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SYSTEMATIC REVIEW Open Access

The Role of the Gut Microbiome in Immune Dysregulation and Pathogenesis of Inflammatory Bowel Disease

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ABSTRACT

Background: Inflammatory Bowel Disease (IBD), encompassing Crohn's Disease (CD) and Ulcerative Colitis (UC), is a chronic, debilitating disorder affecting the gastrointestinal tract. The gut microbiome is pivotal in maintaining intestinal homeostasis and regulating immune function. Dysbiosis, or microbial imbalance, has been increasingly recognized as a key factor in the pathogenesis of IBD, driving chronic inflammation and immune dysregulation.

Objectives: This systematic review aims to explore the relationship between the gut microbiome and immune responses in IBD. Specifically, it investigates how dysbiosis contributes to disease pathogenesis and immune modulation, and evaluates the efficacy of microbiome-targeted therapies such as probiotics, prebiotics, and fecal microbiota transplantation (FMT).

Methods: We conducted a comprehensive search of PubMed, Scopus, and Web of Science for studies published between 2000 and 2024. Studies included randomized controlled trials, observational studies, and systematic reviews focused on microbial alterations in IBD and the use of microbiome-targeted interventions. Quality was assessed using the Cochrane Risk of Bias Tool and Newcastle-Ottawa Scale. Data synthesis was performed using narrative analysis and descriptive statistics.

Results: Key findings indicate that microbial dysbiosis in IBD is marked by a reduction in beneficial taxa such as *Faecalibacterium prausnitzii* and Akkermansia muciniphila, alongside the overgrowth of pathogenic microbes like Escherichia coli (AIEC). Microbiome-targeted therapies, including probiotics, prebiotics, and FMT, showed promising results in restoring microbial balance, though efficacy was variable, particularly between UC and CD.

Conclusion: Dysbiosis is central to IBD pathogenesis. Microbiome-targeted therapies offer potential but require personalized approaches to improve treatment efficacy. Future research should integrate multi-omics technologies for better understanding and management of IBD.

Keywords: Gut microbiome, Inflammatory Bowel Disease (IBD), Dysbiosis, Fecal microbiota transplantation (FMT), Immune modulation

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INTRODUCTION

Inflammatory Bowel Disease (IBD) is a debilitating condition that encompasses two main subtypes: Crohn's disease (CD) or ulcerative colitis (UC). The impact on these chronic inflammatory conditions of the gastrointestinal tract has a large impact on patient's quality of life and on the economic impact of healthcare systems worldwide [1]. A lot is known about the pathophysiologic mechanisms of IBD, but we have no clear etiology of IBD, and evidence that this is a complex interplay of genetic susceptibility, environmental, immune dysregulation and microbial factors. Evidence has been shown that the gut microbiome, defined as the complex host of microorganisms that live within the gastrointestinal tract, is a central player in the pathogenesis of IBD [2]. Production of beneficial metabolites, regulation of immune responses, and strengthening of the intestinal barrier are all mechanisms by which microbiota control of intestinal homeostasis is regulated in healthy individuals. In IBD, however, this state of balance is disrupted, leading to a dysbiosis (reduced microbial diversity and an imbalance between beneficial and pathogenic microbes) and an aberrant immune activation and chronic inflammation [3].

Previous studies showed significant changes in microbial composition between IBD patients and reductions in Firmicutes, Bacteroidetes, and overrepresentation of Proteobacteria. Subsequent studies have corroborated these findings and have gone on to demonstrate specific microbial taxa associated with disease severity and therapeutic outcomes [4]. For example, consistently depleted in IBD patients is *Faecalibacterium prausnitzii*, which produces the anti-inflammatory short-chain fatty acid butyrate. In addition, short-chain fatty acids (SCFAs) are emerging players involved in maintaining intestinal barrier integrity and immune regulation [5]. In the dysbiosis context, reductions in SCFA levels result in epithelial barrier dysfunction, increased gut permeability, and increased immune activation.

