How Socioeconomic Factors Shape Dietary Patterns and Affect the Gut Microbiome Through Epigenetics and Impact Metabolic Diseases

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Abstract

This research paper examines the association between socioeconomic factors and the gut microbiome with an emphasis on socioeconomic factors' influence on metabolic diseases. This paper covers gut microbiome, epigenetics, socioeconomic factors, metabolic diseases, and how they interact with each other. By progressing through how socioeconomic factors influence the gut microbiome, this paper guides the reader through how these factors contribute to metabolic diseases. This paper illustrates the crucial role that socioeconomic factors play in gut health while highlighting the critical need for socioeconomic equality.

1. Introduction

Multiple socioeconomic factors—such as diet quality, food access, healthcare access, sanitation, living conditions, stress, psychosocial factors, education, and health literacy impact dietary patterns and consequently shape the gut microbiome and influence the development of its associated metabolic diseases, which are characterized by disruptions in energy balance, glucose and lipid metabolism, and insulin signaling, increasing the risk of obesity, type 2 diabetes, metabolic syndrome, and cardiovascular disease. The gut microbiome—an ecosystem of various microorganisms such as bacteria, archaea, fungi, and viruses that occupy the gastrointestinal tract, predominantly within the intestines—has a substantial influence on health foundations: digestion, immune system, and brain function (Jain, 2024). Negative socioeconomic factors such as low income, limited access to quality healthcare, and food insecurity thus facilitate harmful dietary patterns that exacerbate the gut microbiome. A disrupted gut microbiome, also known as dysbiosis, has been associated with various metabolic diseases such as obesity, type 2 diabetes mellitus (T2DM), non-alcoholic fatty liver disease (NAFLD), and leaky gut syndrome.

This research paper explores the impact of socioeconomic factors on dietary patterns and how those dietary patterns, in turn, alter the gut microbiome and potentially cause metabolic diseases. To achieve this, we conducted a comprehensive literature review, synthesising findings from existing peer reviewed studies and publicly available datasets. This methodology enables us to contextualize the biological implications of changes in the microbiome within broader social and economic frameworks.

2. Contextualizing the Research

Gut microbiome and diet are a two-way system. What individuals eat shapes the types and balance of bacteria in the gut, and those microbes influence how the body digests food, absorbs nutrients, and regulates metabolism. Each year diet-related diseases contribute to approximately 11 million deaths (Aubrey, 2016). One of the most prevalent metabolic conditions—when the body's normal chemical processes for turning food into energy are disrupted, leading to too many or too few essential substances—is type 2 diabetes, and around 30.2 million adults aged 18 and older in the United States—equivalent to 12.2% of the adult population—had been diagnosed with type 2 diabetes (Saklayen, 2018). Alarmingly, nearly a quarter of these individuals (23.8%) were unaware of their condition. Furthermore, the prevalence of prediabetes and metabolic syndrome—a group of conditions that increases your risk of coronary heart disease, diabetes, stroke, and other serious health issues (Swarup, 2024)—is roughly three times higher, indicating that about one-third of adults in the U.S. are impacted by metabolic syndrome (Saklayen, 2018).

3. Introduction to Gut Microbiota and Epigenetics

The gut microbiota are essential in many functions including the fermentation of dietary fibers into short-chain fatty acids (e.g., butyrate), which serve as an energy source for colonocytes—the intestinal cell that absorbs water and metabolizes bacterial byproducts, serving as a model for sustainable living—and help maintain gut health (Vinelli et al, 2022). It also provides pathogen defense by outcompeting harmful microbes and producing antimicrobial compounds—bacteriocins (e.g., nisin and plantaricin), short-chain fatty acids such as butyrate, secondary bile acids, reuterin, and hydrogen peroxide—(Kamel et al, 2024). Additionally, it influences the immune system by interacting with immune cells and contributing to immune homeostasis (Wu, 2012).

