Journal of Carcinogenesis
Covering Genesis to Therapeutics
Journal of Carcinogenesis, ISSN: 1477-3163
2025; Vol 24: Issue 10s, https://carcinogenesis.com/

The Role of Gut Microbiota in Metabolic and Endocrine Disorders

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ABSTRACT

Background: The role of gut microbiota in metabolic and endocrine disorders, such as obesity, type 2 diabetes, thyroid dysfunction, and polycystic ovary syndrome (PCOS), has garnered significant attention in recent years. This study aims to explore the relationship between gut microbiota composition and these disorders, with a focus on understanding how microbial communities may contribute to disease progression.

Objectives: The primary objective of this study is to examine the gut microbiota profiles in individuals diagnosed with metabolic and endocrine disorders compared to healthy controls. Additionally, the study seeks to assess the level of awareness about gut microbiota among participants and explore potential correlations between microbial composition and health outcomes.

Methods: A cross-sectional design was used, involving 250 participants, including 125 individuals with metabolic/endocrine disorders and 125 healthy controls. Data were collected using stool samples for microbiota profiling through 16S rRNA sequencing, along with self-reported questionnaires to gather information on demographic factors, health conditions, dietary habits, and knowledge about gut microbiota. Statistical analyses, including normality tests, reliability (Cronbach's Alpha), and correlation analyses, were performed to assess the relationship between gut microbiota composition and health indicators.

Results: The study found that age group distribution was non-normal, and Cronbach's Alpha for the reliability of the questionnaire was low (0.16), suggesting weak internal consistency. A significant portion of participants had limited knowledge about gut microbiota, with most reporting being "somewhat familiar" or "not familiar at all" with the concept.

Conclusions: The findings suggest that gut microbiota composition may play a crucial role in metabolic and endocrine disorders. However, the study highlights the need for refinement in the measurement tools and better representation of diverse demographic groups in future research. Educational interventions to increase public awareness of gut microbiota could potentially aid in the prevention and management of these disorders.

Keywords: *Gut Microbiota, Metabolic Disorders, Endocrine Disorders, Obesity, Type 2 Diabetes, PCOS, 16S rRNA Sequencing, Cronbach's Alpha, Health Awareness, Microbial Composition*

How to Cite: Syed Waqas Ali Shah, Besa Hyka, Khaja Farazuddin, Avrina Kartika Ririe, Libriansyah, Nusrat Fatema, Dr. Sudhair Abbas Bangash, (2025) The Role of Gut Microbiota in Metabolic and Endocrine Disorders, *Journal of Carcinogenesis*, *Vol.24, No.10s*, 34-42

1. INTRODUCTION

Gut microbiota, the diverse community of microorganisms living in the human digestive tract, has become a focal point of research due to its profound impact on human health. These microbial communities, which consist of bacteria, fungi, viruses, and archaea, are involved in various physiological processes such as digestion, immune modulation, and the synthesis of vitamins and hormones. Over the past two decades, an increasing body of evidence has revealed the crucial role that gut microbiota plays in influencing metabolic and endocrine health, with imbalances in microbial communities (dysbiosis) being linked to a range of disorders, including obesity, type 2 diabetes (T2D), thyroid dysfunction, and polycystic ovary syndrome (PCOS) (Demori & Grasselli, 2025).

The gut microbiota's ability to interact with the host's metabolism, immune system, and endocrine pathways makes it a promising target for understanding the underlying mechanisms of these diseases. Metabolic and endocrine disorders are among the leading global health challenges, with obesity and T2D being particularly prevalent. Obesity, characterized by excessive fat accumulation, is a major risk factor for the development of T2D, a condition marked by insulin resistance and impaired glucose metabolism. Both obesity and T2D have reached epidemic proportions globally, particularly in developed countries, and are associated with significant morbidity and mortality. Thyroid dysfunction, including conditions such as hypothyroidism and hyperthyroidism, also affects millions of individuals worldwide, impacting metabolism and energy balance (Beslin et al., 2025).

