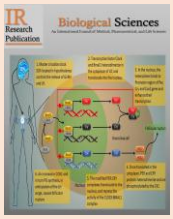
REVIEW ARTICLE

Biological Sciences
(An International Journal of Medical, Pharmaceutical, and Life Sciences)

Journal home: https://irrespub.com/biolsciences/index.php/1/index



Developing an Omics-Driven Computational Framework for Next-Generation Microbiome Therapeutics

Amina Abdulhamid Ahmed*, Ummulkhair Adamu Yusuf, Zainab Hussein Fadlallah, Musa Ojeba Innocent, Mustapha Abdulsalam

Department of Microbiology, School of Science and Information Technology, Skyline University Nigeria

ARTICLE HISTORY

Received: 01-11-2024
Revised: 12-12-2024
Accepted: 15-12-2024
Online: 19-12-2024

KEYWORDS

Microbiome
Omics Technologies
Computational Drug Design
Therapeutics
Research Gaps

ABSTRACT

The human microbiome is critical for health and disease, influencing multiple physiological systems and contributing to a variety of diseases. Advances in omics technologies—including genomes, transcriptomics, proteomics, and metabolomics—have considerably deepened our understanding of the complexity of the microbiome and its interactions with host systems. This study explores the integration of these omics approaches into computational frameworks for the design and discovery of next-generation microbiome therapeutics. Current advancements and case studies highlight the potential of omics-driven methodologies to uncover novel therapeutic targets and enhance the efficacy of microbiome-based interventions. Moreso, critical research gaps in the field are identified, such as the need for more robust data integration techniques and the exploration of unexplored microbial metabolites. Addressing these gaps is essential for advancing microbiome therapeutics and developing personalized medicine strategies. Ultimately, this study underscores the transformative potential of an omics-driven computational framework in revolutionizing the landscape of microbiome-based therapeutics.

**Address for correspondence*
Department of Microbiology, School of Science and Information Technology, Skyline University Nigeria
Email: aminahahmad2003@gmail.com
DOI: https://doi.org/10.55006/biolsciences.2024.4408
Published by IR Research Publication; Copyright ©
2024 by Authors is licensed under CC BY 4.0

Introduction

Microbiome therapeutics is a category of approach with a scope of treating diseases and promoting health by generally manipulating microbiome in human. The human microbiome is defined as a complex community of microorganisms which as bacterial, viral, fungal and archaeal origin and inhabiting the diverse regions of the human body, with an emphasis on the gastrointestinal tract. This microbiota contributes greatly to many aspects of physiological functions including digestive and metabolic functions, immune system, and neurological functions and activities of the brain (1). The interactions of microbes within the host can modulate the host's defenses against pathogens, inflammation, and maybe even homeostasis (2). These conditions are developed from various precursors which distort the biotic equilibrium,

genetic proclivity, environments and lifestyle choices and more.

Modern management strategies aim to enhance the ratio of beneficial bacteria to harmful ones and improve the availability of therapeutic options for patients. Probiotics, which are live bacteria that can be ingested to help restore beneficial bacteria in the body, are an affordable option for this purpose. Prebiotics, on the other hand, are indigestible substances in foods that selectively promote the growth of friendly microorganisms. Another important advancement is fecal microbiota transplantation (FMT), which involves transferring intestinal bacteria from a healthy donor to a patient, thereby restoring the functionality and integrity of the microbiome. These approaches focus on addressing dysbiosis to improve microbial stability and host health (3). With each new finding linking the microbiome to various health disorders, microbiome therapeutics are becoming a crucial aspect of medicine, offering potential for disease prevention and treatment through microbiome manipulation.

Genomics, transcriptomics, proteomics, and metabolomics—-omics techniques are crucial in understanding the dynamic interactions in the microbiome as well as the microbiome and host. These tools enable higher resolution of microbial and functional characterizations, which helps identify target microbial and metabolites related to health and diseases (4). For instance, metagenomics allows assessing the gene content from environmental samples and recognizing the complexity of microbial populations in the microbiota (5). In addition, the transcriptomic and proteomic data elucidate the functional contribution of particular microbial taxa and their metabolic processes along with the potential for designing effective treatments focused on specific microbial targets (6).

This study aims to synthesize current knowledge on the integration of omics technologies into the design and discovery of microbiome therapeutics. By exploring recent advancements and case studies, the study will highlight the potential of omics-driven methodologies to uncover novel therapeutic targets and enhance the efficacy of microbiome-based interventions. Moreso, it will identify critical research gaps within the field, such as the need for more robust data integration techniques and the exploration of unexplored microbial metabolites. Ultimately, the study seeks to provide a comprehensive overview of how an omics-driven computational framework can revolutionize the landscape of microbiome therapeutics, thus advancing personalized medicine strategies.

Understanding the microbiome

Microbiome can therefore be defined as the microbial DNA found in a specific environment, preferably within human beings (7). It mainly consist of the bacteria, Archaea, viruses, Fungi, Protozoa and the largest part of microbiome is gut microbiome. The microbial species are different from each other, associated with the genetics, diet, and age of the individual, and his/her history of exposure (8). It is commonly accepted that the human microbiome is comprised of trillions of microorganisms and that the total microbial biomass of the human body is at least in the same ball park as the total biomass of human cells (9). This highly diverse population is critical for modulation of the physiological condition and for performing several vital processes.

Role of the microbiome in human health

The human microbiome plays important roles in many aspects of the tenants of health, including digestion metabolism as well as immunologic function. It facilitates the splitting of complex carbohydrates, and production of short-chain fatty acids, which selectively serve as energy sources to colonocytes and contain anti-inflammatory properties (10). Furthermore, the microbiome regulates the immune system by boosting immune cell growth and regulating immunological responses, helping the body defend itself against infections (11). So, more evidence suggests that the microbiome influences mood and behavior via the gut-brain axis (12). Overall, sustaining health and preventing disease requires a well-balanced microbiome.

