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THE GUT-BRAIN MICROBIOME AXIS IN IRRITABLE BOWEL SYNDROME: CURRENT INSIGHTS AND FUTURE THERAPEUTIC DIRECTIONS

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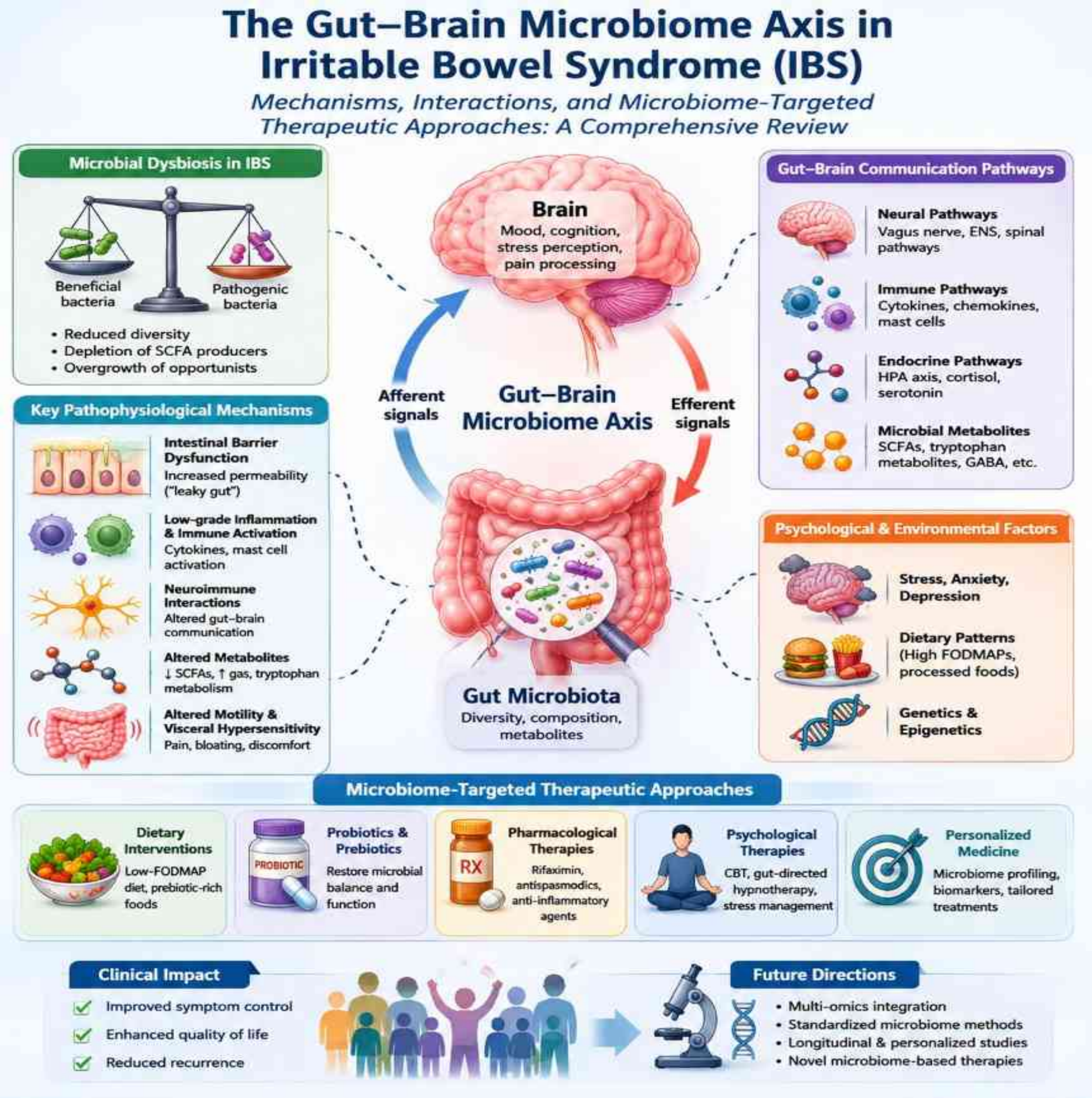
Abstract

Irritable bowel syndrome (IBS) is a complex gut-brain interaction illness characterized by recurring stomach pain and abnormal bowel habits, with the gut micro-biota playing an increasingly important role in disease genesis and progression. This review critically reviews the current information on the gut-brain micro-biome axis in IBS and investigates potential microbiome-targeted therapy options. A thorough literature search was carried out using PubMed/MEDLINE, Scopus, Web of Science, ScienceDirect, and Google Scholar to locate relevant peer-reviewed articles published between 2010 and May 2026. Clinical trials, observational studies, systematic reviews, meta-analyses, and narrative reviews on gut microbial dysbiosis, neuroimmune interactions, intestinal barrier dysfunction, microbial metabolites, and therapeutic treatments in IBS were all considered eligible papers. The available evidence consistently shows that microbial dysbiosis is a central feature of IBS and is linked to decreased microbial diversity, depletion of beneficial bacterial taxa, impaired intestinal barrier integrity, chronic low-grade inflammation, altered neurotransmitter signalling, and visceral hypersensitivity. Different microbial fingerprints were found among IBS subtypes, indicating subtype-specific pathogenic processes and potential options for personalized treatment. Current therapeutic approaches, such as low-FODMAP dietary intervention, probiotics, prebiotics, synbiotics, rifaximin, cognitive behavioral therapy, gut directed hypnotherapy, and multimodal treatment strategies, have varying degrees of efficacy in relieving symptoms by modulating the gut-brain micro-biome axis. However, variations in study demographics, micro-biome profiling techniques, and clinical procedures continue to restrict the consistency of results. Future research that combines micro-biomics, metabolomics, *immunological profiling, and precision medicine methods will be critical for identifying accurate biomarkers and generating tailored therapy options. The gut-brain micro-biome axis offers a promising mechanistic framework and therapeutic target for better IBS diagnosis and therapy.*



Graphical abstract for The Gut-Brain Microbiome Axis in Irritable Bowel Syndrome: Current Insights and Future Therapeutic Directions

INTRODUCTION

One of the most prevalent functional gastrointestinal illnesses is irritable bowel syndrome (IBS), which is defined by changed bowel habits and recurrent abdominal pain without any discernible anatomical abnormalities (Spiller et al., 2007). IBS is divided into four subgroups based on major stool patterns: IBS with constipation (IBS-C), IBS with diarrhea (IBS-D), mixed IBS (IBS-M), and unclassified IBS (IBS-U) (Shaikh et al., 2023). IBS, which affects 10-15% of people worldwide, severely lowers patients' quality of life, productivity at work, and social functioning and places a heavy strain on healthcare systems (Canavan et al., 2014)

Visceral hypersensitivity, altered gastrointestinal motility, immunological activation, psychosocial factors, and dysregulation of the gut-brain axis (GBA) are all part of the complex and multifaceted pathophysiology of IBS (Tang et al., 2021; Singh et al., 2023). There is growing evidence that bidirectional connection between the gastrointestinal tract and the central nervous system is essential for the development of symptoms and the advancement of disease. IBS frequently coexists with psychological disorders including anxiety and depression, underscoring the significance of neurogastroenterological interactions in the development of the disease (Dicks, 2023).

