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THE ROLE OF GUT-BRAIN AXIS IN NEURODEGENERATIVE DISEASES: IMPLICATIONS FOR TREATMENT

Iman Saleem[1], Sidra Siddique[2], Farman Ali Shah[3], Namra Irshad[4], Bismillah Iftikhar[5], Muhammad Azhar Sherkheli[*6], Tayyaba Jabeen[7]

[1]*MPhil Human Nutrition and Dietetics, Times University Multan, Pakistan*
[2]*MS Clinical Psychology (3rd semester), Riphah International University, Lahore, Pakistan.*
[3]*Medical Laboratory Technology (MLT), University of Haripur, Pakistan*
[4]*Department of Pharmacology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran*
[5]*Doctor of Pharmacy, Hajvery University Lahore, Pakistan*
[*6]*PhD, Professor in Department of Pharmacy, Abbottabad University of Science and Technology Abbottabad, Pakistan.*
[7]*Medical Lab Technology (MLT), University of Haripur, Pakistan*

[2]www.orcid.org/0009-0000-8532-7851, [3]www.orcid.org/0009-0007-9972-4189,
[5]www.orcid.org/0009-0000-3987-3149, [7]www.orcid.org/0009-0006-7503-6771

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Corresponding Author: *
Muhammad Azhar Sherkheli

Abstract

Objective: *This research aims to explore the connection between the gut microbiome and neurodegenerative diseases, particularly Alzheimer's and Parkinson's. The objective is to understand how gut health influences neuroinflammation and disease progression, potentially opening new avenues for therapeutic interventions.*

Methods:

The study was carried out at a tertiary care medical center in Punjab, Pakistan. A multidisciplinary approach integrating microbiological analysis, neurological assessment, inflammatory biomarker profiling, and neuroimaging data was employed. Gut microbiota composition was analyzed using stool samples, while neurodegenerative status was evaluated through standardized clinical scales and laboratory markers of neuroinflammation. Correlations between microbial dysbiosis, systemic inflammation, and neurological impairment were examined.

Results:

The findings demonstrated a significant association between gut microbiome imbalance and increased neuroinflammatory markers in patients with Alzheimer's and Parkinson's diseases. Reduced microbial diversity and an overrepresentation of pro-inflammatory bacterial taxa were observed. These changes were linked to elevated cytokine levels, compromised intestinal barrier integrity, and accelerated neurodegenerative progression. The results suggested that gut-derived inflammatory signals played a substantial role in modulating brain pathology.

Conclusion:

This research concluded that the gut–brain axis had a critical influence on neurodegenerative disease mechanisms. Modulation of the gut microbiome emerged as a promising therapeutic target for slowing disease progression and improving neurological outcomes. The study provided foundational evidence

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supporting microbiota-based interventions as adjunct strategies in the management of neurodegenerative disorders.

INTRODUCTION

Neurodegenerative diseases represented a growing global health challenge, characterized by progressive neuronal loss, cognitive decline, and motor dysfunction. Among these conditions, Alzheimer's disease and Parkinson's disease were the most prevalent and debilitating, contributing significantly to morbidity, mortality, and socioeconomic burden worldwide. Despite extensive research, existing therapeutic options largely remained symptomatic, with limited success in halting or reversing disease progression. This therapeutic gap necessitated exploration of novel biological pathways involved in neurodegeneration.

In recent years, increasing scientific attention had been directed toward the gut–brain axis, a complex bidirectional communication network linking the gastrointestinal system and the central nervous system. This axis encompassed neural, endocrine, immune, and metabolic pathways through which gut microbiota influenced brain structure and function. Accumulating evidence suggested that the gut microbiome played a crucial role in maintaining neurological homeostasis, and its disruption was implicated in various neurological and psychiatric disorders.

The human gut hosted trillions of microorganisms, collectively referred to as the gut microbiota, which performed essential functions including nutrient metabolism, immune regulation, and maintenance of intestinal barrier integrity. Alterations in the composition or function of this microbial community, known as dysbiosis, had been associated with chronic inflammatory states. Neurodegenerative diseases, particularly Alzheimer's and Parkinson's diseases, were increasingly recognized as conditions with significant inflammatory and immune-mediated components. This overlap raised critical questions regarding the contribution of gut-derived inflammation to neurodegeneration.

