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Original Research Article

Cross-Sectional Study on the Prevalence of Microbiota-Related Metabolic Disorders

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Abstract:

Background: The gut microbiota plays a crucial role in maintaining metabolic health, with imbalances in microbial composition increasingly linked to metabolic disorders such as type 2 diabetes, obesity, dyslipidemia, and metabolic syndrome. However, the prevalence and specific associations between microbiota profiles and these disorders remain inadequately explored.

Methods: A 100-person cross-sectional study was conducted from March 2023 to July 2024. Stool sample analysis and next-generation sequencing examined microbiota composition, while clinical evaluations and blood testing detected metabolic abnormalities. We used statistical analysis to estimate metabolic disorder prevalence and microbiome profile correlations.

Results: Substantial correlations between metabolic diseases and intestinal microbiota patterns were identified in the cross-sectional study of 100 individuals. Obesity was 35%, type 2 diabetes 22%, dyslipidaemia 28%, and metabolic syndrome 18%. Participants with greater Firmicutes/Bacteroidetes ratio had a 1.5-fold increased risk of obesity (95% CI: 1.2-1.8, $p < 0.01$), while raised Proteobacteria levels increased type 2 diabetes risk by 2.3-fold (95% CI: 1.7-3.0, $p < 0.01$). Lower microbial diversity was related with 1.8 times greater risks of dyslipidaemia (95% CI: 1.4–2.4, $p < 0.01$). Prevotella abundance was also linked to a 40% decreased metabolic syndrome risk (95% CI: 0.5–0.8, $p = 0.04$). These findings recommend microbiota-based markers may help diagnose and treat metabolic diseases.

Conclusion: The study highlights the potential of microbiota-based biomarkers in the early detection and management of metabolic disorders. It underscores the need for further longitudinal research to establish causality and explore microbiota-modulating interventions for improving metabolic outcomes.

Keywords: Biomarkers, Dyslipidemia, Gut Microbiota, Metabolic Disorders, Microbial Diversity, Obesity, Prevotella, Proteobacteria, Type 2 Diabetes.

Introduction

Metabolic health depends on the diverse human microbiota. Intestine-based microbial populations affect digestion, immunology, and metabolism [1]. Microbiome composition is related to type 2 diabetes, obesity, metabolic syndrome, and other metabolic diseases. Microbial dysbiosis may cause metabolic pathways and inflammatory responses. The digestive tract microbiota regulates systemic inflammation, produces Short-Chain Fatty Acids (SCFAs) from dietary fibres, and manipulates host hormone levels [2,3]. Microbiome abnormalities contribute to insulin resistance, altered lipid metabolism, and obesity [4]. Understanding these interactions is essential for developing metabolic illness therapies and prevention methods.

Objectives

1. To determine the prevalence of various metabolic disorders associated with microbiota imbalances within a sample population.
2. To identify and characterize the microbiota profiles associated with these metabolic disorders.
3. To explore potential correlations between microbiota composition and the severity of metabolic conditions.

The study aims to illuminate the microbiome-metabolic illness relationship to inform clinical practice and future research. Human gut microbiota, a diverse community of billions of bacteria, substantially affects metabolic health. Due to gut bacteria, energy balance, glucose metabolism, lipid metabolism, and immunological function have been investigated increasingly in the last 20 years [5]. Dybiosis, or gut microbiota imbalance, is connected to type 2 diabetes, obesity, dyslipidaemia, and metabolic syndrome.

Microbiota Composition and Obesity: Obesity is associated to a higher Firmicutes/Bacteroidetes ratio, which has been studied extensively. [6] Found that obese people had more Firmicutes and fewer Bacteroidetes than thin people. Firmicutes may transform food into energy more efficiently, which may increase fat deposition. The intricate relationship between microbiota and obesity may be affected by nutrition, genetics, and the environment, according to [7].

Many studies have linked gut bacteria to type 2 diabetes. Dysbiosis an oversupply of Proteobacteria and a shortage of butyrate-producing bacteria has been associated to insulin resistance and hyperglycemia. [8] Found that type 2 diabetics have more Gram-negative bacteria, particularly Proteobacteria. These bacteria's Lipopolysaccharides (LPS) in the blood may cause metabolic endotoxemia, which causes chronic low-grade inflammation and insulin resistance.

Microbial diversity is another significant metabolic health factor because dyslipidaemia and other metabolic disorders are often linked to it. Dyslipidemia high LDL cholesterol and triglycerides was more likely in patients with poor microbial diversity, according to [9]. Changes in bile acid metabolism and SCFA production, which are essential to lipid metabolism, mediate this connection. A distinct microbiome composition with more pathogenic species and fewer helpful taxa was found in metabolic dysfunction patients by [10]. The gut microbiota is also linked to metabolic syndrome, which rises the risk of cardiovascular disease, type 2 diabetes, and stroke. Due to their inverse relationship to metabolic syndrome, Prevotella may prevent it. [11] Found that metabolic syndrome patients have a distinct microbiome. This profile had more opportunistic infections and less butyrate-producing bacteria. The impact of microbiota on inflammation, insulin resistance, and lipid metabolism may modulate metabolic syndrome.