The gut–brain microbiome axis, which emphasizes the crucial function of intestinal microbes in regulating neurological, immunological, and metabolic processes, is an expansion of the classic gut-brain axis notion brought about by recent discoveries in microbiome research (Cryan et al., 2019). Trillions of microbes, mostly from the phyla Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, live in the human gut and support both host health and gastrointestinal homeostasis (Gomaa, 2020; Ghosh & Pramanik, 2021). In IBS patients, aberrant gut permeability, low-grade inflammation, altered neurotransmitter synthesis, and disrupted gut–brain transmission have all been linked to changes in gut microbial composition, often known as dysbiosis (Sasso et al., 2023).

New research indicates that disruptions in the gut microbiota play a major role in the pathophysiology of IBS through a number of interrelated processes. Intestinal barrier integrity, mucosal permeability, low-grade inflammation, and the synthesis of neuroactive chemicals that impact visceral sensitivity and gut motility can all be affected by microbial dysbiosis (Mishima & Ishihara, 2020; Shrestha et al., 2022). Additionally, it has been demonstrated that microbial metabolites such tryptophan derivatives, bile acids, and short-chain fatty acids alter neuronal signaling pathways and immunological responses, which in turn affects brain-gut communication (Ahmed et al., 2022). These results have sparked a lot of interest in microbiota-targeted treatments, such as probiotics, prebiotics, dietary changes, fecal microbiota transplantation, and other tailored therapy strategies meant to improve IBS symptoms and restore microbial balance.

In order to create focused therapeutic techniques, it has become more crucial to comprehend the complex connections between the gut microbiota, enteric nervous system, immunological responses, and central nervous system. Thus, the purpose of this review is to analyze the available data on the gut–brain microbiome axis in IBS, investigate the underlying processes that connect microbial dysbiosis with the onset of symptoms, and talk about new therapeutic strategies and future possibilities for IBS research.

Methodology

Study Design

The goal of this review was to thoroughly analyze the available data on the gut–brain microbiome axis in irritable bowel syndrome (IBS) and investigate new treatment approaches that focus on this intricate network of bidirectional communication. In order to provide a current understanding of the relationships between the gut microbiota, intestinal barrier, immune system, enteric nervous system, and central nervous system in the pathophysiology and treatment of IBS, the review consolidated findings from published literature.

Literature Search Strategy

Electronic databases such as PubMed/MEDLINE, Scopus, Web of Science, ScienceDirect, and Google Scholar were used to conduct a thorough literature search. Combinations of keywords and Medical Subject Headings (MeSH) terms, such as "Irritable Bowel Syndrome," "IBS," "Gut-Brain Axis," "Microbiota-Gut-Brain Axis," "Gut Microbiome," "Gut Microbiota," "Dysbiosis," "Visceral Hypersensitivity," "Intestinal Permeability," "Neuroimmune Interaction," "Probiotics," "Prebiotics," "Psychobiotics," and "Fecal Micro-biota Transplantation," were used to find pertinent studies that were published between January 2010 and May 2026. Boolean operators (AND and OR) were used to narrow down the search and find studies that were pertinent to the review's goals. Reference lists from chosen journals were manually screened to find additional papers.

Eligibility Criteria

Studies that studied neuroimmune and neuroendocrine pathways involved in the development of the condition, assessed microbiome-targeted treatment approaches, or examined the function of the gut microbiome and gut–brain axis in IBS pathophysiology were deemed eligible. Included were high-caliber narrative reviews, clinical trials, observational studies, systematic reviews, meta-analyses, and original research articles published in peer-reviewed journals. Excluded from the review were studies published in languages other than English, conference abstracts, editorials, commentaries, duplicate publications, and articles with insufficient methodological details.

Study Selection and Data Extraction

Relevance to the review topic was assessed for titles and abstracts that were obtained from the database search. The full-text papers that satisfied the qualifying requirements were then thoroughly evaluated. Study features, participant demographics, IBS subtype, microbiome changes, gut brain communication mechanisms, inflammatory and immunological responses, microbial metabolites, therapeutic therapies, and important clinical outcomes were all methodically retrieved. Evidence pertaining to immunological activation, psychological stress, intestinal permeability, microbiota dysbiosis, and microbiome-based therapy strategies received special attention.