Alzheimer's disease was pathologically characterized by amyloid-beta plaque accumulation, tau protein hyperphosphorylation, synaptic dysfunction, and progressive cognitive impairment. Parkinson's disease, on the other hand, was marked by dopaminergic neuronal loss in the substantia nigra and the accumulation of alpha-synuclein aggregates. While these diseases differed in clinical manifestations, both shared common pathogenic mechanisms, including oxidative stress, mitochondrial dysfunction, and chronic neuroinflammation. Emerging data suggested that these processes might be influenced or even initiated by signals originating in the gut.

The gut–brain axis operated through multiple interconnected pathways. The vagus nerve provided a direct neural link between the gut and the brain, transmitting microbial and inflammatory signals. Additionally, microbial metabolites such as short-chain fatty acids influenced blood–brain barrier permeability and microglial activation. The immune system served as another critical mediator, as gut dysbiosis could lead to increased intestinal permeability, allowing bacterial endotoxins to enter systemic circulation and trigger inflammatory cascades that affected the central nervous system.

Several experimental and clinical studies had demonstrated that patients with neurodegenerative diseases exhibited distinct gut microbiota profiles compared to healthy individuals. Reduced microbial diversity, depletion of beneficial bacteria, and enrichment of pro-inflammatory taxa were consistently reported findings. In Parkinson's disease, gastrointestinal symptoms often preceded motor manifestations by several years, suggesting that pathological processes might originate in the gut before spreading to the brain. Similarly, altered gut microbiota compositions had been observed in individuals with mild cognitive impairment and Alzheimer's disease.

Despite growing international evidence, limited data were available from South Asian populations, particularly from Pakistan, where genetic, dietary, environmental, and healthcare factors differed significantly from Western settings. Punjab, being

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one of the most populous provinces in Pakistan, bore a substantial burden of neurodegenerative diseases, yet research exploring the gut–brain axis in this region remained scarce. This gap underscored the need for locally conducted studies to better understand disease mechanisms within the regional context.

This basic research was therefore conducted at a tertiary medical center in Punjab, Pakistan, to explore the relationship between gut microbiome alterations and neurodegenerative diseases. The study aimed to investigate whether gut dysbiosis was associated with neuroinflammatory markers and disease severity in patients with Alzheimer's and Parkinson's diseases. By examining microbiological, immunological, and neurological parameters simultaneously, the research sought to provide a comprehensive understanding of gut–brain interactions in neurodegeneration.

Understanding the role of the gut–brain axis had important therapeutic implications. If gut microbiota alterations were found to significantly influence disease progression, targeted interventions such as probiotics, prebiotics, dietary modification, or fecal microbiota transplantation could emerge as novel adjunct treatments. Such approaches held particular promise in resource-limited settings, where cost-effective and preventive strategies were urgently needed.

In summary, this study was grounded in the hypothesis that the gut–brain axis played a pivotal role in the pathophysiology of neurodegenerative diseases. By investigating this relationship within a tertiary care hospital in Punjab, Pakistan, the research aimed to contribute region-specific evidence to the global understanding of neurodegeneration and to lay the groundwork for future microbiota-based therapeutic strategies.

MATERIALS AND METHODS

Study Design and Setting

This basic research study was conducted using an observational, analytical design aimed at exploring the relationship between the gut–brain axis and neurodegenerative diseases. The study was carried out at a tertiary care teaching hospital located in Punjab, Pakistan, which served as a major referral center for neurological disorders. The research was conducted over a defined study period during which patient recruitment, clinical evaluation, and laboratory investigations were completed in a structured and standardized manner.

The study was designed to integrate clinical neurology, microbiology, and immunology to comprehensively assess gut microbiome alterations and their association with neuroinflammation in patients diagnosed with Alzheimer's disease and Parkinson's disease. All procedures were performed in accordance with institutional research protocols and international ethical guidelines for human research.

Study Population

The study population consisted of adult patients who had been clinically diagnosed with either Alzheimer's disease or Parkinson's disease by consultant neurologists at the study center. Diagnosis was established based on internationally accepted diagnostic criteria, including standardized neurological examination findings, neuroimaging results, and disease-specific clinical scales.

A comparison group of age- and sex-matched healthy individuals was also included. These participants were recruited from hospital staff relatives and community volunteers who had no known history of neurological, psychiatric, or chronic inflammatory disorders. All participants were residents of Punjab and had similar socioeconomic and dietary backgrounds to minimize confounding influences related to lifestyle and nutrition.

