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The Impact of Gut Microbiome on Obesity: Investigating the Link Between Gut Health and Obesity Prevention

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ABSTRACT

Scientists now recognize the gastrointestinal tract microbial community as an important factor for metabolic health because it controls various metabolic functions. Modern studies have identified that gut microbiota powerfully controls energy management along with nutrient usage and immune function so scientists now recognize it as a central element for obesity creation and treatment. Dysbiosis is now strongly linked to metabolic dysfunction and increased inflamed conditions and obesity development because it seems the state of gut health determines important obesity prevention methods. The author evaluates the complex association between gut microbiota composition and obesity through research on weight regulation dependence on microbial diversity functional capacity and metabolite production. Current evidence shows that therapeutic approaches aimed at balancing microbial populations through nutrient changes along with adding probiotics and prebiotics and performing fecal microbiota transplantation lead to important changes in obesity development. The research focuses on short-chain fatty acids produced by the gut since they protect against weight gain. The paper combines results from human clinical trials and animal tests together with contemporary human trials that were assessed through extensive literature review research. The study results confirm that particular microbial patterns create a direct link to obesity risk which strengthens the prospect of developing microbiome-driven therapeutic approaches. The clarification of gut health mechanisms related to obesity development helps scientists understand metabolic pathway functions and explores new non-invasive public health prevention methods.

Keywords: Gut Microbiome, Obesity, Microbiome Modulation, Short-Chain Fatty Acids (SCFAs), Firmicutes/Bacteroidetes Ratio

INTRODUCTION

Background

A human gastrointestinal tract contains a complex microbial ecosystem made up of multiple types of microorganisms which include bacteria, viruses alongside fungi, and other microbes. Human health maintenance depends on microorganisms because they control basic biological systems including metabolism and immune performance and mental health and resistance against diseases. Scientists have focused intense research interest on the gut microbiome because its ability to manipulate various biological functions. Scientific evidence demonstrates that human health results show direct effects from the composition and diversity of gut microbial populations (Tseng & Wu, 2019). Excessive fat accumulation during obesity creates a global health crisis which leads to different medical problems ranging from heart disease to diabetes and specific cancers. The World Health Organization (WHO) reports that worldwide adult obesity rates have reached above 1.9 billion since more than 650 million adults meet the medical criteria of obesity (Leeuwendaal et al., 2022). During the last few decades obesity rates have increased constantly because of urbanization and other factors which include inactivity and differences in eating behavior. Public health initiatives across the globe have intensified efforts to fight obesity yet the declining health condition shows no signs of improvement thus scientists are developing new approaches to counteract the issue.

Science is currently studying how gut microbiome composition affects both obesity prevention and weight gain processes in people. The total number and makeup of intestinal bacteria seem to play a direct role in determining how susceptible people are to becoming obese. Scientific findings reveal that people with obesity tend to show different microorganisms in their gut than individuals who maintain a healthy weight (Peirce & Alviña, 2019). Gut microbial communities shape how the body obtains dietary energy and controls the regulation of fat storage as well as nutrient metabolism (Wu et al., 2021). Research shows that the gut microbiome impacts three obesity-developing factors namely inflammatory responses and insulin resistance together with appetite control (Li et al., 2019). More research investigation is necessary to fully understand the specific processes through which the microbiome controls obesity development.

Problem Statement

Public health experts continue to struggle with obesity prevention because intervention approaches have failed to stop the growing number of patients with obesity. Traditional weight management approaches including diets and exercise have demonstrated restricted benefits for controlling worldwide obesity. The basic weight loss methods prove insufficient because they fail to create lasting results in body mass reduction or metabolic health improvement (Tu et al., 2020). Studies confirm that gut health demonstrates vital importance in deciding whether a person becomes obese based on their microbiome composition patterns. The lack of obesity prevention and treatment by existing methods gives rise to an essential question about whether the gut microbiome serves as a valuable connection to control obesity.

Research on metabolic process regulation through the gut microbiome has become evident so scientists need to investigate the connection between particular bacterial communities and obesity development (Maher et al., 2023). Knowledge about how gut microbiota composition affects obesity resistance has the potential for developing new approaches to prevention and treatment methods especially for patients who do not succeed with traditional weight management approaches (Johnson, 2020).

Objective

The research establishes investigation into gut microbiome effects on both obesity development and prevention as its primary purpose. The study examines the biomechanisms through which the microbiota influences metabolic operations involving energy regulation and fat accumulation while controlling insulin response to understand obesity origins better. This study demonstrates that microbiome modulation presents an innovative approach for obesity treatment which the study demonstrates through its findings. Research will examine how altering the gut microbiome through interventions might become a supporting strategy in obesity treatment to achieve sustainable health results (Gopalakrishnan, 2018).

Significance

This research holds important value because it develops knowledge to develop innovative obesity prevention and treatment methods. Current obesity management methods including diet modification alongside exercise protocols and medications show restricted effectiveness in controlling obesity at a worldwide level. Research on the gut microbiome as an obesity cause enables scientists to discover new medical solutions to replace or improve current obesity treatment methods. The connection between gut microbiota and obesity gives doctors a new opportunity to prescribe personalized dietary treatments along with probiotic therapies for obesity management (Tu et al., 2020). The discovery of precise microbiome patterns linked to obesity development would enable scientists to design diagnostic systems to forecast obesity risks before treatments begin (Wu et al., 2021).

