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# The Emerging Role of the Gut Microbiota in the Pathophysiology of Irritable Bowel Syndrome: A Narrative Review

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***Abstract***
*Irritable bowel syndrome (IBS) is a common functional gastrointestinal disorder with a multifactorial pathophysiology. The gut microbiota has recently emerged as a key contributor to symptom generation through its interactions with intestinal permeability, immune activation, and the gut–brain axis. This narrative review summarizes current evidence regarding the role of the gut microbiota in IBS, the mechanisms involved, and therapeutic perspectives based on microbiota modulation. No original data were collected for this article.*
***Keywords****: Irritable bowel syndrome, gut microbiota, dysbiosis, gut–brain axis, probiotics, narrative review.*

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## I. Introduction

Irritable bowel syndrome (IBS) affects 5–10% of the global population and is one of the most frequent reasons for gastroenterology consultations. Its pathophysiology is complex and involves abnormalities in motility, visceral hypersensitivity, low-grade inflammation, and dysregulation of the gut–brain axis.

Advances in metagenomics have strengthened the hypothesis that the gut microbiota plays an essential role in IBS. Qualitative and functional alterations—collectively referred to as dysbiosis—may contribute to the gastrointestinal and extraintestinal symptoms described in IBS patients. This review aims to provide an updated synthesis of current knowledge regarding the role of the microbiota in IBS.

## II. Methods

This narrative review is based on a selection of articles published between 2015 and 2024, identified through PubMed, Scopus, and Google Scholar. Sources include clinical studies, experimental studies, and review articles. No original research data were collected.

**Current Evidence on the Gut Microbiota in IBS**

1. Bacterial dysbiosis

Studies in IBS patients consistently report: a reduction in Lactobacillus, Bifidobacterium, and Faecalibacterium prausnitzii, an increase in certain Firmicutes and Proteobacteria, decreased overall microbial diversity.

These changes are associated with: increased intestinal permeability, persistent low-grade immune activation, altered production of metabolites influencing visceral sensitivity.

2. Interaction between the microbiota and the gut–brain axis

The gut microbiota regulates: neurotransmitter production (serotonin, GABA), vagal nerve activity, stress responses, central pain modulation pathways.

Disruptions in these processes may explain the strong association between psychological stress, anxiety, and symptom exacerbation in IBS.

3. Microbial metabolites and inflammation

Short-chain fatty acids (SCFAs), particularly butyrate, play a key role in: maintaining intestinal barrier integrity, modulating immune responses, regulating gut motility.

Altered SCFA production is frequently observed in IBS patients.

**Microbiota-Targeted Therapeutic Approaches**

1. Probiotics

Effective strains include: Bifidobacterium infantis 35624, multi-strain formulations.

Clinical benefits: reduced abdominal pain, decreased bloating, improved stool consistency.

2. Prebiotics and soluble fibers
Prebiotics enhance beneficial bacteria and improve stool form.
Soluble fibers, especially psyllium, are the most evidence-based.
3. Targeted antibiotics
Rifaximin has shown efficacy in non-constipation IBS (IBS-D), likely through modulation of small intestinal bacterial populations.
4. Fecal microbiota transplantation (FMT)
Results remain inconsistent.
FMT appears beneficial in selected patients, but the lack of standardized protocols limits routine use.

## III. Discussion

Evidence strongly supports a central role of the gut microbiota in IBS pathophysiology. However, no single microbiota profile specific to IBS has been consistently identified. Interindividual variability, methodological heterogeneity, and the complex interplay between psychological, immunological, and microbial factors contribute to these discrepancies.

Future perspectives include: identification of predictive microbial biomarkers, personalized microbiota-based therapeutic strategies, development of next-generation probiotics, precise phenotyping of IBS subgroups.

## IV. Conclusion

The gut microbiota plays a key role in IBS through dysbiosis, low-grade inflammation, and modulation of the gut–brain axis. A deeper understanding of these mechanisms opens the way to innovative microbiota-targeted therapies. Personalized treatment approaches may significantly improve IBS management in the coming years.

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