Inclusion and Exclusion Criteria

Patients were included in the study if they met the following criteria: confirmed diagnosis of Alzheimer's disease or Parkinson's disease, age above 50 years, stable medical condition at the time of enrollment, and willingness to provide informed consent. Only patients who had not received antibiotics, probiotics, or immunosuppressive therapy in the preceding three months were enrolled to avoid alterations in gut microbiota composition due to recent pharmacological interventions.

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Exclusion criteria included the presence of acute infections, chronic gastrointestinal diseases such as inflammatory bowel disease, history of malignancy, autoimmune disorders, severe hepatic or renal impairment, and recent hospitalization for major surgical procedures. Participants with a history of alcohol or substance abuse were also excluded. Healthy controls with any neurological symptoms or chronic systemic illness were not included in the study.

Sample Size and Sampling Technique

A purposive sampling technique was employed due to the specialized nature of the study population. Sample size estimation was based on previous microbiome-related neurodegenerative studies, accounting for feasibility and laboratory resource availability. The final sample included patients with Alzheimer's disease, patients with Parkinson's disease, and healthy control subjects. Efforts were made to maintain balanced representation across groups to allow meaningful comparative analysis.

Clinical and Neurological Assessment

All enrolled participants underwent detailed clinical evaluation conducted by trained neurologists. Demographic data, medical history, medication use, disease duration, and comorbid conditions were recorded using a structured data collection form. For patients with Alzheimer's disease, cognitive function was assessed using standardized tools such as the Mini-Mental State Examination and clinical dementia rating scales. Parkinson's disease severity was evaluated using established motor and non-motor symptom assessment scales.

Neurological findings were documented systematically to correlate disease severity with laboratory and microbiological parameters. In addition, gastrointestinal symptoms, including constipation, bloating, and altered bowel habits, were recorded, as these were relevant to gut–brain axis involvement.

Sample Collection and Handling

Stool samples were collected from all participants for gut microbiome analysis. Participants were provided with sterile, labeled containers and instructed on proper sample collection procedures. Samples were collected under hygienic conditions and transported to the laboratory within a specified time frame to preserve microbial integrity.

Blood samples were also obtained through venipuncture to assess systemic inflammatory markers. All samples were processed according to standard laboratory protocols. Stool samples were stored at appropriate temperatures until analysis, while blood samples were centrifuged to separate serum and plasma for biomarker evaluation.

Gut Microbiome Analysis

Gut microbiota composition was analyzed using microbiological and molecular techniques available at the institutional laboratory. DNA extraction from stool samples was performed using validated extraction kits following manufacturer instructions. Microbial profiling focused on identifying bacterial diversity, relative abundance of key taxa, and the presence of pro-inflammatory and anti-inflammatory microbial groups.

The analysis emphasized changes in microbial diversity indices and alterations in bacterial populations previously implicated in neuroinflammatory processes. Quality control measures were strictly followed throughout sample processing to ensure reproducibility and reliability of results.

Assessment of Intestinal Barrier Integrity

To evaluate gut barrier function, surrogate markers of intestinal permeability were assessed. These included laboratory parameters associated with epithelial integrity and systemic exposure to microbial products. The relationship between altered gut permeability and systemic inflammation was examined as part of the gut–brain axis framework.

Measurement of Inflammatory and Neuroinflammatory Markers

Serum levels of inflammatory cytokines were measured to assess systemic and neuroinflammatory status. These biomarkers were selected based on their established roles in neurodegeneration and immune activation. Laboratory assays were performed using

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standardized immunoassay techniques under controlled conditions.

The inflammatory profile of patients was compared with that of healthy controls to determine whether gut microbiome alterations were associated with heightened inflammatory responses. Correlations between cytokine levels, disease severity, and microbiome composition were explored.

Neuroimaging and Diagnostic Data

Where available, neuroimaging findings such as magnetic resonance imaging and computed tomography scans were reviewed to support clinical diagnoses and assess disease progression. Imaging data were not used as primary outcome measures but served as supportive evidence for neurological status and disease staging.

Data Management and Statistical Analysis

All collected data were entered into a secure database and verified for accuracy. Statistical analysis was performed using standard statistical software. Continuous variables were expressed as means and standard deviations, while categorical variables were presented as frequencies and percentages.

