

# GUT MICROBIOTA-RELATED DIETARY PATTERNS AND THEIR ASSOCIATION WITH METABOLIC SYNDROME AMONG ADULTS: A HOSPITAL-BASED OBSERVATIONAL STUDY

Veeresh Kumar Dhanni<sup>1</sup>

<sup>1</sup>Assistant Professor, Department of Medicine, NCRIMS Meerut, Uttar Pradesh, India

## ABSTRACT

**Background:** Emerging evidence suggests that dietary patterns influence metabolic health through modulation of the gut microbiota. However, data on gut microbiota-related dietary patterns and their association with metabolic syndrome (MetS) among adults remain limited, particularly in hospital-based settings. The objective of the study is to identify gut microbiota-related dietary patterns and examine their association with metabolic syndrome and its components among adults attending a tertiary care hospital.

**Materials and Methods:** A hospital-based cross-sectional study was conducted among 355 adults aged 18–65 years. Dietary intake was assessed using a validated semi-quantitative Food Frequency Questionnaire. Principal Component Analysis (PCA) was used to derive gut microbiota-related dietary patterns. Metabolic syndrome was defined according to the International Diabetes Federation (IDF) 2006 criteria. Multivariable logistic regression was performed to evaluate the association between dietary pattern adherence and metabolic syndrome after adjusting for potential confounders.

**Result:** Three major dietary patterns were identified: Fiber-Rich and Fermented Foods Pattern, Traditional Pattern, and Processed Food Pattern. The overall prevalence of metabolic syndrome was 38.9%. Participants in the highest tertile of adherence to the Fiber-Rich and Fermented Foods Pattern had a significantly lower prevalence of metabolic syndrome compared with those in the lowest tertile (25.4% vs. 51.7%,  $p < 0.001$ ). After adjustment for confounding variables, high adherence to the Fiber-Rich Pattern was associated with lower odds of metabolic syndrome (OR=0.42, 95% CI: 0.24–0.72;  $p = 0.002$ ), whereas high adherence to the Processed Food Pattern was associated with increased odds (OR=2.31, 95% CI: 1.37–3.90;  $p = 0.001$ ). Significant inverse associations were also observed for elevated fasting glucose, triglycerides, blood pressure, and central obesity.

**Conclusion:** Greater adherence to fiber-rich and fermented-food dietary patterns was associated with reduced odds of metabolic syndrome, while processed-food dietary patterns were linked to increased metabolic risk. Microbiota-oriented

Received : 20/01/2026  
Received in revised form : 20/02/2026  
Accepted : 20/03/2026

Corresponding Author:  
**Dr. Veeresh Kumar Dhanni,**  
Email: drvkdhanni91@gmail.com

Source of Support: Nil,  
Conflict of Interest: None declared

*Ann. Clin. Transl. Med*  
2026;1(1); 24-30

**How to cite this article:** Dhanni VK.  
GUT Microbiota-Related Dietary  
Patterns and Their Association with  
Metabolic Syndrome among Adults: A  
Hospital-Based Observational Study.  
*Ann. Clin. Transl. Med.* 2026;1(1):24-  
30.

dietary strategies may contribute to the prevention and management of metabolic syndrome.

**Keywords:** Gut microbiota, Dietary patterns, Metabolic syndrome, Fermented foods, Dietary fiber, Principal component analysis, Obesity, Cardiometabolic health.

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## INTRODUCTION

Metabolic syndrome (MetS) is a multifactorial metabolic disorder characterized by the coexistence of central obesity, insulin resistance, dyslipidemia, hypertension, and impaired glucose metabolism. It has emerged as a major global public health concern due to its strong association with type 2 diabetes mellitus, cardiovascular diseases, and premature mortality.<sup>[1,2]</sup> The prevalence of MetS has increased substantially worldwide, largely driven by unhealthy dietary habits, sedentary lifestyles, and rapid urbanization.<sup>[3,4]</sup>

