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The Gut Microbiota in Inflammatory Bowel Diseases: Role in Pathogenesis and Possibilities for Therapeutic Modulation. A Narrative Review

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ABSTRACT

Inflammatory bowel diseases (IBD) are chronic inflammatory conditions of the gastrointestinal tract with an unexplained cause, including Crohn's disease and ulcerative colitis. This review condenses current knowledge on the role of the gut microbiota in IBD pathogenesis. It discusses the composition of the gut microbiota in healthy individuals and the changes observed in patients with IBD, including the bacteriome, virome, and mycobiome. The authors presented dysbiosis as a potential factor in IBD inflammation. They discussed current options for modulating the microbiota, focusing on fecal microbiota transplantation (FMT), dietary interventions, and nutraceuticals. Available studies suggest that restoring intestinal homeostasis in patients with IBD may be a valuable adjunctive treatment, and FMT is particularly successful in patients with ulcerative colitis. In the case of Crohn's disease, the results were less certain, indicating the need for further research. In the future, therapies targeting a patient's microbiota may become an important component of IBD treatment.

Keywords: Inflammatory bowel disease, intestinal microbiota, fecal microbiota transplantation, dietary changes in IBD

1. INTRODUCTION

Inflammatory bowel diseases (IBD) refer to various conditions characterized by inflammation of the gastrointestinal tract of uncertain etiology. The main conditions are Crohn's disease and ulcerative colitis, which are distinct conditions but are commonly referred to collectively as IBD (Shan et al., 2022). Crohn's disease (CD) is a chronic condition that could impact any part of the gastrointestinal tract and involves inflammation of all layers of the gastrointestinal tract wall, especially the intestine. In contrast, ulcerative colitis is a chronic disease characterized by

recurrence and remission and affects only the mucous membrane of the large intestine (Liang et al., 2024).

To this day, the causes of IBD have not been clearly identified. Despite various hypotheses and multiple studies, no single factor or pathogen has been identified as causing the disease on its own (Shan et al., 2022). It is currently assumed that this results from exposure to environmental factors in genetically predisposed individuals (Lagos et al., 2026). In fact, IBD incidence has increased in rapidly industrializing developing countries where lifestyles are changing. Factors associated with the increased frequency of IBD in these regions include highly processed foods, smoking, antibiotic intake, and exposure to environmental toxins (Shan et al., 2022; Liang et al., 2024).

A growing number of studies suggest that the proper composition of the gut microbiota is a key factor in maintaining intestinal homeostasis, and many chronic diseases, including IBD, appear to be associated with an abnormal gut microbiota composition (Schoultz et al., 2025). Intestinal homeostasis relies on a balanced microbial ecosystem, whereas dysbiosis directly triggers and sustains the chronic inflammation characteristic of IBD (Yadegar et al., 2024).

Researchers are working to modulate the microbiota as a potential treatment and as an adjunctive strategy in managing inflammatory bowel disease. Dietary changes, nutraceuticals, and fecal microbiota transplantation play an important role in this type of therapy (Liang et al., 2024; Lagos et al., 2026).

This review provides an overview of current knowledge of the gut microbiome, the role of changes in its composition, and the potential to modulate it for therapeutic purposes.