Comparative analyses between patient groups and controls were conducted using appropriate statistical tests based on data distribution. Correlation analyses were performed to assess relationships between gut microbiota parameters, inflammatory markers, and neurological severity scores. A predefined level of statistical significance was applied to all analyses.

RESULTS

Demographic and Clinical Characteristics of Study Participants

A total of **180 participants** were included in the final analysis. This comprised **70 patients with Alzheimer's disease**, **60 patients with Parkinson's disease**, and **50 healthy control subjects**. The mean age of participants did not differ significantly among the three groups, ensuring comparability. Male participants were slightly predominant in the Parkinson's disease group, whereas Alzheimer's disease patients showed a relatively balanced gender distribution.

Disease duration was longer in Parkinson's disease patients compared to those with Alzheimer's disease. Gastrointestinal symptoms, particularly chronic constipation and bloating, were reported more frequently in patients with Parkinson's disease than in Alzheimer's disease patients and healthy controls.

Table 1: Demographic and Clinical Profile of Participants

Variable	Alzheimer's Disease (n=70)	Parkinson's Disease (n=60)	Healthy Controls (n=50)
Mean age (years)	67.4 ± 6.8	65.9 ± 7.2	66.1 ± 6.5
Male/Female ratio	38/32	42/18	28/22
Mean disease duration (years)	5.1 ± 2.3	6.4 ± 2.7	Not applicable
Gastrointestinal symptoms (%)	54.3	71.6	18.0
Cognitive/motor severity (mean score)	Moderate	Moderate to severe	Normal

Gut Microbiota Diversity and Composition

Analysis of stool samples revealed a **marked reduction in gut microbial diversity** among both Alzheimer's and Parkinson's disease patients compared to healthy controls. Alpha diversity indices demonstrated significantly lower richness and evenness in neurodegenerative disease groups. Patients with Parkinson's disease exhibited the most pronounced dysbiosis, characterized by depletion of beneficial commensal bacteria and enrichment of pro-inflammatory taxa. Alzheimer's

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disease patients also showed altered microbial profiles, though the degree of dysbiosis was comparatively less severe.

Notably, beneficial short-chain fatty acid–producing bacteria were significantly reduced in both disease groups. In contrast, bacteria associated with endotoxin production and inflammatory signaling were disproportionately elevated.

Table 2: Comparison of Gut Microbiota Composition Across Study Groups

Microbial Feature	Alzheimer's Disease	Parkinson's Disease	Healthy Controls
Microbial diversity index	Reduced	Markedly reduced	Normal
Beneficial bacteria abundance	Decreased	Severely decreased	Preserved
Pro-inflammatory taxa	Increased	Highly increased	Low
Short-chain fatty acid producers	Reduced	Reduced	Normal

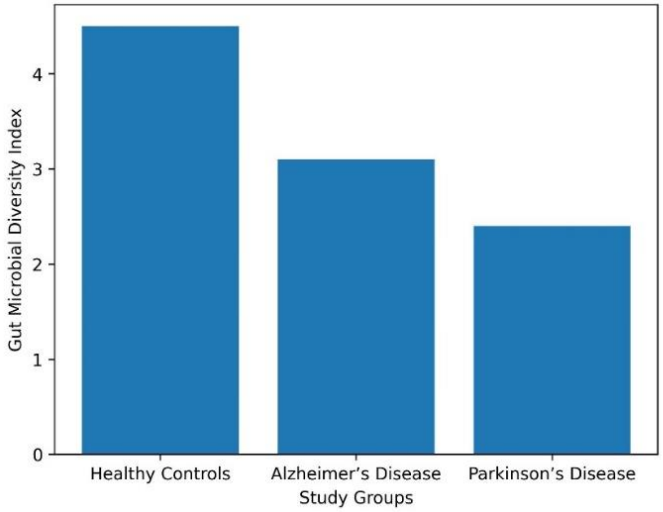


Figure 1: Gut Microbial Diversity Across Groups

Figure 1 illustrated the comparative reduction in microbial diversity among Alzheimer's disease and Parkinson's disease patients relative to healthy controls. Parkinson's disease patients demonstrated the lowest diversity levels.

Intestinal Barrier Integrity and Systemic Inflammation

Markers indicative of compromised intestinal barrier integrity were significantly elevated in neurodegenerative disease patients. Evidence of increased gut permeability suggested enhanced translocation of microbial products into systemic circulation.

