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Correlation Between Gut Microbiome and Mental Health Disorders: A Comprehensive Cross-Sectional Study

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Abstract:
The gut microbiome, which consists of trillions of microorganisms living in the digestive tract, is increasingly recognized as an important factor influencing mental health. Through the gut–brain axis, these microbes can affect brain function, mood, and behavior. This study explored the relationship between gut microbiome composition and mental health disorders, particularly depression and anxiety. In this cross-sectional study, stool samples were collected from adults with depression, anxiety, and from healthy individuals. Microbial analysis was performed using 16S rRNA sequencing, and psychological symptom severity was measured using standard mental health assessment scales. Differences in microbial diversity and abundance were compared across groups, and correlations between specific bacteria and symptom severity were examined. Results showed that individuals with depression and anxiety had lower gut microbial diversity compared to healthy controls. Beneficial bacteria commonly linked to anti-inflammatory effects and healthy brain function were reduced, while some potentially harmful or inflammation-associated bacteria were increased. Several bacterial groups showed meaningful relationships with the severity of depression and anxiety symptoms.These findings suggest that imbalances in gut microbiota may be associated with mental health disorders and support the role of the gut–brain axis in emotional well-being. Understanding these connections may help in developing microbiome-based approaches for prevention and treatment in the future.

Keywords: Gut microbiome, Mental health, Depression, Anxiety, Gut–brain axis.

1. INTRODUCTION

Mental health disorders, particularly depression and anxiety, affect hundreds of millions of individuals worldwide and are among the leading causes of disability and reduced quality of life. These conditions impose a substantial burden on healthcare systems, social structures, and economic productivity. Although their etiology is multifactorial, traditional models primarily focus on genetic vulnerability, psychosocial stressors, and neurochemical imbalances involving neurotransmitters such as serotonin, dopamine, and gamma-aminobutyric acid (GABA). Despite advances in pharmacological and psychological treatments, a significant proportion of patients experience incomplete response or relapse, highlighting the need to explore additional biological mechanisms underlying these disorders.

In recent years, the gut microbiome—the complex community of microorganisms residing in the gastrointestinal tract—has emerged as a potential key player in mental health. These microbes participate in numerous physiological processes, including digestion, immune regulation, and metabolic homeostasis. Importantly, they communicate bidirectionally with the central nervous system through neural, endocrine, and immune pathways, forming what is known as the gut–brain axis. This communication network involves mechanisms such as vagus nerve signaling, microbial production of neuroactive compounds (e.g., serotonin precursors, short-chain fatty acids), and modulation of systemic inflammation, all of which may influence brain function and behavior.

Growing evidence suggests that disruptions in the gut microbial ecosystem, commonly referred to as dysbiosis, may contribute to the pathophysiology of psychiatric disorders. Clinical and preclinical studies have linked altered gut microbial diversity and composition to symptoms of depression, anxiety, and stress-related conditions. For instance, reductions in beneficial bacteria associated with anti-inflammatory and neuroprotective functions have been observed in individuals with mood disorders, while increases in pro-inflammatory taxa have also been reported. However, findings across studies have not always been consistent, possibly due to differences in study design, sample size, dietary patterns, geographic location, and analytical methods used for microbiome profiling.

Given these inconsistencies, further research is necessary to clarify the specific microbial patterns associated with mental health conditions and to understand how these patterns relate to symptom severity. A more comprehensive characterization of the gut microbiome in individuals with depression and anxiety may help identify potential biomarkers and inform microbiome-targeted therapeutic strategies.

2. REVIEW OF LITERATURE

2.1. Cryan & Dinan (2012) – Gut Microbiota and Brain Function

Cryan and Dinan were among the first to strongly propose that gut microorganisms can influence brain function and behavior. Their review highlighted the concept of the gut–brain axis, explaining how gut bacteria communicate with the central nervous system through neural (vagus nerve), endocrine, and immune pathways. They discussed animal studies showing that changes in gut microbiota could alter stress responses, emotional behavior, and neurochemical levels. This work laid the foundation for understanding the microbiome as a potential factor in psychiatric conditions such as anxiety and depression.

2.2. Kelly et al. (2016) – Microbiota and Depression (Human-to-Animal Transfer Study)

Kelly and colleagues conducted a landmark study where gut microbiota from individuals with major depressive disorder were transferred into microbiota-depleted rats. The recipient animals developed behaviors resembling depression, along with altered immune and metabolic profiles. This study provided experimental evidence that gut microbiota changes seen in depressed individuals may play a causal role in depressive-like behaviors.

2.3. Jiang et al. (2015) – Altered Gut Microbiota in Major Depressive Disorder

Jiang and colleagues compared the gut microbiota of patients with major depressive disorder (MDD) and healthy controls. They found that individuals with MDD had reduced microbial diversity and increased levels of certain bacterial groups linked to inflammation. The study also showed that the abundance of specific bacteria correlated with depression severity scores.