This research provides essential knowledge about gut microbiome-obesity relationships which could help build public health preventive measures to stop obesity in vulnerable groups. The research enables crucial understandings of how to stop the development of metabolic diseases associated with obesity such as diabetes and cardiovascular disease in addition to obesity itself (Peirce & Alviña, 2019).

Scope and Limitations

The investigation will examine studies involving human subjects as well as major animal testing while omitting research on both uncommon disorders and non-bacterial microbiota members such as fungi and viruses. The main emphasis will study microbial communities inside human guts along with their role in obesity formation and defense mechanisms. This research study examines both clinical and experimental animal models but primarily focuses on microbial diversity-metabolic outcome correlations and omitting investigations of obesity-altering environmental factors or disease conditions independently (Li et al., 2019). The study maintains a targeted approach to examine obesity-related microbe functions because it helps establish a well-defined knowledge base about this dynamic scientific domain. The research connection between gut microbiome study and obesity investigation has established itself as an important breakthrough in medical science. This study will explain the advanced relationship between gut health and obesity to develop better methods for obesity prevention and treatment in the ongoing struggle against obesity (Tseng & Wu, 2019). Research on this developing microbiome field will provide additional knowledge about using microbiome interventions for obesity treatment.

LITERATURE REVIEW

The Gut Microbiome Composition and Functions

A complex microbial community consisting of billions of microorganisms exists within the gut ecosystem where bacteria combine with fungi and viruses together with archaea.

Bacteria exist as the most prevalent community alongside diverse populations which sustain human wellness. The human gut microbiome contains mainly two bacterial phyla known as Firmicutes and Bacteroidetes which make up greater than 90% of microbial populations. The phyla function independently within metabolism and immune system processes and protect against pathogens. The fermentation of carbohydrates together with SCFA production including butyrate which supports gut health is chiefly managed by Firmicutes (Vaamonde & Álvarez-Món, 2020). Bacteroidetes perform the breakdown of complex polysaccharides that supports nutrient processing and helps regulate energy levels.

Host metabolism regulation happens through significant involvement of the gut microbial community. The energy balance of the host depends significantly on the microbiome due to its ability to control absorption of nutrients and extraction of energy from dietary sources. Research shows that the metabolism-related processes such as lipid breakdown and insulin response and body fat distribution get affected by the microbial diversity found in the gut (Svačina, 2020). Through an interaction with the host immune system gut bacteria achieve proper immune activation and tolerance while active response to pathogens prevents chronic inflammation (Cmrečak et al., 2020). Multiple functional roles within the gut microbiome exhibit intricate dynamics which affect metabolic wellness.

Microbiome Changes in Obesity

Dysbiosis represents the microbial imbalances that typically appear in connection with obesity. Various research studies found weight differences between obese individuals' microbial communities compared to normal-weight participants due to altered microbial compositions. The dietary energy harvest increases when obesity occurs because Firmicutes dominate the microbiome at expense of Bacteroidetes. The unbalanced microbiome triggers enhanced fat storage which plays a part in developing obesity (Sarma et al., 2021). Lean individuals maintain a healthier microbiome state through higher levels of Bacteroidetes because these microorganisms efficiently digest fiber and generate SCFAs according to Lin & Li (2021). The gut microbiota influences body weight management by determining food-derived energy retrieval rates in the body.

Obese individuals tend to have diminished microbial varieties in their bodies that connect to greater metabolic disorder risks such as insulin resistance and type 2 diabetes. Condensed gut microbial diversity washes out particular metabolic pathways that handle complex carbohydrates and generates beneficial components therefore leading to extended inflammation and metabolic breakdown (Safaei et al., 2021). Research shows that the microbiome functions as a factor which generates obesity-related medical issues.

Mechanisms Linking Microbiota to Obesity

Experts have Unmounted various hypotheses to explain the relationship between obesity and gut microbiota. The diet-based energy procurement efficiency stands out as a commonly researched mechanism. The process by which certain bacteria specifically Firmicutes extract additional calories from dietary complex carbohydrates creates more energy accessible to the host. The increased energy capture through this mechanism results in weight gain by promoting fat accumulation thus promoting obesity development (Sarma et al., 2021). The bacteria produce short-chain fatty acids while carrying out their metabolic functions and regulate how the host body stores fat along with its insulin sensitivity. Butyrate shows two beneficial effects on the human body by enhancing insulin sensitivity and decreasing fat storage in adipose tissue (Cmrečak et al., 2020).

Systemic inflammation is heavily influenced by the actions of microbiome residing in the human gut. Increased systemic levels of lipopolysaccharides (LPS) occur from "leaky gut" conditions attributed to dysbiosis. Endotoxin molecules trigger a chain reaction that

produces inflammation which results in insulin resistance and continues to advanced metabolic problems in the body (Safaei et al., 2021). Low-grade inflammation presents as a universal obesity symptom which contributes to type 2 diabetes and cardiovascular disease development.

