

INVESTIGATING THE RELATIONSHIP BETWEEN GUT MICROBIOME AND IBS

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ABSTRACT

Irritable Bowel Syndrome (IBS) is a multifactorial gastrointestinal disorder affecting a significant portion of the global population, characterized by symptoms such as abdominal pain, bloating, and irregular bowel movements. Although there is still much to learn about the pathophysiology of IBS, mounting data has linked the gut microbiota to the onset and progression of the condition. With a focus on microbial diversity, particular bacterial populations, and their impact on gut health and symptoms, this study aims to investigate the connection between gut microbiota makeup and IBS. Stool samples from people with IBS and healthy controls were thoroughly analyzed, and we profiled the microbial communities using next-generation sequencing methods.

Our findings show clear alterations in the relative abundance of specific bacterial species and decreased microbial diversity in the microbiome of IBS patients as compared to controls. In particular, IBS patients showed an overgrowth of pathobionts such *Enterococcus* and *Escherichia coli* together with a decrease of beneficial *Firmicutes* and *Bacteroidetes*. The degree of IBS symptoms, including bloating and stomach pain, was also connected with these alterations. We also looked at how changes in gut motility, visceral hypersensitivity, and low-grade inflammation—three important characteristics of

IBS—may be influenced by microbial dysbiosis.

The results of this study demonstrate the potential use of the gut microbiota as a therapeutic target and diagnostic biomarker for IBS. We can develop new microbiome-based therapies, such as probiotics, prebiotics, and fecal microbiota transplantation, to restore gut health and enhance patient outcomes by comprehending how certain microbial imbalances impact the course of disease. In addition to providing opportunities for individualized therapy based on microbiome profiles, this research emphasizes the significance of microbiome-gut-brain connections in the management of IBS.

Keywords: *Microbiome, gut microbes, IBS, microbial association*

INTRODUCTION:

Irritable Bowel Syndrome (IBS) is a common, chronic gastrointestinal disorder characterized by a group of symptoms that include abdominal pain, bloating, and alterations in bowel habits such as diarrhea, constipation, or a combination of both[1]. IBS is considered a functional disorder, meaning it does not involve any structural abnormalities or visible damage to the digestive system, but instead, the symptoms arise from disturbances in the normal function of the gut. The exact cause of IBS is not well understood, but it is believed to result from a complex interplay of factors, including abnormal gut motility, heightened visceral sensitivity (increased sensitivity to pain in the intestines), dysregulation of the gut-brain axis, alterations in the gut microbiome, psychological stress, and in some cases, post-infectious changes.[16]

IBS can be classified into several subtypes based on the predominant bowel symptom: IBS-D (diarrhea-predominant), IBS-C (constipation-predominant), IBS-M (mixed type), and IBS-U (unsubtyped), which refers to patients whose symptoms do not clearly fit into one of the other categories. The condition affects both men and women, though it is more prevalent in women, and it can be diagnosed using the Rome IV criteria, which emphasize the presence of abdominal pain at least once per week, along with associated changes in bowel movements, over a period of at least three

months.[2]

The diagnosis of IBS is primarily clinical, often requiring the exclusion of other potential causes of gastrointestinal symptoms such as inflammatory bowel disease (IBD), celiac disease, or colorectal cancer[3]. No specific biomarker exists for IBS, which makes the diagnosis challenging and largely reliant on symptom patterns and clinical evaluation.[17] Additionally, IBS symptoms can be highly variable, with some individuals experiencing symptom flares and others going through periods of symptom relief.

Treatment for IBS is multifaceted and aims to manage symptoms rather than cure the condition. It includes dietary modifications such as the Low FODMAP diet, pharmacological interventions like antispasmodics, laxatives, antidiarrheal agents, and antidepressants, as well as psychological therapies such as cognitive behavioral therapy (CBT) and gut-directed hypnotherapy. Probiotics and prebiotics are also often used to help restore balance to the gut microbiome, which is thought to play a crucial role in IBS pathophysiology. While IBS does not lead to serious, life-threatening conditions such as cancer, its impact on daily life and well-being can be profound, with many individuals experiencing significant emotional distress, work limitations, and social isolation due to the unpredictability of symptoms.

GUT MICROBIOME:

The distal small bowel and colon are home to the majority of the 100 trillion bacteria that make up the human gastrointestinal tract. Despite the fact that bacteria have received a lot of attention, it's crucial to keep in mind that viruses, fungi, archaea, and eukaryotes also contribute to the communities that live in the GI tract's microenvironment. More than 2,000 distinct species of bacteria from 12 phyla have been identified by studies; 93.5% of these species belong to the four dominating phyla: Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria. According to recent studies, environmental variables including nutrition, medications, and lifestyle have a bigger impact on the gut flora than genetics. Furthermore, it's possible that the gut

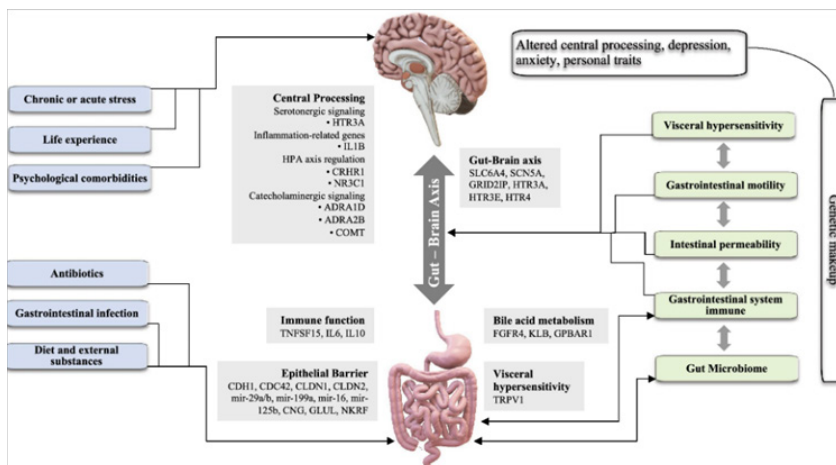
microbiota can predict metabolic variables and clinical phenotypes more accurately than genetics.[4]

