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Dietary Shifts and the Gut Microbiome: The Impact of Westernized Diets on Microbial Composition and Obesity in Mediterranean and Asian Populations

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Abstract

The human gut microbiome, which comprises trillions of microbes, plays an important function in digestion, immunity, and overall health. The current study explored the impact of dietary modifications on the gut microbiome, with a special focus on the Westernized, Mediterranean, and Asian diets and their association with obesity. The rise of obesity has been increasingly linked to changes in the gut microbiome, particularly in relation to dietary patterns. This narrative review and descriptive analysis synthesized findings from 15 studies that compare the gut microbiomes of individuals consuming Western, Mediterranean, and Asian diets, with a focus on Asian populations undergoing dietary transitions due to urbanization or immigration. Following a PRISMA-based guideline, the researcher identified consistent microbiome shifts associated with the Western diet. This namely includes a decrease in *Prevotella* and fiber-degrading bacteria, and an increase in *Firmicutes*, bile-tolerant organisms, and lipopolysaccharide-producing microbes linked to inflammation and metabolic dysfunction. In contrast, Mediterranean and traditional Asian diets promote microbial diversity and anti-inflammatory pathways. Notably, *Prevotella copri DSM 18205* was found to be 73% more prevalent in individuals in Thailand compared to Thai immigrants in the U.S. These findings suggested that Western dietary adoption disrupts protective microbial profiles, contributing to obesity and other modern health outcomes. The rise of obesity and related metabolic disorders has prompted concerns about the role of dietary patterns in shaping the gut microbiome, particularly as Westernized diets become more prevalent globally, which can lead to disruptions in microbial composition.

Keywords: Gut Microbiome, Firmicutes/Bacteroidetes ratio, Obesity, Westernized diet, Inflammation

1. Introduction

On average, the human gut microbiome (human digestive tract-associated microbes) is colonized by around 1.0 x 10^{14} microorganisms in an adult human. These organisms include bacteria, protozoa, viruses, archaea, and fungi as part of our gastrointestinal tract (GI tract) (Matute, 2023). The human gut microbiome consists of two dominant phyla: Firmicutes and Bacteroidetes, which in total, both account for around 90% of all bacteria in our GI tract. The predominant bacteria under the Firmicutes phyla include Lactobacillus, Bacillus, Clostridium, Enterococcus, and Ruminococcus, whereas the most dominant bacteria under the Bacteroidetes phyla include: Bacteroides and Prevotella (Pinart, 2021). Functionally, the Firmicutes are associated with short-chain fatty acid synthesis in the body. Bacteroidetes, the second major group, ferment polysaccharides and "otherwise indigestible carbohydrates" (Pinart, 2021). Although the Firmicutes/Bacteroidetes (F/B) ratio has been proposed as a marker for obesity, its predictive value is debated because functional differences between bacterial subgroups can lead to different metabolic outcomes. Overall, the development and structure of our gut microbiome are shaped by various factors, including genetics, external environment, and most notably, diet.

The Westernized diet, also known as the “standardized American diet,” is a dietary pattern that is categorized by high consumption of saturated fats, carbohydrates, and a low intake of fiber (Statovici, 2017). Driven by the global adoption of Western diets, the imbalance of nutrients in the Westernized diet has not only impacted human health but also contributed significantly to the rising rates of obesity worldwide. Obesity, according to the World Health Organization (WHO), is defined as an “abnormal or excessive fat accumulation that presents a risk to health.” New data from the United States Centers for Disease Control (2023) indicates that in 23 states, more than 35% (or more than one in three people) are documented to exhibit obesity. Based upon the fact that the development and structure of our gut microbiome is shaped to a significant degree by diet, researchers have increasingly turned to quantitative and experimental methods to explore the symbiotic relationship between humans and their gut bacteria. In particular, there has been an emphasis on how a Westernized diet can impact microbiota diversity and the richness of bacterial populations present in traditional diets (Matute, 2021). This study aimed to compare gut microbiome profiles associated with Western, Mediterranean, and Asian diets and to examine how dietary transitions, particularly among Asian populations, are associated with microbiome shifts linked to obesity.

