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Exploring the Impact of High-Fat Diet on Gut Microbiota Composition in Healthy Individuals: A Comprehensive Analysis

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ABSTRACT

The human gut microbiota, composed of diverse microorganisms known as microbiomes, plays a vital role in maintaining human health. The composition and activity of the gut microbiome are influenced by a multitude of factors, including internal factors such as stress and external factors such as nutrition and medication. Understanding the gut microbiota's role in body fatness has gathered significant research attention and public interest. To comprehend the complicated relationship between gut microbes and their hosts, it is essential to characterize the microbiota in healthy individuals. Emerging evidence suggests that alterations in gut microbiota composition, particularly in response to dietary factors, can have profound implications for human health. Of particular interest is the potential impact of a high-fat diet on the gut microbiota, as it has been postulated that such dietary patterns may lead to dysbiosis and subsequent health consequences. Recent research has highlighted the potential impact of dietary factors on the gut microbiota, particularly the association between a high-fat diet and dysbiosis, which may have adverse health effects. This review aims to contribute to the existing knowledge by providing a comprehensive analysis of the microbiomes in healthy individuals compared to those consuming a high-fat diet.
Keywords: Diet regime; Gut microbiome; Health consequences; High-fat diet; Human health.

INTRODUCTION

A biome is a distinct ecosystem characterized by its environment and inhabitants. Human gut, located inside intestines, can be considered a miniature biome as it is populated by trillions of microscopic organisms. These microorganisms include over a thousand species of bacteria, as well as viruses, fungi, and parasites. Human gut microbiome is unique ecosystem that varies from individual to individual. During infancy, newborns acquire their initial gut microbes either through vaginal delivery or breastfeeding (Moore and Townsend, 2019). Additionally, during breastfeeding, the growth of specific microbial communities, including *bifidobacteria*, is enhanced. This is attributed to the presence of oligosaccharides (sugar) in breast milk. *Bifidobacteria*, found in the infant's stomach, play a crucial role in triggering immunological and inflammatory responses, modifying the function of the mucosal barrier, and preventing the growth of harmful organisms. This emphasizes the significant contribution of *bifidobacteria* in maintaining a healthy gut environment and supporting the overall well-being of the infant. As individuals grow older, their diet and other environmental exposures introduce new microbes to their gut biome. However, it is important to note that certain exposures can have adverse effects and lead to the depletion or alteration of the gut microbiota (Mansour *et al*., 2021; Bedani *et al*., 2024).

The human microbiota, consisting of a wide variety of micro-organisms, plays a crucial role in sustaining health and equilibrium in the human body. These microorganisms that inhabiting human gastrointestinal tract have a predominantly symbiotic relationship with their hosts. This symbiosis signifies that both partners which involved derive advantages from this association in which human provide these microorganisms with nourishment and a hospitable environment, while symbiont, in turn; perform important functions that benefit our bodies. One of their key roles is to regulate the growth and activity of potentially harmful micro-organisms, thereby contributing to the maintenance of a harmonious and healthy gut ecosystem.

Diet has emerged as a significant factor influencing the composition of the microbiota, with specific bacterial species thriving in response to distinct nutritional patterns. The consumption of fiber-rich foods, including fruits, whole grains, and vegetables can contribute to the nourishment of beneficial gut bacteria. These foods are known to be high in dietary fiber, which serves as a valuable fuel source for the growth and proliferation of beneficial bacteria in the gut (Aziz *et al*., 2024). By incorporating these fiber-rich foods into the daily diet, individuals can support a healthy gut microbiota, which has been associated with numerous health benefits.

The development of the gut microbiome begins at birth and is primarily completed within the first few years of life. It is important to note that environmental factors, such as diet composition, diet volume, and antibiotic therapy, proved to influence and modify the development and composition of the gut microbiome (Moustafa and Mansour, 2019).

Thus, investigating the contrast in bacterial species between healthy individuals and those following non-healthy ones, especially those high-fat diet regime, presents an interesting avenue for research. This review aims to explore the functionality of the microbiome and compare the characteristics of the microbiota associated with a natural diet versus a high-fat diet. By

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examining the differences in bacterial composition and their potential implications for health, this study seeks to shed light on the impact of dietary choices on the microbiota and its role in maintaining human health and homeostasis.