Recent advances in microbiome research have highlighted the critical role of the gut microbiota in regulating host metabolism and maintaining metabolic homeostasis. The human gastrointestinal tract harbors trillions of microorganisms that participate in nutrient metabolism, immune modulation, and energy balance.<sup>[5]</sup> Alterations in the composition and diversity of gut microbiota, commonly referred to as gut dysbiosis, have been implicated in the pathogenesis of obesity, insulin resistance, chronic low-grade inflammation, and metabolic syndrome.<sup>[6,7]</sup> Several studies have demonstrated that individuals with MetS exhibit distinct microbial signatures compared with metabolically healthy individuals, suggesting a close relationship between gut microbial ecology and metabolic health.<sup>[8,9]</sup>

Diet is considered one of the most influential modifiable factors shaping the gut microbiota. Dietary components such as dietary fiber, whole grains, fruits, vegetables, fermented foods, and polyphenol-rich foods promote the growth of beneficial microbial taxa and the production of short-chain fatty acids, which exert anti-inflammatory and metabolic benefits.<sup>[10,11]</sup> In contrast, Western-style dietary patterns characterized by high consumption of saturated fats, refined carbohydrates, and ultra-processed foods

have been associated with microbial dysbiosis and adverse metabolic outcomes.<sup>[12]</sup> Consequently, the concept of gut microbiota-related dietary patterns has gained increasing attention as a potential link between diet and metabolic disorders. Emerging evidence suggests that dietary patterns capable of modulating gut microbiota composition may influence the development and progression of MetS through mechanisms involving intestinal barrier integrity, microbial metabolite production, bile acid metabolism, and systemic

inflammation.<sup>[13-15]</sup> However, most existing studies have focused either on individual nutrients or microbial taxa, while data examining overall microbiota-related dietary patterns and their association with MetS in adult populations remain limited, particularly in hospital-based settings from developing countries.

Therefore, the present study aimed to identify gut microbiota-related dietary patterns and investigate their association with metabolic syndrome and its individual components among adults attending a tertiary care hospital. Understanding these relationships may provide valuable insights into microbiota-targeted nutritional strategies for the prevention and management of metabolic syndrome.

## MATERIALS AND METHODS

**Study Design and Participants:** This hospital-based cross-sectional study was conducted among adults aged 18–65 years attending the outpatient departments of a tertiary care hospital between January and June 2025. The minimum sample size was calculated using the single population proportion formula, assuming a 30% prevalence of metabolic syndrome, 95% confidence level, and 5% margin of error. After accounting for a 10% non-response rate, 355 participants were required. Participants were recruited consecutively. Individuals with pregnancy, malignancy,

chronic gastrointestinal diseases, or recent antibiotic/probiotic use were excluded. Ethical approval was obtained from the Institutional Ethics Committee, and written informed consent was obtained from all participants.

**Assessment of Gut Microbiota-Related Dietary Patterns:** Dietary intake was assessed using a validated semi-quantitative Food Frequency Questionnaire (FFQ). Food groups were classified according to their reported influence on gut microbial health, including fruits, vegetables, legumes, whole grains, fermented foods, dairy products, and ultra-processed foods. As gut microbiota was not directly measured, the study evaluated gut microbiota-related dietary patterns. Principal Component Analysis (PCA) was used to derive dietary patterns, and participants were categorized into tertiles based on pattern scores.

**Assessment of Metabolic Syndrome:** Anthropometric measurements, blood pressure, and fasting biochemical parameters (glucose, triglycerides, and HDL-C) were obtained using standard procedures. Metabolic syndrome was defined according to the International Diabetes Federation (IDF) 2006 criteria. Information on sociodemographic characteristics, lifestyle factors, and medical history was collected through a structured questionnaire.

**Statistical Analysis:** Data were analyzed using IBM SPSS Statistics version 29.0. Continuous variables were expressed as mean  $\pm$  standard deviation, and categorical variables as frequencies and percentages. Differences across tertiles of dietary pattern scores were assessed using one-way ANOVA and chi-square tests. Multivariable logistic regression was used to evaluate associations between gut microbiota-related dietary patterns and metabolic syndrome after adjusting for potential confounders. Results were presented as odds ratios (ORs) with 95% confidence intervals (CIs), and statistical significance was set at  $p < 0.05$ .