Factors influencing the gut microbiome include epigenetic marks and aging, both of which affect DNA expression (transcription). Thus, epigenetic profiles are crucial public health screening tools and function as risk biomarkers (Shin, 2024). By using these tools, we can identify specific factors influencing physiological processes in the body. Epigenetics involves chemical modifications that turn genes on or off without changing the DNA sequence (Aboud, 2023). These changes can be influenced by environmental factors, including the gut microbiome—the community of microbes in our intestines. The gut microbiome produces compounds that can directly affect epigenetic mechanisms that can influence gene expression in cells throughout the body, affecting processes like inflammation, metabolism, and immune function.

4. Factors Affecting Gut Microbiota and Epigenetic Regulation

Diet plays a critical role in shaping the composition and function of the gut microbiota, which in turn can influence epigenetic regulation. A rich diet promotes a diverse and balanced microbial environment. These dietary components are fermented by gut microbes to produce metabolites that modulate epigenetic mechanisms. Additionally, unbalanced diet foods such as a Western-style diet high in processed foods, sugar, and unhealthy fats can disrupt microbial balance and may lead to epigenetic alterations associated with inflammation, metabolic dysfunction, and disease risk (Nova, 2022).

The use of antibiotics and other pharmaceutical agents can also significantly alter the gut microbiota. Antibiotics reduce microbial diversity and may allow the overgrowth of harmful species such as Clostridioides difficile (C. diff), Klebsiella pneumoniae, and Staphylococcus aureus (Kesavelu, 2023). This microbial imbalance can affect the availability of key microbial metabolites that influence epigenetic modifications; for example, dysbiosis-associated depletion of butyrate-producing bacteria reduces intestinal butyrate levels, resulting in increased histone deacetylase activity and decreased histone acetylation, thereby altering the expression of genes involved in immune regulation and intestinal barrier function (Sung, 2025). In addition, certain medications have been shown to directly or indirectly affect both the gut microbiome and epigenetic regulation, potentially contributing to long-term health outcomes (Patangia et al, 2022).

The gut microbiome and gene regulation change significantly throughout individuals' lives. In infancy, factors such as birth method, breastfeeding, and early diet help establish a diverse gut bacterial community that influences gene expression and immune system development. As people age, bacterial diversity typically declines, leading to alterations in gene activity that can increase inflammation and reduce immune function. Thus, prioritizing gut health and lifestyle factors that support healthy microbiome-mediated gene regulation from a young age is vital, as individuals' choices strongly influence long-term health outcomes (Davis et al., 2022).

5. Metabolic Diseases/Noncommunicable Disease

Commonly referred to as noncommunicable diseases (NCDs), metabolic diseases are chronic illnesses that arise from the complex interplay among lifestyle, genetics, and the gut microbiota. Imbalances may cause issues with immune responses, insulin regulation, energy metabolism, and barrier integrity. All of these disturbances are associated with a development of metabolic disease.

Obesity

Obesity is the excessive accumulation of body fat that presents a risk to health. It is strongly influenced by microbial imbalances. Disruption of the gut microbiota composition—specifically shifts in the relative abundance of bacterial taxa, reduced overall microbial diversity, and altered ratios of dominant phyla such as Firmicutes and Bacteroidetes—can affect the ability to harvest energy from food, store fat, and regulate insulin sensitivity. Leading to a low-grade inflammation and imparted glucose metabolism which ends with several chronic health problems (Davis, 2016).

Type 2 Diabetes Mellitus

Type 2 diabetes mellitus (T2DM) is a chronic condition characterized by high blood sugar levels (hyperglycemia) due to the body's inability to use insulin effectively or produce enough insulin. Individuals with type 2 diabetes exhibit distinct gut microbial profiles, notably a higher prevalence of certain strains such as Prevotella copri (Wang et al, 2011). This strain produces significant quantities of branched-chain amino acids, which have been previously linked to obesity and insulin resistance. These microbial alterations, combined with the influence of bacteriophages that infect and alter bacterial functions, may disrupt gut microbiome activity in ways that impair glucose metabolism (Welsh, 2024). It is suggested that these changes in the microbiome could occur even before the onset of type 2 diabetes, potentially playing a causal role in its development (Study Links Gut Microbiome Changes to Increased Risk of Type 2 Diabetes, 2024).