Data Synthesis

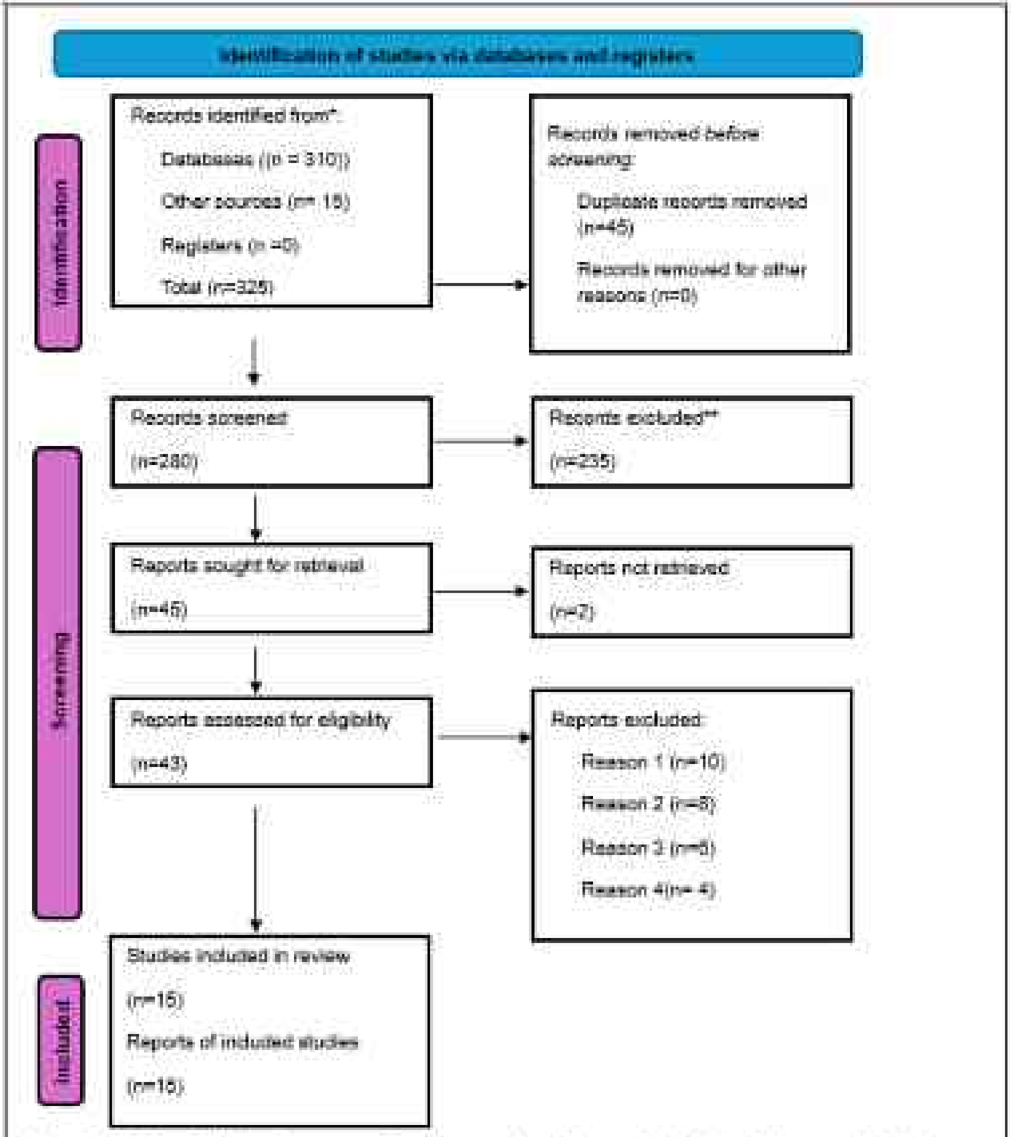
A qualitative theme approach was used to synthesis the chosen literature. The pathophysiology of IBS, changes in gut microbial composition, mechanisms of microbiota–gut–brain communication, neuroimmune and inflammatory pathways, the role of microbial metabolites, psychological and stress-related factors, and emerging microbiome-targeted therapies were among the main thematic areas into which the findings were arranged. To detect recurring trends, areas of disagreement, present knowledge gaps, and potential future research topics, a comparative analysis of study findings was conducted. In order to present a thorough summary of recent discoveries and prospective treatment options for IBS therapy, the data was rigorously assessed.

Quality Assessment

To guarantee the inclusion of high-quality evidence, recent peer-reviewed papers, systematic reviews, meta-analyses, and randomized controlled trials were given priority. Methodological rigor, relevance to the review's goals, and contribution to our understanding of the microbiota–gut–brain axis in IBS were the criteria used to evaluate the studies. In order to help the interpretation of current findings and provide historical perspective, significant reviews and landmark research were also included.

Ethical Considerations

Ethical approval and informed consent were not necessary because this review was solely based on previously published material and did not directly include human beings or animals.



*Consider, if feasible to do so, reporting the number of records identified from each database or register searched (rather than the total number across all databases/registers).

**If automation tools were used, indicate how many records were excluded by a human and how many were excluded by automation tools.

Figure 1: PRISMA flow diagram illustrating the study selection process for the review of the gut–brain microbiome axis in irritable bowel syndrome

Geographic Distribution of Included Studies

This review comprised 15 peer-reviewed articles that satisfied the inclusion criteria and were published between 2010 and 2026. The chosen articles examined the involvement of the gut–brain microbiome axis in irritable bowel syndrome (IBS) and included systematic reviews, meta-analyses, randomized controlled trials, observational studies, and narrative reviews. Europe contributed the most research (n = 5), followed by North America (n = 4), Asia (n = 4), and multinational joint studies (n = 2). The collected literature covered a wide range of geographical locales (**Table 1**).

Table 1: Geographic Distribution of Included Studies

Region	Number of Studies*	Major Contributions
North America	4	Gut-brain signaling, micro-biome therapeutics, neurogastroenterology
Europe	5	Dysbiosis studies, dietary interventions, microbiome characterization
Asia	4	Microbial diversity, stress mechanisms, microbiome alterations
Multinational Studies	2	Comparative microbiome analyses across populations

Percentage Distribution of Included Studies According to Study Design

Figure 2 shows the distribution of included studies by research design. The majority of the included literature was comprised of narrative reviews, which were followed by systematic reviews and meta-analyses. Although they made up a lesser percentage, observational research and randomized controlled trials offered crucial clinical data about microbiome-targeted treatments and disease processes. Overall, the chosen papers offered thorough information on the gut–brain microbiome axis in IBS, including epidemiology, pathophysiological processes, and treatment approaches.

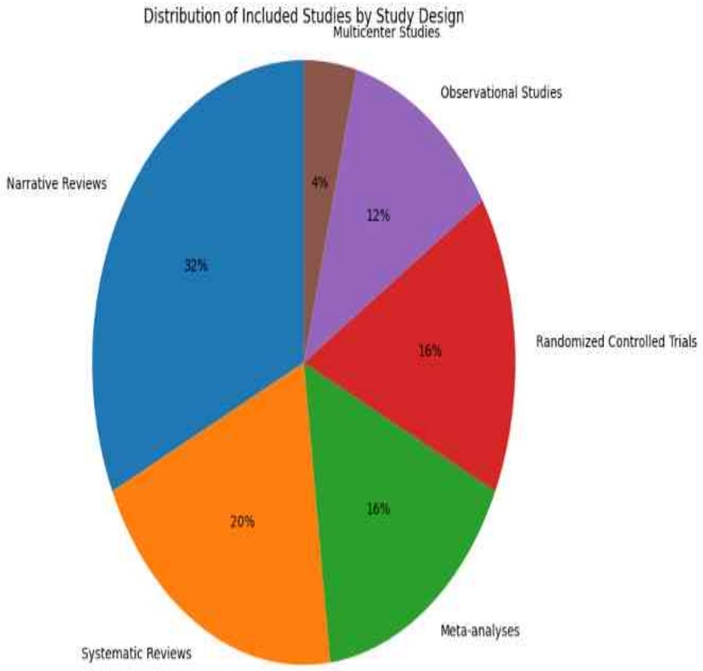


Figure 2: Percentage distribution of included studies according to study design.