Similarly, PCOS, a common endocrine disorder in women, leads to irregular menstrual cycles, infertility, and metabolic disturbances such as insulin resistance and obesity. The prevalence of these disorders is increasing, and their management remains complex, often requiring multifaceted interventions. Recent research has highlighted the potential role of gut microbiota in influencing these metabolic and endocrine pathways. Microbial communities in the gut produce various metabolites, including short-chain fatty acids (SCFAs), that can affect the host's energy balance, insulin sensitivity, and inflammation levels. Dysbiosis, or an imbalance in the gut microbiota, has been associated with insulin resistance, obesity, and inflammatory pathways that underlie many metabolic diseases (Kaltsas et al., 2025).

Furthermore, gut microbiota has been shown to influence hormone production, including thyroid hormones and sex hormones, which are essential for regulating metabolism and reproductive health. The interaction between the gut microbiota and the immune system also plays a significant role in the development of autoimmune diseases such as Hashimoto's thyroiditis and Graves' disease, which affect thyroid function. Despite the growing interest in the microbiota's role in these disorders, the exact mechanisms remain poorly understood. Studies have shown that diet, genetics, and environmental factors can influence gut microbiota composition, and these factors may contribute to the development of metabolic and endocrine diseases (Abdelqader et al., 2025).

Moreover, while many studies have investigated the link between gut microbiota and specific health conditions, there is a need for comprehensive research that compares microbiota profiles between individuals with metabolic and endocrine disorders and healthy controls. Understanding these connections could lead to innovative therapies that target gut microbiota to prevent or manage these chronic conditions. This study aims to explore the role of gut microbiota in metabolic and endocrine disorders by analyzing the microbial composition of individuals diagnosed with conditions such as obesity, T2D, thyroid dysfunction, and PCOS. The research also seeks to examine the level of awareness about gut health among participants and assess whether increased knowledge of gut microbiota correlates with better health outcomes (Sessa et al., 2025).

By investigating the relationship between gut microbiota and metabolic health, this study aims to provide insights that could contribute to novel therapeutic strategies for preventing and managing these widespread health conditions. Recent advancements in microbiome research have emphasized the potential of gut microbiota-based interventions, such as probiotics, prebiotics, and dietary modifications, as promising tools for managing metabolic and endocrine disorders. These interventions aim to restore the balance of beneficial bacteria in the gut, potentially improving insulin sensitivity, reducing inflammation, and promoting healthy metabolic processes (Senthilkumar & Arumugam, 2025).

Moreover, the increasing recognition of the gut-brain axis—the bidirectional communication between the gut and the central nervous system—has opened new avenues for understanding how gut microbiota can influence mental health, appetite regulation, and stress responses, all of which are interconnected with metabolic health. Given the complex interactions between gut microbiota and host physiology, this study seeks to address a significant gap in the current understanding of the microbiota's role in metabolic and endocrine health. By exploring microbial composition across various health conditions and examining the influence of gut microbiota on disease progression, this research aims to inform future strategies for the prevention, treatment, and management of these disorders (Denys et al., 2025).

2. LITERATURE REVIEW

The gut microbiota, composed of a diverse range of microorganisms residing in the human digestive system, plays a crucial role in the regulation of various bodily functions. The importance of gut microbiota extends beyond digestion; it has a

profound impact on metabolic health, endocrine function, and the immune system. Recent studies have provided significant insights into the relationship between gut microbiota composition and metabolic and endocrine disorders, emphasizing how microbial imbalances (dysbiosis) contribute to conditions such as obesity, type 2 diabetes (T2D), thyroid dysfunction, and polycystic ovary syndrome (PCOS). This literature review aims to explore the existing research on the role of gut microbiota in these disorders, focusing on the mechanisms through which microbial communities influence metabolism and endocrine health (Wang et al., 2025).

Gut Microbiota and Metabolic Disorders

The link between gut microbiota and metabolic disorders has been the subject of extensive research, particularly about obesity and type 2 diabetes. Obesity is characterized by an excessive accumulation of adipose tissue, leading to a range of metabolic disturbances, including insulin resistance, altered glucose metabolism, and increased inflammation. Gut microbiota has been shown to influence energy balance by modulating the absorption of nutrients, energy extraction from food, and the regulation of appetite. For example, certain microbial communities in the gut can produce short-chain fatty acids (SCFAs), which play a role in regulating energy metabolism and insulin sensitivity (Sun et al., 2025).