Role of microbiomes in human gut

In general, individuals in good health harbor a diverse microbiota characterized by a well-balanced presence of bacterial phyla, including Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, within their gut. This intricate microbial community plays a crucial role in various physiological functions, such as metabolism, modulation of the immune system, and maintenance of the intestinal barrier (Figure 1), therefore unbalance of these microbiome community can influence the whole metabolic pathways. The key aspects of its real role can be summarized as follow:

Digestion and Nutrient Absorption

The gut microbiome assists in the breakdown and digestion of complex carbohydrates, fiber, and other indigestible molecules that our own digestive enzymes cannot fully process. It helps to extract energy and nutrients from our food, such as vitamins, short-chain fatty acids (Gad *et al*., 2020), and amino acids.

Immune System Regulation

The gut microbiome interacts with the immune system, playing a vital role in immune development and function. It helps educate the immune system, ensuring appropriate responses to pathogens while maintaining tolerance to harmless substances. Imbalances in the gut microbiome can contribute to immune-related disorders.

Metabolism and Energy Balance

The gut microbiome influences the metabolism of various compounds, including bile acids and hormones involved in energy regulation. It has been linked to conditions like obesity and metabolic disorders. Certain gut microbial species can affect the efficiency of energy extraction from food, potentially impacting body weight and overall metabolic health.

Synthesis of Essential Compounds

The gut microbiome plays a fundamental role in the synthesis of essential compounds. One notable example is the production of vitamins, including vitamin K and certain B vitamins. These vitamins are vital for numerous physiological functions, such as blood clotting and energy metabolism. Moreover, the gut microbiome is involved in the synthesis of various bioactive compounds, such as neurotransmitters and short-chain fatty acids. These compounds have the potential to influence brain function and overall health. The ability of the gut microbiome to synthesize these essential compounds highlights its significance in maintaining optimal physiological processes within the human body.

Barrier Function and Gut Integrity

The gut microbiome helps maintain the integrity of the intestinal barrier, preventing the entry of harmful pathogens and toxins into the bloodstream. It also contributes to the production of mucus and strengthens the intestinal lining, providing a physical barrier against pathogens.

Gut-Brain Axis Communication

The gut microbiome communicates bidirectionally with the brain through the gut-brain axis. This interaction influences various aspects of brain function, including mood, behavior, and cognition. The gut microbiome produces neurotransmitters and other molecules that can directly affect the brain.

Disease Prevention and Treatment

Imbalances or disruptions in the gut microbiome have been associated with a range of diseases, including inflammatory bowel disease, allergies, obesity, diabetes, and even mental health disorders. By understanding and manipulating the gut microbiome, researchers hope to develop novel strategies for disease prevention and treatment.