Dysbiosis and disease associations

Dysbiosis refers to an overall disruption in the microbiome or disruption of its normal phsysiological processes or inability to perform the required physiological functions in the right manner possibly resulting in adverse effects on health. It has been associated with such diseases as IBD, obesity, diabetes, allergy, and neurodegenerative diseases (13). For instance, in IBD, alterations in the gut microbiota diversity and composition have been observed, often correlating with disease severity (8). Similarly, obesity has been linked to a decreased diversity of gut microbiota and an overrepresentation of certain bacterial taxa, which may influence energy metabolism and fat storage (14). Understanding the mechanisms underlying dysbiosis and its association with various diseases is critical for developing microbiome-based therapeutic strategies.

Table 1. Health conditions associated with dysbiosis and specific microbial taxa

Health Condition	Associated Microbial Taxa	Description of Dysbiosis
Inflammatory Bowel Disease (IBD)	Decrease in *Firmicutes* (e.g., *Faecalibacterium prausnitzii*); Increase in *Proteobacteria*	Reduced anti-inflammatory bacteria and increased pro-inflammatory bacteria in the gut.
Obesity	Increase in *Firmicutes*; Decrease in *Bacteroidetes*	An altered Firmicutes-to-Bacteroidetes ratio, promoting energy harvest and fat deposition.
Type 2 Diabetes	Increase in *Prevotella*, *Bacteroides*, and *Clostridium* species	Altered gut microbiota composition, contributing to insulin resistance and metabolic changes.
Irritable Bowel Syndrome (IBS)	Increase in *Proteobacteria* (e.g., *Escherichia coli*); Decrease in *Lactobacillus* and *Bifidobacterium*	Disrupted microbial balance leading to gastrointestinal discomfort and altered motility.
Cardiovascular Disease	Increase in *TMAO-producing bacteria* (e.g., *Lachnospiraceae*, *Enterobacteriaceae*)	Gut microbes producing trimethylamine N-oxide (TMAO), which is linked to atherosclerosis.
Allergies	Decrease in *Bifidobacterium* and *Lactobacillus*	Lower diversity in gut microbiota, impairing immune regulation and increasing allergic responses.
Autism Spectrum Disorders (ASD)	Increase in *Clostridia* species; Decrease in *Bacteroides*	Imbalance in gut bacteria associated with gastrointestinal symptoms and behavioral changes.
Colorectal Cancer	Increase in *Fusobacterium nucleatum* and *Bacteroides fragilis*	Dysbiosis promoting inflammation and bacterial genotoxins contributing to tumor development.
Non-Alcoholic Fatty Liver Disease (NAFLD)	Increase in *Firmicutes* and *Proteobacteria*; Decrease in *Bacteroidetes*	Dysbiosis leading to endotoxin release and liver inflammation, promoting liver disease.

Omics technologies in microbiome research

Omics tools have transformed microbiome research by allowing for detailed analysis of microbial communities at multiple levels of biological organization. These technologies offer insights into the structure, function, and dynamics of microbiomes, allowing for a better understanding of their roles in both wellness and disease.

Genomics

Genomics research concentrates on the entire genome of living organisms, involving DNA sequencing and subsequent analysis of the results. In microbiome studies, metagenomic techniques are utilized to investigate genes in microbial population samples from various environments, including the human gastrointestinal tract (15). Illumina and nanopore sequencing have significantly advanced genomics by delivering detailed data on microbial taxa, taxonomy, and functional capabilities (16). Genomic data can reveal the presence of specific genes associated with metabolic pathways, antibiotic resistance, and virulence factors, thereby enhancing the understanding of how these microorganisms contribute to health and disease.

Transcriptomics

Transcriptomics examines RNA transcripts produced by organisms under specific situations to get insights into gene expression and control. Transcriptomic approaches, such as RNA sequencing (RNA-seq), enable microbiome researchers to examine microbial gene expression in response to a variety of environmental stimuli, including food, host interactions, and disease states (17). This data is essential for understanding the functional dynamics of microbial communities and their roles in metabolic processes. Researchers can better understand how changes in the microbiome affect host physiology and disease progression by finding differentially expressed genes.