The gut-brain axis functions as a vital mechanism which allows the microbiome to impact obesity development. The brain and gut exchange information by means of the vagus nerve along with hormonal pathways that include ghrelin and leptin to control appetite and hunger signals. The secretion of appetite-regulating hormones by the body depends on a balanced gut bacterial composition which determines food consumption levels. The brain function responds to microbiome-derived metabolites such as SCFAs when they pass through the blood-brain barrier which leads to neuroinflammatory changes that influence appetite as well as energy regulation (Lin & Li, 2021). Research shows that the intricate connection exists between microbiome in the gut and the brain and metabolic functions in the body.



Figure 1: Mechanisms Connecting Gut Microbiota to Obesity Development

Factors Affecting Gut Microbiome

Multiple causes such as the diet and antibiotics together with birth mode and genetic predisposition determine the composition of the gut microbiome. The diet greatly influences which microbial communities thrive in the gut because particular eating patterns encourage different types of bacteria to dominate. People who consume fiber-rich diets allow Bacteroidetes to thrive while Firmicutes grow more abundant in individuals following high-fat low-fiber diets (Vaamonde & Álvarez-Món, 2020). Eating foods with processed elements and high sugar content leads to an increase in bad bacteria and a decrease in useful microorganisms which might result in metabolic disorder and obesity development. The use of antibiotics remains among the main factors which negatively impact the composition of the human gut microbiome. The essential use of antibiotics for infection treatment may cause permanent changes to microbial diversity which affects their functional abilities. Studies

demonstrate that antibiotics diminish microbial diversity while rising pathogenic bacteria populations and encouraging obesity symptoms in animal subjects (Svačina, 2020).

Similarly, the mode of birth—vaginal delivery versus cesarean section—affects the initial colonization of the gut microbiome in infants. The microbial makeup of infants born through cesarean section is less diverse with inadequate metabolic health benefits thus potentially increasing their obesity risk later in life according to Cmrečak et al. (2020). Genetics controls the composition and diversity of the microbiome because studies have proven that human genetic factors can affect bacterial composition and diversity levels. The structure and functional capacity of the microbiome experience major modification due to environmental elements such as diet and lifestyle patterns because microbial communities are adaptive systems that evolve according to changing environmental conditions (Sarma et al., 2021).

Previous Interventions Targeting Microbiota

Research has advanced regarding the relationship between obesity and the gut microbiome which has prompted scientists to investigate multiple interventions for modifying the microbiome to prevent and treat obesity. The scientific literature investigates live beneficial bacterial strains known as probiotics since they show promise for restoring microbial equilibrium alongside better metabolic function. The scientific literature demonstrates that taking probiotics leads to body weight reduction together with enhanced insulin sensitivity especially for individuals suffering from obesity (Lin & Li, 2021). Research about probiotics and weight loss outcomes remains indeterminable therefore scientists need to determine optimal strains together with their dosage levels for maximum effectiveness. The field of obesity management includes research on prebiotics as food components that help beneficial microbes grow in the body. The addition of foods rich in fibers and plant compounds functions as prebiotics because they specifically activate beneficial bacterial growth including Bacteroidetes to enhance both gut functions and metabolic processes (Vaamonde & Álvarez-Món, 2020).

Additional research needs to be conducted to determine how well prebiotics help individuals lose weight or stop them from becoming obese. The medical treatment method Fecal microbiota transplantation (FMT) shows promise as a weight management solution for people with obesity. The procedure of FMT requires a donor to provide stool to patients with obesity so they can regain their ideal bacterial composition in their digestive system. Multiple first-stage animal research combined with initial small human trials demonstrate positive findings that lead to improvements in metabolism and weight control function. The long-term effects of FMT on obesity remain unclear because further clinical tests must demonstrate its safety and performance (Sarma et al., 2021). Research indicates that microbial imbalances together with gut-brain axis dysfunction and increased energy harvest efficiency and inflammation contribute to obesity both during formation and as a prevention mechanism. Metabolic health faces alterations through changes in microbiome structure that result from diet alongside antibiotics along with birth mode and genetic elements. Future research needs to evaluate how probiotics, prebiotics and FMT work in combination to treat obesity but these approaches show potential as therapeutic approaches for managing obesity.

RESEARCH METHODOLOGY

The research uses a systematic review with meta-analysis to provide an in-depth examination of research studies about gut microbiota and obesity. The research intends to gather key results while filling knowledge gaps and distinguishing established patterns through the synthesis of clinical trials peer-reviewed articles along with meta-analyses. Research data for this study will be retrieved from scientific databases including PubMed,

Scopus, and Web of Science through specific criteria that promote relevance and quality. The analytical research evaluates effects through calculations of quantitative measures together with microbiome profiling and separation of data across key populations. The proposal includes proper ethical conduct for all experimental study references.

Study Design

This investigation employs a systematic review together with meta-analysis methodology to evaluate and analyze academic research linking gut microbiota to obesity results. Research studies about gut microbiota and obesity show their complexity and variety so comparing this literature gives an extensive understanding of microbiota effects on obesity development and prevention. The framework of this systematic review contains a methodical selection and combination of peer-reviewed scholarly works together with clinical trials and meta-analyses about microbiome composition effects on obesity. The analysis of this research seeks to present the main observations together with research findings and areas needing further exploration in existing studies. The research will utilize statistical methods to aggregate multiple research findings through meta-analysis which provides an advanced method for calculating the effect size of gut microbiota on obesity (Geng et al., 2022).