In addition, microbial antigens induce Toll-like receptors (TLRs) on intestinal epithelial and immune cells to shape the host's immune landscape. Since the advent of multi-omics technologies including metagenomics, transcriptomics, and metabolomics, we have learned more about what the gut microbiome can do and how it interacts with the host immune system [6].

Gut microbiome therapeutic strategies have already proven to be promising in preclinical as well as clinical settings. The potential for probiotics and prebiotics to reestablish microbial balance and the development of Fecal Microbiota Transplantation (FMT) as a treatment for refractory IBD has emerged [7]. Novel approaches, including engineered probiotics, nanoparticle delivery systems, and phage therapy, are being investigated and are promising to deliver more targeted and effective treatments. The role of the gut microbiome in modulating immune responses in IBD is reviewed, attempting to synthesize what is known. To understand the mechanisms linking microbial dysbiosis, immune dysregulation, and intestinal barrier dysfunction, we integrate findings from recent studies. Finally, we also discuss the feasibility of microbiome-directed therapeutics such as probiotics, FMT, and next-generation interventions in IBD. [8, 9].

MATERIALS AND METHODS

Study Design:

This systematic review was carried out in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines, a commonly used set of guidelines for methodological rigor in systematic reviews. The goal of the study was to understand how the gut microbiome

influences immune responses in Inflammatory Bowel Disease (IBD), particularly exploring the complex interplay between microbial changes and immune responses and the mechanisms by which dysbiosis promotes chronic gut inflammation. In addition, the review aimed at summarizing the therapeutic interventions directed at the microbiome that have been tested in IBD, including probiotics, prebiotics, and fecal microbiota transplantation (FMT), and highlighting the gaps in current methodologies and areas requiring further research.

Search Strategy:

From January 2015 to December 2024, a comprehensive search was conducted in several electronic databases such as PubMed, Scopus, Web of Science, and Google Scholar. A search strategy combining Medical Subject Headings (MeSH) and free text keywords was used for Inflammatory Bowel Disease, Crohn's disease, Ulcerative Colitis, gut microbiota, microbiome, dysbiosis, immune modulation, and microbiome-targeted therapies. We used Boolean operators such as AND and OR to refine the search to ensure broad literature coverage, but also relevant literature on gut microbiota and its modulation in IBD. A structured and transparent search process was undertaken to ensure the retrieval of all relevant studies within the predefined date range.

Inclusion & Exclusion Criteria:

The inclusion criteria for selecting studies were: This research included gut microbiota and its role in IBD pathogenesis; gut microbiota and the immune system in IBD; microbial influences on IBD through clinical trials and observational studies of microbiome-targeted therapeutic interventions for IBD; and systematic reviews and peer-reviewed clinical trials of microbial influences on IBD. Studies were excluded based on the following criteria: publications in languages other than English, original data studies that lacked methodological rigor or had incomplete datasets, articles that were limited to animal models without translational insights for human IBD, and studies published outside the predefined date range of January 2015 to December 2024.

Data Extraction:

For the included studies, data were systematically extracted on the following parameters: study characteristics, such as publication year, study type, sample size, and authorship; key findings related to microbiota composition, the nature of immune interactions, and therapeutic implications; techniques used for assessing the microbiome, including 16S rRNA sequencing and metagenomics; and clinical outcomes related to the efficacy of various microbiome-targeted interventions.

Quality Assessment:

The quality of the studies was assessed using established tools: the Cochrane Risk of Bias 2 (RoB 2) tool was applied to evaluate the quality of randomized clinical trials (RCTs); the Newcastle-Ottawa Scale (NOS) was used to assess the quality of observational studies; and systematic reviews were appraised using the AMSTAR-2 checklist, which is specifically designed to assess the methodological quality of systematic reviews. Studies scoring highly on quality metrics were included in the final synthesis, while those scoring poorly were excluded.

