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Association Between Gut Microbial Alpha Diversity and Body Mass Index: Evidence from the American Gut Project

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Abstract. Obesity is one of the major global health issues. It has been increasingly connected with alterations in the gut microbiome, and the microbial alpha diversity is often considered a marker of gut ecosystem stability and metabolic health. However, evidence regarding the association between microbial diversity and body mass index (BMI) remains unclear. This article studied the relationship between gut microbial alpha diversity and BMI using data from the American Gut Project. In the analysis, 7021 individuals with available BMI and 16S rRNA sequencing data were included. Data analysis and R were applied to evaluate distributional assumptions, and a linear regression model was used to figure out the association between Shannon diversity and BMI. The results reveal that there is a small negative regression coefficient between Shannon diversity and BMI, suggesting that higher diversity was associated with lower BMI values. However, this association was not statistically significant due to the p value (0.163). The model cannot explain the majority proportion of variance in BMI. What's more, comparisons across BMI categories suggested obvious overlaps in diversity distributions, meaning that there's no clear separation between groups. These findings indicate that overall microbial alpha diversity alone may not be a strong independent predictor of BMI in this study.

Keywords: gut microbiome, alpha diversity, Shannon index, body mass index, obesity

1. Introduction

Obesity has become an epidemic globally and is one of the major public health concerns. High BMI is associated with increased risks of multiple severe diseases, including cardiovascular disease, type 2 diabetes, hypertension, and systemic inflammation. Although excess caloric intake and reduced physical activity are primary reasons, the actual biological mechanisms beneath are unclear and not fully understood.

Over the past decade, people have learned that gut microbiomes have potentially evolved in metabolic regulation. There are trillions of microorganisms in the human gut that influence digestion, nutrient absorption, immune responses, and host metabolism. There are many animal studies that have shown that alterations in gut microbial communities can influence energy harvest efficiency and fat deposition [1].

α diversity reflects the richness and evenness of taxa within an individual sample. The Shannon diversity index accounts for both abundance and distribution of species. Higher α diversity is often

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interpreted as greater ecological stability, which means a higher health level in this situation. However, evidence connecting microbial α diversity and BMI is still unclear. Some studies showed reduced diversity in obese individuals. Other large-scale research analyses have found weak or non-significant associations.

Based on these previous studies and findings, further analysis of large datasets is needed. The American Gut Project provides one of the largest publicly available microbiome datasets [2]. By using statistical analyses, this study aims to evaluate the association between gut microbial α diversity and BMI, including exploratory data analysis and linear regression models.

2. Literature review

Previous studies have discussed the relationship between gut microbiota diversity and obesity. Some research suggests that individuals with obesity tend to have reduced gut microbial diversity compared to individuals with normal weight. For example, Gopep et al. reported that lower microbial diversity is associated with higher BMI and may influence metabolic regulation through the gut–brain axis [3]. Somnuk et al. found that overweight individuals exhibit altered gut microbiota profiles along with metabolic and inflammatory changes [4]. There are also other studies that have shown weak or non-significant associations between microbial diversity and BMI. Davis et al. suggested that dietary patterns may have a stronger influence on gut microbiome composition than BMI itself [5].

Based on these studies, H1 is proposed:

H1: Higher BMI is associated with lower gut microbial α diversity.

3. Methods

3.1. Study population and data source

The data used in this study were collected from the American Gut Project, which is a large public microbiome initiative that collects stool samples and self-reported health information from participants. The dataset includes 16S rRNA gene sequencing data along with demographic and health-related metadata.

All the participants that were included in the analysis had their available BMI values and corresponding microbial diversity measurements. Individuals with missing or incomplete data were excluded. After filtering, a total of 7021 participants remained for the final analysis.

Although the study population covers diverse backgrounds, detailed conditions such as age, sex, diet, and lifestyle were not included in the present analysis. Therefore, these factors may cause potential confusion and should be noticed in the later studies.

3.2. Variable measurement

The outcome variable in this study was body mass index (BMI), calculated from self-reported height and weight. BMI was the continuous variable in the regression analysis. The primary predictor variable was gut microbial α diversity, measured using the Shannon diversity index derived from 16S rRNA sequencing data. The Shannon index takes care of both species' richness and evenness within each sample.

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3.3. Statistical analysis

The study used exploratory data analysis (EDA) to examine the distributions of BMI and Shannon diversity. Histograms and scatter plots were used to evaluate normality and visualize potential associations. A linear regression model was applied to evaluate the relationship between Shannon diversity and BMI. The regression coefficient and corresponding p-value were used to test the strength and statistical significance of the association. BMI categories (underweight, normal weight, overweight, and obese) were examined using boxplots to compare diversity levels and avoid extreme values.