2. Materials and Methods

The methodology used in this study addressed the following question: *How does a Westernized diet impact the gut microbiome, specifically in relation to people consuming Mediterranean and Asian diets, and how do these dietary shifts bridge a gap to modern health outcomes and its association with obesity?* First, a baseline was set for the research question by taking an approach of first breaking the question into component parts resulting in the asking of a series of five questions (Figure 1). The first component step is important in setting the gut microbiome baseline for the three diet profiles: Western, Asian, and Mediterranean.

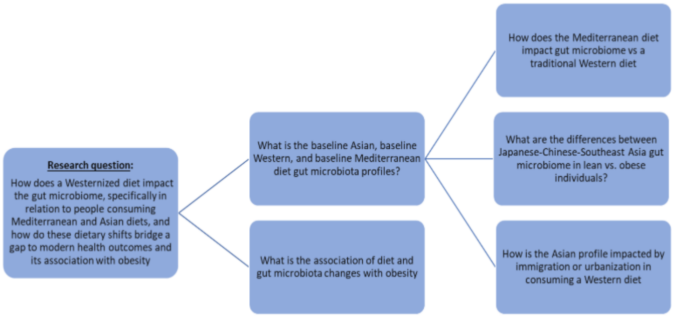

Figure 1. The five sets of data collected in alignment with the research question.

A two-part, mixed-methods study was conducted. This approach allowed for both quantitative and qualitative data extraction from peer-reviewed journals to identify patterns in gut microbiota compositions across different diets. This was important because the mixed methods approach captured details that would not have been revealed if only one component (e.g. narrative review) had been used to gather data and formulate results. The two methods used were a descriptive analysis and a narrative review. As seen in the literature review, some past researchers have conducted a meta-analysis and 16S rRNA (partial bacterial DNA) experiments to determine the sequences of gut microbiome data per dietary culture, but not in a mixed methods approach as in this study. The mixed methods approach combines methods from the literature review and a new qualitative measure of the Asian diet. To address methodological differences across studies, microbiome data were compared descriptively at the phylum level using relative abundance patterns rather than pooled statistical measures, allowing meaningful comparison across Western, Mediterranean, and Asian dietary contexts.

To ensure that differences in methodological approaches between studies could be accounted for, data were compared on taxonomic and analytical levels. More specifically, microbiome comparisons were carried out on the phylum level using ratios of Firmicutes and Bacteroidetes, as presented in Figures 2-4. Obesity was defined based on the original BMI criteria defined within each paper (e.g. Kasai et al. for the Japanese population). Values of relative abundance were used for the presentation of data through pie charts and bar charts instead of actual sequencing values, as presented in Figures 2-5. When actual standardization of the data was not feasible, comparisons were carried out based on immigration associated modifications of microbiome composition (Figure 5).

2.2 Collection of Data for Asian Diet Baseline

First, as part of the descriptive analysis, data for the Asian diet baseline was established using data extracted from a study on Japanese obese versus nonobese individuals conducted by Kasai et al. (Kasai et al., 2015). The study compared the microbiota compositions of obese (BMI ≥25 kg/m²) and non-obese (BMI <20 kg/m²) participants' key bacterial taxa, including Actinobacteria, Firmicutes, and Bacteroidetes, alongside specific genera such as Bifidobacterium, Bacteroides, and Prevotella. The data was systematically assessed from the original table in the research study, which served as the basis for visualizations, and converted into two pie charts in Google Sheets to generate the F/B ratios. The original study's methodology and criteria for defining obesity were strictly followed to maintain consistency.