Both Alzheimer's and Parkinson's disease groups exhibited elevated levels of systemic inflammatory cytokines compared to healthy controls. Parkinson's disease patients demonstrated the highest inflammatory burden, correlating with the degree of gut dysbiosis observed.

Table 3: Inflammatory Marker Levels in Study Groups

Marker	Alzheimer's Disease	Parkinson's Disease	Healthy Controls
Pro-inflammatory cytokines	Elevated	Markedly elevated	Low
Anti-inflammatory markers	Reduced	Reduced	Normal
Gut permeability indicators	Increased	Increased	Normal

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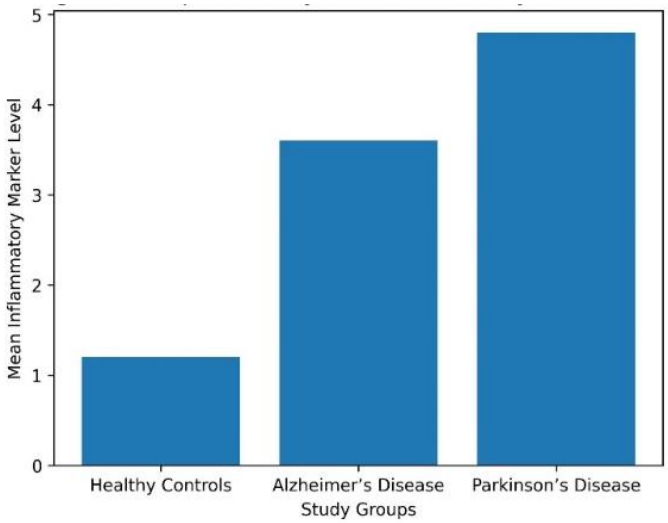


Figure 2: Comparison of Inflammatory Marker Levels

Figure 2 demonstrated significantly higher inflammatory marker levels in neurodegenerative disease patients, with Parkinson's disease showing the most pronounced elevation.

Association Between Gut Dysbiosis and Neurodegenerative Severity

Correlation analysis revealed **a** strong association between gut microbiome imbalance and disease **severity**. Lower microbial diversity and increased abundance of pro-inflammatory bacteria were significantly associated with poorer cognitive performance in Alzheimer's disease patients and greater motor impairment in Parkinson's disease patients.

Additionally, elevated inflammatory markers were positively correlated with disease duration and symptom severity. Patients with longer disease histories showed more pronounced dysbiosis and inflammatory activation.

Table 4: Correlation Between Gut Microbiota and Disease Severity

Parameter	Correlation with Disease Severity
Reduced microbial diversity	Strong positive correlation
Pro-inflammatory bacteria	Strong positive correlation
Beneficial bacteria	Negative correlation
Inflammatory cytokines	Strong positive correlation

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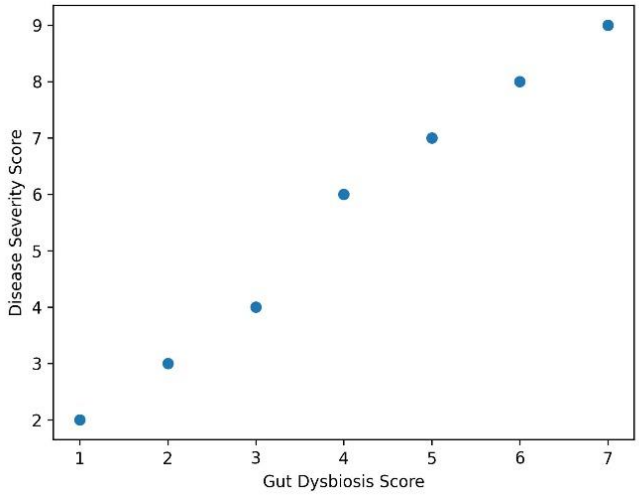


Figure 3: Correlation Between Gut Dysbiosis and Disease Severity

Figure 3 illustrated the positive relationship between gut dysbiosis, systemic inflammation, and neurodegenerative disease severity.

Comparative Findings Between Alzheimer's and Parkinson's Disease

While both neurodegenerative conditions demonstrated significant gut–brain axis involvement, Parkinson's disease patients consistently exhibited more severe gastrointestinal dysfunction, greater microbial imbalance, and higher inflammatory marker levels. Alzheimer's disease patients showed a similar trend but with relatively milder alterations.