All statistical analyses and graphs were performed using R software.

4. Results

4.1. Descriptive statistics

The distribution of BMI showed that most participants were located within the range of 18 to 30, corresponding primarily to normal and overweight categories (Figure 1). The Shannon diversity index approximately followed a normal distribution based on the histogram (Figure 2). Scatter plots exhibited a very weak negative trend between Shannon diversity and BMI. The points were widely dispersed (Figure 3). Boxplot comparisons across BMI categories revealed obvious overlap in Shannon diversity values and thus no clear separation between different groups (Figure 4).

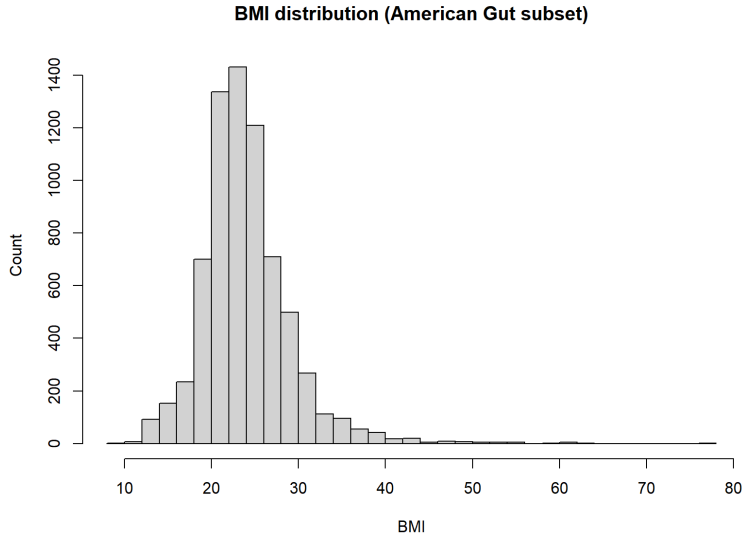

Figure 1. Distribution of body mass index (BMI) among participants

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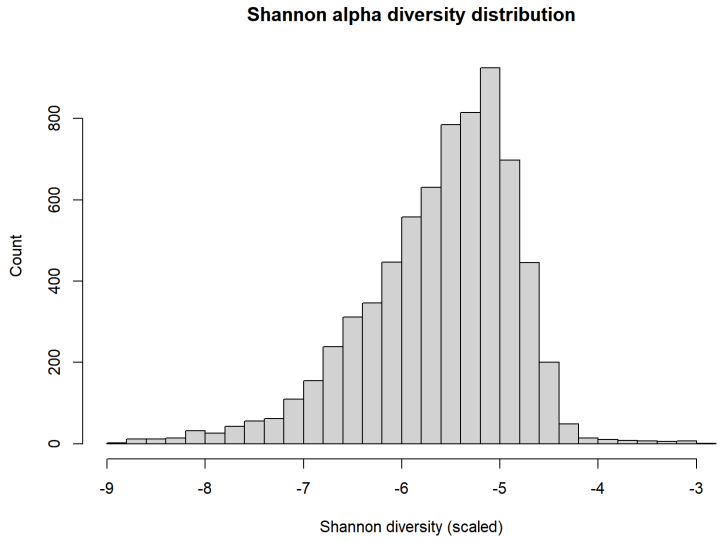