## RESULTS

The characteristics of the study participants are presented in [Table 1]. The study included 355 adults with a mean age of 43.8

years, and approximately half of the participants were female. The overall prevalence of metabolic syndrome was 38.9%, indicating a substantial burden of cardiometabolic risk within the study population.

[Table 2] presents the factor loadings derived from Principal Component Analysis (PCA). Three major gut microbiota-related dietary patterns were identified, namely the Fiber-Rich and Fermented Foods Pattern, Traditional Pattern, and Processed Food Pattern, collectively explaining 57.4% of the total variance in dietary intake.

As shown in [Table 3], the prevalence of metabolic syndrome decreased significantly across increasing tertiles of adherence to the Fiber-Rich and Fermented Foods Pattern. Participants in the highest adherence tertile exhibited approximately half the prevalence of metabolic syndrome compared with those in the lowest tertile.

The multivariable logistic regression results are summarized in [Table 4]. Higher adherence to the Fiber-Rich Pattern was independently associated with lower odds of metabolic syndrome, whereas greater adherence to the Processed Food Pattern was associated with significantly increased odds after adjustment for potential confounding factors.

[Table 5] demonstrates the associations between the Fiber-Rich Pattern and individual components of metabolic syndrome. Significant inverse associations were observed for central obesity, elevated blood pressure, fasting glucose, and triglycerides, while the association with low HDL-C did not reach statistical significance.

The dietary intake data presented in [Figure 1] indicate a progressive increase in the consumption of fruits, vegetables, whole grains, legumes, and fermented foods across tertiles of the Fiber-Rich Pattern. These findings support the dietary characterization of participants with greater adherence to microbiota-supportive eating habits.

[Figure 2] illustrates a gradual increase in the mean metabolic risk score across age groups. Older participants exhibited a higher burden of metabolic abnormalities, suggesting a positive relationship between age and cardiometabolic risk.

The distribution of physical activity levels is depicted in [Figure 3]. Moderate and low physical activity levels accounted for the majority of participants, highlighting the relatively high prevalence of sedentary behavior within the study population.

**Table 1: Sociodemographic and Clinical Characteristics of Participants (n = 355)**

| Variable                 | Mean ± SD / n (%) |
|--------------------------|-------------------|
| Age (years)              | 43.8 ± 11.7       |
| Female sex               | 188 (53.0)        |
| BMI (kg/m <sup>2</sup> ) | 27.4 ± 4.8        |
| Waist circumference (cm) | 92.6 ± 11.9       |
| Systolic BP (mmHg)       | 128.3 ± 15.6      |
| Diastolic BP (mmHg)      | 81.7 ± 10.8       |
| Fasting glucose (mg/dL)  | 108.9 ± 26.5      |
| Triglycerides (mg/dL)    | 171.8 ± 74.2      |
| HDL-C (mg/dL)            | 44.6 ± 10.7       |
| Current smokers          | 62 (17.5)         |
| Physically inactive      | 146 (41.1)        |
| Metabolic syndrome       | 138 (38.9)        |

**Table 2: PCA-Derived Gut Microbiota-Related Dietary Patterns**

| Food Group                | Fiber-Rich Pattern | Traditional Pattern | Processed Food Pattern |
|---------------------------|--------------------|---------------------|------------------------|
| Fruits                    | 0.78               | 0.21                | -0.09                  |
| Vegetables                | 0.82               | 0.18                | -0.14                  |
| Whole grains              | 0.76               | 0.25                | -0.11                  |
| Legumes                   | 0.69               | 0.41                | -0.08                  |
| Fermented foods           | 0.72               | 0.17                | -0.12                  |
| Refined grains            | -0.15              | 0.74                | 0.28                   |
| Red meat                  | -0.09              | 0.58                | 0.44                   |
| Fast foods                | -0.18              | 0.11                | 0.81                   |
| Sugar-sweetened beverages | -0.21              | 0.05                | 0.84                   |
| Processed snacks          | -0.16              | 0.14                | 0.79                   |

Total variance explained = 57.4%.