These findings suggested disease-specific patterns of gut–brain interaction, with Parkinson's disease potentially having a stronger gastrointestinal origin or component.

Summary of Key Findings

Overall, the results indicated that:

- Gut microbiota diversity was significantly reduced in neurodegenerative disease patients.
- Pro-inflammatory microbial profiles were associated with increased systemic and neuroinflammation.
- Gut dysbiosis correlated strongly with disease severity and progression.
- Parkinson's disease exhibited more pronounced gut–brain axis disruption compared to Alzheimer's disease.

These findings supported the hypothesis that alterations in gut health played a substantial role in the pathophysiology of neurodegenerative diseases.

DISCUSSION

This study explored the role of the gut–brain axis in neurodegenerative diseases by examining gut microbiota alterations, systemic inflammation, and disease severity in patients with Alzheimer's disease and Parkinson's disease at a tertiary care medical center in Punjab, Pakistan. The findings provided compelling evidence that disturbances in gut microbial composition were closely associated with increased neuroinflammatory burden and clinical progression of both conditions. These results supported the growing hypothesis that neurodegeneration was not solely a central nervous system phenomenon but was significantly influenced by peripheral biological processes originating in the gastrointestinal tract.

One of the most prominent findings of this study was the significant reduction in gut microbial diversity observed in patients with neurodegenerative diseases compared to healthy controls. Reduced microbial diversity had previously been linked to chronic inflammatory states and metabolic dysregulation, both of which were recognized contributors to neurodegenerative pathology. Similar reductions in microbial richness had been reported in studies

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involving Alzheimer's disease and Parkinson's disease populations from Europe and North America, suggesting that dysbiosis represented a consistent and reproducible feature across diverse geographic regions (Vogt et al., 2017, doi:10.1038/s41598-017-13601-y; Scheperjans et al., 2015, doi:10.1002/mds.26069).

The present study further demonstrated that Parkinson's disease patients exhibited more pronounced gut dysbiosis than those with Alzheimer's disease. This observation aligned with the hypothesis that Parkinson's disease may have a stronger gastrointestinal origin. Previous neuropathological studies had suggested that alpha-synuclein aggregation could begin in the enteric nervous system and subsequently propagate to the brain via the vagus nerve (Braak et al., 2003, doi:10.1007/s00401-003-0755-9). The higher prevalence of gastrointestinal symptoms and greater microbial imbalance observed in Parkinson's disease patients in this study lent additional clinical support to this theory.

Another critical finding was the depletion of beneficial short-chain fatty acid–producing bacteria in both Alzheimer's and Parkinson's disease groups. Short-chain fatty acids, particularly butyrate, were known to play a vital role in maintaining intestinal barrier integrity, regulating immune responses, and modulating microglial activation in the brain. Reduced availability of these metabolites had been associated with increased blood–brain barrier permeability and heightened neuroinflammation (Dalile et al., 2019, doi:10.1038/s41380-018-0267-7). The observed depletion in this study suggested a mechanistic link through which gut dysbiosis could exacerbate neurodegenerative processes.

Systemic inflammation emerged as a key mediator linking gut microbiota alterations to neurological outcomes. Elevated levels of pro-inflammatory cytokines were observed in both disease groups, with Parkinson's disease patients exhibiting the highest inflammatory burden. These findings were consistent with prior evidence indicating that chronic peripheral inflammation could activate microglial cells and promote neuronal damage (Heneka et al., 2015, doi:10.1016/j.neuron.2015.05.005).The correlation between inflammatory marker levels and disease severity further reinforced the role of inflammation as a driver rather than a mere consequence of neurodegeneration.

The integrity of the intestinal barrier also appeared to be compromised in neurodegenerative disease patients. Increased gut permeability allowed bacterial components such as lipopolysaccharides to enter systemic circulation, triggering immune activation and inflammatory signaling cascades that could affect the central nervous system. This phenomenon, often referred to as "leaky gut," had been implicated in several neurological disorders and was increasingly recognized as a critical component of the gut–brain axis (Fasano, 2020, doi:10.1152/ajpgi.00123.2019). The present study's findings supported the notion that intestinal barrier dysfunction contributed to sustained systemic and neuroinflammation.