2.3 Mediterranean Gut Microbiome Baseline

Next, data was extracted from a microbiome study in Spain on individuals consuming a Mediterranean diet conducted by Latorre-Pérez. This study focused on the relative abundance of bacterial phyla, such as Actinobacteria, Firmicutes, and Proteobacteria, as well as specific genera like Collinsella, Eubacterium, and Lachnospiraceae. The relevant data for each phylum from the study's tabular information, using the "Mean Abundance" values for each taxonomic group that were abstracted. These values were then aggregated by phylum, summing the "Mean Abundance" values to determine the total relative abundance for each phylum within the dataset. For example, because there are two instances of Actinobacteria, the mean abundance of 0.178 and 0.543 were combined to generate a total of 0.721 mean abundance. The rest of the phyla were calculated in the same steps and were accumulated into a simple summary table which was used to create a bar chart in Google Sheets of the mean abundance of the phyla. This summarized data visually represented the proportional abundance of each phylum representative of the Mediterranean baseline diet for the sample population.

2.4 Western Gut Microbiome Baseline

For the baseline Western gut microbiome, data was extracted from a *Frontiers in Nutrition* Article conducted by Nagpal et al. in 2018. Based upon the desire to compare the bacterial richness of the major phyla, phyla were aggregated under either of the two major categories of bacteria: Firmicutes or Bacteroidetes. This allowed for comparison of the F/B ratio between the Western, Mediterranean, and Asian diets. For example, *Clostridium alkalicellulosi, Coprococcus eutactus, Erysipelothrix muris, Faecalibacterium prausnitzii, and Lachnospira pectinoschiza*, were all aggregated under the umbrella of Firmicutes. The bacteria under Bacteroidetes are *Bacteroides salanitronis, Bacteroides xylanisolvens, Prevotella multisaccharivorax,* and *Prevotella shahii.* The remaining phyla are considered as individual bacterial strains. The raw data was manipulated and transformed into a pie chart. The phyla were calculated as part of a whole (contribution to the total bacterial richness). All the averages of the Western diet phyla configuration were added to get a total of 7.07. To assess the percentages of each bacterial species in the Western gut profile, each average listed was then divided by the total average (7.07) to get a normalized percent contribution to the total. This data was input into a Google Sheets spreadsheet to be transformed into a pie chart.

It is important to note however that data on the Western microbiome was derived from Nagpal and Shively (2018), a study on non-human primates that consumed a Western diet; thus, this data is considered a comparative measure of Western diet patterns rather than a conclusive measure of a human baseline comparison.

2.5 Effect on Asian Gut Microbiome from Immigration

To address the question of how the Asian gut microbiome changes due to immigration to the U.S., data from a study on the comparison between Hmong Thai (residents in Thailand) and first-generation Thai immigrants conducted by Vangay et al. were used. A data extraction table was collected from the research. The chart indicated the relative difference in the gut microbiomes of people who originated from Thailand (Hmong Thai) and who had immigrated to the United States (Hmong1st). This information was later used to determine the general trend of the gut microbiome changes from an Asian gut microbiome to a Westernized gut microbiome. The *delta. prevalence* values represented the abundance or presence of taxon changes between groups or conditions. The *taxa* column represented the microorganisms being classified. The *qval* (p-value) column represented the statistical significance of the taxon and the *OTUID* is used to help track and distinguish between different microorganisms. The *qval* and OTUID in this case will be excluded from the analysis due to limited resource availability. This part of the raw data was then transformed into a bar chart to illustrate the relative abundance of changes in gut microbiota pre-immigration versus post-immigration of people of Thai descent.

