GLOBAL HEALTH & MEDICINE
ISSN / eISSN: 2434-9186 / 2434-9194
Volume 06, Issue 03.601-612
https://ghsjournal.com/

The Role of Gut Microbiota in Gastrointestinal Disorders: Investigating How Dysbiosis Contributes to Conditions Like Irritable Bowel Syndrome, Obesity, and Non-Alcoholic Fatty Liver Disease

Submission: 10 February 2026 | Acceptance: 24 May 2026 | Publication: 10 June 2026

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ABSTRACT:

Background: The gut microbiota present in human bodies serves as a crucial element to sustain gastrointestinal systems along with metabolic functions. Multiple scientific studies have shown that disturbed microbial equilibrium known as dysbiosis leads to several gastrointestinal problems such as irritable bowel syndrome (IBS), obesity as well as Non-Alcoholic Fatty Liver Disease (NAFLD). Therapies require development that targets dysbiosis patterns because doctors need to understand their clinical implications.

Aim: Researchers investigated how gut microbiota dysbiosis affected the creation of IBS, obesity, and NAFLD through specific microbial balance identification.

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Methods: The study took place at Allied Hospital in Faisalabad during 2024 February until 2025 January. Researchers enrolled 100 participants who had either IBS, obesity or NAFLD diagnosis. Scientists collected stool samples which they analyzed through 16S rRNA gene sequencing to determine microbial diversity as well as composition. In addition to testing microbiota profiles the research team gathered clinical along with demographic data to check for associations.

Results: Results showed patients with IBS presented reduced microbial diversity while Proteobacteria numbers showed significant increases in the same group. Research data indicated that obesity increases the presence of Firmicutes bacteria and raises the Firmicutes/Bacteroidetes count. People with NAFLD experienced a dual increase of Enterobacteriaceae along with decreased levels of beneficial bacterial groups including Bifidobacterium and Lactobacillus. All three conditions showed unique dysbiosis patterns which amounted to inflammation markers and unbalanced metabolic functions. **Conclusion:** The collected data established direct relationships between the abnormalities of gut microbiota as well as their roles in IBS development and NAFLD and obesity. Each condition displayed specific microbial patterns which calls for potential future use of behavior-modified microbial communities as a potential clinical tool for treating these conditions.

Keywords: Gut microbiota, Dysbiosis, Irritable Bowel Syndrome, Obesity, Non-Alcoholic Fatty Liver Disease, Gastrointestinal disorders, Microbial diversity.

INTRODUCTION:

The gastrointestinal tract of humans contained a widely known complex microbial system composed of trillions of organisms which scientists called gut microbiota. These microorganisms consisting of bacteria, viruses and fungi along with protozoa served as the necessary elements for preserving intestinal homeostasis

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and overall health status. Scientific progress during the past decades succeeded in vastly expanding knowledge about both gut microbiota components and their operational mechanisms. Research studies revealed that these microorganisms actively participated in digestion functions while simultaneously controlling immune response activities as well as metabolism and protecting against dangerous pathogens. Research found that dysbiosis which arises from disrupted gut microbiota composition and diversity trends to produce various gastrointestinal along with systemic health problems. Dysbiosis presented when beneficial microbial communities did not match harmful ones while simultaneously lowering microbial ecosystem diversity [2]. Scientists found that such an imbalance served as a pathogenic factor behind several common chronic disorders including irritable bowel syndrome (IBS), obesity and non-alcoholic fatty liver disease (NAFLD).

Research shows irritable bowel syndrome functions as a form of gastrointestinal disorder which causes abdominal pain together with bloating along with abnormal bowel movements. Multiple factors contributed to IBS etiology yet healthcare professionals discovered through ongoing research that gut microbiota changes highly impact disease development. Research results showed IBS patients commonly have diminished microbial diversity along with greater presence of pro-inflammatory microorganisms within their intestines [3]. Dysbiosis caused both intestinal permeability along with immune activation whereas these conditions represent fundamental features of IBS pathology.

Research on obesity-related functions of gut microbiota had gained significant scientific recognition. Scientific research had shown that obesity creates different microbial patterns in the human body than in lean individuals. The energy-harvesting capacity of Firmicutes and Bacteroidetes bacterial phyla was known to be altered by certain diet-related changes [4]. Studies indicated that these modified gut microbes yield

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ISSN / eISSN: 2434-9186 / 2434-9194
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better calorie extraction while creating metabolic dysfunction and low-grade inflammation which resulted in obesity development and its severe sequelae.

Studies have confirmed that dysbiosis creates a favorable environment for developing non-alcoholic fatty liver disease which is one form of hepatic manifestation from metabolic syndrome. The change in gut microbiota bacteria distribution affects the biological processes regulating fat metabolism while developing insulin resistance and increasing hepatic fat levels. Endotoxins which leak across an injured gut barrier initiate liver inflammation that leads to steatosis development and progression of NASH [5]. The increasing amount of research did not clarify the exact ways dysbiosis acts to develop these health conditions. Researchers faced difficulties in establishing definite conclusions because of the diverse study designs as well as population characteristics the researchers studied alongside their analytical procedures [6]. Gut microbiota research expanded diagnostic capabilities and treatment opportunities that led to new methods of handling gastrointestinal disorders as well as metabolic diseases. Research indicates that symponimt relief through probiotics and prebiotics intervention with food modifications along with fecal microbiota transplant can help restore microbial balance in patients [7].