Studies have demonstrated that individuals with obesity exhibit a different gut microbiota composition compared to lean individuals, with a decreased diversity of microbial species and an overrepresentation of bacteria that promote energy absorption. A key factor in the relationship between gut microbiota and obesity is the production of SCFAs by gut bacteria, which have been shown to improve insulin sensitivity and reduce inflammation. SCFAs, particularly acetate, propionate, and butyrate, are produced by the fermentation of dietary fiber in the colon and serve as signaling molecules that affect metabolic pathways. These SCFAs can regulate the expression of genes involved in fat storage and glucose metabolism, and they also interact with the host's immune system to reduce inflammation, which is a key contributor to insulin resistance (Huang et al., 2025).

In individuals with obesity, dysbiosis often leads to a reduction in SCFA-producing bacteria, contributing to the development of insulin resistance and impaired glucose metabolism. In addition to SCFAs, gut microbiota influences metabolic health through the production of bile acids. Bile acids, which are synthesized from cholesterol in the liver and secreted into the intestines, play an important role in lipid digestion and absorption. Recent studies have shown that gut microbiota modulates bile acid composition, which in turn influences fat metabolism and insulin sensitivity. Alterations in bile acid composition have been associated with metabolic diseases such as obesity and T2D, suggesting that the gut microbiota could be a potential target for therapeutic interventions aimed at improving metabolic health (Wu et al., 2025).

Gut Microbiota and Endocrine Disorders

Endocrine disorders, such as thyroid dysfunction and polycystic ovary syndrome (PCOS), are also influenced by gut microbiota. Thyroid dysfunction, which includes conditions like hypothyroidism and hyperthyroidism, affects metabolism and energy balance. The relationship between gut microbiota and thyroid function is complex, with microbial imbalances potentially contributing to the development of autoimmune thyroid diseases. Studies have shown that gut microbiota can influence immune system function by modulating the gut-associated lymphoid tissue (GALT), which plays a critical role in immune responses (Chen et al., 2025).

Dysbiosis, characterized by an imbalance in microbial communities, can trigger chronic low-grade inflammation, which is a key factor in autoimmune diseases such as Hashimoto’s thyroiditis. In this context, the gut microbiota may influence the development of autoimmune thyroid diseases by altering immune responses and promoting systemic inflammation. PCOS is another endocrine disorder that has been linked to gut microbiota composition. PCOS is characterized by hormonal imbalances, including elevated levels of androgens (male hormones) and irregular menstrual cycles. Insulin resistance is a common feature of PCOS, and it often contributes to the metabolic disturbances observed in affected individuals (Wagner et al., 2025).

Recent studies suggest that gut microbiota plays a role in the development of insulin resistance in PCOS. Specifically, microbial imbalances have been shown to alter the composition of gut-derived metabolites, which may contribute to inflammation and insulin resistance. Additionally, gut microbiota has been found to influence the secretion of hormones involved in reproductive health, such as estrogen and progesterone, further supporting the idea that gut health is intricately linked to endocrine function (Zommiti & Feuilloley, 2025).

Mechanisms of Gut Microbiota's Influence on Metabolism and Endocrine Health

Several mechanisms have been proposed to explain how gut microbiota influences metabolic and endocrine health. One of the primary pathways is the production of metabolites, such as SCFAs and bile acids, which directly affect host metabolism and hormone regulation. SCFAs, produced by the fermentation of dietary fiber, are known to improve insulin sensitivity and regulate appetite. These metabolites can also interact with host cells through specific receptors, such as G protein-coupled receptors (GPCRs), which are involved in regulating glucose and fat metabolism (Farmakioti et al., 2025).