2.6 Narrative Review and Voyant Tools Text Analysis on Gut Microbiome versus Obesity

Lastly, to address the question of how the gut microbiome changes with obesity, a narrative review was used. A data extraction table was created, with five columns including, “title”, “author name”, and “key findings”. The tables were author-generated synthesis of five peer-reviewed studies examining the relationship between gut microbiota and obesity. Part 1 summarizes studies focusing on changes in bacterial richness and evenness, while Part 2 highlights studies emphasizing taxonomic shifts, inflammation, and metabolic outcomes. Commonalities were then assessed between obesity impacts on the gut microbiome including bacterial richness and evenness. Key word searches including use of the terms “gut microbiome” and “obesity” were used to find relevant research articles related to the question. The data presented in this table was extracted from five different sources, all associated with the linkage between the gut microbiome and bacterial richness versus evenness. With this narrative approach, *Voyant Tools,* a text-mining application was used to help identify key words and phrases to enumerate the number of instances that the texts provided examples of dysbiosis (imbalance/disruption in the gut microbial composition), obesity, bacterial richness increase/decrease, etc. This was used to specifically track trends, quantify the frequency of specific keywords, and analyze co-occurrence patterns between keywords. The four keywords that were used in the *Voyant Tools* application include: obesity, inflammation, firmicutes, and westernized. A bubble map was then generated to illustrate the trend patterns in the data. When these terms appear frequently, or together, the co-occurrence analysis reinforces a link between the Western diet and gut microbiome inflammation. This table and bubble map was created in part to illustrate a more comprehensive representation of the analysis of multiple literature sources.

The narrative review was conducted following PRISMA reporting principles. PubMed, Web of Science, and Scopus were searched for articles published between January 2014 and December 2024 using the Boolean string (“Western diet” OR “Mediterranean diet” OR “Asian diet”) AND (microbiome OR “gut bacteria”) AND obesity. Studies were included if they involved human adults, reported gut microbiome data using 16S rRNA sequencing, and provided BMI or obesity-related measures; studies were excluded if they focused on pediatric populations, non-dietary interventions, animal-only models (unless used for mechanistic support), or lacked microbiome composition data. Titles and abstracts were screened first, followed by full-text review, with reasons for exclusion recorded; articles that could not be accessed due to subscription restrictions were documented separately as access limitations rather than methodological exclusions.

3. Results

3.1 Descriptive Analysis

Japanese obese versus non-obese microbiome composition data were consolidated into a side-by-side bar graph (Figure 2) as part of the quantitative evaluation of the initial descriptive analysis. The y-axis of the graph focused on 12 different bacterial types and included the two main gut microbiome phyla groups mentioned in the introduction: Firmicutes and Bacteroidetes. Generally, the graphical trend illustrates that the nonobese (red) has a higher incidence of

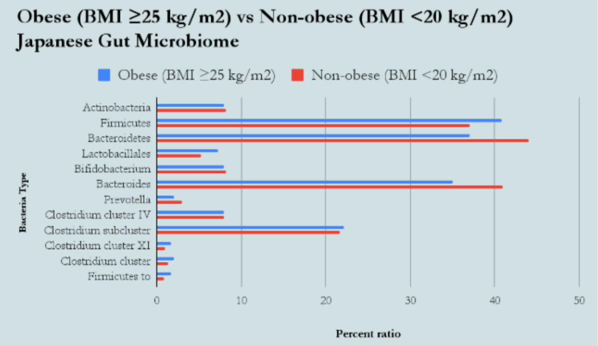

Figure 2. Side-by-Side bar graph showing differences between lean versus obese Japanese gut microbiome.

Bacteroidetes and a lower Firmicutes abundance. For the obese Japanese gut microbiome (blue) however, there was a higher Firmicutes and a lower Bacteroidetes abundance. The percent ratio for the Firmicutes to Bacteroidetes was 1.7 to 0.9 respectively, which further supports the idea that the gut microbiome composition differs significantly between obese and non-obese individuals in the Japanese cohort. The other significant microbiota worth mentioning was Prevotella. There was a reduction in the abundance of Prevotella species from 3% to 2%.

Figure 3 below illustrates the gut microbiome composition of a baseline Mediterranean diet. There are 5 subgroups present. Firmicutes averaged 24.4% of total relative abundance, significantly exceeding Bacteroidetes at 0.712% (p-value= 0.03, Wilcoxon rank-sum; Latorre-Perez et al, 2021). It is evident that Firmicutes dominate in this particular Spanish gut microbiome with Actinobacteria (0.721%), Bacteroidetes (0.712%), and Cyanobacteria (0.357%) with much lower levels.