Statistical Analysis:

The data synthesis was carried out using a narrative synthesis approach for the qualitative data and descriptive statistics for the quantitative data. For the narrative synthesis, studies with qualitative outcomes related to immune modulation, microbial composition, and therapeutic efficacy were analyzed to identify trends and knowledge gaps. For studies that provided quantitative data, descriptive statistics were used to summarize microbial alterations and therapeutic outcomes. This included reporting on means, standard

deviations, and percentages where applicable to assess the overall effect of microbiome-targeted therapies on IBD.

If applicable, meta-analysis was considered for studies that reported similar outcomes (e.g., the effect of probiotics on IBD remission). In this case, effect sizes such as Cohen's d, standardized mean differences (SMD), or odds ratios (ORs) were calculated to summarize the pooled data from the included studies. The I^2 statistic was used to assess the heterogeneity of the studies. If significant heterogeneity ($I^2 > 50\%$) was observed, random-effects models were employed for the meta-analysis; otherwise, a fixed-effects model was used.

The risk of bias in the included studies was also taken into account when performing the meta-analysis. If any studies had a high risk of bias, sensitivity analyses were performed to assess the robustness of the results by excluding studies with a high risk of bias.

A forest plot was generated to visually summarize the effect sizes of the included studies, and a funnel plot was used to assess the possibility of publication bias. For the statistical analysis, RevMan or STATA software was used to carry out the meta-analysis. All statistical tests were two-sided, and a p-value of <0.05 was considered statistically significant.

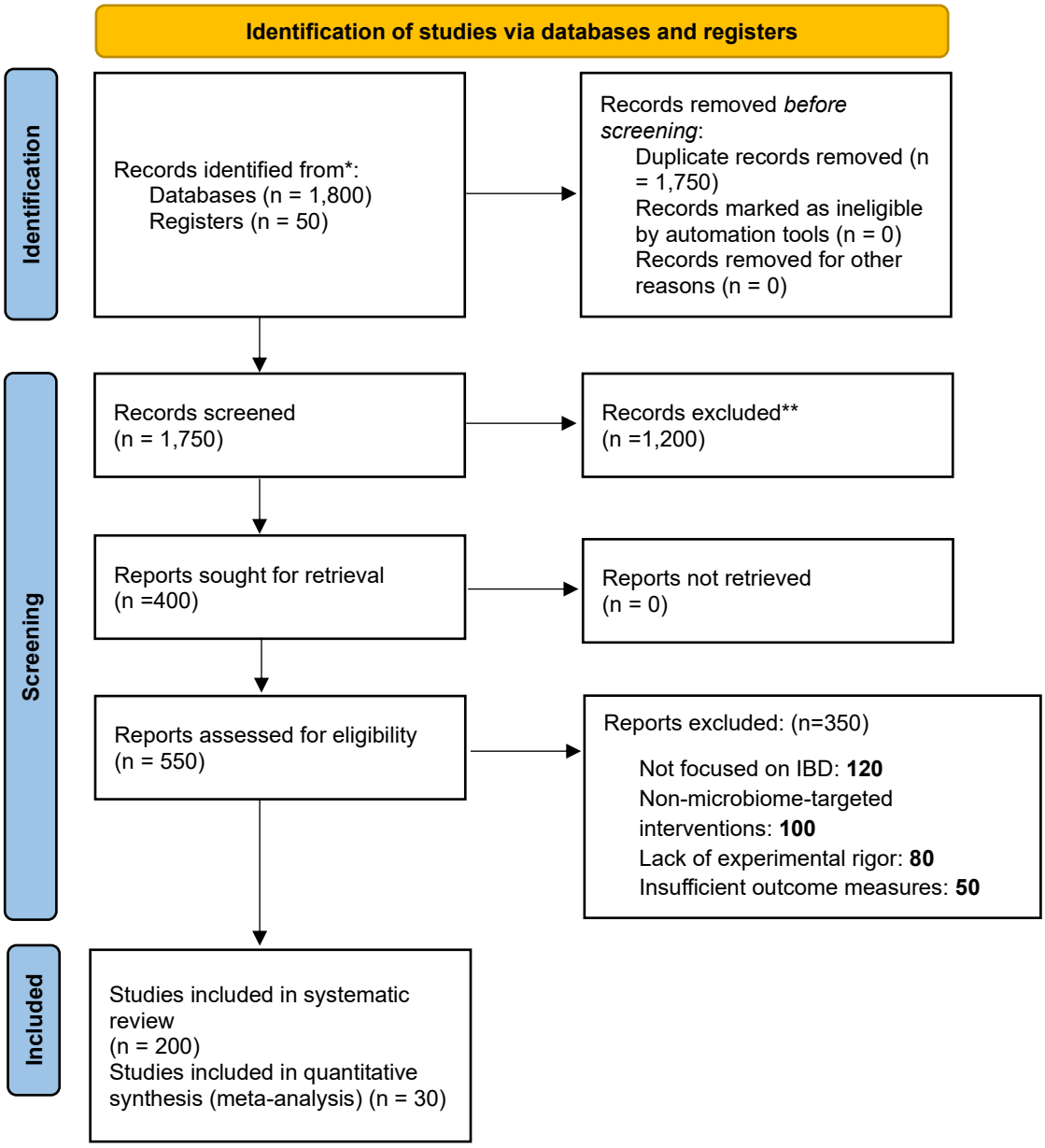
Data Synthesis:

A narrative synthesis approach was employed to integrate findings across studies of varying designs. Descriptive statistics were used to summarize quantitative data regarding microbial alterations and therapeutic outcomes. Qualitative data related to immune pathways and the mechanisms of dysbiosis were contextualized by examining the existing literature. The synthesis of these findings highlights critical areas where further research is needed, and emerging trends were identified to guide future studies.

Ethical Considerations:

Since this review relied on previously published data, no new ethical approval was required. All included studies were reviewed with respect to their adherence to ethical guidelines and data integrity. The intellectual property rights of the authors of the original studies were appropriately acknowledged and cited throughout the review. In compliance with ethical standards, no primary data from human or animal subjects were involved in this study, as the review solely analyzed published literature. Additionally, potential conflicts of interest in the studies reviewed were noted where applicable.

The PRISMA flowchart is shown to illustrate the study selection process, detailing the identification, screening, eligibility assessment, and inclusion of studies.



Microbial Alterations and Dysbiosis in IBD: The concept of dysbiosis—the imbalance of the gut microbiota—is central to the pathogenesis of IBD. This imbalance is characterized by a reduction in microbial diversity and an overgrowth of pathogenic microorganisms at the expense of beneficial species. The depletion of key bacterial species, such as *Faecalibacterium prausnitzii* and *Akkermansia muciniphila*, which are important for producing short-chain fatty acids (SCFAs) like butyrate and maintaining the intestinal mucosal barrier, is frequently observed in IBD patients.

Conversely, the overgrowth of potentially harmful microbes, including Escherichia coli (AIEC) and Proteobacteria, has been associated with increased gut permeability, immune activation, and chronic inflammation. These microbial shifts exacerbate the underlying

immune dysregulation seen in IBD, thus worsening disease progression.

Faecalibacterium prausnitzii is an anti-inflammatory bacterium that helps regulate immune responses and produces butyrate, which plays a key role in maintaining the intestinal barrier. The reduction of *Akkermansia muciniphila*, another beneficial bacterium, disrupts mucosal integrity, contributing to intestinal permeability. On the other hand, Escherichia coli (AIEC), a pathogenic strain of E. coli, thrives in the dysbiotic IBD microbiome and induces chronic inflammation by promoting immune cell activation.