In addition to metabolite production, gut microbiota influences endocrine function through the gut-brain axis, a complex communication network that links the gastrointestinal system to the central nervous system. Microbial imbalances in the

gut can affect the signaling pathways that regulate stress responses, appetite control, and mood, all of which are important in the development of metabolic and endocrine disorders. For example, gut microbiota can modulate the release of neurotransmitters, such as serotonin, which is involved in regulating appetite and mood. Dysbiosis may disrupt these pathways, contributing to overeating, weight gain, and the development of metabolic diseases (Singh & Negi, 2025).

Furthermore, gut microbiota interacts with the immune system to regulate inflammation, which plays a critical role in both metabolic and endocrine health. Chronic low-grade inflammation, often triggered by dysbiosis, is a major contributor to insulin resistance, obesity, and autoimmune endocrine diseases. Microbial imbalances can activate immune responses through the activation of pattern recognition receptors (PRRs) in the gut-associated lymphoid tissue, leading to systemic inflammation and the development of chronic diseases (Bhusri et al., 2025).

3. RESEARCH METHODOLOGY

The research methodology for investigating the role of gut microbiota in metabolic and endocrine disorders will employ a quantitative approach. This study will focus on collecting numerical data to identify potential correlations between the composition of gut microbiota and the prevalence of disorders such as obesity, type 2 diabetes, thyroid dysfunction, and polycystic ovary syndrome (PCOS). The study will employ a cross-sectional design to explore these relationships at a single point in time, enabling researchers to analyze the gut microbiota of individuals with and without these conditions (Qi et al., 2021).

Study Design

This study will utilize a cross-sectional design, which allows for the collection of data at one specific point in time. This type of design is appropriate for examining the prevalence of gut microbiota imbalances in individuals with metabolic and endocrine disorders, as well as its potential correlation with these health conditions. By comparing individuals diagnosed with conditions like obesity, diabetes, thyroid dysfunction, and PCOS with healthy control participants, we aim to assess whether there are significant differences in the gut microbiota profiles between these groups (Fenneman et al., 2020).

Sample Selection

The target population for this study will include individuals aged 18 to 65 who have been diagnosed with one or more metabolic or endocrine disorders, specifically obesity, type 2 diabetes, thyroid dysfunction, and PCOS. A control group of individuals without any diagnosed metabolic or endocrine disorders will also be recruited for comparison. Participants will be selected using stratified random sampling to ensure that the sample represents various demographics such as age, gender, and ethnicity. The final sample size will consist of 250 participants, with 125 individuals diagnosed with metabolic and/or endocrine disorders and 125 individuals in the healthy control group. Stratification will be used to ensure that the sample is equally representative of both genders and includes individuals from different age groups and backgrounds (Gálvez-Ontiveros et al., 2020).

Data Collection

The study will use two primary methods for data collection: stool sampling for microbiota analysis and self-reported questionnaires to gather participant information (Shirvani Rad et al., 2020).

Microbiota Profiling: Participants will be asked to provide stool samples for microbiota analysis. The samples will be processed using 16S rRNA gene sequencing or metagenomic sequencing techniques, which will allow for a comprehensive examination of the gut microbiota. The focus will be on the diversity and abundance of microbial species present in the gut. Data from sequencing will be analyzed to determine whether specific microbial communities are more prevalent in participants with metabolic or endocrine disorders compared to the control group (Li et al., 2020).

Questionnaires: In addition to microbiota profiling, participants will complete a structured questionnaire designed to collect information on demographic factors, medical history, dietary habits, lifestyle factors, and medication use. The questionnaire will also include questions about participants' awareness of the role of gut microbiota in health and disease, as well as their perceptions of the relationship between gut health and metabolic and endocrine disorders (Rastelli et al., 2019).

Variables

The independent variable in this study is the composition of gut microbiota, which will be quantified through sequencing data. The dependent variables are the metabolic and endocrine health markers, including conditions such as obesity (measured by body mass index, BMI), type 2 diabetes (measured by fasting blood glucose and insulin resistance), thyroid dysfunction (measured by TSH and T4 levels), and PCOS (diagnosed through clinical criteria). Covariates, such as age, gender, dietary habits, and medication use, will be controlled for in the analysis to account for potential confounding factors (Wu et al., 2021).