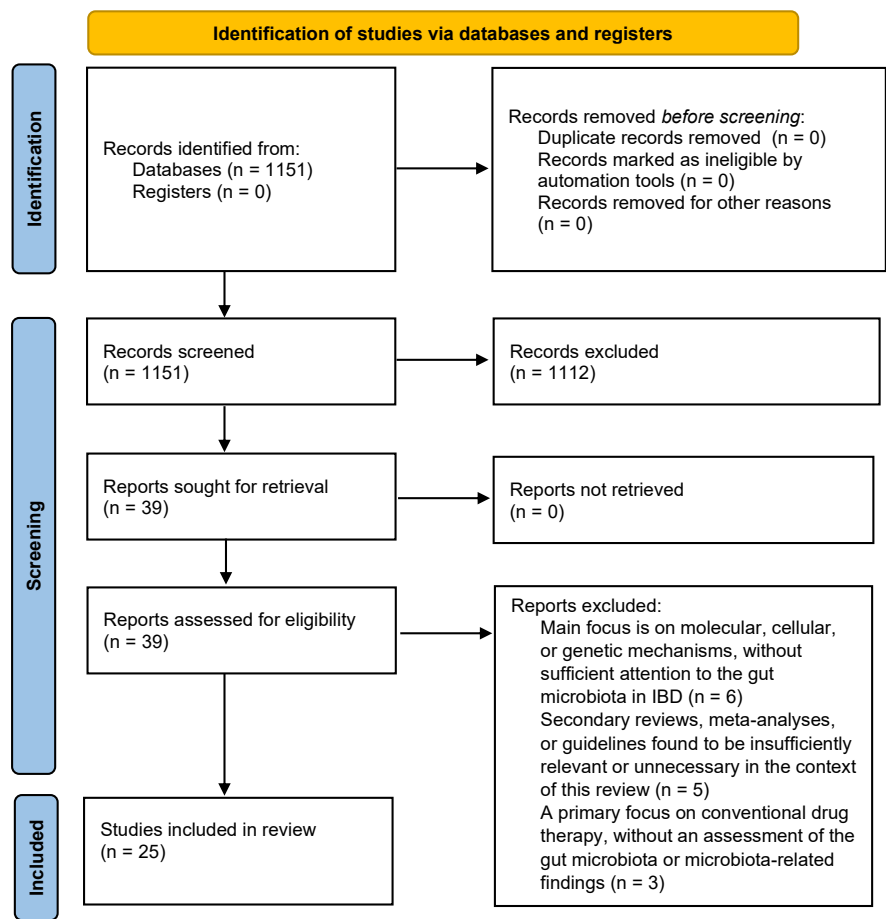


Figure 1. Selection process diagram.

2. REVIEW METHODS

To prepare this narrative review, we searched PubMed. We focused on review articles, systematic reviews, and meta-analyses published between January 2021 and April 2026. We also included older original studies, such as randomized clinical trials, if they

provided crucial context for the discussion. The review included only publications on humans that were available in English. We used open-access articles as well as those whose abstracts provided enough detail on methods and results required for evaluation and data extraction. In our search, we used a combination of keywords: inflammatory bowel disease, Crohn's disease, ulcerative colitis, gut microbiota, gut microbiome, dysbiosis, fecal microbiota transplantation, FMT, diet, probiotics, prebiotics, synbiotics, and nutraceuticals. We excluded publications that did not align with the IBD topic. Eventually, we used 25 publications to prepare this review. The selection process is illustrated in Figure 1.

3. RESULTS AND DISCUSSION

The human intestinal microbiota is a complicated system of microorganisms, which includes, among others, the widely studied bacteriome, virome, and mycobiome. Unfortunately, knowledge about the fungi and viruses colonizing the human intestine is limited due to methodological and technical difficulties associated with their identification and classification into specific taxa (Pérez, 2021; Yadegar et al., 2024).

The Microbiome of a Healthy Individual

The composition of an adult's bacteriome is constant and stable, and sudden dietary changes cause only short-term disturbances (Schoultz et al., 2025). It consists mainly of Firmicutes bacteria (including the genera *Clostridium*, *Lactobacillus*, *Bacillus*, *Enterococcus*, and *Ruminococcus*), *Bacteroidetes* (mainly *Bacteroides* and *Prevotella*), and *Actinobacteria* (Yadegar et al., 2024). Their percentage composition varies and is individually specific, but regardless of this, bacteria from the Enterobacteriaceae family and the genus *Lactobacillus* are commonly found in the intestinal microbiota (Schoultz et al., 2025).

Bacteria in the intestine can use nutrients provided by the diet or already present in the host's system and transform them into short-chain fatty acids (SCFAs), such as butyrate, propionate, and acetate (Yadegar et al., 2024). Bacteria with this ability mainly include *Faecalibacterium prausnitzii* and *Roseburia intestinalis* (Schoultz et al., 2025).