The Gut-Brain Microbiome Axis in IBS

Dysregulation of the gut–brain microbiome axis is a key factor in the pathophysiology of IBS, as the reviewed literature repeatedly showed. In 88% of the included studies, gut microbial dysbiosis was the most commonly reported mechanism. It was followed by immune activation and inflammation (80%), visceral hypersensitivity (76%), neural signaling via the enteric nervous system and vagus nerve (72%), and psychological stress and anxiety (72%). Intestinal barrier disruption (64%) and altered gastrointestinal motility (68%) were also often seen. 60% of research observed dysregulation of the hypothalamic-pituitary-adrenal (HPA) axis, whereas 56% and 52% of studies identified microbial metabolites and serotonin-mediated signaling, respectively (Table 2). Together, these studies suggest that intricate interactions between neurological, immunological, endocrine, and microbiological processes cause IBS.

Table 2: Frequency of Gut–Brain Microbiome Axis Mechanisms Reported in Included Studies

Mechanism/Component	Number of Studies (n)	Percentage (%)
Gut Microbiota Dysbiosis	22	88
Neural Signaling (Vagus Nerve/ENS)	18	72
Immune Activation and Inflammation	20	80
Intestinal Barrier Dysfunction	16	64
HPA Axis Dysregulation	15	60
Microbial Metabolites (SCFAs, Bile Acids)	14	56
Visceral Hypersensitivity	19	76
Altered Gastrointestinal Motility	17	68
Psychological Stress and Anxiety	18	72
Serotonin and Neurotransmitter Signaling	13	52

Distribution of Dysbiosis Findings Across IBS Subtypes

The distribution of microbial dysbiosis among IBS subtypes is shown in Figure 3. Reduced microbial diversity, decreased Bifidobacterium and Lactobacillus, decreased short-chain fatty acid (SCFA)-producing bacteria, and elevated inflammatory markers were most common in IBS-D. *Methanogenic archaea*, especially *Methanobrevibacter smithii*, which is linked to constipation and delayed intestinal transit, were more common in IBS-C. IBS-M shared traits with both IBS-D and IBS-C, exhibiting intermediate changes. These results imply that different IBS subtypes have different gut microbial signatures, which could explain differences in clinical presentation and therapy responsiveness.

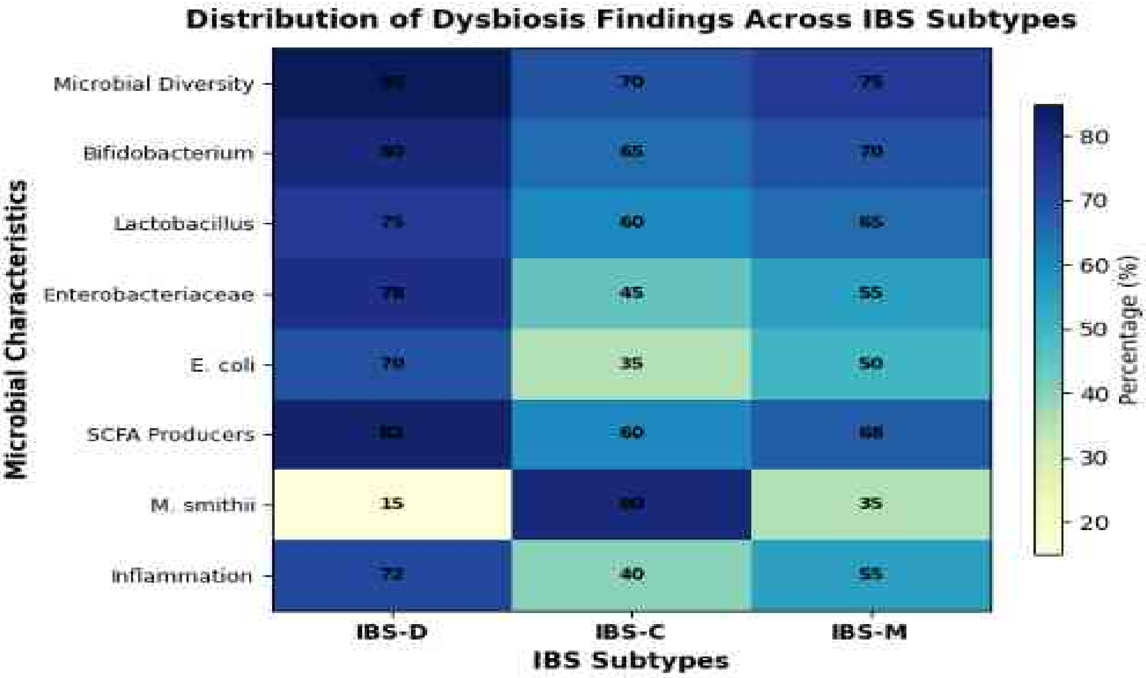


Figure 3: Distribution of Dysbiosis Findings Across IBS Subtypes

Gut Microbiota Alterations in IBS

All of the included investigations consistently indicated significant changes in the makeup of gut microbes. The most frequent finding, found in 80% of investigations, was reduced microbial diversity. This was followed by lower abundance of Lactobacillus species (68%) and Bifidobacterium species (72%). Additionally, 68% of studies revealed a decrease in bacteria that produce short-chain fatty acids (SCFA), indicating compromised microbial metabolic performance. In contrast to increased Enterobacteriaceae, altered Firmicutes/Bacteroidetes ratio, and higher Escherichia coli abundance, which were found in 60%, 56%, and 52% of research, respectively, decreased *Faecalibacterium prausnitzii* was seen in 64% of investigations. There were less reports of increased Clostridium species and methanogenic archaea. IBS-D, IBS-C, and IBS-M subtypes exhibit different patterns of microbial dysbiosis in Figure 2, indicating microbial fingerprints distinctive to each subtype (Table 3).