**Table 3: Prevalence of Metabolic Syndrome Across Tertiles of Dietary Pattern Adherence**

| Dietary Pattern Tertile | Participants (n) | MetS n (%) | p-value |
|-------------------------|------------------|------------|---------|
| T1 (Lowest adherence)   | 118              | 61 (51.7)  |         |
| T2                      | 119              | 47 (39.5)  |         |
| T3 (Highest adherence)  | 118              | 30 (25.4)  | <0.001  |

Participants with higher adherence to the Fiber-Rich and Fermented Foods Pattern exhibited significantly lower prevalence of metabolic syndrome compared with those in the lowest tertile (25.4% vs. 51.7%,  $p < 0.001$ ).

**Table 4: Multivariable Logistic Regression for Metabolic Syndrome**

| Variable                          | Adjusted OR | 95% CI    | p-value |
|-----------------------------------|-------------|-----------|---------|
| Fiber-Rich Pattern (T3 vs T1)     | 0.42        | 0.24–0.72 | 0.002   |
| Traditional Pattern (T3 vs T1)    | 0.88        | 0.55–1.41 | 0.598   |
| Processed Food Pattern (T3 vs T1) | 2.31        | 1.37–3.90 | 0.001   |
| Age (per year)                    | 1.03        | 1.01–1.05 | 0.008   |
| Female sex                        | 0.94        | 0.58–1.53 | 0.812   |
| Physical inactivity               | 1.69        | 1.02–2.79 | 0.041   |

**Table 5: Associations Between Fiber-Rich Dietary Pattern and Individual Components of Metabolic Syndrome**

| Outcome                  | Adjusted OR | 95% CI    | p-value |
|--------------------------|-------------|-----------|---------|
| Central obesity          | 0.63        | 0.39–0.99 | 0.047   |
| Elevated blood pressure  | 0.58        | 0.35–0.95 | 0.031   |
| Elevated fasting glucose | 0.49        | 0.29–0.83 | 0.008   |
| Elevated triglycerides   | 0.46        | 0.27–0.79 | 0.005   |
| Low HDL-C                | 0.67        | 0.40–1.12 | 0.128   |

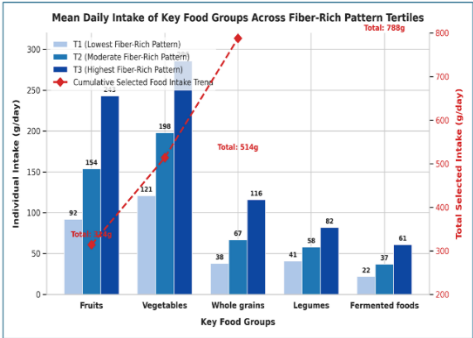


Figure 1: Mean Daily Intake of Key Food Groups Across Fiber-Rich Pattern Tertiles