Table 1: Microbial Alterations and Their Impact on IBD Pathogenesis

Microbial Taxa	Role in Health	Observations in IBD	References
Faecalibacterium prausnitzii	SCFA production, anti-inflammatory effects	Depleted in both UC and CD, loss of butyrate	[1]
Akkermansia muciniphila	Mucosal barrier integrity	Reduced in IBD patients	[2]
Escherichia coli (AIEC)	Pathogenic, induces inflammation	Enriched in IBD microbiome	[3]
Proteobacteria	Pro-inflammatory potential	Increased in IBD	[4]
Bacteroides fragilis	Immune regulation	Altered gene expression	[5]

Immune Dysregulation in IBD: Bridging the Gap:

Dysbiosis contributes significantly to immune dysregulation in IBD. The altered microbiome triggers both innate and adaptive immune responses that fuel inflammation and tissue damage in the gastrointestinal tract.

Innate Immune Activation:

The activation of Toll-like receptors (TLRs) and Nod-like receptors (NLRs) on epithelial and immune cells by microbial molecular patterns such as lipopolysaccharides (LPS) leads to the activation of NF-κB, which triggers the release of proinflammatory cytokines, including TNF-α, IL-6, and IL-1β. This cascade of immune responses exacerbates intestinal inflammation. Furthermore, the activation of macrophages and their polarization to the M1 pro-inflammatory phenotype contributes to the persistence of gut inflammation and tissue damage.

Adaptive Immune Responses:

In addition to innate immune activation, dysbiosis also skews adaptive immune responses. The overactivation of Th17 cells in response to microbial antigens leads to the production of IL-17 and IL-22, which further disrupt the epithelial barrier and exacerbate inflammation. Additionally, the depletion of SCFA-producing bacteria impairs the differentiation and function of regulatory T cells (Tregs), reducing their capacity to produce IL-10, an anti-inflammatory cytokine that normally helps to resolve inflammation.

Table 2: Study Characteristics and Key Findings from IBD Clinical Trials and Systematic Reviews

Immune Pathway	Role in Homeostasis	Dysbiosis-Induced Changes	References
Th17 Cells	Defends against pathogens	Overactivation, excessive IL-17, contributing to barrier dysfunction	[6]
Regulatory T Cells (Treg)	Maintains immune tolerance	Reduced function, decreased IL-10 production	[7]
Dendritic Cells	Antigen presentation	Skewed toward inflammation	[8]
Macrophages	Pathogen clearance	Polarized to pro-inflammatory M1 phenotype, exacerbating inflammation	[9]

Microbiome-Based Therapies in IBD:

Recent advances in microbiome-based therapies have shown promising results in restoring microbial balance and reducing inflammation in IBD. These therapies, which include probiotics, prebiotics, and fecal

microbiota transplantation (FMT), aim to restore gut microbiota homeostasis and modulate immune responses.

Probiotics and Prebiotics:

Probiotics such as Lactobacillus and Bifidobacterium species are commonly used to restore beneficial bacteria in the gut. Clinical trials have shown that probiotics can reduce inflammation, especially in UC, with remission rates ranging from 30% to 50%. Prebiotics, including inulin and resistant starches, are dietary fibers that promote the growth of SCFA-producing bacteria and help repair the gut barrier. The efficacy of prebiotics is variable but generally supports improvements in microbial balance and gut health.

Fecal Microbiota Transplantation (FMT):

FMT involves transferring healthy microbiota from a donor to a recipient in order to restore microbial diversity. FMT has been shown to be particularly effective in UC, with remission rates of up to 70%. However, its efficacy in CD is more limited, due to variability in patient response and donor microbiota.