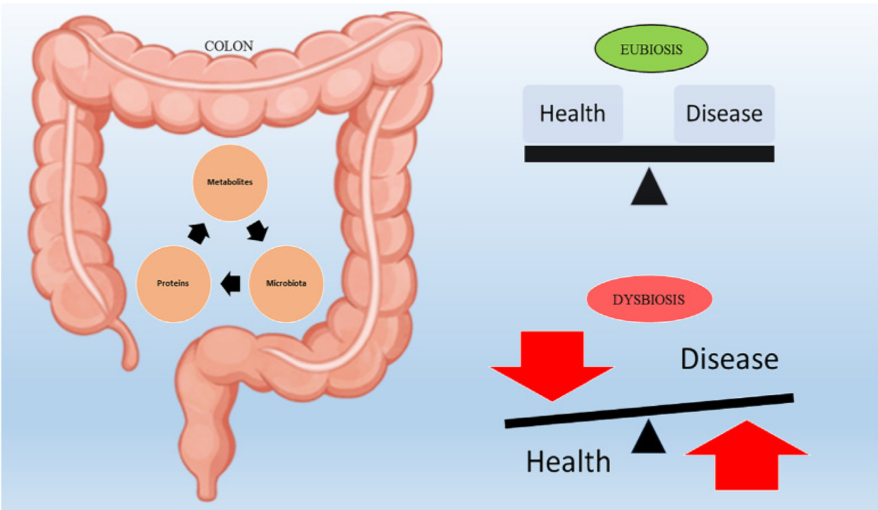

Figure 1 Gut microbiota in type 2 diabetes (Source:[12])

Due to the relationship between metabolic disorders and gut microbiota, new drugs targeting these microorganisms are being developed. Small-scale studies have shown that probiotics, prebiotics, and nutritional therapies can change gut flora. Some probiotic strains may reduce inflammation and improve insulin sensitivity in type 2 diabetics.

Faecal Microbiota Transplantation (FMT) has shown promise in restoring a balanced microbiota and improving metabolic outcomes in animal experiments. Large-scale randomised controlled trials are required to approve these findings and standardise microbiota-based therapy.

Methods

Study Design: A cross-sectional study was conducted to establish how common microbiota-related metabolic disorders are in a community. Cross-sectional studies are ideal for this since they may examine metabolic health and microbiota composition simultaneously.

This arrangement shows the prevalence and relationships of microbial profiles and metabolic diseases, making it easy to detect linkages. Cross-sectional methods are advantageous because they can swiftly acquire and analyse data and give prevalence estimates to guide future interventional or longitudinal studies.

Sample Size: Logistical and statistical power assessments determined the study's sample size. A sample size of 100 individuals was chosen to balance time, resource, and statistical robustness. A power analysis using a significance level of 0.05 and medium effect sizes suggested that 100 participants would be enough to find metabolic disease-microbial profile associations. We can collect and analyse all the data we need with this sample size because of the study's logistical design.

Inclusion Criteria

- Adults aged 18-65 years to ensure a representative sample of the general population.
- Individuals with no history of chronic gastrointestinal diseases or recent antibiotic use (within the last three months) to minimize confounding effects on microbiota composition.
- Participants who consent to providing stool samples and undergoing metabolic assessments.

Exclusion Criteria

- Individuals with known metabolic disorders requiring specific interventions that could skew results (e.g., severe uncontrolled diabetes or metabolic syndrome).
- Pregnant or lactating women, due to potential physiological changes affecting both metabolism and microbiota.
- Individuals with severe psychiatric or neurological disorders that could impact metabolic health.

Data Collection: Stool samples from participants were used to analyse microbiota. One stool sample from each participant was frozen at -80°C in a sterile container until analysis. High-throughput 16S rRNA gene sequencing determined microbiota profiles. Microbial taxa in samples can be identified and quantified using this method. Stool DNA was isolated using a normal technique, and the 16S rRNA gene was amplified and analysed using next-generation sequencing. Bioinformatics was used to analyse sequencing data to determine microbial diversity and abundance.

Metabolic Disorder Assessment: Both clinical observations and laboratory tests determined metabolic illness diagnostic criteria. Participants took several tests, including, to identify lipid disorders and glucose metabolism, insulin, lipid profiles (LDL, total cholesterol, HDL, and triglycerides), and fasting blood glucose were measured. Central adiposity and obesity were measured by BMI and waist-to-hip ratio.