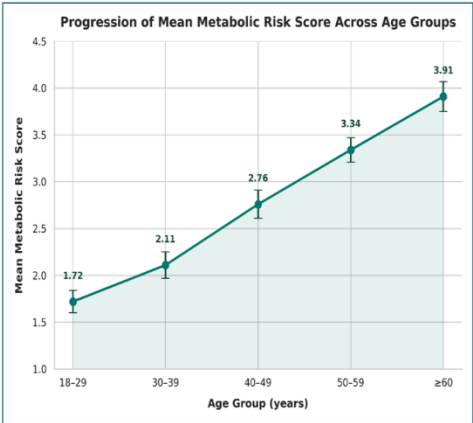


Figure 2: Mean Metabolic Risk Score by Age Group

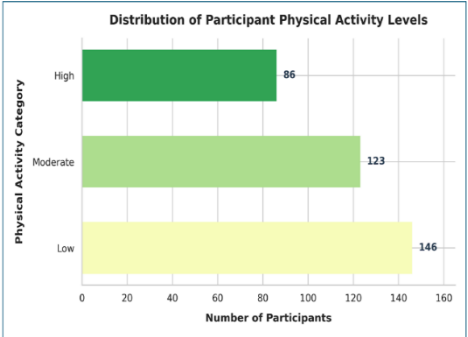


Figure 3: Distribution of Physical Activity Levels

## DISCUSSION

The present hospital-based cross-sectional study investigated the association between gut microbiota-related dietary patterns and metabolic syndrome among adults. The principal findings demonstrated that greater adherence to a Fiber-Rich and Fermented Foods Pattern was associated with a

significantly lower prevalence of metabolic syndrome, whereas adherence to a Processed Food Pattern was associated with increased odds of metabolic syndrome. Furthermore, higher adherence to the fiber-rich pattern was inversely associated with several metabolic syndrome components, including central obesity, elevated blood pressure, fasting glucose, and triglycerides. In the current study, the prevalence of metabolic syndrome was 38.9%, indicating a substantial burden of cardiometabolic risk among adults. This finding is consistent with the growing evidence suggesting that metabolic syndrome is closely linked to alterations in dietary behaviors and gut microbial ecology. Gao et al,<sup>[1]</sup> and Nie et al,<sup>[4]</sup> highlighted that gut microbiota dysbiosis contributes to chronic low-grade inflammation, insulin resistance, and adiposity, which collectively promote the development of metabolic syndrome. Similarly, Singh et al,<sup>[5]</sup> emphasized that disruptions in gut microbial composition may influence metabolic pathways involved in glucose and lipid homeostasis, thereby increasing susceptibility to metabolic disorders.

One of the most important findings of the present study was the inverse association between the Fiber-Rich and Fermented Foods Pattern and metabolic syndrome prevalence. Participants in the highest adherence tertile exhibited substantially lower odds of metabolic syndrome compared with those in the lowest tertile. This observation is in agreement with the findings of Lou et al,<sup>[2]</sup> who reported that dietary patterns rich in fruits, vegetables, whole grains, and other microbiota-supportive foods were associated with favorable metabolic outcomes and reduced obesity risk through modulation of gut microbial composition. Likewise, Asnicar et al,<sup>[10]</sup> demonstrated that habitual consumption of plant-based foods was strongly associated with beneficial microbial profiles and improved metabolic health in a large population cohort. Merra et al,<sup>[14]</sup> further reported that Mediterranean-style dietary patterns rich in fiber and polyphenols positively influence gut microbiota diversity and contribute to improved metabolic regulation.

The beneficial association observed for fiber-rich dietary patterns may be explained by the increased production of short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate, which improve intestinal barrier function, reduce inflammation, and enhance insulin sensitivity. Fan and Pedersen,<sup>[9]</sup> described the central role of microbial metabolites in maintaining metabolic homeostasis, while Ezenabor et al,<sup>[8]</sup> reported that SCFA-producing bacterial communities are associated with reduced cardiometabolic risk. These mechanisms provide biological plausibility for the inverse relationship observed in the current study.

The present study also demonstrated that adherence to the Processed Food Pattern was associated with more than two-fold increased odds of metabolic syndrome. This finding is consistent with the results reported by Shi et al,<sup>[3]</sup> who observed that pro-inflammatory and hyperinsulinemic dietary patterns were linked to unfavorable gut microbiome profiles. Diets characterized by high consumption of refined carbohydrates, processed foods, and sugar-sweetened beverages have been shown to promote microbial dysbiosis, systemic inflammation, and metabolic dysfunction. Lou et al,<sup>[2]</sup> similarly noted that Westernized dietary patterns adversely affect microbial diversity and are associated with obesity and related metabolic disorders.