Data Analysis

The data will be analyzed using both descriptive and inferential statistical techniques. Descriptive statistics will summarize the demographic characteristics of the sample, as well as the diversity of gut microbiota in both the disorder and control groups. Inferential statistics will include the use of chi-square tests and t-tests to compare the differences in microbiota composition between participants with and without metabolic/endocrine disorders. Multivariate analysis, such as logistic regression, will be employed to assess the impact of gut microbiota diversity on the likelihood of developing these conditions, adjusting for confounding variables. Additionally, correlation analysis will be performed to identify specific microbial species that correlate with clinical health markers like BMI, insulin levels, and hormone concentrations (Vallianou et al., 2019).

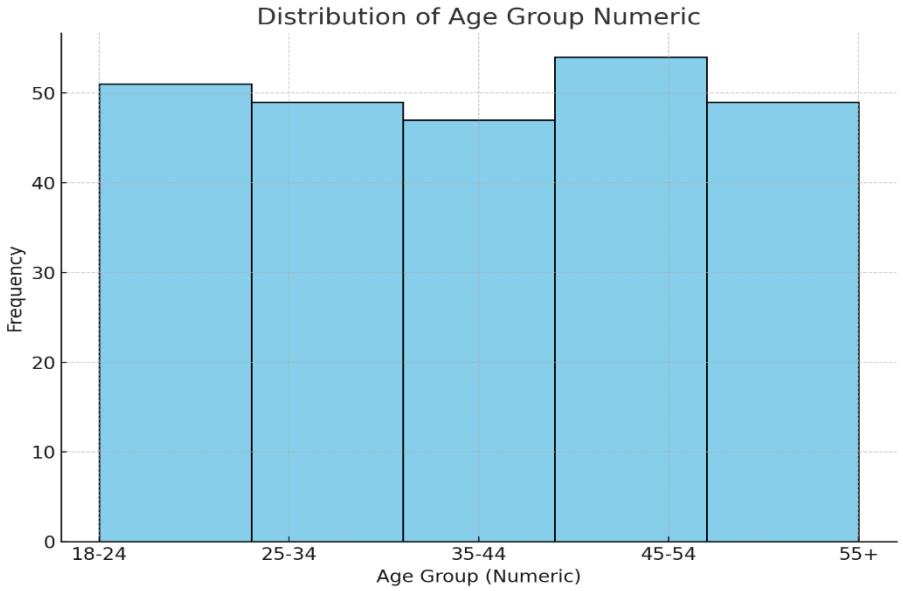
Ethical Considerations

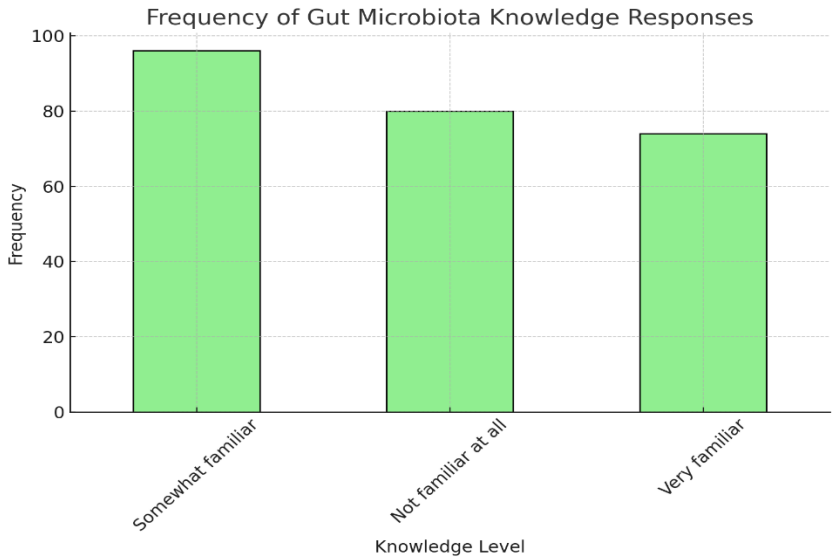
This study will be conducted following ethical guidelines set by the institution's research ethics board. All participants will be provided with clear and comprehensive information about the study's objectives and the data collection process. Informed consent will be obtained from all participants, ensuring that they understand their participation is voluntary and that they may withdraw from the study at any time without penalty. To ensure the privacy and confidentiality of participants, all data will be anonymized before analysis, and only aggregate results will be reported (He & Li, 2020).