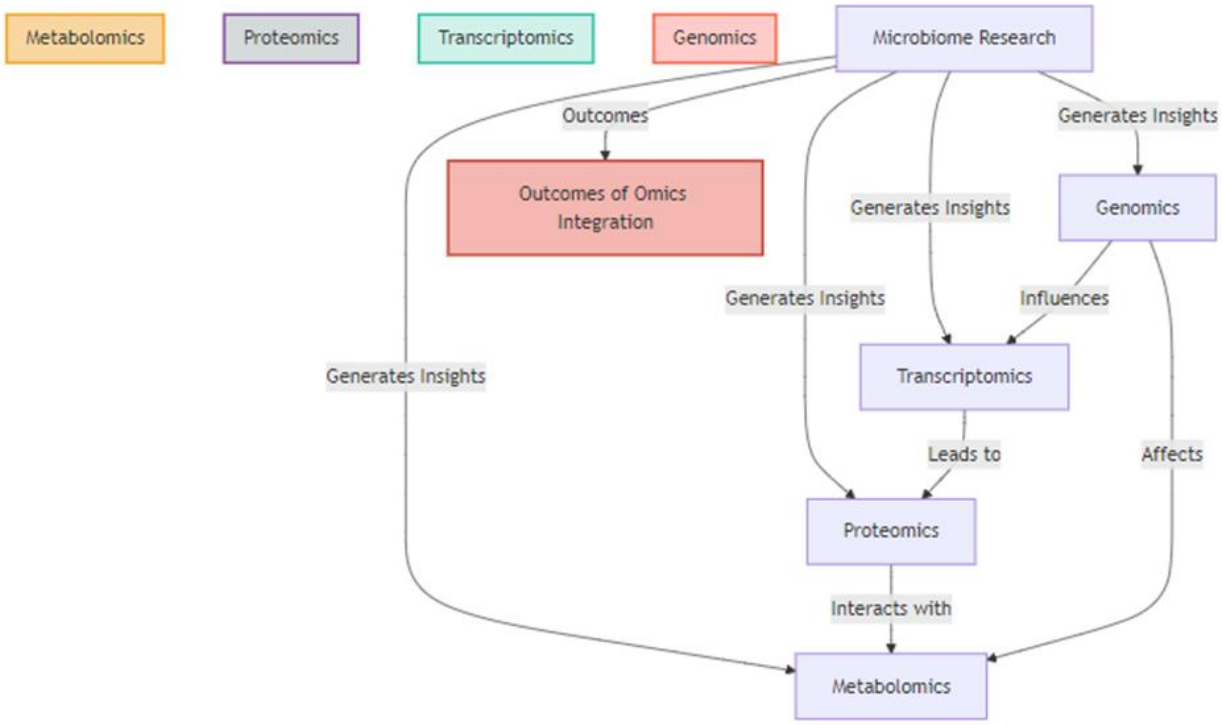


Figure 1. Integration of omics technologies in microbiome research.

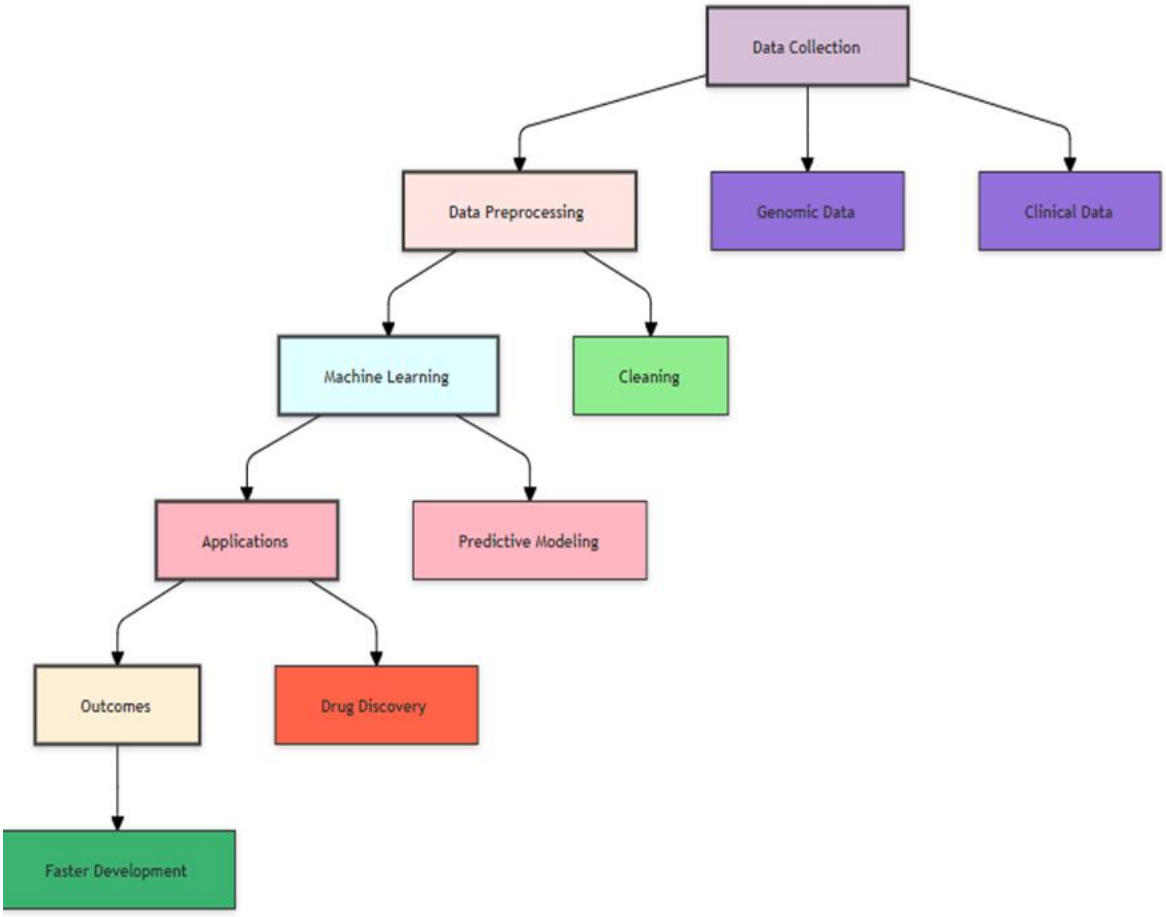


Figure 2. Machine learning and artificial intelligence in drug discovery.

More specifically, proteomics is the large scale study of proteins, paying specific attention to their structural and functional properties. In microbiome investigation, proteomic study determines and measures the abundance of peptides synthesized by microbial populace and thus provide information on their activity and symbiotic relationship with host (18). The tools like mass spectrometry helps in comprehending the multiple protein samples and discover the metabolic pathways as well as biochemical actions that prevail in microbiome. Knowledge of the structure of microbial proteomes could also guide the development of diagnostic and prognostic markers as well as therapeutic targets.