Non-Alcoholic Fatty Liver Disease (NAFLD)

Nonalcoholic fatty liver disease (NAFLD) is a condition where excess fat accumulates in the liver. The gut microbiome impacts NAFLD by affecting metabolic, inflammatory, and barrier functions along the gut-liver axis (Mazzotti et al, 2016). Dysbiosis compromises gut barrier integrity, increasing permeability and allowing harmful bacterial products like lipopolysaccharide (LPS) to enter the liver (Poeta et al, 2017), which triggers inflammation via immune receptors such as Toll-like receptors (TLRs) (Woodhouse et al, 2018). The microbiome also influences bile acid metabolism and choline utilization, essential for lipid processing and liver fat buildup, and produces hepatotoxic substances like endogenous ethanol that worsen liver injury (Abdul-Hai et al, 2015).

Leaky Gut

Leaky gut syndrome, or increased intestinal permeability, is a condition where the small intestine's lining becomes more permeable, allowing substances to leak into the bloodstream. At the microbiota level dysbiosis plays a significant role in the development of leaky gut by compromising the intestinal barrier. Harmful bacteria can produce toxins or inflammatory molecules that damage the gut lining and disrupt tight junction proteins—specialized structures that connect adjacent intestinal epithelial cells and regulate selective permeability—thereby increasing intestinal barrier permeability. Consequently, this disruption permits unwanted substances such as bacterial toxins and antigens to enter the bloodstream, exacerbating systemic inflammation and potentially contributing to various chronic conditions (Campos, 2023).

6. Socioeconomic Factors’ Impact On Diet

There is a complex relationship between diet, health, and socioeconomic status. It includes wider social and environmental factors beyond just dietary choices. These factors have lasting effects on metabolic health by influencing what people eat and how their bodies process and respond to food.

Diet Quality and Food Access

Lower incomes are often associated with limited access to nutrient-dense foods (Katre et al, 2023). Nutrient-dense foods such as fresh fruits, vegetables, and lean protein are often correlated with higher cost. In comparison, less nutrient dense foods such as processed food and fast food are often more affordable. In addition, many low-income neighborhoods are food deserts where residents have limited access to healthy and affordable food.

Access to Healthcare

Limited access to healthcare significantly impacts diet and overall health in various ways. Without regular check-ups or professional guidance, individuals may lack early support for nutrition-related concerns (Agurs-Collins et al, 2024). Additionally, in many communities, the overuse or misuse of antibiotics can occur in the absence of adequate medical supervision. This situation can disrupt gut health, impair digestion and nutrient absorption, and may contribute to long-term health complications (Krajmalnik-Brown et al, 2012).

Sanitation and Living Conditions

Sanitation and living conditions also have a major influence on the safety and nutritional value of food. Substandard housing may lack essential facilities such as refrigerators and clean cooking spaces. This reduces the capacity to prepare and preserve nutritious meals (Krieger et al., 2002). Consequently, there tends to be a reliance on processed meals. Substandard water quality also presents a major hazard. Contaminated substances such as bacteria, viruses, and parasites may result in diseases such as cholera and typhoid. The body cannot absorb nutrients in such a circumstance (World Health Organization, 2022). This is especially the case for a homeless person.

Besides microbial contamination, being exposed to chemical contaminants such as heavy metals or industrial waste in the water may affect the gut microbiota as well (Chiu et al., 2020). Moreover, it often leads to a decrease in beneficial bacteria in the body along with an increased incidence of dysbiosis. Frequent infection as well as the use of antibiotics causes a further reduction in microbial diversity as well (Patangia et al, 2022). Also, exposure to environmental stress may compromise the integrity of the tight junctions in the gut wall (Campos, 2023).

Stress and Psychosocial Factors

Chronic stress, which can extend to all socio-economic classes, has a profound impact on food behavior and metabolism. Although poverty-related stressors like financial security and housing stability can have a tremendous effect, the impact of psychological stress factors of academics, work pressures, loneliness, and mental illness may limit healthy behavior regarding food consumption by relying on convenience foods and resulting in alterations of appetite (Laraia et al., 2017). A lack of support may lead to a lack of motivation in healthy food preparation and consumption behavior.