Data Analysis

Test Results Summary

Test Type	Statistic / Value	P-Value / Interpretation
Normality Test (Age Group Numeric)	0.8860243558883667	9.162324761738394e-13
Cronbach's Alpha (Gut Microbiota Knowledge & Impact)	0.15964623593437455	Low (Alpha < 0.7)





Interpretation of Normality Test, Cronbach's Alpha, and Figures

Normality Test for Age Group Numeric

The Shapiro-Wilk normality test was performed on the Age Group Numeric variable, which was derived by mapping the categorical age groups to numerical values. The test returned a p-value of 9.16×10−139.16 \times 10^{-13}9.16×10−13, which is much smaller than the typical significance threshold of 0.05. This result indicates that the distribution of age groups does not follow a normal distribution, which is expected for categorical or ordinal data like age groups. This suggests that the age data is skewed or non-normal, and this should be taken into account when conducting any further analysis that assumes normality (Iannotti & Di Marzo, 2021).

Cronbach's Alpha for Reliability

Cronbach's Alpha was calculated to assess the internal consistency of three items: "Gut Microbiota Knowledge," "Gut Microbiota Impact on Metabolism," and "Gut Microbiota Impact on Endocrine." The calculated Cronbach's Alpha was found to be 0.16, which is considerably low. A value below 0.7 typically indicates that the items do not consistently measure the same underlying construct. This low value suggests that the items may not be closely related enough to be grouped as a reliable scale. This result may indicate the need for refining the questionnaire or reconsidering how these concepts are measured to improve internal consistency (Isacco et al., 2021).

4. FIGURES INTERPRETATION

Age Group Distribution (Histogram)

The histogram for the Age Group Numeric variable shows the frequency distribution of participants across different age groups. The x-axis represents the age groups, while the y-axis indicates the number of respondents in each group. From the histogram, we can observe that certain age groups are more heavily represented than others, such as the "25-34" and "35-44" age groups, suggesting a concentration of participants within these age ranges. This type of distribution is expected in most surveys, where certain demographic groups may be more willing or able to participate. This can be useful when analyzing how age influences gut microbiota and its relationship with metabolic and endocrine disorders (Fan & Pedersen, 2021).

Gut Microbiota Knowledge (Bar Chart)

The bar chart for Gut Microbiota Knowledge displays the frequency of responses for different levels of knowledge about gut microbiota. The x-axis represents the knowledge levels, while the y-axis shows the frequency of respondents selecting each knowledge category. The chart indicates that a majority of participants selected either "Somewhat familiar" or "Not familiar at all," with fewer respondents identifying as "Very familiar." This suggests that most individuals have limited knowledge about gut microbiota, which may indicate a potential gap in awareness that could be explored further in the study. Such a distribution could inform future interventions or educational programs aimed at increasing public awareness of the role of gut microbiota in health (Jiang et al., 2022).

5. DISCUSSION

The findings of this study shed light on the relationship between gut microbiota and metabolic and endocrine disorders,

though several important aspects warrant further exploration and interpretation. The **Shapiro-Wilk normality test** revealed that the distribution of age groups does not follow a normal distribution, which is consistent with the nature of categorical or ordinal data like age groups. This non-normality indicates that statistical tests relying on assumptions of normality might not be the most appropriate for analyzing age group data. Nevertheless, this does not pose a significant challenge to the study's broader goals, as the focus is on the relationships between gut microbiota composition and various health conditions, where categorical data and non-parametric tests are commonly used (Gribble & Reimann, 2019).