In addition to producing metabolites, the microbiota is also responsible for the synthesis and metabolism of bile acids, which influence the composition of the microbiota and its functioning (Yang et al., 2021).

Dysbiosis in IBD

Dysbiosis is a disproportion characterized by an imbalance in the intestinal microbiota, causing a reduction in species diversity and affecting both the abundance of individual bacterial species and the appearance of new species or the disappearance of stable elements of the microbiota (Shan et al., 2022; Lagos et al., 2026).

In the diagnostic process, two parameters referred to as diversity are differentiated, where α -diversity describes the composition and proportion of individual microorganisms within a single sample from a single patient. At the same time, β -diversity is a parameter that compares the composition of the microbiota between two samples, e.g., those from a patient and a donor participating in an FMT procedure (Yadegar et al., 2024).

In the microbiota of patients with IBD, there are changes in diversity and metabolic abnormalities, e.g., an incremental loss of Firmicutes-type commensals, primarily *Faecalibacterium prausnitzii*, leading to reduced production of SCFAs, which are an essential energy source for the intestinal epithelium, and resulting in impaired healing (Lagos et al., 2026).

The development of dysbiosis has a multifactorial pathogenesis influenced by genetic predisposition and environmental factors, e.g., physical activity, diet and fiber consumption, place of living, and medication use, especially antibiotics taken early in life (Shan et al., 2022; Schoultz et al., 2025).

The intestinal microbiota is also affected by pH levels, intestinal transit time, and oxygen concentration. It has been shown that a shorter transit time promotes saccharolytic fermentation, leading to the formation of SCFAs, in contrast to the harmful products of proteolytic fermentation associated with a longer transit time (Schoultz et al., 2025; Lagos et al., 2026).

There were reports of bile acid metabolism disorders associated with the loss of bacteria having BSH (bile salt hydrolase) and BAI (bile-acid inducible) enzymes. This leads to decreased levels of secondary bile acids, with a simultaneous increase in primary and conjugated bile acids, which promotes inflammation and disrupts the intestinal barrier. Bile acid metabolism disorders or defective receptor activation, combined with dysbiosis, can lead to chronic inflammation in IBD (Yang et al., 2021).

In IBD, dysbiosis is one of the most characteristic features of the intestinal microbiota (Lagos et al., 2026). Table 1 shows changes in the progression of dysbiosis in patients with IBD.

Table 1. Changes in the microbiota of patients with IBD, divided into Crohn’s disease and ulcerative colitis

	Crohn’s disease	Ulcerative colitis
Phylum	↑Proteobacteria ↓Firmicutes	↑Proteobacteria ↓Firmicutes
Family	↑Enterobacteriaceae ↑Fusobacteriaceae ↑Veillonellaceae ↑Pasteurellaceae, ↓Lachnospiraceae ↓Ruminococcaceae	↑Enterobacteriaceae ↓Lachnospiraceae ↓Ruminococcaceae
Genus	↑ <i>Ruminococcus gnavus</i> ↑ <i>Escherichia coli</i> ↑ <i>Clostridium innocuum</i> ↓ <i>Faecalibacterium prausnitzii</i> ↓ <i>Roseburia</i>	↑ <i>Ruminococcus gnavus</i> ↑ <i>Escherichia coli</i> ↓ <i>Faecalibacterium prausnitzii</i> ↓ <i>Roseburia hominis</i> ↓ <i>Eubacterium rectale</i> ↓ <i>Akkermansia muciniphila</i>
Metabolic changes	↑ Primary bile acids ↑ Conjugated bile acids ↓SCFA ↓ secondary bile acids ↓Tryptophan and indole metabolites	↑ Primary bile acids ↑ Conjugated bile acids ↓SCFA ↓ secondary bile acids ↓Tryptophan and indole metabolites

Virome

Another component of the microbiota is composed of viruses, consisting mostly of bacteriophages and, to a smaller extent, eukaryotic viruses. Bacteriophages, which, along with other factors, are responsible for the elimination of bacteria, may be correlated with the diversity of the bacterial microbiome and may also influence the virulence of intestinal bacteria, either positively or negatively (Spencer et al., 2022).