Normal gut growth and health depend on bacteria. For instance, as compared to animals grown in a typical laboratory setting, germ-free mice exhibit reduced cycling and propagation of the migrating motor complex, delayed intestinal transit and stomach emptying, and decreased expression of the enteric nervous system genes GABA and VAP-33. By supplying vital amino acids, vitamins, and short-chain fatty acids, as well as encouraging the healthy growth and operation of the gut immune system, bacteria help support the host's health.

Mircobial association with IBS:

The integrated actions and communication between the microbiota and the autonomous nervous system are central players in the perpetuation of IBS symptoms. This signaling pathway is called the Gut-Brain Axis (GBA). The GBA is a bidirectional neurohumoral communication system that integrates brain and GI functions, such as gut motility, appetite and weight and here the microbiota plays a critical role.[5] Changes in gastrointestinal or central nervous system physiology may result in an altered habitat, which again may cause changes in the composition of the microbiota.

Dysbiosis, a disruption of the physiologic symbiotic interaction (eubiosis) between the human host and the microbiota, is thought to be a fundamental cause in the onset and maintenance of IBS in most patients. Evidence now available indicates that IBS is actually a problem of the microbiota and the GBA, since the dysbiosis seen in IBS and the immunological reaction that follows may cause and maintain the gastrointestinal symptoms of IBS.[6] It is unknown if gut alterations are caused by brain abnormalities or whether vagal and sympathetic pathways in the brain impact how the stomach functions.



Microbiome in healthy individual vs individual affected by IBS

In an initial investigation including 80 IBS patients and 65 matched controls who did not have IBS, Jeffery and associates discovered that *Ruminococcus gnavus* and *Lachnospiraceae* were abundant, but *Coprococcus catus* and *Barnesiella intestinihominis* were less prevalent [7]. IBS patients had lower abundance of *Bifidobacterium*, *Lactobacillus*, and *Faecalibacterium prausnitzii*, according to a meta-analysis of 13 publications [8]. A different meta-analysis that included 16 publications and 777 IBS patients discovered that, at the phylum level, there were more Firmicutes and less Bacteroidetes (with a higher Firmicutes:Bacteroidetes ratio). At lower taxonomic levels, they also found several alterations, such as a rise in Clostridiales and *Clostridium* and a fall in Bacteroidia and Bacteroidales [9]. Similarly, in the gut microbiome analysis of IBS patients compared to healthy controls, researchers found lower levels of *Lactobacillus* and *Bifidobacterium* and highly abundant *E. coli* and *Enterobacter* in subjects with IBS, but no difference in fecal Bacteroides or Enterococcus [10].

The majority of research have failed to identify substantial differences across IBS subtypes, despite evidence that the

microbiome of IBS patients and controls vary [9,11,12,13]. It should be noted that a lack of standardized techniques may contribute to the difficulty to identify meaningful variations in microbiome phenotypes in individuals with IBS. The current standard for analyzing gut microbial assemblages is whole shotgun metagenomics; however, this method depends on bioinformatic methods to interpret the data, which have drawbacks of their own [14,15]. When examining these functional characteristics, it's also critical to use metagenomics, metatranscriptomics, and metabolomics since taxonomic composition alone might not be sufficient to explain individual variances.

Conclusion:

In Conclusion, there is a complicated and multidimensional link between the gut microbiota and irritable bowel syndrome (IBS). There is mounting evidence that the pathophysiology of IBS may be significantly influenced by changes in the variety and composition of the gut microbiota. IBS patients have been shown to have dysbiosis, or an imbalance in the microbial community, with bacterial populations differing between IBS patients and healthy controls. IBS symptoms have been linked to certain microbial groups, including Firmicutes, Bacteroidetes, and species like *Faecalibacterium prausnitzii*.

Though a direct cause is still unknown, it is known that the gut microbiota can affect inflammation, visceral sensitivity, and gut motility—all of which are important aspects of IBS. IBS symptoms can also be caused by interactions between the microbiota and other factors including heredity, stress, and food. Though more study is required to completely understand the role of the microbiome and to create more effective, tailored medicines for IBS, personalized methods to therapy, such as dietary modifications, probiotics, and antibiotics, are showing promise.

A number of interesting techniques for controlling IBS are being investigated at the moment, including therapeutic treatments that target the gut flora. By restricting items that worsen bloating and pain, dietary interventions—in particular, the low FODMAP diet—have been shown to be useful in lowering

the symptoms of IBS. Although the benefits vary depending on the strain, probiotics like *Bifidobacterium* and *Lactobacillus* can help restore microbial balance and reduce symptoms. Prebiotics, which promote the growth of good bacteria, could also be helpful, but their usage must be carefully managed to prevent symptoms from getting worse. Fecal microbiota transplantation (FMT) is being researched as a possible therapy for people with refractory IBS, while antibiotics such as rifaximin have demonstrated promise in controlling IBS-D by lowering small intestine bacterial overgrowth (SIBO).

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