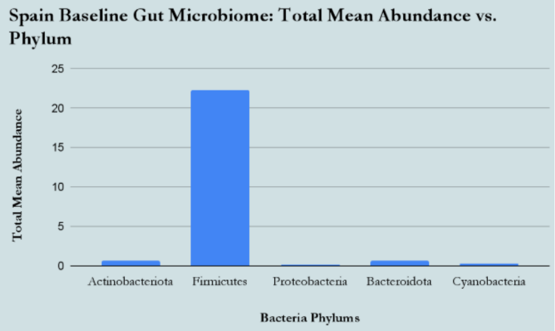

Figure 3. Bar graph of baseline mediterranean diet.
Aggregate phylum composition of Spanish adults adhering to a Mediterranean diet (n=130).
Firmicutes (24.4%) were significantly more abundant than Bacteroidota (0.7%), p = 0.03 (Wilcoxon rank-sum) (Latorre-Pérez et al., 2021).

Figure 4 illustrates the baseline Western diet gut microbiome composition. There are 9 total subgroups identified. All these bacteria shown in the graph are under either the Firmicutes or Bacteroidetes phylum. *Lachnospira pectinoschiza*, *Faecalibacterium prausnitzii*, *Erysipelothrix muris*, *Coprococcus*, *Eutactus*, and *Clostridium alkalicellulosi* are all under the Firmicutes phyla. The rest are under the Bacteroidetes phylum. Summing the percentages of bacteria in the Firmicutes phyla indicated that it encompassed 78.4% of all the bacteria present in the Western gut microbiome.

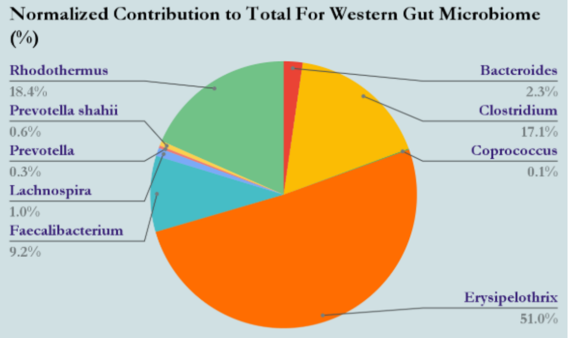

Figure 4. Pie chart for baseline western data.

Figure 5 is a comprehensive side-by-side bar chart breakdown of the gut microbiome changes from an original Hmong Thai group showing relative changes representative of their immigration to the U.S. As evident in the chart, most of the bacterial composition is part of the Prevotella subgroup. Based on visual inspection of the descriptive bar chart (Figure 5), Prevotella copri DSM 18205 appears substantially reduced among U.S. Hmong immigrants; however, this observed difference was not statistically tested and should be interpreted as an approximate, descriptive comparison rather than a validated effect size. In other words, US immigrants experienced a major decline in the prevalence of *Prevotella copri* compared to their counterparts in Thailand. The bar chart also shows the phylum of Coprococcus. Coprococcus is under the phylum Firmicutes and in this case demonstrates a 59% decrease after US immigration.

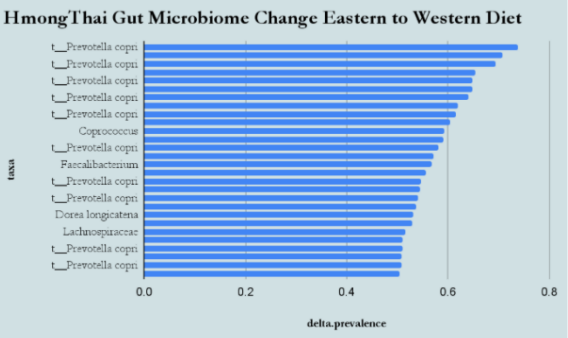

Figure 5. Side by side bar-graph comparison after US immigration for Thai ethnicity.