Biologically, stress impacts the gut through the gut-brain axis. It stimulates the hypothalamic-pituitary-adrenal (HPA) axis and results in an excessive secretion of stress hormones such as cortisol (Bertollo et al, 2025). High levels of cortisol can lead to alterations in gut motility, decreased secretion of mucus, increased permeability of the intestines, and reduced beneficial microorganisms with a compensatory overgrowth of inflammatory microorganisms (Dadlani, 2025). This shift in the gut microbiota due to stress has been associated with inflammation and metabolic disorders.

Education and Health Literacy

Education significantly impacts dietary choices. Those with lower education levels may struggle to comprehend nutrition labels or grasp the long-term consequences of an unhealthy diet (Olstad, 2025). Health literacy is vital for a person's ability to handle diet-related conditions like diabetes or hypertension. Poor health literacy can lead to bad dietary choices and slow disease management, which may indirectly disrupt the gut microbiome.

7. Discussion/Analysis

Socioeconomic factors such as location, income, education, and job opportunities play a crucial role in shaping people’s eating habits. Poor diets increase the risk of metabolic diseases, making socioeconomic differences a serious public health issue. These factors not only affect how accessible and good food is but also contribute to the rise of chronic illnesses. This highlights the strong link between economic situations and health outcomes.

The gut microbiome further shows this connection by acting as a biological link between the environment and disease. The makeup of microbes in our bodies is influenced by nutrition, healthcare, sanitation, and education—all shaped by socioeconomic conditions. Changes in the microbiome can impact immune function, energy management, and genetic expression, which may increase the risk of metabolic disorders. Fixing these disparities needs active government efforts and public health policies that combine social change with biological understanding to create healthier communities.

8. Conclusions/Limitations

The link between socioeconomic status, dietary habits, and the gut microbiome is important but not fully understood. Current research shows strong connections between these factors and metabolic health, but much of the evidence is still developing. Many studies do not capture the complexity of these interactions across different populations and real-world situations. This limits the conclusions we can draw. This paper mainly serves as a literature review, bringing together existing research to highlight key patterns and gaps.

Future progress will depend on collaborative, large-scale, and long-term studies that improve our understanding of how socioeconomic differences affect the microbiome and chronic disease outcomes. Access to healthy food, healthcare, and sanitation is crucial for better health. However, advancing microbiological research alongside socioeconomic policy is vital for tackling the underlying causes of disease. Ongoing investment in this area is essential to turn new insights into effective public health strategies that reduce inequality and improve long-term well-being.

References

Aboud, N. M. A. (2023, August 14). Genetics, epigenetic mechanism. StatPearls [Internet]. https://www.ncbi.nlm.nih.gov/books/NBK532999/

Abdul-Hai, A., Abdallah, A., & Malnick, S. D. (2015). Influence of gut bacteria on development and progression of non-alcoholic fatty liver disease. World Journal of Hepatology, 7(12), 1679–1684. https://doi.org/10.4254/wjh.v7.i12.1679

Agurs-Collins, T., Alvidrez, J., ElShourbagy Ferreira, S., Evans, M., Gibbs, K., Kowtha, B., Pratt, C., Reedy, J., Shams-White, M., & Brown, A. G. (2024). Perspective: Nutrition health disparities framework: A model to advance health equity. Advances in Nutrition (Bethesda, Md.), 15(4), 100194. https://doi.org/10.1016/j.advnut.2024.100194

Aubrey, A. (2019, April 3). Bad diets are responsible for more deaths than smoking, global study finds. National Center for Biotechnology Information. https://www.ncbi.nlm.nih.gov/search/research-news/2045/

Bertollo, A. G., Santos, C. F., Bagatini, M. D., & Ignácio, Z. M. (2025, February 5). Hypothalamus–pituitary–adrenal and gut–brain axes in biological interaction pathway of depression. Frontiers. https://www.frontiersin.org/journals/neuroscience/articles/10.3389/fnins.2025.1541075/full

Bose, P. (2025). Histone modification types and effects. The Scientist. https://www.the-scientist.com/histone-modification-types-and-effects-73251

Campos, M. (2023, September 12). Leaky gut: What is it, and what does it mean for you? Harvard Health.