Another noteworthy finding was the inverse association between the Fiber-Rich Pattern and individual metabolic syndrome components, particularly fasting glucose and triglycerides. Participants with greater adherence to the fiber-rich dietary pattern exhibited significantly lower odds of hyperglycemia and hypertriglyceridemia. These findings are supported by Gao et al,<sup>[1]</sup> who highlighted the potential of microbiota-targeted dietary interventions to improve glucose metabolism and lipid profiles. Likewise, Antony et al,<sup>[7]</sup> reported that modulation of the gut microbiome through dietary and microbial interventions may improve insulin sensitivity and cardiometabolic markers. The umbrella review conducted by Aleali et al,<sup>[6]</sup> further demonstrated that gut microbiome

modulation is associated with improvements in anthropometric and metabolic parameters among individuals with metabolic syndrome.

Fermented food consumption emerged as an important component of the protective dietary pattern identified in this study. Previous evidence suggests that fermented foods may enhance microbial diversity and increase the abundance of beneficial bacterial taxa. Li et al,<sup>[13]</sup> reported that fermented foods are associated with favorable cardiometabolic outcomes through modulation of microbial composition and metabolic signaling pathways. These observations support the role of fermented foods as potential dietary strategies for metabolic syndrome prevention.

The findings of the present study collectively reinforce the growing evidence that dietary patterns exert their metabolic effects, at least in part, through interactions with the gut microbiota. Recent reviews by Nie et al,<sup>[4]</sup> Singh et al,<sup>[5]</sup> and Ezenabor et al,<sup>[8]</sup> have emphasized the bidirectional relationship between diet, gut microbial ecology, and metabolic health. Our results extend these observations by demonstrating that microbiota-related dietary patterns are significantly associated with metabolic syndrome and several of its clinical components in an adult hospital-based population.

The study has several strengths, including the assessment of overall gut microbiota-related dietary patterns using Principal Component Analysis and the evaluation of multiple metabolic syndrome components using standardized criteria. However, several limitations should be acknowledged. First, the cross-sectional design precludes causal inference between dietary patterns and metabolic syndrome. Second, dietary intake was self-reported and may be subject to recall bias. Third, direct gut microbiota profiling through stool sequencing was not performed; therefore, microbiota-related dietary patterns were used as proxy indicators rather than direct microbial measurements. Finally, the hospital-based sample may limit the generalizability of the findings to the broader population.

## CONCLUSION

Higher adherence to a Fiber-Rich and Fermented Foods Pattern was associated with lower odds of metabolic syndrome and several of its components, whereas adherence to a Processed Food Pattern was associated with increased metabolic risk. These findings support the potential role of microbiota-oriented dietary strategies in the prevention and management of metabolic syndrome. Future prospective studies incorporating direct microbiome profiling are warranted to further elucidate the mechanisms linking dietary patterns, gut microbiota, and metabolic health.