Metabolomics

Metabolomics is defined as the global analysis of small-molecule metabolites produced by the organism creating a snapshot of what a particular metabolism is currently doing in the biological system. In the context of microbiome research, metabolomic assessment can be useful in characterization of metabolites synthesised by the microbial consortium and the manner in which they alter the host physiology (19). High through put methods include the GC-MS and LC-MS where by the metabolism products of the microbiomes can be determined. Awareness of these metabolic cross-talk is crucial to enhance understanding of host-microbiome interactions because metabolites play a role in modulating host immune responses and inflammation and influence the development of disease.

Integrative omics approaches

Integrative omics approaches combine genomics, transcriptomics, proteomics and metabolomics data to explain the intricate behaviour of microbial communities and their impact on the host (20). This way, Next-Generation Sequencing (NGS) researchers can develop various intertwined layers of biological data that will help find out what contributes to health and what contributes to disease in microbial behavior and dynamics schemas. They allowed us to obtain more information about the systems biology of microbiome and how the latter might impact the host physiology. This study provides a compelling support that integration of omics data is central to the continuous advancement of microbiota derived products and precision medicine strategies. The figure 1 below shows the integration of omics technologies in microbiome research enables full understanding of microbial communities, genotype, gene expression, protein expression and function, and metabolomics data links to genomics to enable identification of biochemical functions and drug targets.

Computational Frameworks for Drug Design

Computational frameworks for drug design leverage advanced computational techniques to streamline the discovery and development of new therapeutic agents. These approaches are essential in the context of microbiome therapeutics, where traditional drug discovery methods may be insufficient to address the complexity and variability of microbial communities.

Overview of computational drug design

Computational drug design aims at design of drug and optimization of the chemical or biological compound through the use of computer tools. This unionized strategy unites concepts from chemistry, biology, and informatics to anticipate the specialized relationships between drugs and their target organisms (21). These include molecular docking, quantitative structure-activity relationship modeling as well as virtual screening. Molecular docking try to predict how the drug interacts with the molecular target with a view of determining potential inhibitors based on the performance of the simulation (22). QSAR modeling maps chemical structures to biological activities, and thus allows the effects of new compounds to be predicted from a database (23). Virtual screening is the computational based process of passing chemicals to filters designed to rank the libraries of compounds by their likelihood to exhibit biological activity (24). In summary, these computational methods have effectively shortened and decrease the cost of time originating from the conventional mode of drug discovery, which, in one way, offer a better process towards the discovery of new drugs.

Machine learning and artificial intelligence in drug discovery

Machine learning (ML) and artificial intelligence (AI) are disrupting the drug discovery industry in a way that allows for big data analysis and the identification of intricate patterns that might be difficult to observe otherwise (25). When existing drug data is fed into ML algorithms, these models can then be trained to estimate the biological activity of new chemical compositions, improve the lead optimization process, and optimize virtual screening processes. For example, deep learning techniques, which form the subcategory of ML, have been used to study chemical structures and find out how the chemical compounds interact with target proteins (26). Moreover, AI platforms can handle many types of data at once, from genomics, proteomics, and metabolomics data, in an attempt to discover new targets in microbiome studies (27). The ability of AI to analyze and learn from complex

datasets facilitates the discovery of novel compounds and improves the efficiency of drug development processes, potentially leading to more effective microbiome-targeted therapeutics. The figure 2 below illustrates how machine learning (ML) and artificial intelligence (AI) streamline drug discovery by processing genomic and clinical data, using predictive modeling to drive applications like drug discovery, and ultimately achieving faster development, aligning with the advanced AI-driven integration of diverse data types in microbiome research.

Integration of omics data in computational models

The integration of omics data—encompassing genomics, transcriptomics, proteomics, and metabolomics—into computational models is crucial for understanding the multifaceted interactions within microbiomes and their implications for drug design. By combining omics data with computational frameworks, researchers can create more accurate models that reflect the complexity of biological systems (28). For instance, genomic data can provide insights into the genetic basis of microbial functions, while transcriptomic data can reveal how these functions are regulated under various conditions (29). Proteomic and metabolomic data further enhance this understanding by elucidating the active biochemical pathways and metabolic products involved in host-microbe interactions. Integrative computational models that utilize omics data enable the identification of potential therapeutic targets and biomarkers, facilitating the development of personalized medicine strategies (30). Moreover, these models can be employed to simulate the effects of microbiome modulation through drug interventions, ultimately guiding the design of more effective microbiome-targeted therapies.

Current advances in omics-driven microbiome therapeutics

Omics-driven approaches have significantly advanced the field of microbiome therapeutics by providing insights into the complex interactions between microorganisms and their hosts. These advancements have led to the development of innovative therapeutic strategies aimed at modulating the microbiome to improve health outcomes.

Case studies and success stories

There are several examples of omics-driven microbiome therapeutics as the concept for practical use in clinics. For instance, Fecal Microbiota Transplantation (FMT) have been advocated for its use in the management of recurrent Clostridium difficile infection (CDI) with more authors reporting a success of over 90 percent in restoration of the microbiome and eradication of the infection (31). Metagenomics and metabolomics have been applied to describe the anthropofauna before and after FMT, focusing on the post-FMT microbiota features that predict successful treatments (32). One more success story of the application of a probiotic and a prebiotic is managing the inflammatory bowel disease (IBD). Different studies hold evidence that particular strains can help in biodiversity of gut and therefore relief of IBD patients. (33). By employing omics technologies, researchers have identified the metabolic pathways and interactions involved in the beneficial effects of probiotics, paving the way for personalized probiotic therapies tailored to individual patients' microbiomes (34). These case studies underscore the promise of integrating omics-driven insights into therapeutic interventions targeting the microbiome.

