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Human Microbiome and Disease Associations: Exploring Microbial Dysbiosis, Host Interactions, and Implications for Precision Medicine

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Abstract
The human microbiome represents a complex ecosystem of microorganisms inhabiting various anatomical sites, playing essential roles in physiological homeostasis, immune regulation, metabolic processes, and protection against pathogenic organisms. Advances in microbiome research have revealed significant associations between microbial composition and the development of various diseases. This cross-sectional analytical study examines the relationship between human microbiome composition and disease susceptibility across 244 microbiome-related clinical observations and health records. Microbial diversity demonstrated the strongest statistical association with disease prevalence ($F=7.84$, $p=0.001$), followed by antibiotic exposure ($F=6.53$, $p=0.002$) and dietary factors ($F=5.97$, $p=0.004$). Disruptions in microbial diversity microbial dysbiosis are strongly associated with inflammatory bowel disease, obesity, metabolic syndrome, and autoimmune disorders. AI-powered microbiome profiling, precision nutrition, and targeted therapeutic interventions offer promising pathways for microbiome-based disease prevention and treatment.
Keywords: Human microbiome, microbial dysbiosis, gut microbiota, precision medicine, probiotics, metagenomics, AI microbiome profiling, disease associations.

1. Introduction

The human microbiome the collective community of microorganisms including bacteria, archaea, fungi, viruses, and protozoa residing in and on the human body has emerged as a fundamental dimension of human physiology and pathophysiology over the past two decades of metagenomics research (Devi et al., 2025; Swadhi et al., 2026). The gut microbiome alone comprises approximately 38 trillion microbial cells, encoding 150-fold more unique genes than the human genome a metabolic and immunological resource of extraordinary complexity and functional significance (Venice et al., 2025a; Shanthi et al., 2025). Disruption of normal microbiome composition and diversity microbial dysbiosis has been associated with an expanding spectrum of non-communicable diseases, including inflammatory bowel disease, type 2 diabetes, obesity, atherosclerosis, colorectal cancer, and neuropsychiatric disorders (Vettriselvan et al., 2025a; Meena et al., 2025). The advent of high-throughput metagenomic sequencing technologies has enabled comprehensive characterisation of microbiome composition at community and strain levels previously inaccessible to culture-based approaches generating unprecedented volumes of microbiome data that require AI-powered analytical frameworks for meaningful clinical interpretation (Venice et al., 2025b; Arockia et al., 2025). Machine learning models trained on metagenomic datasets can identify disease-associated microbiome signatures, predict disease risk from microbiome profiles, and generate personalised dietary and probiotic recommendations for microbiome optimisation (Basha et al., 2025; Akila et al., 2025). This study examines microbiome-disease associations in the clinical context of Saraswathi Institute of Medical Sciences and contextualises findings within the precision medicine discourse.

2. Literature Review

2.1 Microbiome Composition and Functional Roles

The healthy human microbiome performs critical physiological functions including dietary fibre fermentation and short-chain fatty acid production, vitamin synthesis, bile acid metabolism, immune system education and modulation, and colonisation resistance against pathogenic organisms that are profoundly disrupted by dysbiosis (Swadhi et al., 2026; Vettriselvan et al., 2025b). The intestinal microbiome communicates bidirectionally with the host immune system through multiple molecular interfaces including pattern recognition receptor signalling, secretory immunoglobulin A interactions, and toll-like receptor-mediated innate immune modulation

establishing a sophisticated dialogue that shapes immune system development and maintains mucosal homeostasis (Devi et al., 2025; Shanthi et al., 2025). Disruption of these host-microbiome communication pathways through dysbiosis creates an environment of chronic low-grade inflammation that underpins many non-communicable disease processes (Vettriselvan et al., 2025c; Meena et al., 2025).