## REFERENCES

- Gao Y, Li W, Huang X, Lyu Y, Yue C. Advances in Gut Microbiota-Targeted Therapeutics for Metabolic Syndrome. *Microorganisms*. 2024 Apr 24;12(5):851. doi: 10.3390/microorganisms12050851. PMID: 38792681; PMCID: PMC11123306.
- Lou X, Li P, Luo X, Lei Z, Liu X, Liu Y, Gao L, Xu W, Liu X. Dietary patterns interfere with gut microbiota to combat obesity. *Front Nutr*. 2024 Jun 17;11:1387394. doi: 10.3389/fnut.2024.1387394. PMID: 38953044; PMCID: PMC11215203.
- Shi N, Nepal S, Hoobler R, Menni C, Playdon MC, Spakowicz D, Wells PM, Steves CJ, Clinton SK, Tabung FK. Pro-inflammatory and hyperinsulinaemic dietary patterns are associated with specific gut microbiome profiles: a TwinsUK cohort study. *Gut Microbiome (Camb)*. 2024 Dec 5;5:e12. doi: 10.1017/gmb.2024.14. PMID: 39703541; PMCID: PMC11658949.
- Nie P, Hu L, Feng X, Xu H. Gut Microbiota Disorders and Metabolic Syndrome: Tales of a Crosstalk Process. *Nutr Rev*. 2025 May 1;83(5):908-924. doi: 10.1093/nutrit/nuae157. PMID: 39504479.
- Singh A, Verma A, Ashraf S, Sarfraz Sheikh D, Irfan H, Riaz R, Venjhray F, Meghwar S, Kumar R, Tariq MD, Hamza HM, Ahsan A, Satapathy P. Role of gut microbiota in the pathogenesis of metabolic syndrome: an updated comprehensive review from mechanisms to clinical implications. *Ann Med Surg (Lond)*. 2025 Jul 29;87(9):5851-5861. doi: 10.1097/MS9.0000000000003656. PMID: 40901177; PMCID: PMC12401419.
- Aleali MS, Mahapatro A, Maddineni G, Paladiya R, Jeanty H, Mohanty E, Mirchandani M, Jahanshahi A, Devulapally P, Alizadehasl A, Tariq MD, Hosseini Jebelli SF, Aliabadi AY, Hashemi SM, Amini-Salehi E. The impact of gut microbiome modulation on anthropometric indices in metabolic syndrome: an umbrella review. *Ann Med Surg (Lond)*. 2025 Mar 7;87(4):2263-2277. doi: 10.1097/MS9.0000000000003140. PMID: 40212162; PMCID: PMC11981403.
- Antony MA, Chowdhury A, Edem D, Raj R, Nain P, Joglekar M, Verma V, Kant R. Gut microbiome supplementation as therapy for metabolic syndrome. *World J Diabetes*. 2023 Oct 15;14(10):1502-1513. doi: 10.4239/wjcd.v14.i10.1502. PMID: 37970133; PMCID: PMC10642415.
- Ezenabor EH, Adeyemi AA, Adeyemi OS. Gut Microbiota and Metabolic Syndrome: Relationships and Opportunities for New Therapeutic Strategies. *Scientifica (Cairo)*. 2024 Jul 15;2024:4222083. doi: 10.1155/2024/4222083. PMID: 39041052; PMCID: PMC11262881.
- Fan Y, Pedersen O. Gut microbiota in human metabolic health and disease. *Nat Rev Microbiol*. 2021 Jan;19(1):55-71. doi: 10.1038/s41579-020-0433-9. Epub 2020 Sep 4. PMID: 32887946.
- Asnicar F, Berry SE, Valdes AM, Nguyen LH, Piccinno G, Drew DA, et al. Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. *Nat Med*. 2021 Feb;27(2):321-332. doi: 10.1038/s41591-020-01183-8. Epub 2021 Jan 11. PMID: 33432175; PMCID: PMC8353542.
- Leeming ER, Johnson AJ, Spector TD, Le Roy CI. Effect of Diet on the Gut Microbiota: Rethinking Intervention Duration. *Nutrients*. 2019 Nov 22;11(12):2862. doi: 10.3390/nu11122862. PMID: 31766592; PMCID: PMC6950569.
- Aslam, H., Trakman, G., Dissanayake, T. et al. Dietary interventions and the gut microbiota: a systematic literature review of 80 controlled clinical trials. *J Transl Med* 24, 39 (2026). <https://doi.org/10.1186/s12967-025-07428-9>
- Li KJ, Burton-Pimentel KJ, Vergères G, Feskens EJM, Brouwer-Brolsma EM. Fermented foods and cardiometabolic health: Definitions, current evidence, and future perspectives. *Front Nutr*. 2022 Sep 20;9:976020. doi: 10.3389/fnut.2022.976020. PMID: 36204374; PMCID: PMC9530890.
- Merra G, Noce A, Marrone G, Cintoni M, Tarsitano MG, Capacci A, De Lorenzo A. Influence of Mediterranean Diet on Human Gut Microbiota. *Nutrients*. 2020 Dec 22;13(1):7. doi: 10.3390/nu13010007. PMID: 33375042; PMCID: PMC7822000.
- Valdes AM, Walter J, Segal E, Spector TD. Role of the gut microbiota in nutrition and health. *BMJ*. 2018 Jun 13;361:k2179. doi: 10.1136/bmj.k2179. PMID: 29899036; PMCID: PMC6000740.