Limitations of current approaches

Despite the significant advancements in omics-driven microbiome therapeutics, several limitations persist. One major challenge is the inter-individual variability in microbiome composition and function, which can complicate the development of standardized therapies (35). Personalized medicine approaches are often necessary, yet they require comprehensive omics profiling, which can be resource-intensive and time-consuming. Moreover, the complexity of microbial interactions poses difficulties in predicting therapeutic outcomes. The dynamic nature of the microbiome means that changes in one part of the community can have cascading effects on others, making it challenging to isolate the effects of specific interventions (36). Moreso, there are regulatory and ethical considerations surrounding the use of microbiome-based therapies, particularly with novel interventions like FMT, which can complicate their clinical adoption (37). Addressing these limitations is crucial for advancing the field and ensuring the safe and effective implementation of microbiome therapeutics.

Future perspectives in therapeutic applications

Prospective of omics driven Microbiome therapeutics are very bright in the coming years. The availability of new high-throughput sequencing techniques and new tools based on machine learning will allow for the quick analysis of microbiome data and the discovery of new targets for treatments and diagnostic markers (38). In addition, the application of omics technologies,

genomics, transcriptomics, proteomics, and metabolomics for integrated analysis, will enhance the understanding of the different microbial functions and their host interactions and may open up avenues for new therapies (39). The development of next-generation probiotics, designed based on specific microbiome profiles, represents an exciting avenue for future research. These tailored probiotics could enhance the efficacy of microbiome modulation therapies by targeting individual patients' unique microbial landscapes (40). Moreso, the exploration of bacteriophage therapy as a complement or alternative to traditional antibiotics offers a novel approach to manipulating the microbiome to combat drug-resistant infections (41).

Research gaps in omics-driven microbiome therapeutics

Despite significant advances in omics-driven microbiome therapeutics, several research gaps persist that warrant further exploration. Addressing these gaps is crucial for the continued development and application of microbiome-based interventions.

Identification of unexplored areas

One major gap in current research is the limited understanding of the interactions between microbiomes and various environmental factors, including diet, lifestyle, and medications. While some studies have explored the impact of diet on the gut microbiome (42), many dietary components and their effects on microbial communities remain unexplored. For instance, the role of fiber types or specific food components in modulating the microbiome and subsequent health outcomes requires more rigorous investigation (43). Furthermore, there is a need for more extensive research into the functional roles of understudied microbial species within the microbiome. Many studies focus on a few dominant species, neglecting the functional contributions of less abundant but potentially important microorganisms (44). This gap in knowledge limits the potential for identifying novel therapeutic targets and understanding the full scope of microbial interactions. Another unexplored area is the investigation of the microbiome's role in drug metabolism and pharmacokinetics. The influence of microbiomes on the efficacy and safety of various drugs remains inadequately characterized (45). Understanding how microbiomes can affect drug metabolism could lead to the development of personalized therapeutic strategies, optimizing drug dosing based on individual microbiome profiles. The figure 3 illustrates key unexplored areas in omics-driven microbiome research, highlighting the implications of microbiome-drug interactions, longitudinal studies, and personalized therapies for enhancing therapeutic outcomes.

Implications for future research directions

Addressing the identified research gaps holds significant implications for future investigations in omics-driven microbiome therapeutics. Firstly, a comprehensive understanding of the interplay between microbiomes and environmental factors can inform the development of personalized dietary recommendations and interventions that leverage microbiome modulation for improved health outcomes (46). Research focusing on specific dietary components and their effects on microbial diversity and function may uncover novel therapeutic approaches. Moreover, Future study should focus on the functional roles of underrepresented microbial species in the microbiome. Using advanced metagenomic and meta transcriptomic approaches, researchers can acquire insights into the contributions of these species to microbial community dynamics and host relationships (47). This understanding could lead to the identification of new therapeutic targets and the development of innovative microbiome-based interventions. Moreso, investigating the microbiome's impact on drug metabolism and pharmacokinetics could revolutionize personalized medicine. Future studies should aim to elucidate the mechanisms by which microbiomes influence drug efficacy and toxicity, potentially guiding the development of microbiome-informed drug therapies that maximize therapeutic benefits while minimizing adverse effects (48).

Challenges and considerations

As the field of omics-driven microbiome therapeutics continues to advance, several challenges and considerations arise that need to be addressed to ensure successful implementation and efficacy of these approaches. These challenges include data integration and interpretation, as well as ethical and regulatory issues surrounding microbiome research and therapies.

Data integration and interpretation

The human microbiome plays important roles in many aspects of the tenants of health, including digestion metabolism as well as immunologic function. It facilitates the splitting of complex carbohydrates, and production of short-chain fatty acids, which selectively serve as energy sources to colonocytes and contain anti-inflammatory properties (49). Combination of these datasets is crucial in providing an enriched understanding of the microbial activities and its associated