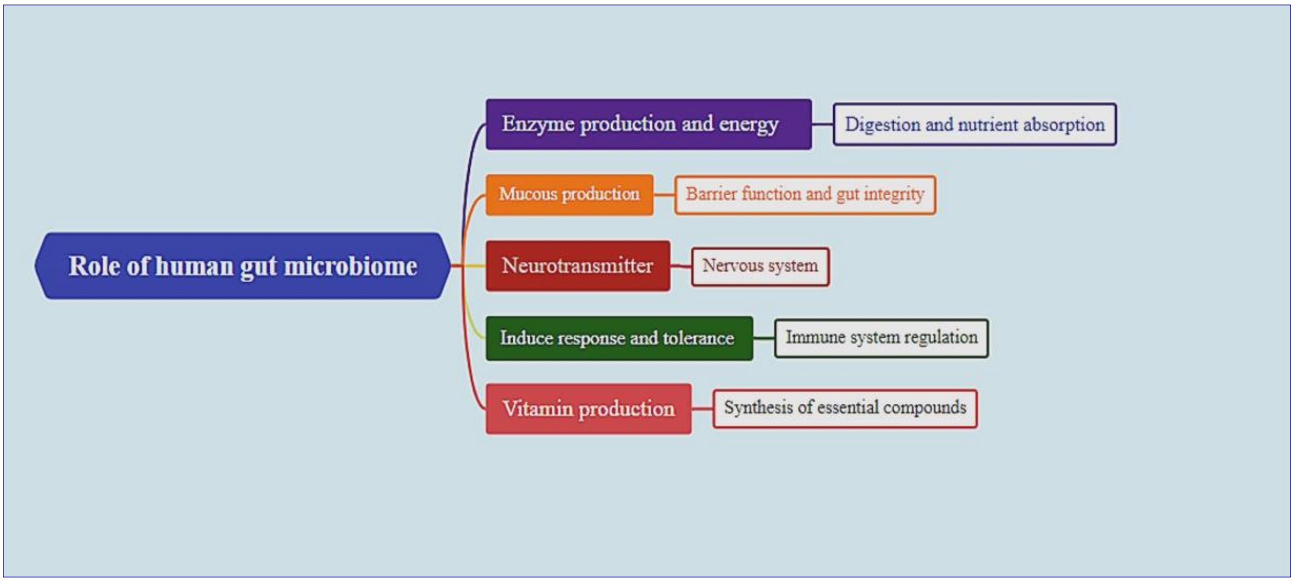

Figure (1): The vital Role of gut microbiota in maintaining human health.

Comparison of microbiome composition and diversity

Healthy individuals

The composition of the gut microbiota varies among individuals, but certain bacterial species are commonly found in the gastrointestinal tract of healthy individuals. These species include:

Bacteroides fragilis: It is a common inhabitant of the human colon and contributes to the breakdown of complex carbohydrates, thus maintaining a balanced gut environment (Cheng *et al*., 2020).

Bifidobacteria: Known for their ability to ferment dietary fibers, Bifidobacteria produce short-chain fatty acids (SCFAs) that have positive effects on the host's health (Ashaolu *et al*., 2021).

Akkermansia muciniphila: This mucin-degrading bacterium resides in the mucus layer of the gut and is associated with a healthy gut. It plays a crucial role in maintaining the integrity of the gut barrier (Aggarwal *et al*., 2022).

Faecalibacterium prausnitzii: This species is one of the most abundant bacteria in the human colon and possesses anti-inflammatory properties (Dikeocha *et al*., 2022).

Roseburia sp.: Certain species within this genus are involved in the fermentation of dietary fibers, thereby producing SCFAs that contribute to gut health (Portincasa *et al*., 2022).

Enterococcus faecalis: A Gram-positive bacterium, Enterococcus faecalis plays a role in maintaining the microbial balance in the gut (Han *et al*., 2023).

Prevotella sp.: Involved in the metabolism of various carbohydrates, *Prevotella* species contribute to the diversity of the gut microbiota (Betancur-Murillo *et al*., 2022). The collective diversity and equilibrium of these microbial communities play a crucial role in sustaining the stability and functionality of the gut microbiota, thereby contributing to overall human health.

Individuals consuming high fat diet

Conversely, individuals consuming a high-fat diet may experience significant changes in the composition of their gut microbiota (Lamichhane *et al.,* 2024). Such diets have been associated with variations in microbial diversity and an increase in specific bacterial species that are adept at metabolizing dietary fats (Maher *et al*., 2023). These alterations can have an impact on the host's metabolism, potentially leading to metabolic disorders, inflammation, and an increased risk of conditions such as obesity and metabolic syndrome.

Understanding the specific bacterial species that thrive or decline in response to a high-fat diet is crucial for comprehending the intricate interplay between diet, microbiota, and health outcomes.

Microbial communities-High fat diet

Studies have shown that high-fat diets can lead to an increase in the relative abundance of Firmicutes. An elevated Firmicutes to Bacteroidetes ratio has been observed in individuals with obesity, although the relationship is complex and not universally applicable (Houtman *et al*., 2022).

Bacteroidetes abundance can also be affected by high-fat diets. Some studies suggest a decrease in Bacteroidetes, which may influence the overall metabolic profile of the gut microbiota (Du *et al*., 2023).

Certain strains of *Escherichia coli* (*E. coli*) have been associated with a high-fat diet. An increased abundance of *E. coli* may contribute to inflammation and metabolic disturbances (Ju *et al.,* 2023). Additionally, some studies indicate that a high-fat diet could reduce the abundance of *Akkermansia muciniphila*, and lower levels of this bacterium have been linked to metabolic disorders (Keane *et al*., 2023).

Certain bacteria within the *Clostridium* clusters, such as members of *Clostridium* cluster XIVa and IV, have been implicated in the metabolism of dietary fibers. Changes in the abundance of these clusters may occur in response to alterations in diet composition, including high-fat intake (Enriquez *et al*., 2022).