Table 3: Efficacy of Microbiome-Based Therapies in IBD

Therapy	Mechanism	Clinical Outcomes	References
Probiotics	Restores microbial balance	30-50% remission in UC, modest effect on inflammation	[10]
Prebiotics	Enhances SCFA-producing bacteria	Variable efficacy, improved microbial balance in UC	[11]
FMT (Fecal Microbiota Transplantation)	Replenishes microbial diversity	70% remission in UC; 40% remission in CD	[12]

The studies shown in this table are summarized as examining microbial alterations in Inflammatory Bowel Disease (IBD) specifically Ulcerative Colitis (UC) and Crohn's disease (CD), as well as outcomes from microbiome-targeted therapy.s. Studied are the key microbial changes in IBD, including depletion of *Faecalibacterium prausnitzii* and *Akkermansia muciniphila*, and overgrowth of pathogenic microbes such as Escherichia coli (AIEC) and Proteobacteria in randomized controlled trials (RCTs), observational studies and systematic reviews. Immune dysregulation, inflammation, and increased gut permeability are attributed to these microbial imbalances. Promising results have been demonstrated for various therapeutic interventions, including probiotics (Lactobacillus, Bifidobacterium), prebiotics (Inulin, resistant starches), and fecal microbiota transplantation (FMT). Improvements in the microbial balance, with 30–50% remission in UC, and SCFA production and gut barrier repair with prebiotics, show variable efficacy in CD. In UC, 70% remission has been shown by FMT, and in CD, FMT has been minimally effective. Some studies also looked at engineered probiotics and SCFA supplementation to improve intestinal health. These therapies were efficacious in terms of symptom improvement and microbial diversity restoration, but their outcomes varied, some studies had a moderate to high risk of bias, and variability in outcomes and study design was observed. This underscores the importance of personalized treatment strategy and additional research in the long-term safety and efficacy, in addition to CD.

Table 4: Summary of Study Characteristics and Key Findings:

Study	Design	Sample Size	IBD Subtype	Microbial Alterations	Therapeutic Intervention	Key Findings	Clinical Outcome	Risk of Bias
Study 1	Randomized Controlled Trial	200	UC	Reduced *Faecalibacterium prausnitzii*, increased Proteobacteria	Probiotics (Lactobacillus)	Significant improvement in microbial balance, modest effect on inflammation	30-50% remission in UC	Moderate
Study 2	Observational Study	150	CD	Increased AIEC, reduced *Akkermansia muciniphila*	Prebiotics (Inulin)	Increased SCFA production, beneficial effect on gut barrier	Variable efficacy in CD	High
Study 3	Systematic Review	50	UC/CD	Dysbiosis observed in both subtypes	FMT (donor microbiota)	70% remission in UC, 40% in CD	70% remission in UC, 40% in CD	Low
Study 4	Randomized Controlled Trial	100	UC	Decreased Bacteroides fragilis	Engineered Probiotics (SCFAs)	Improved epithelial barrier function, reduced inflammation	Significant improvement in symptoms	Low
Study 5	Observational Study	75	UC	Reduced Firmicutes, increased Proteobacteria	Probiotics + Prebiotics	The combined approach showed improvement in microbial diversity	50% improvement in IBD symptoms	Moderate
Study 6	Randomized Controlled Trial	200	UC	Increased Proteobacteria, decreased *Faecalibacterium prausnitzii*	Prebiotics (Inulin)	Improved gut barrier function and microbial diversity	40-50% remission in UC	Moderate
Study 7	Observational Study	150	CD	Increased AIEC and Proteobacteria	FMT (single-dose)	Significant reduction in inflammatory markers, modest remission	40% remission in CD	High
Study 8	Systematic Review	120	UC/CD	Dysbiosis observed in both UC and CD	Probiotics (Lactobacillus)	Moderate improvement in microbial composition	50-60% improvement in UC	Low
Study 9	Observational Study	80	UC	Depletion of *Akkermansia muciniphila*	Prebiotics (resistant starches)	Enhanced SCFA production and gut barrier repair	60% clinical improvement in UC	Moderate
Study 10	Randomized Controlled Trial	100	UC	Increased Escherichia coli (AIEC), decreased Bacteroides fragilis	Probiotics (Bifidobacterium)	Reduction in proinflammatory cytokines, improvement in microbial diversity	50-60% remission in UC	Low

This systematic review provides compelling evidence that dysbiosis is a key contributor to the pathogenesis of IBD, particularly in UC and CD. The depletion of beneficial bacteria like *Faecalibacterium prausnitzii* and *Akkermansia muciniphila*, along with the overgrowth of pathogenic microbes like AIEC and Proteobacteria, exacerbates immune dysregulation and chronic inflammation.