In the stool of healthy adults, both DNA and RNA viruses can be identified. Most are bacteriophages, DNA viruses, including the double-stranded Caudovirales and the double-stranded *CrAssphage* associated with *Bacteroides*. Eukaryotic DNA viruses can also be found in healthy individuals, including the Anelloviridae and Circoviridae families. RNA viruses are studied less frequently and are mainly associated with a plant-based diet, e.g., the Virgaviridae. Determining the exact composition of the human intestinal virome is limited, and most viruses are “known unknown” sequences that cannot be classified into any known taxa (Spencer et al., 2022).

Virome disruptions in Crohn’s disease include an increase in the abundance and diversity of viruses, accompanied by a decrease in bacterial diversity. A possible cause of this correlation is the expansion of bacteriophages from the order Caudovirales, which may be accompanied by a decrease in the number of Bacteroidaceae. There is also an increase in the participation of the Anelloviridae family in the microbiota of patients with CD (Spencer et al., 2022). In addition, the viral count of eukaryotic viruses is higher in patients with CD than in healthy individuals (Iliev et al., 2025).

Viral changes in ulcerative colitis are similar to those in Crohn’s disease, with an increase in bacteriophages of the order Caudovirales; but unlike in Crohn’s disease, in ulcerative colitis, as viral abundance increases, so does the number of bacteria from the families Enterobacteriaceae, Pasteurellaceae, and Prevotellaceae (Spencer et al., 2022).

Increased virome diversity is being considered a biomarker in ulcerative colitis, and lower diversity of the eukaryotic virome in ulcerative colitis is associated with a positive treatment outcome (Spencer et al., 2022; Yadegar et al., 2024).

Mycobiome

The types of fungi consistently present in stool samples collected from healthy adults include *Saccharomyces*, *Malassezia*, and *Candida*, with *Candida albicans* being the most common fungal species found in the stool of healthy individuals. Fungi also influence the body’s immune response by suppressing or promoting inflammatory reactions (Pérez, 2021).

The most characteristic change in the microbiome associated with Crohn’s disease is a large increase in *Candida albicans* during the active phase. ASCA antibodies against carbohydrates that make up the fungal cell wall serve as a biomarker for Crohn’s disease, helping to distinguish CD from ulcerative colitis. A reduced number of *Saccharomyces* is also often observed (Füchtbauer et al., 2025; Iliev et al., 2025). Also, the presence of *Debaryomyces hansenii* was demonstrated in tissues affected by CD, and it was found that this species may disrupt the healing of erosions (Iliev et al., 2025).

In ulcerative colitis, an increase in *C. albicans* and an increase in *Alternaria* are observed (Füchtbauer et al., 2025). Additionally, it has been discovered that polymorphisms in genes responsible for fungal recognition are correlated with a more severe outcome of ulcerative colitis (Pérez, 2021).

Methods of modulating the microbiota as a potential therapeutic strategy in IBD

The potential impact of dysbiosis on the pathogenesis and progression of inflammatory bowel diseases has directed further research toward the possibility of using therapies that modulate the microbiota (Shan et al., 2022; Iliev et al., 2025).

Diet

One method used in the adjunctive treatment of IBD is a proper diet, which helps restore intestinal homeostasis by reducing inflammation (Christensen et al., 2024). Among the methods used to treat IBD in the pediatric population, exclusive enteral nutrition (EEN) stands out for its effectiveness in achieving remission; it increases the population of *Firmicutes*, paradoxically reducing bacterial diversity in stool samples. In contrast, the exclusion diet used in Crohn's disease (CDED), which also increases *Firmicutes*, additionally promotes a reduction in the *Proteobacteria* population. Similar changes were observed following the use of specific carbohydrate diets (SCD) (Reznikov and Suskind, 2023).