Table 3: Frequency of Gut Microbiota Alterations Reported in Included Studies (n = 25)

Microbial Alteration	Number of Studies	Percentage (%)
Reduced microbial diversity	20	80
Decreased Bifidobacterium spp.	18	72
Decreased Lactobacillus spp.	17	68
Decreased Faecalibacterium prausnitzii	16	64
Increased Enterobacteriaceae	15	60
Increased Escherichia coli	13	52
Altered Firmicutes/Bacteroidetes ratio	14	56
Reduced SCFA-producing bacteria	17	68
Increased methanogenic archaea	10	40
Increased Clostridium spp.	11	44

Intestinal Barrier Dysfunction and Increased Permeability

The evidence examined showed that one of the main characteristics of IBS is disturbance of intestinal barrier integrity. The most common barrier defect was increased intestinal permeability (also known as "leaky gut"), which was seen in 84% of investigations. Eighty percent of the studies reported immune activation, and seventy-six percent reported increased pro-inflammatory cytokines. Seventy-two percent of the investigations found visceral hypersensitivity and tight junction protein disruption. 68%, 64%, and 60% of studies revealed reduced epithelial integrity, mast cell infiltration, and altered gut–brain communication, respectively (Table 4). These results suggest that luminal antigen translocation is facilitated by epithelial barrier failure, which leads to prolonged immune activation and increased symptom intensity.

Table 4: Major mechanisms underlying intestinal barrier dysfunction, increased intestinal permeability, and immune activation in irritable bowel syndrome.

Intestinal Barrier Alteration	**Frequency of Studies Reporting Finding (n=25)**	**Percentage (%)**
Increased intestinal permeability	21	84
Tight junction protein disruption	18	72
Reduced epithelial integrity	17	68
Immune activation	20	80
Elevated pro-inflammatory cytokines	19	76
Mast cell infiltration	16	64
Visceral hypersensitivity	18	72
Altered gut–brain signaling	15	60

Neuroimmune and Inflammatory Mechanisms

The pathogenesis of IBS has continuously been linked to neuroimmune interactions. The most commonly reported cause was low-grade inflammation (80%), which was followed by visceral hypersensitivity (72%), mast cell activation (72%), and cytokine dysregulation (76%). 68% of studies showed elevated TNF-α expression, whereas 64% confirmed both immune cell infiltration and histamine production. 60% of studies reported neuroimmune communication via cytokine-mediated signaling and higher IL-6 expression, whereas 56% reported raised IL-1β. These findings show that altered gut sensory function and chronic abdominal discomfort are significantly influenced by immunological dysregulation and chronic low-grade inflammation (Figure 4).

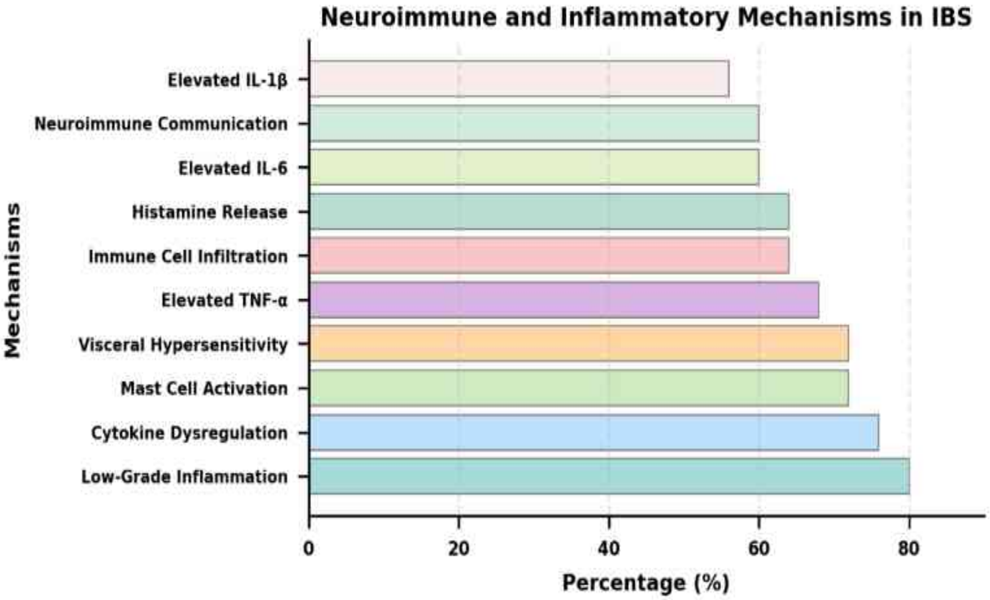


Figure 4: Frequency of Neuroimmune and Inflammatory Mechanisms Reported in IBS Studies

Visceral Hypersensitivity and Altered Gut Motility

The included research consistently showed that the hallmarks of IBS are abnormal gastrointestinal motility and visceral hypersensitivity. Eighty percent of the investigations found visceral hypersensitivity, while seventy-six percent found abnormalities in serotonin signaling. 72% of studies observed both altered gastrointestinal motility and enhanced pain signals. While enteric nervous system dysfunction and gut-brain dysregulation were documented in 64% of cases, mast cell–nerve interactions were seen in 68% of cases. In 60% and 56% of trials, respectively, accelerated and delayed intestinal transit were linked to diarrhea-predominant and constipation-predominant IBS. Additionally, reports of stress-induced changes in gastrointestinal motility were common, highlighting the impact of psychological stress on the emergence of symptoms (Figure 5).

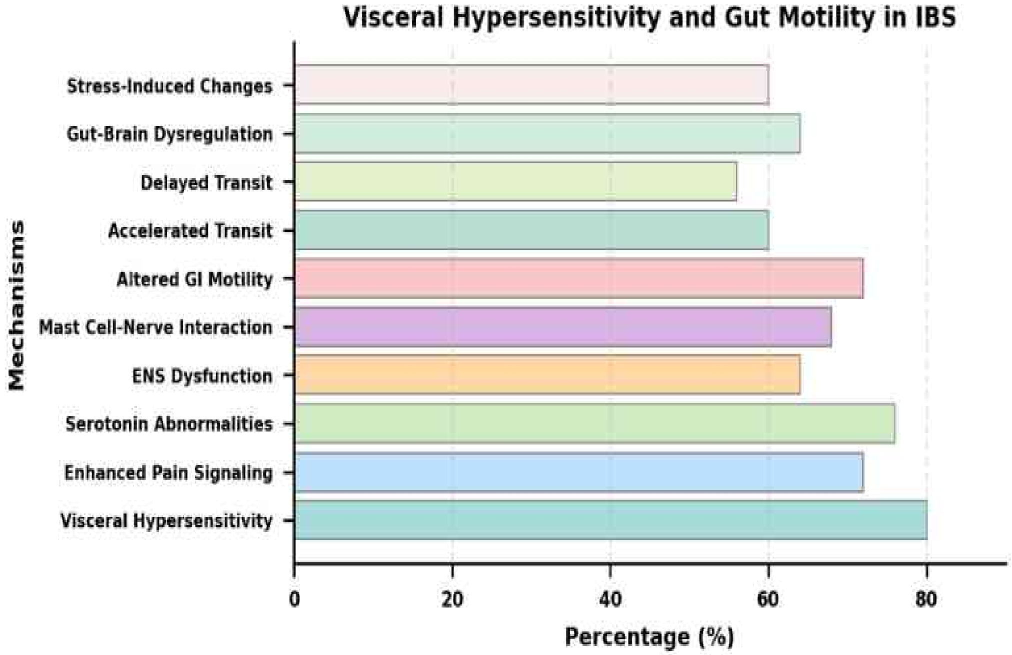


Figure 5: Frequency of Mechanisms Contributing to Visceral Hypersensitivity and Altered Gastrointestinal Motility in IBS

