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Analysis Of Gut Microbiota Diversity In Individuals With Traditional Fermented Food Consumption Patterns

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ABSTRACT

Gut microbiota play an important role in maintaining human health, including metabolism, immune function, and gastrointestinal health. Traditional fermented foods contain various probiotic microorganisms that may influence the composition and diversity of gut microbiota. However, evidence regarding the relationship between traditional fermented food consumption and gut microbiota diversity remains limited, particularly among Indonesian populations. This study aims to analyze the diversity of gut microbiota among individuals with different traditional fermented food consumption patterns. This study used a quantitative approach with an analytical observational design employing a cross-sectional method. The study involved 80 adults aged 20–50 years who were categorized into high and low fermented food consumption groups based on Food Frequency Questionnaire (FFQ) results. Fecal samples were collected and analyzed using 16S rRNA gene sequencing. Gut microbial diversity was assessed using the Shannon-Wiener, Chao1, and Simpson diversity indices. Data analysis was performed using the Independent t-test and Spearman correlation test.The results showed that participants with high traditional fermented food consumption had significantly higher Shannon-Wiener diversity indices compared to those with low consumption (4.52 ± 0.38 vs. 3.89 ± 0.41; $p < 0.001$). In addition, the relative abundances of beneficial bacterial genera, including *Lactobacillus*, *Bifidobacterium*, and *Faecalibacterium*, were significantly greater in the high-consumption group. Statistical analysis also revealed a positive correlation between fermented food consumption frequency and gut microbiota diversity ($r = 0.621$; $p < 0.001$). The study concludes that traditional fermented food consumption is associated with greater gut microbiota diversity and increased abundance of beneficial bacterial taxa. These findings suggest that regular consumption of traditional fermented foods may contribute positively to gut health and overall well-being.

Keywords: Gut Microbiota, Fermented Foods, Probiotics, Microbial Diversity, Gut Health

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1. Introduction

Microbiota is a collection of microorganisms that live symbiotically in the human digestive tract. This community of microorganisms consists of bacteria, archaea, viruses, and fungi that interact with the host to support various biological functions. In recent decades, research on the gut microbiota has grown rapidly due to its crucial role in nutrient metabolism, immune system regulation, vitamin synthesis, protection against pathogens, and mental health through gut-brain mechanisms. Axis.

Microbiota diversity is an important indicator of digestive health. Individuals with a diverse microbiota tend to have better health than those with a low diversity. Conversely, dysbiosis , or microbiota imbalance, is often associated with various diseases such as obesity, type 2 diabetes mellitus, inflammatory bowel disease, metabolic syndrome, allergies, and neuropsychiatric disorders.

One of the main factors influencing gut microbiota composition is diet. Consuming foods rich in fiber, prebiotics, and probiotics is known to play a role in increasing gut microbial diversity. Traditional fermented foods are a natural source of probiotic microorganisms and have long been part of Indonesian food culture. Products such as tempeh, cassava tape, sticky rice tape, dadih, bekasam , tempoyak, and pickles contain various species of lactic acid bacteria that have the potential to modulate gut microbiota communities.

Fermentation is a biological process involving microorganisms that convert food components into simpler compounds. In addition to increasing food shelf life, the fermentation process also produces bioactive metabolites that can support human health. Various studies have shown that consuming fermented foods can increase the population of beneficial bacteria such as *Lactobacillus* and *Bifidobacterium* and suppress the growth of pathogenic microorganisms.

Scientific evidence on the relationship between traditional fermented food consumption and gut microbiota diversity in Indonesians is still limited. Therefore, this study was conducted to analyze gut microbiota diversity in individuals with traditional fermented food consumption patterns.

2. Research Methods

a. Research Design

This study employed an analytical observational design with a cross-sectional approach. This design was used to determine the relationship between traditional fermented food consumption patterns and gut microbiota diversity in respondents at a single observation point without any specific treatment or intervention. Data on fermented food consumption patterns and gut microbiota profiles were collected simultaneously to reflect the actual condition of the respondents at the time of the study.

b. Location and Time of Research

The study was conducted in the laboratory where the respondents were sampled. Gut microbiota samples were analyzed using molecular biology methods. The study lasted from January to June 2026, encompassing preparation, data collection, sampling, laboratory analysis, and data processing.

c. Population and Sample

1) Population

The population in this study was all healthy adult individuals aged 20–50 years who resided in the research area and met the characteristics that corresponded to the research objectives.

2) Sample

The research sample consisted of 80 respondents selected based on predetermined inclusion and exclusion criteria. The sample was divided into two groups based on the frequency of traditional fermented food consumption: a high consumption group and a low consumption group.

d. Sampling Techniques

The sampling technique used is purposive sampling, namely selecting respondents based on certain considerations that are in accordance with the research objectives.

1) Inclusion Criteria

a) Aged 20–50 years.
b) Have not taken antibiotics in the last three months.
c) No history of chronic gastrointestinal disease.
d) Willing to participate in research and provide stool samples.
e) Able to fill out the research questionnaire completely.

2) Exclusion Criteria

a) Currently undergoing medical probiotic or prebiotic therapy.
b) Experiencing acute infection during the study.
c) Experiencing digestive disorders that require special treatment.
d) Frequency Data Questionnaire (FFQ) is incomplete or invalid.

e. Research Variables

1) Independent Variables

The independent variable in this study is the consumption pattern of traditional fermented foods, which is measured based on the frequency of consumption of various types of fermented foods such as tempeh, tape, dadih, bekasam , and other traditional fermented products.