High-fat diets have also been associated with an increase in the abundance of sulfate-reducing bacteria, such as *Desulfovibrio* sp. These bacteria can produce hydrogen sulfide, which may have implications for gut health (Singh *et al.,* 2023). Furthermore, additional bacterial and *Candida* species from the previously stated genera have been linked to high-fat diets and may have a negative impact on an individual's health. Some of these recorded genera can be reported, for example:

Enterobacteriaceae: This family of bacteria includes various genera such as *Enterobacter, Klebsiella*, and *Citrobacter.* High-fat diets have been linked to an increased abundance of Enterobacteriaceae, which may promote inflammation and metabolic dysfunction (Lobionda *et al*., 2019). A recent study done by Zheng *et al*., (2024) revealed that intestinal farnesoid X receptor (FXR) is responsible for the regulation of lipid metabolism in diet-induced dyslipidemia mediated by gut microbiota-bile acid crosstalk.

Streptococcus mutans: This bacterium is primarily linked to dental caries, but studies have indicated that high-fat diets may increase the bacterium's abundance, which may contribute to oral health problems (Wang *et al.,* 2018) and may be a causative agent of cardiovascular disease (Nomura *et al.,* 2020). A growing body of research indicates that oral bacterial pathogens may be associated with a variety of systemic diseases, including bacterial pneumonia, low birth weight, diabetes mellitus, cardiovascular diseases, and infective endocarditis (Neculae *et al*., 2023).

Candida albicans: *Candida albicans* is a species of yeast that normally resides in the human gut. However, overgrowth of Candida albicans, known as candidiasis, can occur with high-fat diets. This overgrowth may lead to various health problems, including gastrointestinal disturbances (Peroumal *et al*., 2022).

Fusobacterium nucleatum: Although mainly linked to periodontal disease, *Fusobacterium nucleatum* has also been observed to be more prevalent in people who consume a high-fat diet. This bacterium has been linked to inflammation and potential contributions to gut dysbiosis (Kenneth *et al.*, 2023). It's worth noting that the effects of these bacterial and Candida species on health outcomes may vary among individuals and warrant additional research. It's important to note that the impact of these bacterial species and Candida species on health outcomes may vary among individuals and require further research. Additionally, the relationship between high-fat diets and specific microbial changes is complex and multifactorial. Further studies are needed to fully understand the mechanisms and implications of these associations.

Mechanism of dysfunction of metabolism due to high fat diet

High-fat diets can lead to disruption of microbial diversity that means a decrease in microbial variation of existing genera and species within the gut microbiota. This reduction in diversity can also result in an imbalance of microbial populations, favoring certain species over others. This dysbiosis can negatively impact the overall functioning and stability of the microbiome. This can alter the metabolic activities of the gut microbiota. Where, the increased intake of dietary fats can promote the growth of bacteria that specialize in metabolizing fats, leading to an overrepresentation of fat-metabolizing microbes (Figure 2) This shift in microbial metabolism can affect the production of beneficial metabolites and disrupt the intricate balance of microbial functions. Therefore, we can summarize the consequences as follow:

Altered Gut Microbiota Composition

High-fat diets can disrupt the balance of the gut microbiota, leading to dysbiosis. This dysbiosis is characterized by changes in the relative abundance of specific bacterial species and genera, as mentioned earlier. The altered microbial composition can impact the intestinal environment, leading to inflammation, impaired gut barrier function, and metabolic disturbances.

Increased Intestinal Permeability

High-fat diets have been associated with increased intestinal permeability, also known as "leaky gut." The disruption of the gut barrier allows the translocation of bacteria, bacterial components, and toxins from the intestine into the bloodstream. This can trigger an immune response and chronic inflammation (in low-grade), contributing to the development of metabolic disorders (Rohr *et al*., 2020).

Inflammation and Immune Activation

High-fat diets can induce inflammation in the intestine through various mechanisms. The dysbiosis microbiota and increased intestinal permeability can activate immune cells in the gut, such as macrophages and dendritic cells, leading to the release of pro-inflammatory cytokines (Silva *et al*., 2020). Chronic inflammation in the intestine can disrupt normal physiological processes and contribute to the development of conditions like inflammatory bowel disease (IBD) and metabolic syndrome (Moustafa and Mansour, 2019, Kwon *et al*., 2024).

Disrupted Energy Metabolism

High-fat diets are rich in calories and can lead to excessive energy intake. The increased intake of dietary fats can result in elevated levels of free fatty acids in the intestine. These free fatty acids can trigger inflammation, impair insulin signaling, and disrupt energy metabolism in the intestinal cells. This disruption can contribute to metabolic dysfunction and insulin resistance that leads to diabetic-type 2 disease development (Luo *et al*., 2020).