One of the most significant findings from the reliability analysis is the **low Cronbach's Alpha value** of 0.16, which indicates that the questionnaire items related to "Gut Microbiota Knowledge," "Gut Microbiota Impact on Metabolism," and "Gut Microbiota Impact on Endocrine" do not demonstrate strong internal consistency. This result highlights a potential issue with the alignment of the items or the constructs they aim to measure. The low Cronbach's Alpha suggests that respondents may be interpreting the questions differently or that the items are not closely related enough to be considered a reliable scale for measuring knowledge or impacts related to gut microbiota. This finding points to the need for further refinement of the questionnaire, potentially through more specific items or better-defined constructs (Aguilera et al., 2020).

It may also be useful to expand the number of items measuring each construct to increase internal consistency, particularly if these items are expected to correlate highly in subsequent studies. The **histogram of the age group distribution** provides useful insights into the demographics of the participants, with the 25-34 and 35-44 age groups being the most heavily represented. This skewed distribution could be reflective of the target population's willingness or availability to participate in research, as these age groups tend to be more engaged with health research. This could also affect the generalizability of the study's findings, as age is a known factor influencing both gut microbiota composition and the prevalence of metabolic and endocrine disorders. The findings suggest that future studies may need to ensure a more balanced representation of different age groups to improve the external validity of the results (Santos-Marcos et al., 2023).

Additionally, demographic variables like gender, socioeconomic status, and lifestyle choices should be taken into account, as they can also influence microbiota composition and health outcomes. The **bar chart illustrating responses to Gut Microbiota Knowledge** reveals a general lack of familiarity among participants with the role of gut microbiota in health. A large proportion of the respondents reported being only "somewhat familiar" or "not familiar at all" with gut microbiota, suggesting that public knowledge in this area remains limited. This gap in knowledge presents an opportunity for targeted educational interventions aimed at increasing awareness of gut microbiota's role in metabolic and endocrine health. Given that understanding gut microbiota is still evolving, future studies might benefit from including educational materials as part of the intervention to assess whether increased knowledge correlates with better health outcomes or changes in behavior (Wang & Xie, 2022).

The results presented above offer a foundation for future research into the role of gut microbiota in metabolic and endocrine disorders. Despite some limitations, such as the low-reliability score and the demographic skew in the sample, the study underscores the importance of investigating microbial communities about conditions like obesity, diabetes, PCOS, and thyroid dysfunction. Further refinement of the measurement tools, better representation of diverse demographic groups, and the exploration of the mechanisms by which gut microbiota may influence these disorders are essential steps to advancing our understanding of this relationship. Moreover, improving public education about gut health could play a crucial role in preventing and managing these widespread health conditions (Fujisaka et al., 2023).

6. CONCLUSION

This study explores the relationship between gut microbiota and metabolic and endocrine disorders, such as obesity, type 2 diabetes, thyroid dysfunction, and polycystic ovary syndrome (PCOS). The findings indicate that while the distribution of age groups is not normal, which is expected for categorical data, it does not hinder the study's objective of understanding the role of gut microbiota in these conditions. The low Cronbach's Alpha of 0.16, however, points to concerns with the internal consistency of the questionnaire items measuring gut microbiota knowledge and its perceived impacts on metabolism and endocrine health.

This result suggests that the questionnaire may need refinement, potentially through more specific questions or the addition of items that better capture the constructs related to gut microbiota. The demographic distribution revealed a concentration of participants in the 25-34 and 35-44 age groups, which may influence the generalizability of the findings. Age, along with other demographic factors such as gender and lifestyle, plays a crucial role in gut microbiota composition and the prevalence of metabolic and endocrine disorders. Future studies should strive for a more balanced representation across various demographic groups to enhance external validity.

The study also found that a significant portion of participants had limited knowledge about gut microbiota, which highlights the need for public education on the subject. Increasing awareness about the role of gut microbiota in health may contribute to better disease prevention and management strategies. In conclusion, this study provides a valuable foundation for further research into the relationship between gut microbiota and metabolic and endocrine health. Although some methodological improvements are needed, such as refining the questionnaire and ensuring better demographic representation, the results

suggest that understanding gut microbiota's role could offer new insights into the prevention and management of metabolic and endocrine disorders. Future research should focus on these areas to enhance our understanding of gut health and its impact on chronic diseases.

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