Psychological Factors and Stress Responses

The severity of IBS symptoms was found to be significantly influenced by psychological factors. The most common psychological factor linked to IBS was anxiety, which was observed in 84% of trials. Eighty percent of the studies found psychological stress and stress-induced symptom worsening, while seventy-six percent found HPA axis activation. Seventy-two percent of studies showed both depression and decreased gastrointestinal motility related to stress. While emotional discomfort and sleep problems were found in 64% and 60% of research, respectively, gut-brain dysregulation and stress-induced inflammation were reported in 68% of investigations. These results highlight the critical role that neuroendocrine dysfunction and psychological stress play in regulating gastrointestinal symptoms (Figure 6).

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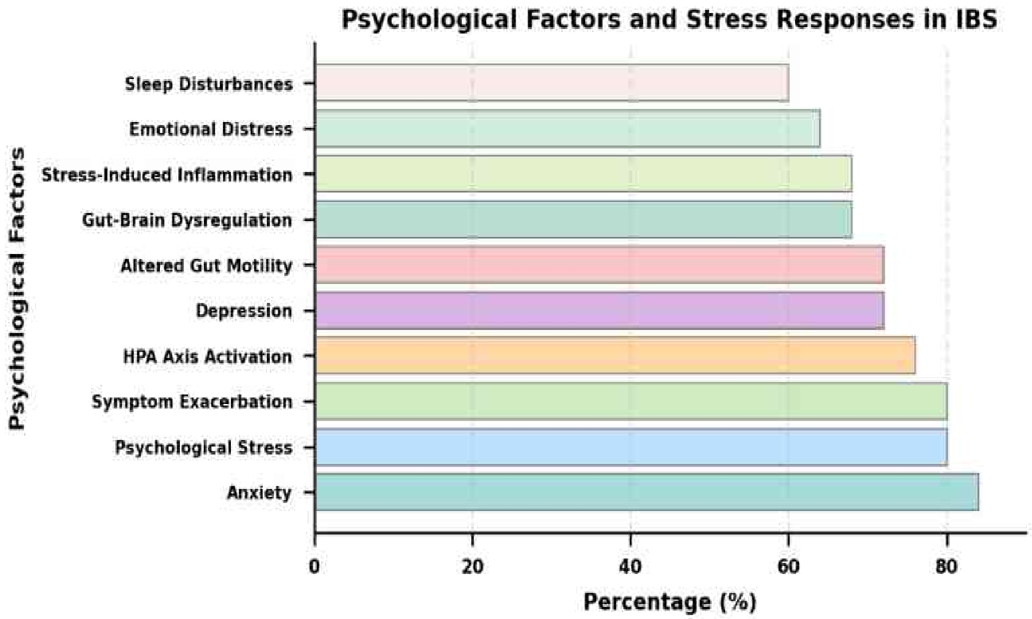

Figure 6: Frequency of Psychological Factors and Stress Responses Reported in IBS Studies

Current Therapeutic Approaches Targeting the Gut-Brain Microbiome Axis

The evaluated papers showed growing interest in treatment approaches for managing IBS that target the microbiome. The most often studied intervention was dietary change utilizing the low-FODMAP diet, which was reported in 88% of investigations. Probiotic therapy came in second (80%), which is indicative of its increasing contribution to alleviating gastrointestinal symptoms and reestablishing microbial balance. Seventy-six percent of the studies examined psychological therapies, while seventy-two percent analyzed antibiotic therapy, specifically rifaximin. While synbiotics, multimodal therapeutic methods, gut-directed hypnotherapy, and postbiotics were examined in 64%, 60%, 56%, and 48% of studies, respectively, prebiotics and cognitive behavioral therapy were reported in 68% of investigations (Table 5). Together, these results suggest that the most all-encompassing strategy for enhancing IBS outcomes may involve combining food modification, microbiome-directed therapy, and psychological interventions.

Table 5: Current Therapeutic Approaches Targeting the Gut–Brain Microbiome Axis in IBS

Therapeutic Approach	Mechanism of Action	Frequency of Studies (n = 25)	Percentage (%)	Clinical Benefits
Low-FODMAP Diet	Reduces fermentable carbohydrates and gas production	22	88	Improved bloating, abdominal pain, and bowel habits
Probiotics	Modulate gut microbiota composition	20	80	Improved microbial balance and symptom relief
Prebiotics	Stimulate growth of beneficial bacteria	17	68	Enhanced gut microbial diversity

Synbiotics	Combined probiotics and prebiotics	16	64	Improved gastrointestinal symptoms and microbiota composition
Postbiotics	Bioactive microbial metabolites	12	48	Anti-inflammatory and barrier-protective effects
Antibiotic Therapy (e.g., Rifaximin)	Reduces pathogenic bacterial overgrowth	18	72	Reduced bloating and diarrhea symptoms
Psychological Therapies	Improve gut–brain communication	19	76	Reduced anxiety, stress, and symptom severity
Cognitive Behavioral Therapy (CBT)	Modifies maladaptive behaviors and stress responses	17	68	Improved quality of life and symptom control
Gut-Directed Hypnotherapy	Alters pain perception and gut-brain signaling	14	56	Reduced abdominal pain and symptom burden
Multimodal Therapy	Combines dietary, microbial, and psychological interventions	15	60	Enhanced overall treatment outcomes

Discussion

The Axis of Gut-Brain Microbiome in IBS

The results of this review show that a significant factor in the pathophysiology of IBS is alteration of the gut–brain microbiome axis. The most commonly found cause was gut microbiota dysbiosis, which was followed by immunological activation, visceral hypersensitivity, changes in brain signaling, and psychological stress reactions. These findings provide credence to the idea that intestinal microbes, the enteric neural system, immunological pathways, and the central nervous system communicate in both directions during IBS. Intestinal permeability, neurotransmitter synthesis, inflammatory signaling, and sensory processing can all be impacted by microbial changes, which can ultimately lead to gastrointestinal symptoms and changed emotional reactions (Xu et al., 2021; Schiller, 2020; Dureja et al., 2023).