3.2 Narrative Review and Voyant Tools Text Analysis

The qualitative analysis (narrative review and *Voyant Tools*), was used to analyze the second branch of the research question: *What is the association between gut microbiota and obesity?* Reiterating the PRISMA guidelines followed, the researcher searched PubMed, Web of Science, and Scopus (January 2014 – December 2024) using the string ('Western diet' OR 'Mediterranean diet' OR 'Asian diet') AND (microbiome OR 'gut bacteria') AND obesity. From 654 records, 31 met inclusion criteria (human adults, 16S rRNA data, BMI reported). After removing the 8 papers that were behind pay walls, the remaining 23 informed the narrative synthesis. From these, 5 studies were selected for in-depth narrative review based on relevance to the research question. Based on the five papers (listed in references), the key findings were summarized and resulting features shown in Part 1 and Part 2. Each study was reviewed in full, with particular attention given to reported changes in bacterial richness and evenness. To ensure consistency in data extraction, key observations were documented in a structured format, which included study identifiers (author, year), sample population characteristics (e.g., human or murinae models, obesity status), and reported shifts in microbial richness and evenness. This process facilitated the identification of common trends across studies, particularly regarding the decline in bacterial diversity in obese subjects. Thus, after summarizing all of the research papers, there were five key details that were found to be common factors between gut microbiota association and obesity: bacterial richness decrease, bacterial evenness decrease, the establishment of a causative link between richness and evenness in obesity, a higher F/B ratio, and increased gut dysbiosis. Most of the study designs that were included were clinical, with one being a pre-clinical study done on mice. This preclinical study design was chosen because it complements clinical studies that may not be as easily observed in human trials due to ethical or logistical concerns. These findings indicate that transitioning to a Westernized diet profoundly affects the gut microbiome, which can support a tendency towards obesity through reduced microbial diversity and disrupted microbial equilibrium.

Table 1. Data extraction table (part 1)

Microbiota Features	**Study Design**	**Population/Subjects**	**Key Findings**	**References**
Bacterial Richness Decreased	Clinical	Obese adults (Westernized diet)	Obese individuals typically exhibit lower bacterial richness, with a decreased diversity in their gut microbiome. This reduction may contribute to obesity-related inflammation and metabolic disorders.	Liu BN et al., 2021; Tsigalou et al., 2021
Bacterial Evenness Decreased	Clinical	Children (Obesity)	A decrease in evenness, with dominant populations of Firmicutes, was observed in obese children. A shift toward dysbiosis that can exacerbate weight gain.	Noor et al., 2023
Richness and Evenness Linked to Obesity	Preclinical	Mice (High-fat diet)	In mice, a high-fat diet led to decreased microbial richness and an uneven distribution of bacteria, favoring obesity-associated microbiota. This change was linked to disrupted metabolic processes.	LI, Xuan et al., 2017

Data extraction table (part 2)

Increased Dominance of Firmicutes/Bacteroidetes	Clinical	Obese adults (Various diets)	The F/B ratio increased, often at the cost of other microbial groups, which reduced overall microbial diversity and impacted both richness and evenness in obese subjects.	Koumpouli et al., 2024
Dysbiosis and Reduced Richness	Clinical	Obese Mediterranean diet individuals	The shift to a Westernized diet in individuals with a Mediterranean background resulted in reduced gut microbiome richness, particularly in beneficial bacteria like Bifidobacteria.	Tsigalou et al., 2021

Lastly, as part of the narrative review, *Voyant Tool*s was used to evaluate the correlation between four key terms most common in the 10 research papers that were analyzed: *obesity, inflammation, Firmicutes, and Westernized,* which is shown in Figure 7. A quick note to state is that co-occurrence was assessed using Voyant Tools' built-in-term co-occurrence and proximity analysis, which identifies the frequency with which selected keywords appear within the same document and within close textual proximity. Keywords were considered co-occurring when they appeared within the same text segment (paragraph-level context) rather than requiring direct adjacency. No minimum frequency threshold was imposed beyond inclusion of the predefined keywords, allowing all observed co-occurrence patterns across the corpus to be captured. "Obesity" is represented in purple, "Firmicutes" is represented in green, "Inflammation" is represented in red, and "Westernized" is represented in pink. This allows for the illustration that the higher the incidence and ratio of these terms, the more likely that they are associated with each other. The trend on the bubble map illustrates that obesity is the most common word along with little bubbles of inflammation interspersed. In the bubble map created from the 10 research papers (on the y-axis) which were analyzed, obesity was mentioned 648 times, along with inflammation (118 times), Westernized (20 times), and Firmicutes (62 times).