2.4. Zheng et al. (2016) – Gut Microbiome and Metabolic Changes in Depression

This study demonstrated that gut microbiota alterations in depressed patients were associated with changes in metabolic pathways, particularly those related to neurotransmitter synthesis and inflammation. When microbiota from depressed patients were transplanted into germ-free mice, the animals exhibited depressive-like behaviors and metabolic disturbances.

2.5. Simpson et al. (2021) – Gut Microbiota in Anxiety Disorders

Simpson and colleagues reviewed studies examining gut microbiota in anxiety disorders. They reported consistent findings of reduced beneficial bacteria such as *Lactobacillus* and *Bifidobacterium*, along with increased pro-inflammatory microbes. The review also discussed how microbiota-targeted interventions, including probiotics and dietary changes, showed promise in reducing anxiety symptoms in some clinical trials.

3. MATERIALS AND METHODS

3.1 Study Design and Participants

This cross-sectional study recruited 150 adults aged 18–60 from outpatient clinics and the community. Group assignment:

Group	Number	Diagnostic Criteria
Depressed	50	DSM-5 diagnosis of MDD
Anxious	50	DSM-5 diagnosis of GAD
Control	50	No psychiatric diagnosis

Exclusion Criteria: Antibiotic use in past 3 months, probiotics/prebiotics use, chronic gastrointestinal diseases, severe medical illnesses.

3.2 Clinical Assessments

Assessment	Purpose
BDI-II	Measures depressive symptom severity
HAM-A	Measures anxiety severity
BMI	Body mass index, potential confounder

3.3 Sample Collection and Sequencing

- Fecal samples collected at baseline
- DNA extraction using QIAamp DNA Stool Mini Kit
- 16S rRNA gene amplification (V3–V4 region)
- Sequencing on Illumina MiSeq platform

3.4 Bioinformatics and Statistical Analysis

- **QIIME2** for sequence processing
- **α-diversity** (Shannon index) and **β-diversity** (Bray–Curtis dissimilarity)
- Differential abundance using **LEfSe**
- Correlation analysis (Spearman's rho) between microbial taxa and symptom scores

4. RESULTS

4.1 Participant Characteristics

Table 1. Participant Demographics and Clinical Scores

Variable	Depressed (n=50)	Anxious (n=50)	Controls (n=50)	p-value
Age (mean ± SD)	34.8 ± 9.2	33.5 ± 10.1	35.1 ± 8.7	0.78
Female (%)	58	60	56	0.89
BMI (mean ± SD)	24.5 ± 3.8	23.9 ± 4.1	24.1 ± 3.7	0.72
BDI-II Score	28.7 ± 7.4	10.2 ± 4.5	7.5 ± 3.1	<0.001*
HAM-A Score	14.3 ± 5.1	24.6 ± 6.3	8.1 ± 2.9	<0.001*

*Significant at $p < 0.05$

4.2 α- and β-Diversity

- **α-diversity (Shannon index)** was significantly lower in depressed and anxious groups compared to controls ($p < 0.01$).
- **β-diversity analysis** (PCoA plots) showed distinct clustering of microbiome profiles between groups (PERMANOVA $p < 0.001$).

Three clusters represent control, depression, and anxiety groups indicating significant group separation.

4.3 Differential Taxa Abundance

Table 2. Differentially Abundant Taxa Among Groups

Taxa	Higher in Group	Fold Change	p-value
Bifidobacterium	Controls > Depressed	2.3	0.005
Lactobacillus	Controls > Anxious	1.8	0.012
Alistipes	Depressed > Controls	1.9	0.008
Enterobacteriaceae	Anxious > Controls	2.1	0.003

4.4 Correlation with Symptom Severity

Table 3. Correlations Between Microbial Abundance and Clinical Scores

Taxa	BDI-II Correlation (ρ)	HAM-A Correlation (ρ)
Bifidobacterium	-0.46**	-0.32*
Lactobacillus	-0.39*	-0.35*
Alistipes	+0.42*	+0.28

$p < 0.05$; ** $p < 0.01$

5. DISCUSSION

5.1 Key Findings

1. Reduced microbial diversity in depressed and anxious individuals suggests gut dysbiosis.
2. Beneficial genera (*Bifidobacterium*, *Lactobacillus*) were less abundant, consistent with prior work linking these taxa to positive mood regulation.
3. Pathogenic or pro-inflammatory taxa (e.g., *Alistipes*, *Enterobacteriaceae*) were elevated in mental health disorder groups.

5.2 Biological Mechanisms

- **Neuroactive metabolite production:** Gut microbes influence serotonin and short-chain fatty acid production.
- **Immune modulation:** Dysbiosis may increase inflammatory cytokines that affect the central nervous system.
- **Neural pathways:** Vagus nerve communication connects gut signaling with the brain.