Figure 2. Distribution of Shannon diversity index

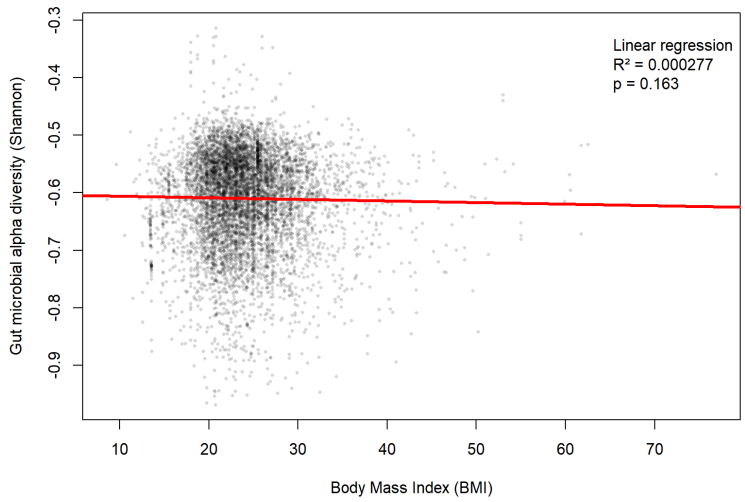

Figure 3. Scatter plot of BMI versus Shannon diversity

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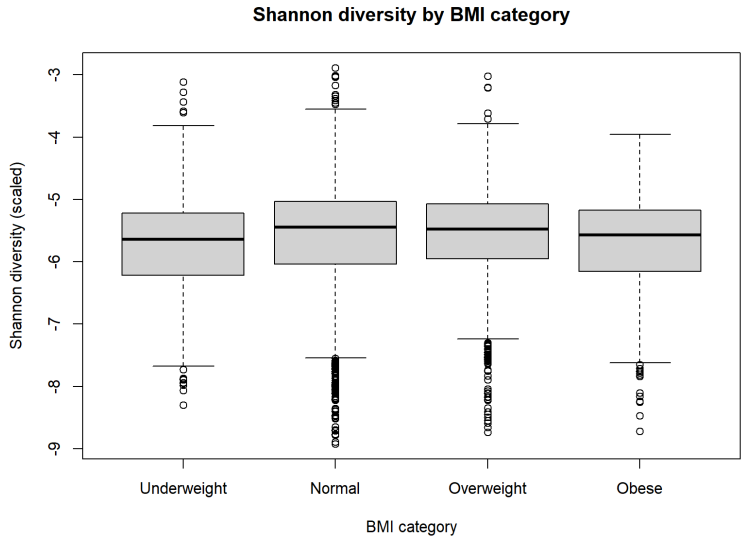

Figure 4. Shannon diversity across BMI categories

4.2. Regression analysis

Linear regression analysis was performed to evaluate the association between Shannon diversity and BMI. The estimated regression coefficient was small and negative. It indicates that higher microbial diversity was associated with slightly lower BMI values, but this association was not statistically significant ($p = 0.163$). The regression model explained only a very small proportion of the variance in BMI ($R^2 = 0.000277$) (Figure 3).

5. Discussion

This study examined the association between gut microbial α diversity and BMI using the data of a large number of participants from the American Gut Project. Although a slight negative trend was observed, the association was not statistically significant. The regression model also explained only a small proportion of the variation in BMI and suggested that microbial diversity alone may not be a strong predictor of BMI in this dataset.

These findings are similar to previous studies that reported no significant relationships between microbial diversity and BMI according to Nenrot S Gopep et al. [3] However, there are also some earlier studies that have suggested different conclusions. Somnuk et al. reported that adults with only overweight issues exhibit metabolic and inflammatory disturbances [4]. Davis et al. [4] observed that Western dietary patterns may initiate early microbial shifts leading to metabolic risk. Differences in study design, population characteristics, sequencing methods, and analytical approaches could all contribute to these inconsistencies.

One possible explanation for the weak relationships observed in this study is that overall microbial diversity may be too general. Obesity probably only reacts to certain microbial taxa or functional pathways rather than overall richness and evenness. Wang et al. suggested that early evaluation of microbial and causal pathways helps clarify how gut variations influence BMI and metabolic health [6]. In that case, specific microbials may play more direct roles in influencing BMI than global diversity measures.

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Several limitations should be considered. First, BMI was calculated from self-reported height and weight, which may introduce measurement bias. Second, potential variables such as diet, medication use, and lifestyle factors were not controlled for in this analysis. Third, the health conditions other than obesity for participants were not taken into consideration as well.

Despite these limitations, the large sample size strongly supports the findings. If future studies can introduce more data, such as longitudinal data, functional metagenomic analysis, and more detailed phenotypic information, it could better clarify the relationship between gut microbiota and obesity.

6. Conclusion

In summary, this study focuses on the relationship between gut microbiota α diversity and BMI using data from the American Gut Project. While there was a weak negative correlation between them, this relationship was still not statistically significant, and the regression model was also basically unable to explain the variation in BMI. These findings suggest that gut microbiota α diversity alone may not be a very strong independent predictor of BMI. If possible, future research combining functional microbiota analysis and longitudinal data may be able to provide a deeper understanding of the complex interplay between gut microbiota and obesity.

There are several limitations of this study. First, BMI values were calculated from self-reported height and weight. The accuracy of the data is questionable and can't avoid measurement bias. Second, confounding variables were not controlled or monitored, such as the participants' dietary patterns, medication use, physical activity, and lifestyle factors. Third, the data used for this study is not strong enough to infer causal relationships between microbial diversity and BMI. α diversity is a relatively broad metric that can only represent more of a microbiome community than the specific microbial taxa or functional pathways that are actually making the influence.

Future research should focus on integrating and analyzing more detailed and comprehensive data. If the future studies could take additional variables such as diet, host genetics, and environmental exposures into consideration, they may improve model performance and provide a more related understanding of the gut microbiome–host interaction. Research like this could all possibly contribute to more targeted and effective strategies for obesity prevention and intervention.

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