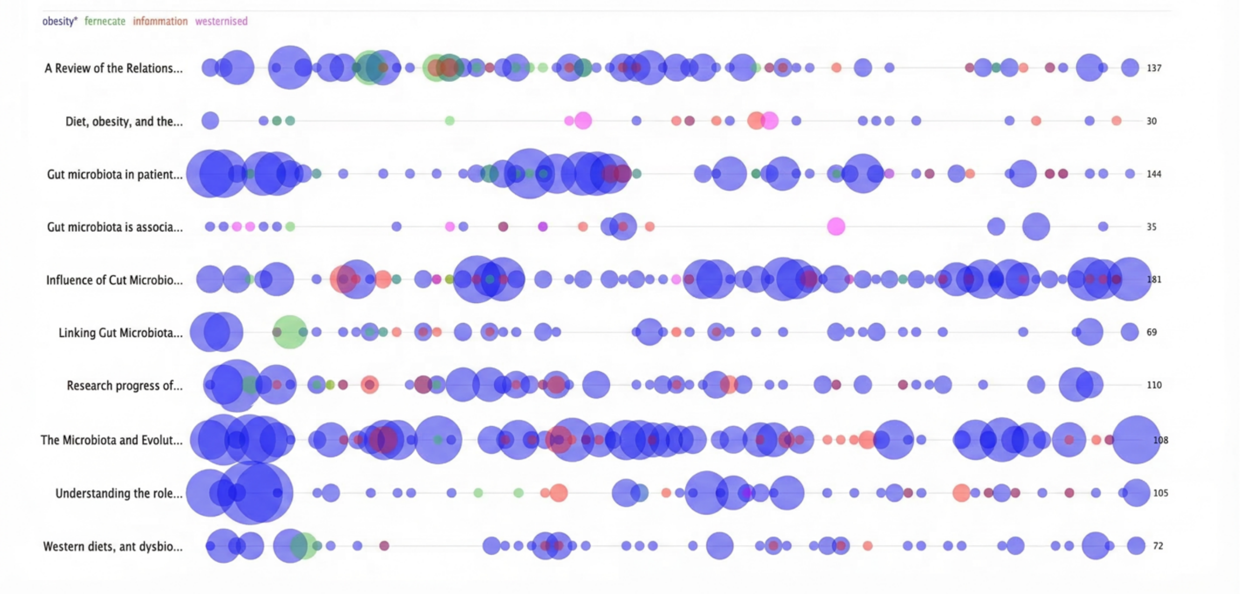

Figure 7. Bubble map correlation.

4. Discussion

A side-by-side bar graph comparison of Japanese lean versus obese gut microbiota allowed for a clearer evaluation of whether this falls in line with the F/B ratio hypothesis (a disputed topic), and how this contributes to the prevalence of certain gut microbiota in relation to obesity. Generally, Bacteroidetes are often associated with lean body mass and a higher fiber intake, which can lead to the production of short-chain fatty acids, which may regulate and lower inflammation. Typically, a higher Firmicutes abundance is generally associated with increased fat storage, reduced gut diversity, and overall increased inflammation and metabolic health issues such as higher rates of diabetes, strokes, and heart disease. There is a reduction in *Prevotella* species in the obese group (from 3% to 2%) which could potentially indicate a lower fiber intake and is often associated with a Westernized dietary influence.