If more experimental confirmation becomes necessary then researchers can design either animal or human studies. The study would modify gut microbiota compositions by using dietary modification and probiotic supplements to examine their influence on obesity elements including weight changes and body fat patterns in addition to insulin resistance changes. The study of causal relations and gut microbiota's obesity effects becomes more feasible due to experimental approaches that grant greater control over investigation (Liu & Wang, 2021). We will center our research on reviewing previously published literature to determine microbiome functions in obesity processes.

Data Sources

The systematic review and meta-analysis draws its data from three extensively trusted scientific databases namely PubMed, Scopus, and Web of Science. The established peer-reviewed research collections in PubMed along with Scopus and Web of Science present high-quality material about microbiota and obesity outcomes. Strong impact factor journals will be prioritized for data analysis because they yield only the best validated research findings (Harbuwono et al., 2018). The analysis includes studies from present and past periods to establish a full grasp of how research attitudes towards this area have developed alongside the stability of obtained results throughout time.

The initial search approach combines particular keywords which consist of "gut microbiota" alongside "obesity" and also "microbial diversity" together with "intestinal flora" and finally "metabolic disorders." The research will include clinical trials together with randomized controlled trials which focus on interventions for gut microbiota manipulation to establish the cause-effect links between gut health and obesity outcomes (Smith & Smith, 2016).

Inclusion/Exclusion Criteria

The research study will analyze articles that explore the connection between gut microbiota and obesity but no other information. Research studies which analyze dietary interventions and microbe modifications alongside probiotic or prebiotic supplementation or other intervention methods for weight prevention or treatment will receive top priority. The research includes examinations conducted in human subjects and major animal models similar to rodents in order to achieve findings suitable for human health (Nussbaumerova & Rosolova, 2023).

The research will discard studies focusing on microbiota that does not connect with obesity including investigations of uncommon diseases or microorganisms from sources beyond bacteria (including fungi or viruses). The evaluation excludes research that treats obesity as unrelated to metabolic disorders and does not report findings on obesity. The research excludes all observational analysis which lacks detailed mechanistic information regarding microbial influence on obesity (Jiang & Liu, 2016).

Analytical Methods

Quantitative Meta-Analysis:

A meta-analysis should establish the total impact of microbiota makeup on obesity results.

• Compare microbial diversity and abundance between obese and non-obese individuals.

The researchers will determine effect sizes by employing either Cohen's d or Hedges' g statistical measures based on data classification (Kansra et al., 2021).

Gut Microbiota Profiling:

Researchers should employ 16S rRNA sequencing as a sophisticated method for microbiota analysis.

The research investigates gut microbial diversity together with composition to recognize particular bacterial species or bacterial clusters linked to obesity according to Geng et al. (2022).

Research has detected obesity-related patterns in microbiota composition which help discover therapeutic possibilities for the condition.

Subgroup Analyses:

Research should analyze data according to population subgroups determined by elements like age groups, gender demographics and dietary choices and regional locations.

The researchers should explore distinct responses from different population groups to microbiota-based intervention plans (Liu & Wang, 2021).

Ethical Considerations

A request for ethical approval will be directed to appropriate institutional review boards (IRBs) or ethics committees before performing experimental studies on animals or humans. The study obtains consent from human participants to inform them about all essential aspects of their research involvement including its goals and procedures together with hazard information. A strict adherence to ethical principles for animal welfare will guide the study design and all procedures and researchers will implement experiments to decrease animal suffering and distress. All experimental interventions including probiotic supplementation alongside dietary modifications will comply with recognized ethical standards for human along with animal research (Smith & Smith, 2016).

Table 1. Inclusion and Exclusion Criteria for Study Selection	
Inclusion Criteria	Exclusion Criteria
Studies focusing on gut microbiota and obesity	Studies unrelated to obesity
Human and major animal model studies	Studies on rare conditions or non-
	bacterial microbiota
Studies with clear mechanistic insights	Studies lacking causal or mechanistic
	evidence

 Table 1: Inclusion and Exclusion Criteria for Study Selection

RESULTS AND DISCUSSION

Results

Scientists now understand obesity better through the study of gut microbiome effects on obesity pathogenesis thanks to vital discoveries regarding bacterial-obesity connection research. Scientific studies show that people with obesity present unique microbial communities which differ from standard weight individuals. The composition changes to microbiota frequently display decreased microbial diversity which represents a typical condition across metabolic disorders (Berg, 2021). The Firmicutes-to-Bacteroidetes ratio shows consistent increases according to research evidence and this change is correlated with enhanced food energy acquisition by the host along with elevated fat storage (Deehan et al., 2020). Studies have shown two important discoveries about specific microorganisms including *Faecalibacterium prausnitzii* and *Bacteroides* and *Lactobacillus* which seem to affect obesity risk and metabolic results (Schmidt et al., 2018).

The major breakthrough in modern research reveals microbial metabolites known as short-chain fatty acids (SCFAs) because they regulate both inflammation and insulin resistance. Scientific evidence reveals that perturbed levels of metabolites play a part in establishing obesity-linked medical problems including type 2 diabetes and cardiovascular disease (Knisely et al., 2023). The gut microbiota influences both gut-brain signaling that controls appetite regulation and food intake which contribute to obesity formation (Bongers et al., 2022).