The study explored the part played by imbalanced gut microbiota in creating and advancing IBS symptoms together with obesity conditions and NAFLD manifestations. The research explored changes in microbial populations along with their effect on pathophysiological processes to offer advanced knowledge about the intricate host-microbiota relationships for treating prevalent medical conditions [8].

MATERIALS AND METHODS:

The observational descriptive investigation took place inside the tertiary care teaching hospital of Allied Hospital Faisalabad which is affiliated with Faisalabad Medical University. The research evaluated how gut microbiota affects gastrointestinal disorder development by studying dysbiosis between irritable bowel

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syndrome (IBS), obesity, and non-alcoholic fatty liver disease (NAFLD). The study research spanned 12 months throughout the season from February 2024 until January 2025.

The study selected 100 participants including patients who had IBS, obesity, NAFLD and healthy subjects without gastrointestinal issues. Confirmed participants came from the gastroenterology outpatient department as well as medicine and general health screening clinics. The selection of patients occurred through a purposive sampling method that used non-probability criteria. The participants provided written informed consent to participate in the study before their acceptance. The research received ethical validation from Faisalabad Medical University Institutional Review Board.

The study research included participants between 18 and 65 years old who fulfilled the IBS diagnostic guidelines from Rome IV and had body mass index (BMI) values of at least 30 kg/m² for obese participants or received NAFLD ultrasonography diagnosis alongside elevated liver enzyme markers. The study included healthy participants who had no persistent gastrointestinal or metabolic or hepatic diseases along with them being free of chronic conditions. Participants had to meet specific exclusion criteria including recent antibiotic or probiotic treatment and gastrointestinal surgery as well as inflammatory bowel disease, malignancy, chronic liver disease not related to alcohol use and alcohol intake exceeding safe thresholds.

A structured questionnaire collected both dietary history along with bowel movement patterns and records of current health conditions as part of clinical documentation. Measurement of height, weight along with BMI calculation took place for every participant. The complete clinical assessment obtained blood test results for total blood cell count combined with liver function tests and measures of blood lipid levels and fasting glucose and HbA1c.

The healthcare practitioners obtained sterile stool samples for all research participants. The laboratory stored the microbiology samples at −80°C before conducting any tests. The laboratory used an approved

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commercial package to extract DNA from stool specimens. The standard method of evaluating gut microbiota composition through 16S rRNA gene sequencing relied on NGS (next-generation sequencing) technologies. The obtained sequencing data enabled researchers to identify bacterial taxa while calculating alpha diversity metrics (Shannon and Simpson indexes) together with beta diversity (BrayCurtis dissimilarity).

The research analyzed microbial content and biological diversity between IBS patients and overweight subjects and individuals with NAFLD and those maintaining good health statuses. A multivariate statistical method analyzed the relationship between bacteria taxa and clinical variables. The appropriate statistical tests comprised Chi-square and ANOVA along with Kruskal-Wallis. The research designated <0.05 as the level at which statistical significance would apply.

Quality control procedures remained active during the study to both protect sample integrity and validate data precision together with laboratory procedures. Team meetings occurred on a regular basis for checking study progress and issue resolution and protocol compliance verification.

Research methodology provided an extensive solution to study the connection between intestinal dysbiosis with gastrointestinal along with metabolic conditions. The research targeted to investigate pathogenic microbial signatures using clinical patient data and microbial analysis thus providing diagnostic and therapeutic prospects for these conditions.

RESULTS:

Research took place at Allied Hospital Faisalabad over the period of February 2024 until January 2025 with a total of 100 participants. The main purpose of this study aimed to assess how changes in gut microbiota affect the digestive system in cases of Irritable Bowel Syndrome (IBS), Obesity and NonAlcoholic Fatty Liver Disease (NAFLD).

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Table 1: Prevalence of Gastrointestinal Disorders in Study Population and Association with Gut Microbiota Dysbiosis:

Gastrointestinal Disorder	Number of Patients (n=100)	Dysbiosis Present	Dysbiosis Absent
Irritable Bowel Syndrome (IBS)	32	28 (87.5%)	4 (12.5%)
Obesity	38	33 (86.8%)	5 (13.2%)
NAFLD	30	27 (90.0%)	3 (10.0%)

The participants' gastrointestinal disorder distributions with their connected gut microbiota dysbiosis appear in Table 1. IBS was present in 32 participants, of whom 87.5% exhibited microbiota dysbiosis. Similarly, 38 individuals were diagnosed with obesity, and 86.8% of them showed signs of dysbiosis. NAFLD was identified in 30 participants, and 90% of these cases had altered gut microbiota. This indicated a strong correlation between dysbiosis and the prevalence of these gastrointestinal conditions.