As evident in the Spanish baseline gut microbiome bar graph, Firmicutes has the highest total mean abundance levels. However, not all Firmicutes are associated with obesity. Many subgroups, such as Lachnospiraceae, Ruminococcaceae, and Butyricicoccus, produce short-chain fatty acids that support gut health and reduce inflammation. This illustrates that the F/B ratio alone is an oversimplified indicator, and the functional roles of bacterial subgroups must be considered when interpreting microbiome-diet relationships. As discussed earlier, there is debate that a higher incidence of Firmicutes is often linked to a higher prevalence of obesity, but this is not always the case. The presence of high levels of the Firmicutes phylum is not inherently negative, and under this subgroup there is a variety of beneficial microbiota that exist in the baseline Mediterranean Diet. The Mediterranean diet gut microbiome shows a high presence of Firmicutes, but it's dominated by beneficial, short-chain fatty acid-producing families like *Lachnospiraceae*, *Ruminococcaceae*, *Butyricicoccus*, and *Anaerovoracaceae*, which all promote gut health, reduce inflammation, and support metabolic regulation. *Peptostreptococcacea*e could be pro-inflammatory when present in excess, but if at balanced levels, might not be associated with a significant adverse impact. Despite the high Firmicutes levels, the Mediterranean diet's gut microbiome benefits from fiber fermentation and anti-inflammatory effects, which appear to lead to better health outcomes compared to the Western diet.

The baseline Western gut microbiome is associated with higher F/B ratios, more calorie extraction (expenditure), and a greater association with obesity. One of the Clostridium subgroups is particularly known for gut barrier disruption, which in simple terms means a leaky gut. The "leaky gut" impairs an individual's intestinal lining, which further exacerbates the potential for inflammation and obesity.

The change in the gut microbiome for Thai immigrants demonstrates a decrease in Coprococcus. This is significant because it aligns with previous findings wherein Bacteroidetes-dominant microbiomes (typical of healthy, fiber-rich diets) are replaced by Firmicutes-dominant microbiomes. Prevotella is under the Bacteroidetes microbiome, and this evidence of a decrease of Prevotella when Hmong Thai people switched to a Western diet may support the observation of a potential increase in the prevalence of obesity associated with the higher F/B ratio. Although this may be equivocal, it is a part of the beneficial bacteria in the Firmicutes phylum and its decline suggests less fiber fermentation and reduced short-chain fatty acid production, which may contribute to inflammatory and metabolic health issues.

The 648:62 ratio of "obesity" to "Firmicutes" points to the strong association between this bacterial phylum and obesity-related discussions in the literature. There is also a strong association between “obesity” and “inflammation,” with the ratio being 648:118. While Firmicutes were mentioned far less frequently, their repeated presence in obesity-related research suggests their relevance in metabolic dysregulation.

5. Conclusion/Future Direction

One of the most important findings developed because of this research was the ability to both synthesize and analyze compositions across different dietary profiles. The quantitative approach (developed using descriptive analysis) was effective in analyzing the gut microbiota variations among Japanese obese and non-obese individuals, Mediterranean diet adherents, Western diet consumers, and Hmong Thai immigrants to the United States. The qualitative approach (developed using a narrative review and Voyant Tools) aided in the process of incorporating not only qualitative analysis but also provided a deeper context along with the descriptive analysis.

An unexpected discovery was the stark 73% decline in *Prevotella copri DSM 18205* in Hmong Thai immigrants who transitioned to a Western diet. This shift strongly supported Davenports’ research suggesting that a diet low in fiber and high in processed foods alters the gut microbiome and promotes obesity. Additionally, the text mining analysis with Voyant Tools revealed a strong association between the terms Firmicutes and obesity, further reinforcing the association of the gut microbiota's role in metabolic health especially from a research perspective.

Future research should explore specific Firmicutes subgroups rather than relying solely on the F/B ratio, as certain strains do have beneficial metabolic effects while others may contribute to long-term obesity. Conducting longitudinal studies that track microbiome changes in individuals transitioning to a Western diet could also provide valuable insights into how these dietary shifts influence gut bacteria and obesity over time. However, this research ran into limited sources for a baseline Western gut microbiome in the research realm. Additionally, standardizing microbiome dataset methodologies across studies would improve comparability, potentially through bioinformatics tools or machine learning. If data can be standardized in the near future, this would make it feasible to simplify statistical analyses and perform higher-quality meta-analyses.

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