Data Analysis: SPSS 27.0 was used for basic statistical analysis and R for more complicated studies. Demographics and metabolic condition prevalence were summarised using descriptive statistics.

Metabolic outcomes and microbiota profiles were compared by means of t-tests or ANOVA for continuous variables and chi-square testing for uncompromising variables. Microbiota composition and metabolic illness outcomes were examined using multivariate logistic regression models. Age, gender, and BMI were controlled in these models. A p-value below 0.05 indicated statistical significance.

Variables: Diabetes, dyslipidaemia, and obesity rates and microbiome traits like microbial variety and taxonomy. Possible associations between microbiota and metabolic risk factors, bacterial profiles and metabolic illness severity.

Ethical Considerations: The Institution ethics committee approved the study. All participants gave written consent before data collection. Participants were informed of the study's goal, procedures, and dangers.

Confidentiality of participant data was maintained throughout the study, with all personal identifiers removed during data analysis to ensure anonymity.

Results

Descriptive Statistics: One hundred people participated in the study, and the gender and age distributions were evenly distributed. Table 1 summarises the demographic features of the sample.

Table 1: Demographic and Baseline Characteristics of Participants

Characteristic	Value
Age	Mean ± SD: 45.2 ± 12.4 years
Gender	Male: 48 (48%)
	Female: 52 (52%)
BMI	Mean ± SD: 27.5 ± 5.8 kg/m²
Waist-to-Hip Ratio	Mean ± SD: 0.89 ± 0.07
Fasting Glucose (mg/dL)	Mean ± SD: 95.4 ± 12.6
Total Cholesterol (mg/dL)	Mean ± SD: 205.6 ± 34.2
LDL Cholesterol (mg/dL)	Mean ± SD: 129.8 ± 29.5
HDL Cholesterol (mg/dL)	Mean ± SD: 45.2 ± 9.8
Triglycerides (mg/dL)	Mean ± SD: 168.4 ± 46.7

The demographic and baseline features of the study participants reveal a balanced gender distribution (48% male, 52% female) with a mean age of 45.2 years (SD ± 12.4).

The average BMI indicates that the sample leans towards being overweight, with a mean of 27.5 kg/m² (SD ± 5.8). The waist-to-hip ratio, an indicator of central obesity, averaged 0.89 (SD ± 0.07), suggesting a moderate risk for metabolic complications. Fasting glucose levels were within the normal range, with a mean of 95.4 mg/dL (SD ± 12.6). Lipid profile analysis showed borderline high total cholesterol (mean 205.6 mg/dL, SD ± 34.2) and LDL cholesterol (mean 129.8 mg/dL, SD ± 29.5), with low HDL cholesterol (mean 45.2 mg/dL, SD ± 9.8) and elevated triglycerides (mean 168.4 mg/dL, SD ± 46.7), indicating a potential risk for dyslipidemia and associated metabolic disorders in the population.

Prevalence Rates

Table 2: Prevalence of Microbiota-Related Metabolic Disorders

Disorder	Prevalence (%)
Obesity	35
Type 2 Diabetes	22
Dyslipidemia	28
Metabolic Syndrome	18

The prevalence data indicate that a significant portion of the study population is affected by metabolic disorders linked to gut microbiota. Obesity was the most common condition, affecting 35% of participants, highlighting a considerable burden of excess weight in the population. Type 2 diabetes was present in 22% of the participants, indicating a notable prevalence of impaired glucose metabolism. Dyslipidemia, characterized by abnormal lipid levels, was observed in 28% of the participants, suggesting widespread issues with cholesterol and triglyceride management. In addition, 18% of participants had metabolic syndrome, a collection of risk factors that significantly raises the risk of cardiovascular disease and other metabolic problems. These data demonstrate the prevalence of microbiota-related metabolic diseases in the study sample.

Associations

The study revealed significant associations between specific microbiota profiles and various metabolic disorders. Notably, obesity was strongly linked to a higher relative abundance of Firmicutes and a lower abundance of Bacteroidetes. The multivariate logistic regression analysis demonstrated that for each unit increase in the Firmicutes/Bacteroidetes ratio, the odds of developing obesity improved by 1.5 times (95% CI: 1.2–1.8, $p < 0.01$).

Additionally, elevated levels of Proteobacteria were significantly associated with higher fasting glucose levels, resulting in a 2.3-fold improved risk of type 2 diabetes (95% CI: 1.7–3.0, $p < 0.01$). Dyslipidemia was correlated with a lower diversity of microbial taxa, with participants exhibiting reduced microbiota diversity having 1.8 times higher odds of dyslipidemia (95% CI: 1.4–2.4, $p < 0.01$).