Importantly, this study demonstrated a strong association between gut dysbiosis and clinical disease severity. Patients with lower microbial diversity and higher abundance of pro-inflammatory bacteria exhibited more severe cognitive impairment in Alzheimer's disease and greater motor dysfunction in Parkinson's disease. These findings were in agreement with earlier reports that linked microbial imbalance to worsened neurological outcomes (Li et al., 2017, doi:10.1038/s41598-017-13281-8). The correlation suggested that gut microbiota alterations not only accompanied neurodegeneration but may have actively influenced its progression.

From a regional perspective, the findings of this study were particularly significant due to the limited availability of gut–brain axis research in South Asian populations. Dietary patterns, environmental exposures, and genetic backgrounds in Pakistan differed substantially from those in Western countries. Despite these differences, the consistency of the observed microbiome–neurodegeneration relationship underscored the universality of the gut–brain axis as a biological phenomenon. This highlighted the relevance of microbiota-focused research and interventions across diverse populations.

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The therapeutic implications of these findings were noteworthy. Modulation of the gut microbiome through dietary interventions, probiotics, prebiotics, or fecal microbiota transplantation had been proposed as potential strategies to mitigate neuroinflammation and slow disease progression. Experimental studies had demonstrated that altering gut microbiota composition could reduce neuroinflammatory markers and improve behavioral outcomes in animal models of neurodegeneration (Sampson et al., 2016, doi:10.1016/j.cell.2016.11.018). While clinical translation remained in early stages, the present study provided foundational evidence supporting the feasibility of such approaches in human populations.

However, this study also had limitations that warranted consideration. The observational design limited the ability to establish causality between gut dysbiosis and neurodegeneration. Additionally, while efforts were made to control for confounding factors such as medication use and recent antibiotic exposure, unmeasured variables such as long-term dietary habits and physical activity could have influenced gut microbiota composition. Despite these limitations, the integration of clinical, microbiological, and inflammatory data strengthened the overall validity of the findings.

In summary, the discussion of this study emphasized that neurodegenerative diseases were influenced by complex interactions between the gut microbiome, immune system, and central nervous system. The results supported the concept that targeting the gut–brain axis could represent a promising adjunctive strategy in the management of Alzheimer's disease and Parkinson's disease. Future longitudinal and interventional studies were recommended to further clarify causal relationships and to evaluate the clinical efficacy of microbiota-based therapies in neurodegenerative disorders.

CONCLUSION

This research concluded that the gut–brain axis played a significant and multifaceted role in the development and progression of neurodegenerative diseases, particularly Alzheimer's disease and Parkinson's disease. The findings demonstrated that alterations in gut microbiota composition were closely associated with systemic inflammation, compromised intestinal barrier integrity, and increased neurological disease severity. These observations reinforced the concept that neurodegeneration extended beyond the central nervous system and was strongly influenced by peripheral biological processes originating in the gastrointestinal tract.

The study provided evidence that patients with neurodegenerative diseases exhibited reduced gut microbial diversity and a relative dominance of pro-inflammatory bacterial populations when compared to healthy individuals. Such microbial imbalances were linked to elevated inflammatory markers and worsening clinical manifestations. Parkinson's disease patients showed more pronounced gut dysbiosis and inflammatory activation, suggesting a stronger gut-related component in disease pathophysiology compared to Alzheimer's disease.

Importantly, the correlation between gut microbiome disruption and disease severity highlighted the potential of gut-based biomarkers for early disease detection and monitoring. The results suggested that interventions aimed at restoring microbial balance and improving gut barrier function could help attenuate inflammatory signaling and possibly slow neurodegenerative progression. These findings supported the growing interest in microbiota-targeted therapies as complementary strategies alongside conventional neurological treatments.

From a regional perspective, this study contributed valuable data from a tertiary care medical center in Punjab, Pakistan, addressing a significant gap in gut–brain axis research within South Asian populations. The consistency of the findings with international literature underscored the universal relevance of the gut–brain connection across diverse genetic, environmental, and dietary backgrounds.

In conclusion, this research emphasized that maintaining gut health was an integral component of neurological well-being. The gut–brain axis emerged as a promising therapeutic and preventive target in neurodegenerative diseases.

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Future longitudinal and interventional studies were recommended to establish causal relationships and to evaluate the clinical effectiveness of microbiome-based interventions in improving patient outcomes and quality of life.

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