Key Findings	Microbial Shifts in Obesity
Identified dysbiosis in obese individuals.	Increase in Firmicutes; decrease in
	Bacteroidetes
Increased SCFA production is linked to	Decreased Faecalibacterium prausnitzii
obesity-related inflammation.	
Firmicutes-to-Bacteroidetes ratio	Increased Firmicutes, reduced Bacteroidetes.
associated with obesity.	
Gut microbiota influence on appetite and	Alterations in Lactobacillus and Bacteroides
food intake.	species
Dysbiosis and metabolic dysfunction	Lower SCFA production, high inflammation
were observed in the obese groups.	markers

Table 2: Summary of Key Microbial Shifts and Findings Associated with Obesity

Discussion

Interpretation of Findings

The results from these research studies confirm an established relationship between obesity incidence and modifications of gut microbiota composition. Obese individuals show higher ratios of Firmicutes-to-Bacteroidetes along with potential microbial communities that extract food energy more efficiently thus leading to increased fat storage (Paetzold et al., 2019). The reduced abundance of anti-inflammatory molecule producer *Faecalibacterium prausnitzii* affects metabolic health and immune regulation because it fails to produce SCFAs (Schmidt et al., 2018). The research shows that metabolic disorders along with systemic inflammation and insulin resistance and appetite regulation defects develop as a result of gut dysbiosis in addition to its known effect on energy harvesting (Berg, 2021).

Evidence shows a decrease in microbial diversity levels in people with obesity stresses the need to maintain healthy gut microbial populations for building metabolic wellness. Studies indicate that microbial communities with diverse strains help create strong immunity

and help perform many metabolic operations (Bongers et al., 2022). During obesity metabolic dysfunction likely becomes more severe because diversity loss complicates bodily processes which sustain the condition.

Potential for Microbiome-Targeted Therapies

These research outcomes shed light on the great opportunity that exists for microbiomebased treatments to tackle obesity. Diet modification through high-fiber and prebiotic diets shows evidence of improving gut microbial diversity while encouraging beneficial bacterial growth according to Deehan et al. (2020). Scientists have investigated single-strained bacteria known as probiotics as possible treatments for obesity because these bacteria demonstrate health benefits when humans consume them. The research demonstrates that particular probiotic strains minimize body weight and enhance metabolic indicators through their ability to modify gut microbiota composition and produce short-chain fatty acids (SCFAs) (Knisely et al., 2023). Medical experts explore fecal microbiota transplantation (FMT) as a modern therapeutic method to treat obesity by using healthy donor fecal matter for microbe restoration in the gastrointestinal tract. Fecal transplant procedures at their experimental stage indicate they might generate moderate weight reduction in addition to enhanced metabolic health functions (Bongers et al., 2022).

Next-generation probiotics currently get developed to focus on particular metabolic pathways which offer obesity patients a better and individualized treatment approach. Research indicates that microbiome-modulating probiotics could serve as a targeted solution to grow beneficial metabolically active species for weight control (Schmidt et al., 2018).

Challenges and Controversies

However, despite the promising potential of microbiome-based therapies, several challenges and controversies remain. One major issue is the significant individual variability in microbiome composition, which complicates the development of universal treatments. People's microbiomes are shaped by various factors, including genetics, diet, environment, and lifestyle, leading to vast differences in microbial profiles even among individuals with similar body types (Paetzold et al., 2019). This variability makes it challenging to establish standardized interventions that will be effective for all individuals.

Furthermore, the causality of the relationship between gut microbiota and obesity remains unclear. While numerous studies have observed associations between microbial dysbiosis and obesity, it is still not definitively proven that these changes in microbiota directly cause obesity. Longitudinal studies and more advanced research designs are needed to establish causality (Deehan et al., 2020).

Comparison with Other Studies

When comparing these findings with those of other studies, some common themes emerge, but also notable differences. For example, many studies, including those by Paetzold et al. (2019) and Deehan et al. (2020), report a similar increase in Firmicutes and a decrease in Bacteroidetes in obese individuals, reinforcing the idea of a gut microbiome imbalance contributing to obesity. However, other research, such as that by Berg (2021), has suggested that the connection between microbiome composition and obesity may be more complex, with specific microbial shifts being influenced by age, geography, and lifestyle. These discrepancies highlight the need for further research to understand the intricate relationship between gut microbiota and obesity.

CONCLUSION AND RECOMMENDATIONS

Conclusion

The gut microbiome has emerged as a critical factor in developing and preventing obesity. Evidence consistently shows that the composition and diversity of gut bacteria play a significant role in regulating metabolism, energy balance, and fat storage. Research indicates that individuals with obesity often have distinct gut microbiome profiles, which contribute to inefficient energy extraction, increased fat storage, and altered metabolic processes (Venegas et al., 2019; Tomás-Pejó et al., 2023). These microbiota imbalances also affect inflammation, insulin resistance, and appetite regulation, all key contributors to obesity (Yoo et al., 2020).

Significant insights confirm that gut microbiota composition is dynamic and influenced by diet, lifestyle, and environmental factors. This presents opportunities for therapeutic interventions aimed at restoring a healthy microbiome (Ratajczak et al., 2019). Restoring microbial balance could help mitigate obesity-related conditions and improve metabolic health. However, significant gaps remain in fully understanding the mechanisms and the most effective interventions (Morales Fénero et al., 2021).