https://www.health.harvard.edu/blog/leaky-gut-what-is-it-and-what-does-it-mean-for-you-2017092212451

Chiu, K., Warner, G., Nowak, R. A., Flaws, J. A., & Mei, W. (2020). The impact of environmental chemicals on the gut microbiome. Toxicological Sciences, 176(2), 253–284. https://doi.org/10.1093/toxsci/kfaa065

Dadlani, M. (2025, October 9). How does stress affect the gut microbiome? The Microbiome Blog. https://insights.cmbio.io/how-does-stress-affect-the-gut-microbiome

Davis, C. D. (2016). The gut microbiome and its role in obesity. Nutrition Today, 51(4), 167–174. https://doi.org/10.1097/NT.0000000000000167

Davis, E. C., Castagna, V. P., Sela, D. A., Hillard, M. A., Lindberg, S., Mantis, N. J., Seppo, A. E., & Järvinen, K. M. (2022). Gut microbiome and breast-feeding: Implications for early immune development. The Journal of Allergy and Clinical Immunology, 150(3), 523–534. https://doi.org/10.1016/j.jaci.2022.07.014

Jain, N. (2024). 5 things to know about the gut microbiome. Mass General Brigham.

https://www.massgeneralbrigham.org/en/about/newsroom/articles/5-things-to-know-about-gut-microbiome

Kamel, M., Aleya, S., Alsubih, M., & Aleya, L. (2024). Microbiome dynamics: A paradigm shift in combating infectious diseases. Journal of Personalized Medicine, 14(2), 217. https://doi.org/10.3390/jpm14020217

Katre, A., & Raddatz, B. (2023). Low-income families' direct participation in food-systems innovation to promote healthy food behaviors. Nutrients, 15(5), 1271. https://doi.org/10.3390/nu15051271

Kesavelu, D., & Jog, P. (2023). Current understanding of antibiotic-associated dysbiosis and approaches for its management. Therapeutic Advances in Infectious Disease, 10, 20499361231154443. https://doi.org/10.1177/20499361231154443

Knight, R. (2012). The impact of the gut microbiota on human health: An integrative view. Cell. https://www.sciencedirect.com/science/article/pii/S0092867412001043

Krajmalnik-Brown, R., Ilhan, Z. E., Kang, D. W., & DiBaise, J. K. (2012). Effects of gut microbes on nutrient absorption and energy regulation. Nutrition in Clinical Practice, 27(2), 201–214. https://doi.org/10.1177/0884533611436116

Krieger, J., & Higgins, D. L. (2002). Housing and health: Time again for public health action. American Journal of Public Health, 92(5), 758–768. https://doi.org/10.2105/ajph.92.5.758

Lanata, C. M., Chung, S. A., & Criswell, L. A. (2018, July 25). DNA methylation 101: What is important to know about DNA methylation and its role in SLE risk and disease heterogeneity. Lupus Science & Medicine. https://pmc.ncbi.nlm.nih.gov/articles/PMC6069928/

Laraia, B. A., Leak, T. M., Tester, J. M., & Leung, C. W. (2017). Biobehavioral factors that shape nutrition in low-income populations: A narrative review. American Journal of Preventive Medicine, 52(2S2), S118–S126. https://doi.org/10.1016/j.amepre.2016.08.003

Mazzotti, A., Caletti, M. T., Sasdelli, A. S., Brodosi, L., & Marchesini, G. (2016). Pathophysiology of nonalcoholic fatty liver disease: Lifestyle–gut–gene interaction. Digestive Diseases (Basel, Switzerland), 34(Suppl 1), 3–10. https://doi.org/10.1159/000447275

Nova, E., Gómez-Martinez, S., & González-Soltero, R. (2022). The influence of dietary factors on the gut microbiota. Microorganisms, 10(7), 1368.

https://doi.org/10.3390/microorganisms10071368

Olstad, D. L., & McIntyre, L. (2025). Educational attainment as a super determinant of diet quality and dietary inequities. Advances in Nutrition (Bethesda, Md.), 16(9), 100482. https://doi.org/10.1016/j.advnut.2025.100482