Impaired Gut Hormone Regulation:

The gut produces various hormones that regulate appetite, satiety, and glucose homeostasis (Vu *et al.*, 2023). High-fat diets can disrupt the secretion and signaling of these gut hormones, such as peptide YY (PYY), glucagon-like peptide-1 (GLP-1), and ghrelin. This disruption can lead to increased food intake, reduced satiety, and impaired glucose regulation (Koliaki *et al*., 2020).

Shift in Bile Acid Metabolism

High-fat diets can impact bile acid metabolism in the gut. Bile acids, which are synthesized in the liver and modified by the gut microbiota, play a role in lipid digestion and absorption (Lin *et al*., 2019, Hu *et al*., 2024). Alterations in the gut microbiota composition can affect bile acid metabolism, potentially leading to imbalances in lipid metabolism and absorption (Ocvirk and O'Keefe, 2021).

These mechanisms collectively contribute to the dysfunction of the gut microbiome resulting from a high-fat diet regime. It's important to note that these mechanisms are interconnected and can influence each other, exacerbating the negative effects on gut health. Additional research is needed to fully understand the intricate mechanisms and relationships between high-fat diets, the gut microbiome, and associated health outcomes. This research will target these interventions to mitigate the adverse effects of high-fat diets on intestinal health. Moreover, interventions aimed at modulating the gut microbiota, such as prebiotics, probiotics, and dietary modifications, may hold promise in mitigating the negative effects of high-fat diets on gut health. In summary, this comprehensive analysis highlights the detrimental effects of high-fat diets on gut microbiota composition and emphasizes the need for further research to understand the underlying mechanisms and develop strategies for maintaining a healthy gut microbiota in the context of high-fat dietary patterns.

CONCLUSION

In conclusion, this comprehensive analysis has shed light on the impact of high-fat diets on gut microbiota composition in healthy individuals. The findings suggest that high-fat diets lead to alterations in the abundance and diversity of bacterial genera and *Candida* species in the gut microbiota. These changes have implications for metabolic health, inflammation, and gut dysbiosis. The observed increase in Firmicutes and Enterobacteriaceae, along with the decrease in Bactero-