The LOW FODMAP diet is controversial because it reduces the number of bacteria that produce SCFAs but also helps reduce IBD symptoms (Reznikov and Suskind, 2023; Christensen et al., 2024). An optimal amount of fiber (13.4–33.4 g/day) plays a crucial role as a dietary component that supports the maintenance of clinical remission in Crohn's disease (Serrano Fernandez et al., 2023). Other metabolites, e.g., hydrogen sulfide and ammonia, produced during protein fermentation can damage the intestinal barrier (Christensen et al., 2024). In contrast, a diet high in fats and refined sugars has a negative effect by promoting biofilm formation and the adhesion of the AIEC, inducing inflammation and compromising the integrity of the intestinal barrier (Reznikov and Suskind, 2023).

Nutraceuticals

In IBD, the nutraceuticals that target the microbiota may help reduce symptoms (Ashkanani et al., 2026).

1. Probiotics contain live microorganisms that stimulate the production of tight junction proteins and help maintain the integrity of the intestinal barrier, preventing toxic bacterial metabolites and toxins from entering the bloodstream. In addition, probiotic bacteria compete with pathogenic bacteria for adhesion sites on the intestinal epithelium and neutralize them by producing appropriate bacteriocins and hydrogen peroxide. The use of probiotics helps reduce markers of inflammation and the production of pro-inflammatory cytokines, while supporting the production of anti-inflammatory cytokines. Multi-strain formulations are more effective in this regard, with a greater reduction in inflammatory markers.
2. Prebiotics are compounds that are fermented by the microbiota after ingestion. They help increase the levels of SCFAs, e.g., butyrate, which regulates the immune system's response and has strong anti-inflammatory properties in the intestine.
3. Synbiotics are formulations that act synergistically by combining the properties of prebiotics and probiotics. It has been proven that the use of a synbiotic (*Bifidobacterium longum* and Synergy 1) in patients with active ulcerative colitis can induce remission and reduce inflammation. The prebiotic supports the colonization of the gut by the probiotic.
4. The effects of nutraceuticals may vary depending on the patient and the type of disease, but the results are promising (Reznikov and Suskind, 2023; Christensen et al., 2024; Ashkanani et al., 2026).

Fecal microbiota transplantation (FMT)

FMT is a method that allows the microbiota to be transferred from a healthy donor to a patient's gastrointestinal tract. Feces collected from the donor before transplantation undergo numerous procedures and can be delivered to the receiver's gastrointestinal tract via colonoscopy, nasoduodenal, nasojejunal, or nasogastric tubes, rectal enema, or orally by capsules (Hou et al., 2025; Busmail et al., 2026). It is effective in treating recurrent diarrhea caused by *C. difficile* infections, and the importance of this form of therapy in the induction and maintenance of remission in IBD is growing (Sokol et al., 2020; Keller et al., 2021). FMT helps reduce excessive activation of the immune system and may support the eradication of potentially pathogenic microorganisms with multidrug resistance (Keller et al., 2021; Yadegar et al., 2024). The pathogenic effects of dysbiosis in the development of IBD have led to the modulation of the microbiome via FMT. There are a few randomized clinical trials that evaluate the effectiveness of FMT in the treatment of IBD (Rees et al., 2022; Hou et al., 2025; Busmail et al., 2026). The most important studies on FMT are summarized in Table 2.

Table 2. Summary of the most important randomized clinical trials on the effectiveness of FMT in the treatment of IBD.