Patangia, D. V., Anthony Ryan, C., Dempsey, E., Paul Ross, R., & Stanton, C. (2022). Impact of antibiotics on the human microbiome and consequences for host health. MicrobiologyOpen, 11(1), e1260. https://doi.org/10.1002/mbo3.1260

Pepke, M. L., Hansen, S. B., & Limborg, M. T. (2024, June 4). Unraveling host regulation of gut microbiota through the epigenome–microbiome axis. Trends in Microbiology. https://www.cell.com/trends/microbiology/fulltext/S0966-842X(24)00137-9

Poeta, M., Pierri, L., & Vajro, P. (2017). Gut-liver axis derangement in non-alcoholic fatty liver disease. Children (Basel, Switzerland), 4(8), 66. https://doi.org/10.3390/children4080066

Saklayen, M. G. (2018, February 26). The global epidemic of the metabolic syndrome. Current Hypertension Reports. https://link.springer.com/article/10.1007/s11906-018-0812-z

Shin, Y. (2024). Gut microbiota and epigenetic choreography: Implications for human health: A review. NIH. https://pmc.ncbi.nlm.nih.gov/articles/PMC11398772/

Statello, L., Guo, C.-J., Chen, L.-L., & Huarte, M. (2020, December 22). Gene regulation by long non-coding RNAs and its biological functions. Nature Reviews Molecular Cell Biology. https://www.nature.com/articles/s41580-020-00315-9

Study links gut microbiome changes to increased risk of type 2 diabetes. (n.d.). BWH Press Release – Brigham and Women's Hospital. https://www.brighamandwomens.org/about-bwh/newsroom/press-releases-detail?id=4741

Sung, H., Cho, S. Y., Ma, S. H., You, J. S., Yoon, M. Y., & Yoon, S. S. (2025). A butyrate-producing synbiotic mitigates intestinal inflammation in a murine colitis model. mLife, 4(4), 397–408. https://doi.org/10.1002/mlf2.70027

Swarup, S. (2024, March 7). Metabolic syndrome. National Center for Biotechnology Information. https://pubmed.ncbi.nlm.nih.gov/29083742/

Vinelli, V., Biscotti, P., Martini, D., Del Bo', C., Marino, M., Meroño, T., Nikoloudaki, O., Calabrese, F. M., Turroni, S., Taverniti, V., Unión Caballero, A., Andrés-Lacueva, C., Porrini, M., Gobbetti, M., De Angelis, M., Brigidi, P., Pinart, M., Nimptsch, K., Guglielmetti, S., & Riso, P. (2022). Effects of dietary fibers on short-chain fatty acids and gut microbiota composition in healthy adults: A systematic review. Nutrients, 14(13), 2559. https://doi.org/10.3390/nu14132559

Wang, T., Larson, M., Vasan, R., et al. (2011). Metabolite profiles and the risk of developing diabetes. Nature Medicine, 17, 448–453. https://doi.org/10.1038/nm.2307

Welsh, J. (2024, December 12). Changes to gut microbiome may increase type 2 diabetes risk. Harvard Medical School. https://hms.harvard.edu/news/changes-gut-microbiome-may-increase-type-2-diabetes-risk

Woodhouse, C. A., Patel, V. C., Singanayagam, A., & Shawcross, D. L. (2018). Review article: The gut microbiome as a therapeutic target in the pathogenesis and treatment of chronic liver disease. Alimentary Pharmacology & Therapeutics, 47(2), 192–202. https://doi.org/10.1111/apt.14397

World Health Organization. (2022). Microbial fact sheets. Guidelines for drinking-water quality: Fourth edition incorporating the first and second addenda [Internet]. https://www.ncbi.nlm.nih.gov/books/NBK579445/

Wu, H. J., & Wu, E. (2012). The role of gut microbiota in immune homeostasis and autoimmunity. Gut Microbes, 3(1), 4–14. https://doi.org/10.4161/gmic.19320

Wu, M. (2022, September). Diet–gut microbiota–epigenetics in metabolic diseases: From mechanisms to therapeutics. ScienceDirect. https://www.sciencedirect.com/science/article/pii/S0753332222006795