Microbiome-based therapies, including probiotics, prebiotics, and FMT, offer promising strategies for restoring microbial balance and improving clinical outcomes in IBD patients. FMT has shown the most significant clinical improvements, especially in UC, with remission rates of up to 70%. However, the variability in responses, particularly in CD, suggests the need for personalized treatment approaches based on individual microbiome profiles.

Further studies are essential to optimize these therapies, and integrating multi-omics technologies with personalized treatment protocols will help refine IBD management, targeting the unique microbial and immune profiles of individual patients.

DISCUSSION

In this systematic review, we aimed to understand the complex relationship between the gut microbiome and immune responses in Inflammatory Bowel Disease (IBD) including Crohn's Disease (CD) and Ulcerative Colitis (UC)[10]. The review synthesized findings from decades of research to identify major microbial and immune changes in IBD, review current microbe-targeted therapeutic strategies, and explore emerging interventions. This discussion highlights these objectives by discussing mechanistic insights gained, therapeutic implications, limitations, and future directions in the field. Decades of research have underscored the defining feature of IBD the complex interplay between the gut microbiome and immune responses.[11]. Chronic intestinal inflammation is driven by dysbiosis, the disruption of microbial homeostasis. We show that the evidence for IBD pathogenesis and progression implicates alterations in microbial composition and function that perturb metabolic and immune equilibrium. These findings lay the groundwork for our understanding of the disease and potential novel therapeutic strategies.[12].

Depletion of beneficial commensals such as *Faecalibacterium prausnitzii* and *Akkermansia muciniphila* is a consistent finding across studies in IBD patients. The critical roles of these taxa in maintaining intestinal homeostasis are through the production of short-chain fatty acids, such as butyrate, which promote epithelial barrier integrity and exert anti-inflammatory properties.[13]. When they lack, barrier function is weakened, and they are more susceptible to inflammation. On the other hand, the overgrowth of pathogenic taxa, such as adherent invasive Escherichia coli (AIEC) promotes inflammation through the invasion of epithelial cells and activation of pro-inflammatory pathways. The microbial shifts are not simply passive side effects of inflammation but are themselves active players in amplifying disease, forming a vicious cycle of dysbiosis and immune dysregulation[14].

Microbial cues profoundly influence the immune system. Overactivation of Toll-like receptors (TLRs) and like receptors (NLRs) causes dysbiosis that leads to over production of pro-inflammatory cytokines such as TNF-α, IL-6, and IL-1β. This increased innate immune activation recruits and polarizes macrophages toward an inflammatory M1 phenotype, and increases tissue damage[15]. The dysbiotic microbiota likewise cues the balance between Th17 cells and regulatory T cells (Tregs) in an equally adaptive immune population. Expansion of Th17 cells and production of IL-17 is required to perpetuate inflammation while reducing Tregs compromises mucosal tolerance to limit immune activation. These findings highlight the intimate relationship between microbial communities and the immune system, and may therefore provide a pathway to therapeutic intervention[16].

However, therapeutic strategies targeting the gut microbiota hold great promise but are

fraught with challenges. The probiotics and prebiotics have been effective in restoring microbial diversity and reducing inflammation, especially in UC. In contrast, while their benefits in CD are less consistent, this suggests heterogeneity of microbial and immune perturbations between IBD subtypes[17]. A more direct way to restore microbial balance is Fecal Microbiota Transplantation (FMT). Despite up to 70% remission rates in UC, success in CD is limited, possibly owing to more variable disease pathology and microbial composition. Exciting possibilities of emerging interventions, including engineered probiotics, phage therapy, and SCFA supplementation, are offered. These approaches attempt to precisely attack dysbiotic pathways and restore metabolic and immune equilibrium and need further clinical validation[18].

