associated with autoimmune diseases and chronic inflammatory conditions. These findings support the hypothesis that intestinal dysbiosis may function as an important environmental factor capable of interacting with genetic susceptibility and promoting immune-mediated pathology.

From a therapeutic perspective, microbiota-targeted interventions including probiotics, prebiotics, synbiotics, dietary modification, postbiotics, and fecal microbiota transplantation demonstrated promising clinical potential. Although several studies reported beneficial effects involving inflammatory reduction and restoration of microbial balance, important limitations remain regarding standardization, individualized responses, long-term safety, and reproducibility of therapeutic outcomes. Consequently, further clinical investigations and translational studies remain necessary before microbiome-based therapies can be fully integrated into routine medical practice.

The growing prevalence of chronic noncommunicable diseases worldwide, particularly in developing regions undergoing rapid nutritional and epidemiological transitions such as Mexico, Colombia, and Ecuador, further emphasizes the importance of understanding microbiota-associated disease mechanisms. Lifestyle factors including dietary habits, sedentary behavior, antibiotic exposure, and environmental changes may significantly influence intestinal microbial diversity and systemic health outcomes.

Despite the substantial advances achieved in microbiome research, several scientific challenges persist. Methodological heterogeneity, interindividual microbial variability, and the complexity of host–microbiome interactions continue to limit definitive interpretation of causal relationships between dysbiosis and systemic disease. Future investigations should therefore prioritize longitudinal research, mechanistic studies, standardized analytical methods, and development of reliable microbial biomarkers capable of improving clinical applicability.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Ultimately, the evidence reviewed throughout this article supports the concept that gut microbiota should be considered a central regulator of systemic health and disease. Continued multidisciplinary research integrating gastroenterology, immunology, neurology, microbiology, nutrition, and translational medicine will be essential for advancing understanding of microbiome-associated pathology and developing innovative preventive and therapeutic strategies for chronic disease management in modern medicine.

REFERENCES

1. Y. Fan and O. Pedersen, "Gut microbiota in human metabolic health and disease," *Nature Reviews Microbiology*, vol. 19, no. 1, pp. 55–71, 2021, doi: 10.1038/s41579-020-0433-9.
2. S. V. Lynch and O. Pedersen, "The human intestinal microbiome in health and disease," *New England Journal of Medicine*, vol. 375, no. 24, pp. 2369–2379, 2016, doi: 10.1056/NEJMra1600266.
3. J. F. Cryan *et al*., "The microbiota-gut-brain axis," *Physiological Reviews*, vol. 99, no. 4, pp. 1877–2013, 2019, doi: 10.1152/physrev.00018.2018.
4. J. S. Loh *et al*., "Microbiota–gut–brain axis and its therapeutic applications in neurodegenerative diseases," *Signal Transduction and Targeted Therapy*, vol. 9, article 37, 2024, doi: 10.1038/s41392-024-01743-1.
5. Z. Ma *et al*., "A systematic framework for understanding the microbiome in human health and disease: from basic principles to clinical translation," *Signal Transduction and Targeted Therapy*, vol. 9, article 237, 2024, doi: 10.1038/s41392-024-01946-6.
6. S. P. Wiertsema, J. van Bergenhenegouwen, J. Garssen, and L. M. J. Knippels, "The interplay between the gut microbiome and the immune system in the context of infectious diseases throughout life and the role of nutrition in optimizing treatment strategies," *Nutrients*, vol. 13, no. 3, article 886, 2021, doi: 10.3390/nu13030886.
7. Y. Belkaid and T. W. Hand, "Role of the microbiota in immunity and inflammation," *Cell*, vol. 157, no. 1, pp. 121–141, 2014, doi: 10.1016/j.cell.2014.03.011.
8. N. Kamada, S. U. Seo, G. Y. Chen, and G. Núñez, "Role of the gut microbiota in immunity and inflammatory disease," *Nature Reviews Immunology*, vol. 13, no. 5, pp. 321–335, 2013, doi: 10.1038/nri3430.
9. W. Yang and Y. Cong, "Gut microbiota-derived metabolites in the regulation of host immune responses and immune-related inflammatory diseases," *Cellular & Molecular Immunology*, vol. 18, pp. 866–877, 2021, doi: 10.1038/s41423-021-00661-4.
10. F. Di Vincenzo *et al*., "Gut microbiota, intestinal permeability, and systemic inflammation: a narrative review," *International Journal of Molecular Sciences*, vol. 25, no. 4, article 2297, 2024.
11. J. Correale, M. Farez, and M. Gaitán, "The role of the gut microbiota in multiple sclerosis," *Nature Reviews Neurology*, vol. 18, pp. 544–558, 2022.
12. A. Rutsch, J. B. Kantsjö, and F. Ronchi, "The gut-brain axis: how microbiota and host inflammasome influence brain physiology and pathology," *Frontiers in Immunology*, vol. 11, article 604179, 2020, doi: 10.3389/fimmu.2020.604179.
13. H. Ullah *et al*., "The gut microbiota–brain axis in neurological disorder," *Frontiers in Neuroscience*, vol. 17, article 1225875, 2023, doi: 10.3389/fnins.2023.1225875.
14. C. L. Hsu and B. Schnabl, "The gut–liver axis and gut microbiota in health and liver disease," *Nature Reviews Microbiology*, vol. 21, pp. 719–733, 2023.
15. F. C. Ross *et al*., "The interplay between diet and the gut microbiome: implications for health and disease," *Nature Reviews Microbiology*, vol. 22, pp. 671–686, 2024, doi: 10.1038/s41579-024-01068-4.
16. T. P. M. Scheithauer *et al*., "Gut microbiota as a trigger for metabolic inflammation in obesity and type 2 diabetes," *Frontiers in Immunology*, vol. 11, article 571731, 2020.
17. R. Sanchez-Gimenez *et al*., "Gut microbiota-derived metabolites and cardiovascular disease risk: a systematic review of prospective cohort studies," *Nutrients*, vol. 14, no. 13, article 2654, 2022.
18. W. H. W. Tang, T. Kitai, and S. L. Hazen, "Gut microbiota in cardiovascular health and disease," *Circulation Research*, vol. 120, no. 7, pp. 1183–1196, 2017, doi: 10.1161/CIRCRESAHA.117.309715.
19. A. F. Peery *et al*., "AGA clinical practice guideline on fecal microbiota-based therapies for select gastrointestinal diseases," *Gastroenterology*, vol. 166, no. 3, pp. 409–434, 2024.

20. B. H. Mullish *et al*., “The use of faecal microbiota transplant as treatment for recurrent or refractory Clostridioides difficile infection and other potential indications: joint British Society of Gastroenterology and Healthcare Infection Society guidelines,” *Gut*, vol. 73, no. 3, pp. 409–434, 2024.

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal

Issue 3, Year 2, Volume 1, No. 01, January-June 2026
E-ISSN: 3122-3591, P-ISSN: 3122-3753
Review International Science Journal