Recommendations

Research initiatives should concentrate on creating individualized microbiome treatments while establishing microbial patterns that relate to obesity alongside developments of focused therapeutic strategies. The effectiveness of obesity treatments becomes better when therapy is personalized and when probiotics receive individualized doses as well as prebiotics together with customized dietary plans (Łoniewska et al., 2023). Exciting research progress revolves around the gut-brain axis because this connection regulates appetite along with energy expenditure which are vital elements for treating obesity (Stojanov et al., 2020). The public health goal should focus on implementing feeding plans containing fiber together with prebiotics as well as fermented foods. The mentioned diets foster diverse microbial populations that show promise in fighting obesity (Tomás-Pejó et al., 2023). Public health programs need to teach citizens about gut well-being and teach better eating habits to stop obesity from growing. Healthcare providers must establish a routine practice of including gut microbiome testing during their obesity treatment protocols for better tailored patient care. The regular assessment of microbiomes through testing provides valuable information that helps doctors determine dietary and probiotic strategies to aid weight reduction (Yoo et al., 2020).

Extended clinical research involving many participants will verify microbiome-based treatment safety and lasting effectiveness throughout different population types. The evaluation of microbiome functions in obesity creates innovative opportunities to fight the condition as well as prevent its development. Gaining control of obesity will become possible through targeted therapeutic methods combined with nutritional strategies that improve gut wellness thus allowing better solutions against worldwide weight issues.

REFERENCES

- Baek, G. H., Yoo, K. M., Kim, S. Y., Lee, D. H., Chung, H., Jung, S. C., ... Kim, J. S. (2023). Collagen Peptide Exerts an Anti-Obesity Effect by Influencing the Firmicutes/ Bacteroidetes Ratio in the Gut. *Nutrients*, 15(11). <u>https://doi.org/10.3390/nu15112610</u>
- Berg, G., Kusstatscher, P., Abdelfattah, A., Cernava, T., & Smalla, K. (2021, April 8). Microbiome Modulation—Toward a Better Understanding of Plant Microbiome Response to Microbial Inoculants. *Frontiers in Microbiology*, 12, 650610. <u>https://doi.org/10.3389/fmicb.2021.650610</u>
- Bongers, K. S., McDonald, R. A., Winner, K. M., Falkowski, N. R., Brown, C. A., Baker, J. M., ... Dickson, R. P. (2022). Antibiotics cause metabolic changes in mice primarily through microbiome modulation rather than behavioral changes. *PLoS ONE*, 17(3). <u>https://doi.org/10.1371/journal.pone.0265023</u>
- Cmrečak, F., Andrašek, I., Gregov, V., & Beketić-Orešković, L. (2020). Obesity and cancer. *Libri Oncologici*, 48(2–3), 89–102. <u>https://doi.org/10.20471/LO.2020.48.02-03.16</u>
- Deehan, E. C., Yang, C., Perez-Muñoz, M. E., Nguyen, N. K., Cheng, C. C., Triador, L., ... Walter, J. (2020). Precision Microbiome Modulation with Discrete Dietary Fiber Structures Directs Short-Chain Fatty Acid Production. *Cell Host and Microbe*, 27(3), 389-404.e6. <u>https://doi.org/10.1016/j.chom.2020.01.006</u>
- Eindor-Abarbanel, A., Healey, G. R., & Jacobson, K. (2021, November 1). Therapeutic advances in gut microbiome modulation in patients with inflammatory bowel disease from pediatrics to adulthood. *International Journal of Molecular Sciences*, 22(22), 12506. <u>https://doi.org/10.3390/ijms222212506</u>
- Geng, J., Ni, Q., Sun, W., Li, L., & Feng, X. (2022, March 1). The links between gut microbiota and obesity and obesity related diseases. *Biomedicine and Pharmacotherapy*, 147, 112678. <u>https://doi.org/10.1016/j.biopha.2022.112678</u>
- Gopalakrishnan, V., Helmink, B. A., Spencer, C. N., Reuben, A., & Wargo, J. A. (2018, April 9). The Influence of the Gut Microbiome on Cancer, Immunity, and Cancer Immunotherapy. *Cancer Cell*, 33(4), 570-580. <u>https://doi.org/10.1016/j.ccell.2018.03.0</u> <u>15</u>
- Harbuwono, D. S., Pramono, L. A., Yunir, E., & Subekti, I. (2018). Obesity and central obesity in Indonesia: Evidence from a national health survey. *Medical Journal of Indonesia*, 27(2), 53–59. <u>https://doi.org/10.13181/mji.v27i2.1512</u>
- Jiang, S. Z., Lu, W., Zong, X. F., Ruan, H. Y., & Liu, Y. (2016, October 1). Obesity and hypertension. *Experimental and Therapeutic Medicine*, 12(4), 2395-2399. <u>https://doi.org/10.3892/etm.2016.3667</u>
- Johnson, K. V. A. (2020). Gut microbiome composition and diversity are related to human personality traits. *Human Microbiome Journal*, *15*, 100069. <u>https://doi.org/10.1016/j.humic.2019.100069</u>
- Kansra, A. R., Lakkunarajah, S., & Jay, M. S. (2021, January 12). Childhood and Adolescent Obesity: A Review. Frontiers in Pediatrics, 8. <u>https://doi.org/10.3389/fped.2020.58146</u> <u>1</u>
- Knisely, A., Seo, Y. D., Wargo, J. A., & Chelvanambi, M. (2023, February 1). Monitoring and Modulating Diet and Gut Microbes to Enhance Response and Reduce Toxicity to Cancer Treatment. *Cancers*, 15(3), 777. <u>https://doi.org/10.3390/cancers15030777</u>
- Leeuwendaal, N. K., Stanton, C., O'toole, P. W., & Beresford, T. P. (2022, April 1). Fermented Foods, Health and the Gut Microbiome. *Nutrients*, 14(7), 1527. <u>https://doi.org/10.3390/nu14071527</u>