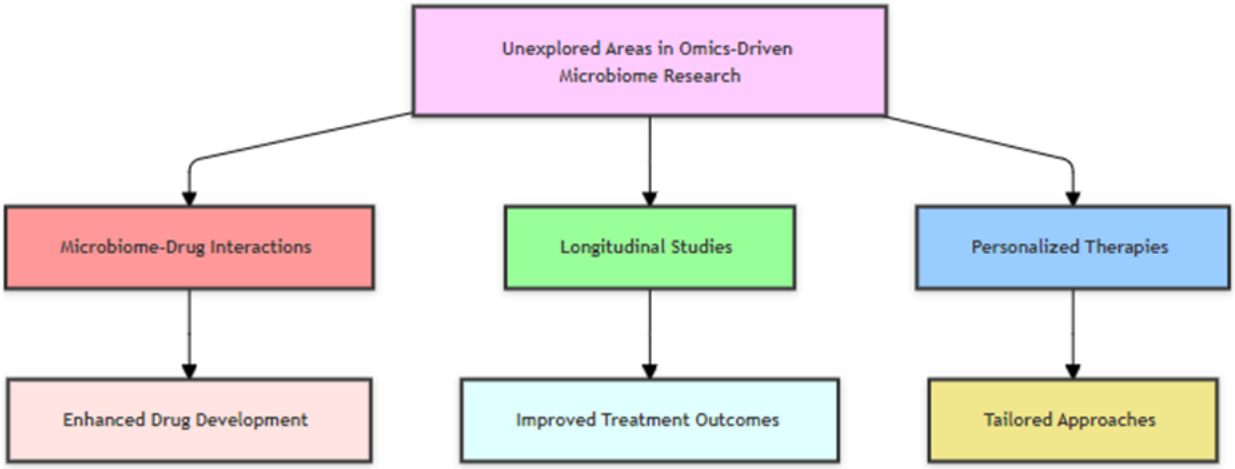


Figure 3. Unexplored areas in omics-driven microbiome research and their implications

consequences on health. However, data integration poses significant challenges due to the heterogeneity of the data, differences in measurement techniques, and variations in data quality (50). Researchers must develop robust computational frameworks and bioinformatics tools capable of processing and analyzing these complex datasets effectively. Moreso, the interpretation of integrated omics data requires advanced statistical methods and algorithms to identify meaningful patterns and relationships that can inform therapeutic strategies (51). The complexity of microbiome interactions further complicates data interpretation, as microbial communities exhibit dynamic and context-dependent behaviors. Therefore, there is a need for sophisticated modeling approaches that can account for the intricacies of microbial ecology and host-microbe interactions (52). Addressing these data integration and interpretation challenges is crucial for advancing the field of microbiome therapeutics.

Ethical and regulatory issues

Ethical and regulatory issues are significant considerations in the development and application of omics-driven microbiome therapeutics. One primary concern is related to the use of human subjects in microbiome research, particularly in studies involving fecal microbiota transplantation (FMT) and other interventions. Ensuring informed consent and the ethical treatment of participants is essential to maintain public trust and uphold ethical standards (53). Moreso, the long-term effects of microbiome-based therapies on individual health and the potential for unintended consequences must be carefully evaluated. For instance, altering a patient's microbiome could have unforeseen effects on their immune system or susceptibility to diseases (54). To mitigate hazards, patients undergoing microbiome-targeted medicines must undergo extensive safety studies and monitoring. The regulatory frameworks governing microbiome research and treatments are likewise developing. The US Food and Drug Administration (FDA) and the European Medicines Agency (EMA) are developing criteria for evaluating microbiome-based products (55). However, these regulations are still in their infancy, and there is a need for clear and comprehensive regulatory procedures that address the unique problems associated with microbiome therapeutics, including standardized manufacturing methods and product labeling.

Conclusion

This study focuses on utilizing omics-based approaches to understand and modulate the human microbiota in relation to treatment. Genomic, transcriptomic, proteomic, and metabolomic methods have provided integrative insights into microbial communications and the relationships between microbes and humans. These findings are paving the way for novel therapeutic strategies that aim to modify the microbiome to address various diseases, including inflammatory bowel diseases, obesity, and metabolic disorders. Moreso, combining omics data has become essential for enhancing the efficacy of microbiome interventions. Employing machine learning and artificial intelligence can improve the prediction of therapeutic outcomes and facilitate the discovery of new microbial targets for drug development. Contemporary applications, such as fecal microbiota transplantation and its long-term effects on recurrent Clostridium difficile infection, serve as valuable examples. However, challenges related to dual use, data integration, interpretation, and ethical issues in microbiome research remain significant concerns. Addressing these areas is crucial for the ongoing advancement and responsible application of microbiome

therapeutics. The information presented suggests a promising future for microbiome therapies based on omics technologies. Continued advancements in sequencing tools and algorithms will enhance our understanding of the complex interactions within the microbiome and their impact on health. Ultimately, as researchers deepen their understanding of microbial functions, the development of personalized microbiome therapies tailored to individual health profiles is expected to transform treatment approaches. Furthermore, collaboration among microbiologists, bioinformaticians, clinicians, and relevant organizations will be vital in addressing emerging challenges and advancing omics research. By fostering interdisciplinary cooperation and innovation, we can fully realize the potential of omics technologies to revolutionize microbiome therapy, improve health outcomes, and deepen our appreciation of the microbiome's role in human health and disease.

Contribution of authors

Amina Abdulhamid Ahmed: Leads literature review on genomics and metagenomics, focusing on key findings and innovations in microbiome analysis. Ahmed synthesizes data from these areas to support the development of therapeutic frameworks. Ummulkhair Adamu Yusuf: Focuses on articles related to proteomics and metabolomics in microbiomes, identifying relevant biomarkers and therapeutic pathways. Yusuf contributes insights on integrating multi-omics data for therapeutic applications. Zainab Hussein Fadlallah: Contributes expertise in microbiology, sourcing and reviewing studies that provide experimental and clinical insights. Fadlallah evaluates findings from lab-based studies and discusses their potential applications in microbiome therapeutics. Musa Ojeba Innocent: Compiles computational methods and tools from reviewed articles, highlighting advances in microbiome data analysis and applications in therapeutics. Innocent curates and synthesizes computational strategies relevant to the framework. Mustapha Abdulsalam: Oversees all research activities, including conceptualization, project administration, and the integration of omics perspectives. Abdulsalam ensures comprehensive coverage of computational approaches in microbiome therapeutics.