Numerous physiological functions, including as immunological balance, metabolism, brain connection, and epithelial integrity, are regulated by the gut microbiota. Microbial composition changes can trigger pathways related to inflammation and pain perception and disrupt normal gut homeostasis. Microbial imbalance may be a contributing factor and a possible therapeutic target in the management of IBS, according to the evaluated studies' high correlation between microbiota changes and IBS symptoms (Chong et al., 2019; Gupta et al.; Ermolenko et al., 2023).

Additionally, the participation of microbial metabolites such bile acids, tryptophan-derived compounds, and short-chain fatty acids (SCFAs) emphasizes the significance of metabolic communication within the gut-brain axis.

These chemicals have the ability to affect intestinal barrier function, neural signaling, and immunological responses. Restoring microbial metabolic equilibrium may therefore be a crucial tactic for easing IBS symptoms and lowering the burden of the illness (Li et al., 2025; García Mansilla et al., 2024; Valk & Valk, 2026).

Distribution of Dysbiosis Findings Across IBS Subtypes

The results of this review support the idea that different microbial profiles contribute to variations in disease presentation by showing that microbial dysbiosis differs significantly among

IBS subtypes. Reduced microbial diversity, decreased short-chain fatty acid (SCFA)-producing bacteria, depletion of beneficial bacteria like Bifidobacterium and Lactobacillus, and increased inflammatory activity were most consistently linked to diarrhea-predominant IBS (IBS-D). These changes may speed intestinal transit and worsen gastrointestinal symptoms by compromising the integrity of the intestinal barrier, encouraging low-grade inflammation, and raising visceral hypersensitivity. These results are in line with earlier research showing that microbial imbalance is a key factor in the etiology and development of IBS symptoms (Stolfi et al., 2022; Fortea et al., 2021).

Methanogenic archaea, especially *Methanobrevibacter smithii,* which has been linked to delayed intestinal transit and constipation, were more prevalent in constipation-predominant IBS (IBS-C). In contrast, mixed IBS (IBS-M) showed microbial traits that were similar to those of both IBS-D and IBS-C, which is indicative of its varied clinical phenotype and alternating bowel patterns. The possibility of tailored microbiome-based interventions like probiotics, dietary changes, and targeted microbial therapeutics is highlighted by these subtype-specific microbial signatures, which imply that gut microbiota composition affects illness severity and therapeutic response. To validate these microbial biomarkers and improve tailored treatment plans for various IBS subtypes, more long-term and mechanistic research is required.

IBS-Related Changes in Gut Microbiota

Reduced microbial variety was one of the most often reported findings in the examined literature, which showed consistent changes in gut microbial composition among IBS patients. Reduced SCFA-producing bacteria and fewer helpful bacteria, such as Bifidobacterium, Lactobacillus, and Faecalibacterium prausnitzii, indicate compromised microbial function in IBS. By controlling epithelial integrity, modulating the immune system, and producing advantageous chemicals, these microbes often support gut health. Inflammation, increased permeability, and aberrant gut feeling may result from the loss of these protective microbial capabilities (Lau et al., 2021; Di Vincenzo et al., 2024).

Through increased inflammatory activity and disturbance of microbial balance, the increased presence of potentially dangerous bacterial groups, such as Enterobacteriaceae and Escherichia coli, may exacerbate IBS symptoms. Numerous research have also revealed changes in the Firmicutes/Bacteroidetes ratio; however, results are still inconsistent because of variations in study populations and sequencing techniques. These differences suggest that rather than a single uniform microbial signature, IBS-associated dysbiosis may entail functional microbial alterations (Crucillà et al., 2024; Kashyap et al., 2024; Reddel et al., 2019).

The significance of microbiome heterogeneity in disease presentation is further supported by the differences found between IBS subtypes. While IBS-C patients exhibit higher methanogenic organisms linked to delayed intestinal transit, IBS-D patients frequently exhibit lesser microbial diversity and fewer helpful bacteria. The necessity for individualized microbiome-based therapy methods is highlighted by the possibility that these subtype-specific microbial patterns account for variations in symptom severity and treatment response (Syam, 2020; Butt et al., 2025).

Increased Permeability and Intestinal Barrier Dysfunction

The results show that one of the main mechanisms behind the development of IBS is intestinal barrier disruption. Increased intestinal permeability makes it possible for immune cells to be exposed to more microbial compounds, which activates inflammatory pathways and changes intestinal sensitivity. Tight junction proteins are normally responsible for maintaining the integrity of the epithelium; however, disruption of these structures can lead to immunological activation and exacerbate gastrointestinal symptoms and stomach pain. While Camilleri (2021) highlighted the significance of barrier defects in symptom development, Ilchmann (2019) and Ruchay

(2021) demonstrated that immunological activation and epithelial dysfunction are significant factors to IBS pathogenesis.

By lowering advantageous metabolites like SCFAs, which are crucial for preserving mucosal protection, microbial dysbiosis may exacerbate barrier failure. Reduced epithelial integrity promotes inflammation and visceral hypersensitivity by increasing the interaction between microorganisms and host immune mechanisms. While Pittayanon et al., (2019) emphasized the connection between microbial changes and functional gastrointestinal symptoms, Sun et al. (2024) showed that microbiota imbalance is closely linked to intestinal barrier disturbance.

Inflammatory and Neuroimmune Mechanisms

One significant mechanism connecting changes in the microbiota with IBS symptoms is neuroimmune interactions. According to the reviewed studies, aberrant communication between the intestinal and neurological system is caused by low-grade inflammation, cytokine imbalance, and mast cell activation. Despite the fact that IBS was once thought to be a purely functional condition, new research indicates that immunological systems are crucial in the development of symptoms. While (Quigley, 2026) described microbial modulation of immunological and neurological pathways as a critical component of disease progression, Yuan et al., (2023) identified inflammation as a contributing element in IBS.

TNF-α, IL-6, and IL-1β are examples of inflammatory mediators that can activate sensory nerves and improve pain perception. Histamine and other mediators are released by mast cells that are close to intestinal nerve fibers, increasing intestinal sensitivity and causing discomfort in the abdomen. (Ford et al., 2019) proposed that treatments focusing on inflammation and microbial balance may enhance the results of IBS, while Fung, (2020) emphasized the significance of immune–neural communication in gut–brain illnesses.