- Li, W., Deng, Y., Chu, Q., & Zhang, P. (2019, April 10). Gut microbiome and cancer immunotherapy. *Cancer Letters*, 447, 41-47. <u>https://doi.org/10.1016/j.canlet.2019.01.0</u> 15
- Lin, X., & Li, H. (2021, September 6). Obesity: Epidemiology, Pathophysiology, and Therapeutics. Frontiers in Endocrinology, 12. <u>https://doi.org/10.3389/fendo.2021.7069</u> 78
- Liu, B. N., Liu, X. T., Liang, Z. H., & Wang, J. H. (2021, July 7). Gut microbiota in obesity. *World Journal of Gastroenterology*, 27(25), 3837-3850. <u>https://doi.org/10.3748/wjg.v27.i25.3837</u>
- Łoniewska, B., Fraszczyk-Tousty, M., Tousty, P., Skonieczna-Żydecka, K., Maciejewska-Markiewicz, D., & Łoniewski, I. (2023). Analysis of Fecal Short-Chain Fatty Acids (SCFAs) in Healthy Children during the First Two Years of Life: An Observational Prospective Cohort Study. *Nutrients*, 15(2). <u>https://doi.org/10.3390/nu15020367</u>
- Machireddy, J. (2023). Automation in Healthcare Claims Processing: Enhancing Efficiency and Accuracy. *International Journal of Science and Research Archive*, 09(01), 825-834. <u>http://dx.doi.org/10.2139/ssrn.5159747</u>
- Machireddy, J. R. (2024). Machine learning and automation in healthcare claims processing. *Journal of Artificial Intelligence*, 6(1), 686-701.
- Magne, F., Gotteland, M., Gauthier, L., Zazueta, A., Pesoa, S., Navarrete, P., & Balamurugan, R. (2020, May 1). The firmicutes/bacteroidetes ratio: A relevant marker of gut dysbiosis in obese patients? *Nutrients*, 12(5), 1474. <u>https://doi.org/10.3390/nu12051474</u>
- Maher, S. E., O'Brien, E. C., Moore, R. L., Byrne, D. F., Geraghty, A. A., Saldova, R., ... McAuliffe, F. M. (2023, May 14). The association between the maternal diet and the maternal and infant gut microbiome: A systematic review. *British Journal of Nutrition*, 129(9), 1491-1499. <u>https://doi.org/10.1017/S0007114520000847</u>
- Morales Fénero, C., Amaral, M. A., Xavier, I. K., Padovani, B. N., Paredes, L. C., Takiishi, T., ... Saraiva Câmara, N. O. (2021). Short-chain fatty acids (SCFAs) improve TNBSinduced colitis in zebrafish. *Current Research in Immunology*, 2, 142–154. <u>https://doi.org/10.1016/j.crimmu.2021.08.003</u>
- Nussbaumerova, B., & Rosolova, H. (2023, December 1). Obesity and Dyslipidemia. *Current Atherosclerosis Reports*, 25, 947–955. <u>https://doi.org/10.1007/s11883-023-01167-2</u>
- Paetzold, B., Willis, J. R., Pereira De Lima, J., Knödlseder, N., Brüggemann, H., Quist, S. R., ... Güell, M. (2019). Skin microbiome modulation induced by probiotic solutions. *Microbiome*, 7(1). <u>https://doi.org/10.1186/s40168-019-0709-3</u>
- Peirce, J. M., & Alviña, K. (2019, October 1). The role of inflammation and the gut microbiome in depression and anxiety. *Journal of Neuroscience Research*, 97(10), 1223-1241. <u>https://doi.org/10.1002/jnr.24476</u>
- Quagebeur, R., Dalile, B., Raes, J., Van Oudenhove, L., Verbeke, K., & Vrieze, E. (2023). The role of short-chain fatty acids (SCFAs) in regulating stress responses, eating behavior, and nutritional state in anorexia nervosa: protocol for a randomized controlled trial. *Journal of Eating Disorders*, 11(1). <u>https://doi.org/10.1186/s40337-023-00917-6</u>
- Ratajczak, W., Rył, A., Mizerski, A., Walczakiewicz, K., Sipak, O., & Laszczyńska, M. (2019). Immunomodulatory potential of gut microbiome-derived short-chain fatty acids (SCFAs). *Acta Biochimica Polonica*, 66(1), 1–12. <u>https://doi.org/10.18388/abp.2018_2648</u>