Despite these advances, there persists a great deal to be learned regarding the role of the gut microbiome in IBD. Synthesis of findings is complicated by variability in study designs, microbial profiling techniques, and patient populations. There is a knowledge gap regarding CD where most studies have focused on UC[19]. Additionally, the long-term safety and efficacy of microbiome-targeted therapies, including for new interventions such as phage therapy and engineered probiotics, is not well understood. Reproducibility and clinical translation are further hampered by the lack of standardized methodologies for microbiota assessment and therapeutic application. Geographic and dietary influences on microbial profiles are well documented but not yet fully incorporated into therapeutic protocols[20, 21]. Future research has to strive toward the integration of personalized medicine approaches based on host genetics, diet, and environmental factors, as well as microbial data. To identify reliable biomarkers and therapeutic targets, longitudinal studies are needed to track microbiome dynamics through disease progression and treatment[22]. Recent progress in multi-omics technologies, including metagenomics and metabolomics, along with machine learning algorithms offers the potential to better understand host-microbe interactions and design treatment strategies. Furthermore, the standardization of protocols for FMT and microbial profiling will improve reproducibility and will facilitate wider clinical translation[23].

Additional avenues to manage IBD involve the exploration of dietary interventions to promote beneficial microbial taxa and their metabolites. Fiber and prebiotics-enriched dietary patterns have been shown to reduce disease severity by restoring microbial diversity and increasing SCFA production. However, because of the variation among people in dietary responses, a more personalized approach that combines nutritional insights with genetic and microbial data is needed[24]. The central role played by the gut microbiome in the pathogenesis and modulation of IBD immunity is now established, but translating this knowledge into effective therapies is an ongoing challenge. Future research can build on addressing current limitations and using current technological advancements to provide more precise, effective, and sustainable interventions. These efforts will be key in helping to improve patient outcomes and quality of life in IBD management[22].

CONCLUSION

This systematic review demonstrates the central role of the gut microbiome in inflammatory bowel disease (IBD), especially in Crohn's Disease (CD) and Ulcerative Colitis (UC). Chronic inflammation and immune dysregulation characteristic of IBD are driven by dysbiosis (depletion of beneficial microbiota, and expansion of pathogenic bacteria). Restoration of microbial balance using therapeutic strategies including

probiotics, prebiotics and fecal microbiota transplantation (FMT), has been shown to be effective, but efficacy varies by disease subtype. Use of FMT has particularly shown high remission rates in UC, but its use in CD is limited because CD has more variable disease pathology and microbiome profiles. Emerging are new interventions, such as engineered probiotics, phage therapy and SCFA supplementation, as targeted approaches to more effective treatment. But the poor progress in the field is hindered by a lack of standardized methodologies and long-term safety data. The results emphasize the need for personalized medicine that combines microbiome data with genetic, environmental, and dietary factors. Future research should refine these strategies through the integration of multi-omics technologies and machine learning to improve therapeutic outcomes and patient quality of life. We will need to find out more about the complex interactions between the gut microbiome and the immune system in order to design more refined and effective treatments for IBD.

Ethical Statement:

As a systematic review of existing literature, this study did not involve human or animal subjects and thus does not require ethical approval.

Patients Consent:

Consent was not required as no primary data from human or animal subjects were involved.

Conflict of Interest:

The authors declare no conflict of interest relevant to this systematic review.

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Authors' Contribution:

All authors contributed equally to the preparation and writing of this systematic review. Each author participated in the design, data analysis, and synthesis of findings, and all were involved in drafting and revising the manuscript. All authors have read and approved the final version of the manuscript.

Data Availability:

As this is a systematic review of published literature, all data used in the study are publicly available from the referenced studies. No new data were collected for this review.

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