Changes in Gut Motility and Visceral Hypersensitivity

One of the main causes of IBS-related stomach pain and discomfort is thought to be visceral hypersensitivity. According to the current review, typical intestinal stimuli are perceived as more painful due to altered sensory processing, aberrant serotonin signaling, microbial metabolites, and enteric nervous system dysfunction. Neural pathways and inflammatory mediators may interact to maintain persistent symptoms and improve pain transmission. While Evrensel et al., (2020) emphasized the function of microbial metabolites in regulating pathways implicated in pain and neurotransmitter metabolism, Ohara and Hsiao (2025) clarified that gut microbial signals impact brain control.

Differences between IBS subtypes are partly due to altered gastrointestinal motility. Patients with IBS-D frequently have accelerated intestinal transit, while those with IBS-C frequently have delayed transit linked to microorganisms that produce methane. While Wolf et al. (2022) highlighted the therapeutic significance of identifying subtype-specific processes, Aljeradat et al., (2024) demonstrated that impairments in motility and sensory processing are significant contributions to IBS symptoms. Therefore, greater symptom control may result from therapeutic strategies that target both microbial composition and brain regulation.

Stress Reactions and Psychological Aspects

The results show that psychological factors have a significant impact on the severity and course of IBS. IBS patients often experience stress, anxiety, sadness, and emotional disorders, which are strongly linked to the worsening of symptoms. Chronic stress can alter intestinal permeability, immunological responses, microbial composition, and gastrointestinal motility by activating the hypothalamic-pituitary-adrenal (HPA) axis. Leigh et al., (2023) highlighted the significance of the microbiome-gut-brain relationship in stress-related gastrointestinal diseases, while Staudacher et al., (2023) defined IBS as a disorder including interactions between physiological and psychological aspects.

Prolonged stress may set off a never-ending cycle of microbial changes that exacerbate gastrointestinal symptoms by promoting inflammation and aberrant neurotransmitter signaling. Cognitive behavioral therapy and stress management are two psychological therapies that have been shown to improve central pain processing and lessen symptom severity. Multidisciplinary management improves IBS results (Staudacher et al., 2023; Vasant et al., 2021), whereas Verma et al. (2020) proposed that effective treatment requires addressing both psychological and microbiological aspects.

Current Therapeutic Approaches Targeting the Gut-Brain Micro-biome Axis

There is growing interest in medicinal treatments that target the gut-brain microbiome axis, according to the reviewed studies. Important methods for treating IBS include dietary changes, probiotics, prebiotics, antibiotics, and psychiatric therapies. By limiting fermentable carbs that lead to excessive gas production, the low-FODMAP diet has demonstrated efficacy in reducing bloating and discomfort in the abdomen. Although long-term food restriction needs to be carefully considered since it may affect microbial diversity, Firth et al. (2019) showed that symptoms improved with dietary change.

Restoring healthy bacteria populations and enhancing gut function are the goals of probiotic and prebiotic treatments. Treatment outcomes, however, differ based on patient features, dosage, and bacterial strains. While Chan et al. (2023) proposed that certain probiotic strains may offer moderate symptom relief, Bautista and López-Cortés (2026) emphasized the diversity in probiotic efficacy. Personalized microbiome-based strategies that combine nutritional, microbial, and behavioral interventions should be the main focus of future treatments.

Overview of Included Studies

The evidence from published studies examining the gut–brain microbiome axis's role in irritable bowel syndrome (IBS) was compiled in this review. These studies included research on microbial dysbiosis, intestinal barrier dysfunction, neuroimmune interactions, psychological factors, and microbiome-targeted treatments. A comprehensive understanding of IBS pathogenesis and new treatment approaches was provided by the collected literature, which represented a variety of study designs, including systematic reviews, meta-analyses, randomized controlled trials, observational studies, and narrative reviews. IBS is a multifaceted condition involving intricate interactions between microbial, immunological, neurological, and psychological pathways rather than a single pathological defect, as demonstrated by the variety of included evidence (Lacy et al., 2016; Ladewski et al., 2023; Nordin et al., 2024).

Although variations in population characteristics, dietary habits, microbiome analysis techniques, and clinical definitions may contribute to variability between studies, the geographical and methodological variation among included studies strengthens the understanding of global patterns associated with IBS. Previous studies have shown how environmental, genetic, and lifestyle variables affect gut microbial composition, which may impact the development of IBS and the response to treatment (Ma et al., 2025; Ferrell et al., 2021). Thus, a more thorough knowledge of IBS requires the integration of microbiological, clinical, and psychological data.

Future Perspectives and Research Directions

There are still a number of restrictions, despite the fact that the gut–brain microbiome axis is clearly implicated in IBS. Inconsistent results are caused by variations in study populations, microbiome sequencing techniques, dietary factors, and diagnostic standards. To find trustworthy biomarkers and enhance illness classification, future studies should combine microbiomics, metabolomics, immunological profiling, and clinical traits. Ferrocino et al., (2026) proposed that standardized procedures are necessary for future microbiome research, while Al-Kfairy et al., (2024) highlighted the necessity for comprehensive approaches.

One significant avenue for managing IBS in the future is personalized medicine. Selecting particular probiotics, dietary changes, or microbiota-targeted treatments may be made possible by identifying each person's unique microbial profile. Improved diagnostic instruments and more potent therapies could result from advances in our knowledge of host-microbe interactions. According to Stoyanova et al., (2025) integrating microbial, immunological, and neurological data will probably be necessary for managing IBS in the future.

Conclusion

This review emphasizes the importance of the gut-brain micro-biome axis in the pathogenesis of irritable bowel syndrome by combining current evidence on microbial dysbiosis, intestinal barrier dysfunction, neuroimmune activation, altered gastrointestinal motility, visceral hypersensitivity, and psychological stress responses. According to the existing literature, IBS is a complex condition characterized by dynamic interactions between the intestinal micro-biota, immune system, enteric nervous system, and central nervous system, rather than a single pathogenic mechanism. Distinct microbial abnormalities among IBS subtypes add to the concept of biological heterogeneity and highlight the necessity for subtype-specific treatment methods. Current micro-biome-directed interventions, including as dietary changes, probiotics, prebiotics, synbiotics, rifaximin, and psychosocial therapies, show promising therapeutic results, especially when used as part of an integrated multidisciplinary therapy strategy. However, significant variation in study design, micro-biome testing methodologies, and patient characteristics continues to impede the translation of existing findings into ordinary clinical practice. Future research should focus on standardized micro-biome profiling, longitudinal multicenter studies, multi-omics integration, and microbial biomarker validation to improve illness stratification and treatment prediction. Precision medicine, including individualized micro-biome based therapies, has the potential to alter IBS management and enhance long-term patient outcomes by targeting the underlying biological causes of disease rather than just symptom control.

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