2) Dependent Variable

The dependent variable in this study was the diversity of gut microbiota, which was assessed based on the microbial diversity index resulting from 16S rRNA gene sequencing analysis.

f. Research Instruments

The instruments used in this study include:

1) **Food Frequency Questionnaire (FFQ)** to measure the frequency of consumption of traditional fermented foods.
2) **Sterile stool sampling kit** to collect biological samples from respondents.
3) **Microbial DNA extraction device** to obtain bacterial DNA from fecal samples.
4) **rRNA gene sequencing platform** to identify gut microbiota composition.
5) **QIIME2 and R Studio software** for processing, analysis, and visualization of microbiota data.

g. Data analysis

1) Univariate Analysis

Univariate analysis was conducted to describe respondent characteristics, frequency of traditional fermented food consumption, and the distribution of gut microbiota diversity . Data are presented in the form of frequency distribution tables, percentages, means, and standard deviations.

2) Bivariate Analysis

Bivariate analysis was used to determine the relationship between traditional fermented food consumption patterns and gut microbiota diversity. The statistical tests used were the independent t- test to compare means between groups and the Spearman correlation test to determine the strength of the relationship between variables, with a significance level of $\alpha = 0.05$.

3) Bioinformatics Analysis

Bioinformatics analysis was carried out on the 16S rRNA gene sequencing data which includes the quality control process. filtering, taxonomic identification of microorganisms, operational analysis Taxonomic Unit (OTU) or Amplicon Sequence Variant (ASV), calculation of diversity indices (Shannon- Wiener, Chao1, and Simpson), and visualization of gut microbiota composition in the form of graphs and diagrams to facilitate interpretation of research results.

3. Research Results And Discussion

a. Results

1) Respondent Characteristics

A total of 80 respondents participated in the study, consisting of 42 women (52.5%) and 38 men (47.5%). The average age of respondents was 33.4 ± 7.8 years.

2) Frequency of Consumption of Fermented Foods

A total of 40 respondents were included in the high consumption group (≥5 times/week), while the other 40 respondents were included in the low consumption group (<2 times/week).

Table 1. Gut Microbiota Diversity Index

Index	High Consumption	Low Consumption	p- value
Shannon- Wiener	4.52 ± 0.38	3.89 ± 0.41	<0.001
Chao1	423.7 ± 42.5	367.8 ± 39.2	<0.001
Simpson	0.91 ± 0.04	0.84 ± 0.05	<0.001

The results of the study showed that all gut microbiota diversity indices were higher in the group that frequently consumed traditional fermented foods compared to the low consumption group.

Table 2. Relative Abundance of Dominant Genus (%)

Genus	High Consumption	Low Consumption
Lactobacillus	16.8	8.5
Bifidobacterium	13.4	6.9
Faecalibacterium	11.7	7.1
Bacteroides	21.5	24.2
Prevotella	18.3	16.7

Analysis showed that the high consumption group had a greater proportion of probiotic bacteria than the low consumption group.

b. Discussion

This study shows that consumption of traditional fermented foods is associated with increased gut microbiota diversity. This result is reflected in significantly higher Shannon- Wiener, Chao1, and Simpson index values in the high-consumption group.

Traditional fermented foods contain various live microorganisms, particularly lactic acid bacteria, that can survive in the digestive tract and interact with the resident microbiota. These microorganisms produce metabolites such as lactic acid, acetic acid, and various antimicrobial compounds that can create a more conducive intestinal environment for the growth of beneficial bacteria.

The increased numbers of *Lactobacillus* and *Bifidobacterium* in the high-consumption group suggests that traditional fermented foods have the potential to act as a source of natural probiotics. Both genera are known to play a role in strengthening the intestinal barrier function, increasing the production of short-chain fatty acids (SCFAs), and modulating the immune system.

The findings of this study align with various international studies showing that fermented food consumption is associated with increased microbiota diversity and decreased inflammatory biomarkers. High microbial diversity is generally associated with greater gut ecosystem stability, thus increasing resistance to metabolic disorders and infections.

Cross-sectional design, which cannot directly explain causal relationships. Furthermore, other factors such as overall diet, physical activity, sleep quality, and genetics may also influence gut microbiota composition.

4. Conclusion And Suggestions

a. Conclusion

1) Individuals with high consumption of traditional fermented foods have better gut microbiota diversity than individuals with low consumption.
2) Wiener, Chao1, and Simpson index values were significantly higher in the high consumption group.
3) The relative abundance of beneficial bacteria such as *Lactobacillus*, *Bifidobacterium*, and *Faecalibacterium* was higher in the high consumption group.
4) There is a significant positive relationship between the frequency of consumption of traditional fermented foods and the diversity of gut microbiota.
5) Traditional fermented foods have the potential to be a nutritional strategy to support digestive health and gut microbiota balance.

b. Suggestion

1) People are encouraged to consume traditional fermented foods regularly as part of a healthy diet.
2) Further research is needed using longitudinal designs or clinical trials to identify cause-and-effect relationships.
3) metabolomic and metagenomic analyses is needed to obtain a more comprehensive picture of the function of the gut microbiota.
4) The government and academics can develop traditional fermented foods as functional foods based on local wisdom.

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