Acknowledgments

I am profoundly grateful to the Head of the Department of Microbiology at Skyline University Nigeria for his steadfast support and invaluable guidance throughout this research. I also extend my sincere appreciation to the Vice Chancellor of Skyline University Nigeria for his ongoing encouragement and for cultivating an environment that promotes academic growth and achievement. Their dedication to advancing research has been essential to the completion of this work.

Conflict of Interest

The author declares no conflict of interest.

Funding

No funding was received for this research.

References

1. Ochoa-Repáraz, J., Ramelow, C. C., & Kasper, L. H. (2020). A gut feeling: the importance of the intestinal microbiota in psychiatric disorders. Frontiers in Immunology, 11, 510113.
2. Acevedo-Román, A., Pagán-Zayas, N., Velázquez-Rivera, L. I., Torres-Ventura, A. C., & Godoy-Vitorino, F. (2024). Insights into Gut Dysbiosis: Inflammatory Diseases, Obesity, and Restoration Approaches. International Journal of Molecular Sciences, 25(17), 9715.
3. Quaranta, G., Guarnaccia, A., Fancello, G., Agrillo, C., Iannarelli, F., Sanguinetti, M., & Masucci, L. (2022). Fecal microbiota transplantation and other gut microbiota manipulation strategies. Microorganisms, 10(12), 2424.
4. Abdulsalam, M., & Ila, M. A. (2023). Closing the Gap: Artificial Intelligence Integration for Advancing Chikungunya Virus Studies in Africa. Biological Sciences, 3(4), 493-502.
5. Fadiji, A. E., & Babalola, O. O. (2020). Metagenomics methods for the study of plant-associated microbial communities: a review. Journal of microbiological methods, 170, 105860.
6. Chen, B., Zhang, D., Wang, X., Ma, W., Deng, S., Zhang, P., & Liang, S. (2017). Proteomics progresses in microbial physiology and clinical antimicrobial therapy. European Journal of Clinical Microbiology & Infectious Diseases, 36, 403-413.
7. Blum, H. E. (2017). The human microbiome. Advances in medical sciences, 62(2), 414-420.
8. Innocent, M. O., Mustapha, A., Abdulsalam, M., Livinus, M. U., Samuel, J. O., Elelu, S. A., & Muhammad, A. S. (2024). Soil Microbes and Soil Contamination. In Soil Microbiome in Green Technology Sustainability (pp. 3-35). Cham: Springer Nature Switzerland.

9. Zhu, B., Wang, X., & Li, L. (2010). Human gut microbiome: the second genome of human body. Protein & cell, 1(8), 718-725.
10. Fusco, W., Lorenzo, M. B., Cintoni, M., Porcari, S., Rinninella, E., Kaitsas, F., & Ianiro, G. (2023). Short-chain fatty-acid-producing bacteria: key components of the human gut microbiota. Nutrients, 15(9), 2211.
11. Kogut, M. H., Lee, A., & Santin, E. (2020). Microbiome and pathogen interaction with the immune system. Poultry science, 99(4), 1906-1913.
12. Skonieczna-Żydecka, K., Marlicz, W., Misera, A., Koulaouzidis, A., & Łoniewski, I. (2018). Microbiome–the missing link in the gut-brain axis: focus on its role in gastrointestinal and mental health. Journal of clinical medicine, 7(12), 521.
13. Das, B., & Nair, G. B. (2019). Homeostasis and dysbiosis of the gut microbiome in health and disease. Journal of biosciences, 44, 1-8.
14. Gérard, P. (2016). Gut microbiota and obesity. Cellular and molecular life sciences, 73(1), 147-162.
15. Fadiji, A. E., & Babalola, O. O. (2020). Metagenomics methods for the study of plant-associated microbial communities: a review. Journal of microbiological methods, 170, 105860.
16. Tedersoo, L., Albertsen, M., Anslan, S., & Callahan, B. (2021). Perspectives and benefits of high-throughput long-read sequencing in microbial ecology. Applied and environmental microbiology, 87(17), e00626-21.
17. Sudhagar, A., Kumar, G., & El-Matbouli, M. (2018). Transcriptome analysis based on RNA-Seq in understanding pathogenic mechanisms of diseases and the immune system of fish: a comprehensive review. International journal of molecular sciences, 19(1), 245.
18. Abdulsalam, M., Salihu, A. T., Usman, H. Y., & Usman, M. Y. (2024). Protein Biosynthesis in Microorganisms: Mechanisms, Regulation, and Biotechnological Applications. World Journal of Advanced Research and Reviews, 21(1), 869-881.
19. Bhosle, A., Wang, Y., Franzosa, E. A., & Huttenhower, C. (2022). Progress and opportunities in microbial community metabolomics. Current Opinion in Microbiology, 70, 102195.
20. Chetty, A., & Blekhman, R. (2024). Multi-omic approaches for host-microbiome data integration. Gut Microbes, 16(1), 2297860.
21. Abdulsalam, M., Hamisu, A. A., Ahmad, A. M., Wakili, F. B., Rabiu, I. B., Burodo, R. A., & Iliyas, N. A. (2024). Synergies at the Intersection: Exploring the Role of Bioinformatics in Enhancing Physiotherapy and Nursing Practice. Biological Sciences, 4(3), 712-724.
22. Decherchi, S., & Cavalli, A. (2020). Thermodynamics and kinetics of drug-target binding by molecular simulation. Chemical Reviews, 120(23), 12788-12833.
23. Nantasenamat, C., Isarankura-Na-Ayudhya, C., & Prachayasittikul, V. (2010). Advances in computational methods to predict the biological activity of compounds. Expert opinion on drug discovery, 5(7), 633-654.
24. Abdulsalam, M. (2024). Exploring the Therapeutic Promise of Cationic Antibacterial Peptides. Biological Sciences, 4(3), 692-700.
25. Musa, I. O., Isibor, P. O., Samuel, J. O., Mustapha, A., Mustapha, A., Akande, S., & Adeniji, H. (2024). Introduction to Nanotoxicology. In Environmental Nanotoxicology: Combatting the Minute Contaminants (pp. 1-22). Cham: Springer Nature Switzerland.
26. Saheed, Y. K., Balogun, B. F., Odunayo, B. J., & Abdulsalam, M. (2023). Microarray gene expression data classification via Wilcoxon sign rank sum and novel Grey Wolf optimized ensemble learning models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 20(6), 3575-3587.
27. D'Urso, F., & Broccolo, F. (2024). Applications of Artificial Intelligence in Microbiome Analysis and Probiotic Interventions– An Overview and Perspective Based on the Current State of the Art. Applied Sciences, 14(19), 8627.
28. Wörheide, M. A., Krumsiek, J., Kastenmüller, G., & Arnold, M. (2021). Multi-omics integration in biomedical research–A metabolomics-centric review. Analytica chimica acta, 1141, 144-162.
29. Manzoni, C., Kia, D. A., Vandrovcova, J., Hardy, J., Wood, N. W., Lewis, P. A., & Ferrari, R. (2018). Genome, transcriptome and proteome: the rise of omics data and their integration in biomedical sciences. Briefings in bioinformatics, 19(2), 286-302.
30. Collin, C. B., Gebhardt, T., Golebiewski, M., Karaderi, T., Hillemanns, M., Khan, F. M., & Kuepfer, L. (2022). Computational models for clinical applications in personalized medicine–guidelines and recommendations for data integration and model validation. Journal of personalized medicine, 12(2), 166.
31. Khanna, S. (2021). Microbiota restoration for recurrent Clostridioides difficile: Getting one step closer every day!. Journal of Internal Medicine, 290(2), 294-309.