5.3 Clinical Implications

Altered microbiome profiles could:

- Serve as biomarkers for depression and anxiety.
- Inform microbiome-targeted therapies (e.g., probiotics, diet modulation).

5.4 Limitations

Despite the meaningful findings, several limitations should be considered when interpreting the results. First, the cross-sectional design restricts the ability to determine causality. While associations between gut

microbiome composition and mental health symptoms were identified, it remains unclear whether microbial changes contribute to the development of psychiatric disorders or arise as a consequence of them.

Second, dietary habits, physical activity, sleep patterns, medication use, and lifestyle factors were not fully controlled and may have influenced microbiome composition. Since gut microbial communities are highly responsive to environmental inputs, these variables could act as confounding factors.
Third, the study relied on 16S rRNA sequencing, which provides taxonomic information but limited insight into microbial functional activity. Metagenomic or metabolomic approaches would offer a more comprehensive understanding of microbial metabolic pathways involved in neurobiological processes.
Additionally, the sample size, although adequate for detecting group differences, may not capture the full heterogeneity of microbiome profiles across diverse populations. Cultural, geographic, and genetic factors could influence the generalizability of the findings.

5.5 Future Directions

Future research should focus on longitudinal study designs to monitor microbiome changes over time, particularly before and after the onset of psychiatric symptoms or during treatment. Such designs would help clarify causal relationships and temporal dynamics.
There is also a need for interventional trials investigating targeted microbiome modulation strategies, including specific probiotics, prebiotics, synbiotics, dietary interventions, and fecal microbiota transplantation. These approaches may reveal whether altering gut microbial composition can improve mental health outcomes.

Moreover, integrating multi-omics technologies (metagenomics, metabolomics, transcriptomics) with neuroimaging and immunological markers would provide a more holistic understanding of the biological pathways linking the gut microbiome and the brain.
Finally, personalized approaches considering individual microbiome profiles, diet, and lifestyle factors may contribute to the development of precision psychiatry strategies in the future.

6. CONCLUSION

This study adds to the growing body of evidence demonstrating a significant association between gut microbiome composition and mental health disorders. Distinct microbial patterns were linked to depression and anxiety severity, supporting the concept that gut microbial imbalance may play a role in psychiatric symptomatology. These findings reinforce the importance of the gut–brain axis as a biologically plausible pathway connecting intestinal microbial ecology with emotional and cognitive processes.
Although causality cannot yet be established, the results highlight the potential of the gut microbiome as a source of novel biomarkers and therapeutic targets. Continued research in this field may open new avenues for preventive, diagnostic, and treatment strategies that complement existing mental health interventions.

REFERENCES:

1. Cryan JF, Dinan TG. Mind-altering microorganisms: the impact of the gut microbiota on brain and behaviour. *Nat Rev Neurosci*. 2012;13(10):701-12.
2. Kelly JR, et al. Breaking down the barriers: the gut microbiome, intestinal permeability and stress-related psychiatric disorders. *Front Cell Neurosci*. 2015;9:392.
3. Dinan TG, Cryan JF. The microbiome–gut–brain axis in health and disease. *Gastroenterol Clin North Am.* 2017;46(1):77–89.

4. Foster JA, Neufeld KM. Gut–brain axis: how the microbiome influences anxiety and depression. *Trends Neurosci.* 2013;36(5):305–12.
5. Jiang H, Ling Z, Zhang Y, Mao H, Ma Z, Yin Y, et al. Altered fecal microbiota composition in patients with major depressive disorder. *Brain Behav Immun.* 2015;48:186–94.
6. Zheng P, Zeng B, Zhou C, Liu M, Fang Z, Xu X, et al. Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the host's metabolism. *Mol Psychiatry.* 2016;21(6):786–96.
7. Clarke G, Stilling RM, Kennedy PJ, Stanton C, Cryan JF, Dinan TG. Minireview: gut microbiota: the neglected endocrine organ. *Mol Endocrinol.* 2014;28(8):1221–38.
8. Sampson TR, Mazmanian SK. Control of brain development, function, and behavior by the microbiome. *Cell Host Microbe.* 2015;17(5):565–76.
9. Wallace CJ, Milev R. The effects of probiotics on depressive symptoms in humans: a systematic review. *Ann Gen Psychiatry.* 2017;16:14.
10. Bastiaanssen TFS, Cowan CSM, Claesson MJ, Dinan TG, Cryan JF. Making sense of… the microbiome in psychiatry. *Int J Neuropsychopharmacol.* 2019;22(1):37–52.
11. Liu RT, Walsh RFL, Sheehan AE. Prebiotics and probiotics for depression and anxiety: a systematic review and meta-analysis of controlled clinical trials. *Neurosci Biobehav Rev.* 2019;102:13–23.
12. Sherwin E, Sandhu KV, Dinan TG, Cryan JF. May the force be with you: the light and dark sides of the microbiota–gut–brain axis in neuropsychiatry. *CNS Drugs.* 2016;30(11):1019–41.