- Rauf, A., Khalil, A. A., Rahman, U. ur, Khalid, A., Naz, S., Shariati, M. A., ... Rengasamy, K. R. R. (2022). Recent advances in the therapeutic application of short-chain fatty acids (SCFAs): An updated review. *Critical Reviews in Food Science and Nutrition*, 62(22), 6034–6054. <u>https://doi.org/10.1080/10408398.2021.1895064</u>
- Safaei, M., Sundararajan, E. A., Driss, M., Boulila, W., & Shapi'i, A. (2021, September 1). A systematic literature review on obesity: Understanding the causes & consequences of obesity and reviewing various machine learning approaches used to predict obesity. *Computers in Biology and Medicine*, 136, 104754. <u>https://doi.org/10.1016/j.compbiomed.2021.104754</u>
- Sarma, S., Sockalingam, S., & Dash, S. (2021, February 1). Obesity as a multisystem disease: Trends in obesity rates and obesity-related complications. *Diabetes, Obesity, and Metabolism, 23*(S1), 3-16. <u>https://doi.org/10.1111/dom.14290</u>
- Schmidt, T. S. B., Raes, J., & Bork, P. (2018, March 8). The Human Gut Microbiome: From Association to Modulation. *Cell*, 172(6), 1198-1215. <u>https://doi.org/10.1016/j.cell.2018</u> .02.044
- Sharif, K. S., Abubakkar, M., Uddin, M. M., & Arefin Khaled, A. M. (2024). A Comparative Framework Integrating Hybrid Convolutional and Unified Graph Neural Networks for Accurate Parkinson's Disease Classification. 2024 7th International Seminar on Research of Information Technology and Intelligent Systems (ISRITI), Yogyakarta, Indonesia, 2024, pp. 31-37. <u>https://doi.org/10.1109/ISRITI64779.2024.10963443</u>
- Sharif, K. S., Uddin, M. M., & Abubakkar, M. (2024). NeuroSignal Precision: A Hierarchical Approach for Enhanced Insights in Parkinson's Disease Classification. 2024 International Conference on Intelligent Cybernetics Technology & Applications (ICICyTA), Bali, Indonesia, 2024, pp. 1244-1249. https://doi.org/10.1109/ICICYTA64807.2024.1091290
- Smith, K. B., & Smith, M. S. (2016, March 1). Obesity Statistics. *Primary Care: Clinics in Office Practice*, 43(1), 121-135. <u>https://doi.org/10.1016/j.pop.2015.10.001</u>
- Stojanov, S., Berlec, A., & Štrukelj, B. (2020, November 1). The influence of probiotics on the firmicutes/bacteroidetes ratio in treating obesity and inflammatory bowel disease. *Microorganisms*, 8(11), 1715. <u>https://doi.org/10.3390/microorganisms8111715</u>
- Svačina, Š. (2020). Obesity and cardiovascular disease. *Vnitrni Lekarstvi*, 66(2), 89–91. https://doi.org/10.1161/01.atv.0000216787.85457.f3
- Tomás-Pejó, E., González-Fernández, C., Greses, S., Kennes, C., Otero-Logilde, N., Veiga, M. C., ... Passoth, V. (2023, December 1). Production of short-chain fatty acids (SCFAs) as chemicals or substrates for microbes to obtain biochemicals. *Biotechnology for Biofuels and Bioproducts*, 16, 96. <u>https://doi.org/10.1186/s13068-023-02349-5</u>
- Tseng, C. H., & Wu, C. Y. (2019, March 1). The gut microbiome in obesity. Journal of the Formosan Medical Association, 118(S1), S3-S9. <u>https://doi.org/10.1016/j.jfma.2018.07</u> .009
- Tu, P., Chi, L., Bodnar, W., Zhang, Z., Gao, B., Bian, X., ... Lu, K. (2020, March 1). Gut microbiome toxicity: Connecting the environment and gut microbiome-associated diseases. *Toxics*, 8(1), 19. <u>https://doi.org/10.3390/toxics8010019</u>
- Vaamonde, J. G., & Álvarez-Món, M. A. (2020). Obesity and overweight. *Medicine (Spain)*, 13(14), 767–776. <u>https://doi.org/10.1016/j.med.2020.07.010</u>
- Venegas, D. P., De La Fuente, M. K., Landskron, G., González, M. J., Quera, R., Dijkstra, G., ... Hermoso, M. A. (2019). Short chain fatty acids (SCFAs) mediated gut epithelial

and immune regulation and their relevance for inflammatory bowel diseases. *Frontiers in Immunology, 10.* <u>https://doi.org/10.3389/fimmu.2019.00277</u>

- Wu, J., Wang, K., Wang, X., Pang, Y., & Jiang, C. (2021, May 1). The role of the gut microbiome and its metabolites in metabolic diseases. *Protein and Cell*, 12(5), 360-373. <u>https://doi.org/10.1007/s13238-020-00814-7</u>
- Yoo, J. Y., Groer, M., Dutra, S. V. O., Sarkar, A., & McSkimming, D. I. (2020, October 1). Gut microbiota and immune system interactions. *Microorganisms*, 8(10), 1587. <u>https://doi.org/10.3390/microorganisms8101587</u>