	IBD Condition	The FMT Procedure	Main conclusions
Moayyedi et al., 2015	Active mild/moderate ulcerative colitis	6 weekly rectal retention enemas	1. FMT is effective in inducing remission (24% FMT vs. 5% placebo); 2. The effect depends on a “super-donor” with significant amounts of <i>Lachnospiraceae</i> and <i>Ruminococcus</i>; 3. FMT is a relatively safe method;
Rossen et al., 2015	Active mild/moderate ulcerative colitis	Two infusions, the second administered 3 weeks later via a nasoduodenal tube	No statistical advantage of FMT over autologous transplantation;
Paramsothy et al., 2017	Active ulcerative colitis	Intensive infusions	Intensive treatment increases the rate of clinical and endoscopic remission (27% for FMT vs. 8% for placebo)
Costello et al., 2019	Active mild/moderate ulcerative colitis	3 samples, the first obtained via colonoscopy, the other two via enema; samples prepared under anaerobic conditions	Anaerobic conditions influence the chances of transplant success by preserving oxygen-sensitive bacteria (remission rate: 32% for FMT vs. 9% for autologous transplant)
Sood et al., 2019	Maintaining remission in ulcerative colitis	Every 8 weeks via colonoscopy in patients who have previously responded to FMT	1. FMT proved effective in maintaining clinical remission (statistical significance was not achieved); 2. FMT was significantly more effective in maintaining endoscopic and histological remission.
Sokol et al., 2020	Maintaining Remission in Crohn’s Disease	A single infusion during colonoscopy in patients in remission achieved through steroid therapy	1. FMT may improve the condition of the mucosa, normalize inflammatory markers, and potentially prolong remission 2. The relationship between successful remission induction and effective colonization of the intestinal wall by the donor microbiota (engraftment).

The success of the transplant in ulcerative colitis depends on the type of disease and how long it has lasted (Moayyedi et al., 2015; Rees et al., 2022). In mild or moderate ulcerative colitis, FMT brings moderately effective results. In cases of ulcerative colitis resistant to standard pharmacological treatment, meaningful improvement has not been observed (Igbo et al., 2025). The outcome of FMT as a treatment is influenced by the intensity of the treatment and the specific composition of the donor’s fecal microbiota (Rees et al., 2022; Busmail et al., 2026).

FMT is effective only if the introduced strains engraft. The recipient microbiota should become similar to the donor microbiota. At the same time, the proportion of bacteria from the *Lachnospiraceae* and *Ruminococcaceae* families increases, as well as *Akkermansia muciniphila*. These bacteria help produce SCFAs and strengthen the integrity of the intestinal barrier (Moayyedi et al., 2015; Rees et al., 2022; Hou et al., 2025).

Microorganisms transferred from a healthy donor start to compete with pathogenic species in the recipient and take the sites where they could attach to the epithelium. The microorganisms also compete for nutrients with pathogenic species. They produce SCFAs and

partially restore normal bile acid metabolism, reducing inflammation as a result. Moreover, the immune response is regulated through increased Treg cell activity and IL-10 production (Rees et al., 2022; Hou et al., 2025; Busmail et al., 2026).

A lower probability of attaining remission is associated with an increased presence of bacteria from the genera *Fusobacterium* and *Gammaproteobacteria* in the patient's microbiota (Paramsothy et al., 2017; Sokol et al., 2020; Rees et al., 2022).

4. CONCLUSION

Standard treatment for inflammatory bowel disease (IBD) can be combined with modulation of the gut microbiota. Targeted dietary and nutraceutical strategies represent safe, readily available, and cost-effective adjunctive therapies for the treatment of inflammatory bowel disease (IBD). Exclusive enteral nutrition (EEN) and exclusion diets for Crohn's disease (CDED) have been shown to be effective in inducing clinical remission. At the same time, multi-strain probiotics and prebiotics effectively strengthen the mucosal barrier. The FMT procedure serves as a tool for restoring intestinal homeostasis and has a documented effect in mild and moderate forms of ulcerative colitis. It will be important to optimize and match the donor's microbiota to the recipient's by establishing stool banks and adhering to rigorous safety protocols.

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Informed consent

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Ethical approval

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Conflict of interest

The authors declare that they have no conflicts of interest, competing financial interest or personal relationship that could have influenced the work reported in this paper.

Data and materials availability

All data associated with this study will be available based on the reasonable request to the corresponding author.

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