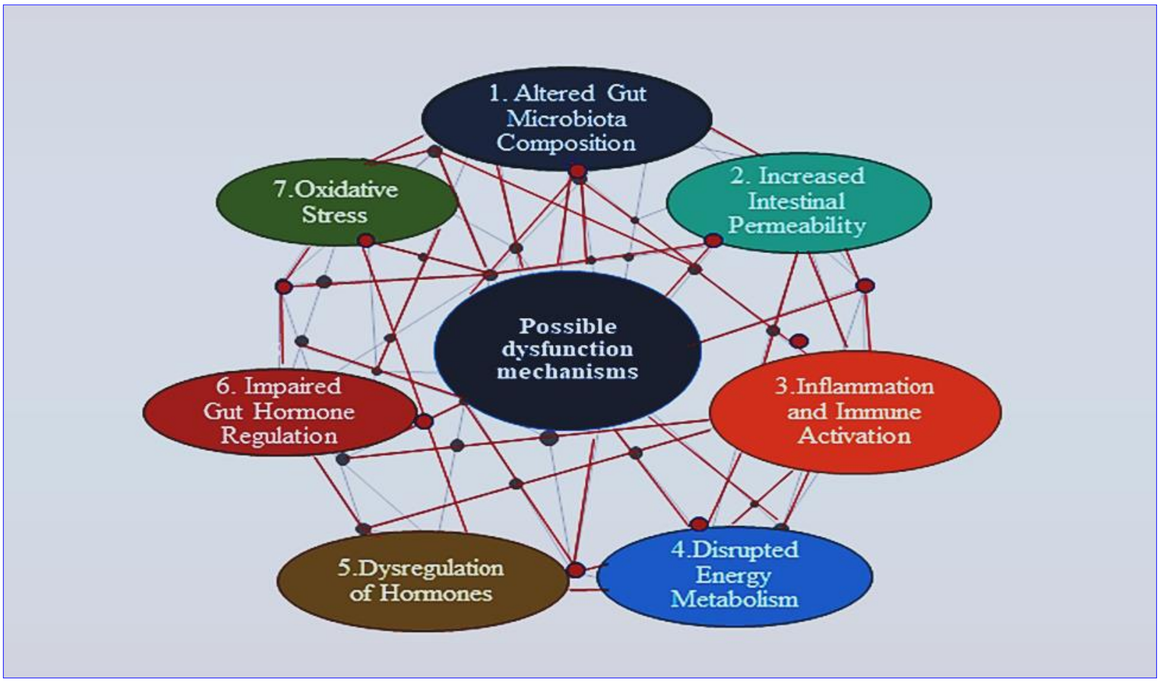

Figure (2): Mechanism of dysfunction of metabolism due to high fat diet. The figure provides a comprehensive overview of the interplay between potential mechanisms underlying metabolic dysfunction caused by a high-fat diet. The diagram illustrates these mechanisms using lines and nodes, wherein the size of each node represents the magnitude of its influence on metabolic function.

idetes and *Akkermansia muciniphila*, indicates an unfavorable gut microbiota profile associated with high-fat diets. Additionally, the presence of *Strepto*coccus *mutans*, *Candida albicans*, *Fusobacterium nucleatum* and certain *Lactobacillus* strains highlights the potential negative impacts on oral health and gut microbial balance. However, it is important to note that individual variations, diet composition, and other factors can influence these associations. Further research is needed to unravel the underlying mechanisms and develop strategies to mitigate the potential health risks associated with high-fat diets and gut microbiota dysbiosis. Previous research has shown that microbiome composition correlates more closely with the consumption of individual foods rather than just nutrient intake. Therefore, future investigations should consider analyzing the co-variation between diet and the microbiome by focusing on individual foods rather than relying solely on established nutrient composition variables. Furthermore, it is crucial to consider the long-term effects of high-fat diets on gut microbiota composition and overall health. The current analysis provides valuable insights into the immediate impact of high-fat diets on the gut microbiota in healthy individuals. However, longitudinal studies are needed to examine how these changes evolve over time and whether they contribute to the development of chronic conditions such as obesity, diabetes, and cardiovascular disease.

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استكشاف تأثير النظام الغذائي عالي الدهون على ميكروبيوم الامعاء في الأفراد الأصحاء: تحليل شامل

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الملخــص العــربى

تتكون بكتيريا الأمعاء للانسان من مجموعة متنوعة من الكائنات الدقيقة التي تُعرف باسم "الميكروبيوم"، وتلعب أدوارًا حيوية في الحفاظ على صحة العامة للانسان. وتتأثر تركيبة ونشاط هذه الميكروبات بعوامل عديدة، منها عوامل داخلية كالتوتر وعوامل خارجية مثل التغذية والأدوية. و أصبح فهم دور بكتيريا الأمعاء في زياده وزن الجسم محط اهتمام كبير بين الباحثين. وللاستيعاب الكامل للعلاقة المعقدة بين الميكروبات وأجسامنا، من الضروري تحديد خصائص هذه البكتيريا لدى الأفراد الأصحاء. حيث تشير الأدلة الناشئة إلى أن التغيرات في تركيبة بكتيريا الأمعاء، خاصة استجابة للعوامل الغذائية، يمكن أن يكون لها آثار عميقة على صحة الإنسان. ومن الأمور التي تحظى باهتمام خاص التأثير المحتمل للنظام الغذائي الغني بالدهون على بكتيريا الأمعاء، حيث يُفترض أن مثل هذه الأنماط الغذائية قد تؤدي إلى خلل في التوازن البكتيري (dysbiosis) وما يترتب عليه من عواقب صحية. أبرزت الأبحاث الحديثة التأثير المحتمل للعوامل الغذائية على بكتيريا الأمعاء، وخاصة الصلة بين النظام الغذائي الغني بالدهون والخلل البكتيري، والذي قد تكون له آثار صحية ضارة. تهدف هذه المقالة إلى المساهمة في المعرفة الحالية من خلال تقديم تحليل شامل للميكروبيوم لدى الأفراد الأصحاء مقارنةً بأولئك الذين يتناولون نظامًا غذائيًا غنيًا بالدهون وذلك من خلال استكشاف التنوع النسبي والوفرة لمجموعات بكتيرية مختلفة، والبحث عن ارتباطات محتملة مع المؤشرات الصحية، تهدف هذه المقالة إلى توسيع فهمنا للدور الذي يلعبه النظام الغذائي في تشكيل بكتيريا الأمعاء، والآليات الكامنة وراء ذلك. نتوقع أن يكون لهذه النتائج تأثيرات بعيدة المدى على تطوير استراتيجيات غذائية جديدة لصحة الأمعاء العامة.