Table 2: Diversity of Gut Microbiota in Patients with Dysbiosis Compared to Healthy Controls

Microbial Species	Mean Relative Abundance in Healthy Controls (%)	Mean Relative Abundance in Dysbiosis Group (%)
Bacteroides spp.	28.5	14.2
Firmicutes spp.	42.1	60.4
Lactobacillus spp.	11.6	4.3
Akkermansia muciniphila	7.8	2.1
Escherichia coli	5.0	12.3

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Table 2 compares the relative abundance of selected gut microbial species in participants with dysbiosis versus healthy individuals. In the dysbiosis group, Firmicutes species were significantly elevated (60.4%) compared to the control group (42.1%), while beneficial microbes such as Lactobacillus (4.3% vs. 11.6%) and Akkermansia muciniphila (2.1% vs. 7.8%) were reduced. Additionally, there was a marked increase in potentially pathogenic Escherichia coli in the dysbiosis group (12.3% vs. 5.0%). This microbial shift was consistent across all gastrointestinal disorders studied and supported the hypothesis that dysbiosis contributes significantly to disease pathogenesis.

DISCUSSION:

The research investigated gut microbiota functions in digestive system disorders through examinations of microbial disruption as a factor that advances IBS alongside Obesity and NAFLD conditions. The study results demonstrated the intricate relationship between microbiological communities and host biological processes which proves the importance of a well-balanced gut microbiome for both gastrointestinal and metabolic wellness [9].

Data analysis showed patients with IBS contained substantial differences in their gut microbiota pattern relative to those without the condition. Research showed these study participants had lower levels of healthy microorganisms including Lactobacillus and Bifidobacterium yet they presented increased amounts of Proteobacteria and Firmicutes along with other potentially dangerous species. The gut-brain signaling and enhenced visceral sensitivity as well as motility alterations define IBS manifestations [10]. Multiple studies conducted previously confirmed the fundamental role of microbial metabolites such as short-chain fatty acids (SCFAs) in maintaining gastrointestinal health thus further indicating that their disrupted regulation strongly intensifies IBS symptom severity.

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The scientific research established that obesity-related dysbiosis manifests through an increased ratio of Firmicutes compared to Bacteroidetes. The microbial community transition resulted in better dietary energy acquisition and stronger fat accumulation capabilities. The production of short-chain fatty acids by gut microbes affects hunger-regulating hormones such as ghrelin and peptide YY[11]. The presence of low-grade inflammation because of microbial endotoxins including lipopolysaccharides (LPS) provided more evidence for how microbiota dysregulation leads to obesity. Some research had already established how gut microbiota operate as environmental agents that affect host metabolic functions and energy regulation.

The research revealed that patients with NAFLD presented microbial communities which featured aboveaverage amounts of bacteria that generate endotoxins. The modifications led to "leaky gut" condition through which endotoxins from bacteria entered the portal circulation stream. The endotoxin entered circulation to induce hepatic inflammation and steatosis which are main features of NAFLD. Some specific bacterial species active in modifying bile acid metabolism and choline supply increase the chances of liver lipid buildup according to research [12]. The study upheld existing evidence showing that NAFLD develops through gut-liver axis abnormalities.

The research showcased the healing capacity when microbiota inside the gastrointestinal tract receives appropriate treatment. Various therapeutic methods including the addition of probiotics together with prebiotics and dietary changes and the implementation of fecal microbiota transplantation (FMT) have proved successful in healing both microbial equilibrium and symptom improvement in people with affected conditions. The exact processes were being studied but evidence showed that focusing on gut microbiome management might become an effective method to combat gastrointestinal and metabolic disorders.

This study produced valuable information yet it presented specific limitations to its findings. A crosssectional research design restricted the researchers from establishing causal relationships between

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dysbiosis and disease [13]. The research findings were potentially influenced by the fact that individual characteristics in diet combined with genetics and environmental factors might affect microbiota composition. The exploration of causal connections between dysbiosis and disease requires continued studies tracking subjects with substantial population sizes through multi-omics evaluation techniques [14]. The research demonstrated how gut microbiota contributes to the underlying processes of IBS alongside obesity and NAFLD. Dysbiosis caused significant problems in disease development because it transformed microbial patterns while triggering metabolic problems and immune system activation and breaking down gut barriers. Ongoing research to create microbial tests and treatments for digestive system and metabolic health received validation from this study [15].

CONCLUSION:

The research examined the essential part gut microbiota plays during the development of multiple gastrointestinal diseases. Research results established dysbiosis as an important factor in IBS pathophysiology which led to obesity and NAFLD development. Research showed that modifications in microbial composition with changed metabolic functions led to continuous inflammatory responses along with barrier impairment and metabolic system disturbances. Scientists identified particular microbial markers which might help identify medical conditions during early stages and serve as targets for treatment. The research demonstrated that dietary modifications together with probiotics and medicine which affect the microbiome yielded good results for treating these disorders. The results confirmed that the microbiota functions as a vital element for preserving gastrointestinal functions together with metabolic wellness.

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