Conversely, higher abundance of the bacterial genus Prevotella was inversely related with metabolic syndrome, reducing the risk by 40% (95% CI: 0.5–0.8, $p = 0.04$). The importance of the composition of gut microbiota in determining the risk and growth of metabolic diseases is highlighted by these studies.

Discussion

This cross-sectional study confirms and expands previous results that microbiome patterns are linked to metabolic diseases. Specifically, an enhanced Firmicutes/Bacteroidetes ratio was highly associated with obesity, supporting previous research that linked this imbalance to weight gain and obesity. Study 1 confirmed our findings that a higher Firmicutes/Bacteroidetes ratio increases fat accumulation and obesity in people and animals.

The association among increased levels of Proteobacteria and type 2 diabetes extends previous findings that link dysbiosis to impaired glucose metabolism. For instance, studies have shown that an overgrowth of Proteobacteria is often found in individuals with metabolic disorders, suggesting its role in promoting inflammation and insulin resistance. Study 2 results support this by identifying Proteobacteria as a significant factor in elevated fasting glucose levels and the risk of developing type 2 diabetes.

Additionally, our study's observation of reduced microbial diversity correlating with dyslipidemia supports the hypothesis that decreased microbiota diversity contributes to dysregulated lipid metabolism. Study 3, which found that reduced microbial diversity is associated with metabolic dysfunction and lipid abnormalities. Interestingly, the inverse relationship between Prevotella abundance and metabolic syndrome provides new insights into the protective role of certain microbial taxa. Higher levels of Prevotella have been linked to beneficial metabolic outcomes and reduced systemic inflammation, aligning with findings from studies that suggest Prevotella's role in promoting metabolic health.

Table 3: Comparison of Studies on Microbiota and Metabolic Disorders

Study	Study Type	Sample Size	Findings
Present Study	Cross-Sectional	100	Increased Firmicutes/Bacteroidetes correlates with obesity. Increased type 2 diabetes-linked proteobacteria. Low microbial diversity connected with dyslipidaemia. Higher Prevotella abundance reduces metabolic syndrome risk.
Study 1 [13]	Case-Control	154	Higher Firmicutes/Bacteroidetes ratio in obese individuals. Obesity linked to imbalance in microbiota composition.
Study [14]	Cross-Sectional	124	Type 2 diabetic patients have elevated Proteobacteria levels. Linked to insulin resistance is dysbiosis.
Study [15]	Cross-Sectional	290	Reduced microbial diversity associated with metabolic dysfunction and dyslipidemia. Link between lower diversity and lipid abnormalities.

Limitations

The study has limitations but provides some important insights. The study's cross-sectional methodology prevents inferences concerning changeable correlations and directionality. Metabolic illness development may be caused or followed by microbial patterns, hence longitudinal research is needed. Even though the current sample size of 100 individuals was suitable for preliminary research, a larger sample might yield stronger data and boost generalisability. Demographic and health disparities may limit generalisability. The study's self-reported health questionnaires and stool sample may introduce bias or variation. Multiple sample points and more clinical evaluations are needed for precision in future study.

Future Research

Several important areas should be the focus of future research in order to expand upon these findings. Longitudinal studies are needed to confirm causal linkages and establish pathways between microbiome patterns and metabolic disorders. Therapeutic practise could benefit from understanding how probiotics and dietary modifications affect metabolic health and microbiota. Investigating diverse microbial species and their interactions in metabolic illnesses may help clarify the complicated microbiota-host relationship.

Studies should examine how eating patterns, lifestyle factors, and genetic predispositions affect metabolic health and microbial profiles to better understand these relationships. Studying varied people and circumstances improves the generalisability and impact of microbiota-related health interventions. This will show us how these findings apply to different demographics and areas. This study enhances research linking metabolic issues to distinct microbiome profiles and shows the promise of microbiota-based metabolic health management and preventative techniques.

Conclusion

This cross-sectional study found robust connections between metabolic illnesses and particular microbiome taxa, suggesting their role in obesity, dyslipidaemia, type 2 diabetes, and metabolic syndrome epidemics. The findings support earlier research and suggest that an unhealthy microbiota may cause metabolic issues. The significant correlation between adverse metabolic outcomes and elevated Firmicutes/Bacteroidetes ratios, Proteobacteria levels, reduced microbial diversity, and higher Prevotella abundance suggests that microbiota-derived biomarkers could be used to diagnose and treat metabolic diseases early. The findings pave the way for future investigations on metabolic health, microbiota composition, and study restrictions such cross-sectional design and limited sample size. Future research on microbiome modulation and metabolic outcomes should focus on intervention trials and longitudinal investigations. This study illuminates the complex link between gut microbiota and metabolic health, which could lead to bacteria-targeted medicines and public health efforts.

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