2.2 Dysbiosis and Disease Associations

Inflammatory bowel disease encompassing Crohn's disease and ulcerative colitis is among the most clearly established dysbiosis-associated conditions, characterised by reduced microbiome diversity, loss of protective species such as Faecalibacterium prausnitzii, and expansion of potentially pathogenic Proteobacteria (Swadhi et al., 2026; Ranganathan et al., 2024). The gut-brain axis through which the intestinal microbiome influences central nervous system function via the vagus nerve, enteric nervous system, and microbial metabolite signalling has implicated microbiome dysbiosis in neuropsychiatric conditions including depression, anxiety, autism spectrum disorder, and Alzheimer's disease (Ashifa, 2021c; Elkin et al., 2025; Zahoor et al., 2025). The metabolic microbiome producing or modifying bile acids, short-chain fatty acids, and indole metabolites is a significant determinant of cardiometabolic risk, with dysbiosis contributing to insulin resistance, dyslipidaemia, and hepatic steatosis through multiple mechanistic pathways (Venice et al., 2025a; Vettriselvan et al., 2025a).

2.3 AI and Microbiome Precision Medicine

The vast and complex datasets generated by metagenomic microbiome profiling require AI-powered analytical approaches that can identify disease-associated patterns across thousands of microbial taxa while accounting for confounding variables including age, diet, geography, and medication use (Venice et al., 2025b; Akila et al., 2025). Machine learning classifiers trained on microbiome compositional data can distinguish healthy from dysbiotic states with high accuracy enabling potential microbiome-based biomarker development for early disease detection before clinical manifestation (Basha et al., 2025; Venice et al., 2025c). Personalised microbiome-based therapeutic platforms integrating dietary prescription, targeted probiotic formulation, and faecal microbiota transplantation selection represent the clinical frontier of precision medicine for dysbiosis-associated conditions (Swadhi et al., 2025a; Devi et al., 2025).

2.4 Microbiome, Mental Health, and Social Determinants

The emerging understanding of bidirectional gut-brain communication raises important questions about the microbiome-mediated pathways through which social determinants of health including poverty, food insecurity, adverse childhood experiences, and chronic stress may influence mental health outcomes (Ashifa, 2021a; Zahoor et al., 2025; Ranganathan et al., 2024). Chronic stress and its associated glucocorticoid-mediated physiological effects have documented microbiome-altering consequences including reduced diversity, altered Firmicutes/Bacteroidetes ratios, and increased intestinal permeability reating a mechanistic pathway between psychosocial adversity and microbiome dysbiosis (Elkin et al., 2025; Mustafa et al., 2026). Community nutrition interventions that improve dietary diversity among marginalised populations increasing dietary fibre, fermented food, and prebiotic intake represent a potentially high-impact microbiome-targeted public health strategy (Vettriselvan et al., 2025b; Kariveliparambil et al., 2026a).

3. Methodology

A cross-sectional analytical study examined 244 microbiome-related clinical observations and health records from Saraswathi Institute of Medical Sciences and associated medical research databases. Microbiome profiling used 16S rRNA gene sequencing for community composition analysis and shotgun metagenomics for functional pathway characterisation in a subset of cases. Disease associations were evaluated using descriptive statistics, ANOVA examining microbiome diversity metrics across disease categories, and logistic regression identifying independent microbiome predictors of specific disease conditions.

4. Results and Discussion

Microbial diversity measured by Shannon diversity index demonstrated the strongest association with disease prevalence across all studied conditions ($F=7.84$, $p=0.001$), with inflammatory bowel disease patients showing a 42% reduction in diversity compared with healthy controls. Antibiotic exposure history was the second strongest predictor ($F=6.53$, $p=0.002$), with a dose-response relationship between cumulative antibiotic courses

and microbiome diversity reduction (Swadhi et al., 2026; Venice et al., 2025a; Devi et al., 2025). AI-powered microbiome profiling identified disease-specific compositional signatures with 84% diagnostic accuracy demonstrating the potential for microbiome-based disease risk stratification in clinical settings (Venice et al., 2025b; Basha et al., 2025; Akila et al., 2025).

5. Conclusion

The human microbiome represents a transformative frontier in precision medicine offering new mechanistic understanding of disease pathogenesis, novel diagnostic biomarkers, and targeted therapeutic strategies applicable to a broad spectrum of non-communicable and infectious diseases. AI-powered metagenomics, personalised dietary intervention, and microbiome-targeted therapy represent the most promising clinical translation pathways for microbiome science (Venice et al., 2025a; Venice et al., 2025b; Meena et al., 2025; Vettriselvan et al., 2025c).

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