32. Lee, J. W. J., Plichta, D., Hogstrom, L., Borren, N. Z., Lau, H., Gregory, S. M., & Ananthakrishnan, A. N. (2021). Multi-omics reveal microbial determinants impacting responses to biologic therapies in inflammatory bowel disease. Cell host & microbe, 29(8), 1294-1304.
33. Yang, J., Qin, S., & Zhang, H. (2022). Precise strategies for selecting probiotic bacteria in treatment of intestinal bacterial dysfunctional diseases. Frontiers in Immunology, 13, 1034727.
34. Al-Fakhrany, O. M., & Elekhnawy, E. (2024). Next-generation probiotics: the upcoming biotherapeutics. Molecular Biology Reports, 51(1), 505.
35. Abdulsalam, M., Hamisu, A. A., Ahmad, A. M., Wakili, F. B., Annu, F. S., & Garba, M. M. (2024). Microbiome Dynamics and Strategic Management Strategies: Exploring Synergies between Integrative Medicine Modalities and Microbial Balance. Biological Sciences, 4(3), 725-735.
36. Tiamiyu, B. B., Lateef, A. A., Ajadi, I., Adeyemi, S. B., Owolabi, P. O., Sagaya, A., & Mustapha, O. T. (2024). Bioclimatic Modeling of Current Geographic Distribution and Future Range Shifts of Selected Edible Mushrooms in Nigeria. Sahel Journal of Life Sciences FUDMA, 2(1), 51-61.
37. Gulliver, E. L., Young, R. B., Chonwerawong, M., D'Adamo, G. L., Thomason, T., Widdop, J. T., & Forster, S. C. (2022). The future of microbiome-based therapeutics. Alimentary Pharmacology & Therapeutics, 56(2), 192-208.
38. Saheed, Y. K., Salau-Ibrahim, T. T., Abdulsalam, M., Adeniji, I. A., & Balogun, B. F. (2024). Modified bi-directional long short-term memory and hyperparameter tuning of supervised machine learning models for cardiovascular heart disease prediction in mobile cloud environment. Biomedical Signal Processing and Control, 94, 106319.
39. Abdulsalam, M., Ubah, F. Z. Y., Ahmed, H. U., Tafida, U. A., & Nasir, A. W. (2024). Deciphering the Genetic Code: Mechanisms, Evolution, and Implications for Biotechnology. World Journal of Advanced Research and Reviews, 21(1), 858-868.
40. Abdulsalam, M., Natour, S., Rabiu, I. B., & Abdulazeez, M. (2024). Microbial Magic: Decoding the Impact of Hypoxia on Exercise Physiology through Microbiota Dynamics. Biological Sciences, 4(3), 736-745.
41. Abdulsalam, M., Abdulrazaq, I., Tiamiyu, B. B., & Salam, O. L. (2023). Comparative Antimicrobial Properties of a Consortium of Nauclea latifolia Sm. and Ocimum gratissium L. Extracts with Their CuO. Biological Sciences, 3(1), 386-393.
42. Beam, A., Clinger, E., & Hao, L. (2021). Effect of diet and dietary components on the composition of the gut microbiota. Nutrients, 13(8), 2795.
43. Livinus, M. U., Bala, S. Z., Abdulsalam, M., Innocent, M. O., Hassan, M., Elelu, S. A., & Kini, P. (2024). Role of Microbes in Soil Food Webs and Vegetation Development. In Soil Microbiome in Green Technology Sustainability (pp. 107-132). Cham: Springer Nature Switzerland.
44. Musa, I. O., Samuel, J. O., Adams, M., Abdulsalam, M., Nathaniel, V., Maude, A. M., & Tiamiyu, A. G. T. (2024). Soil Erosion, Mineral Depletion and Regeneration. In Prospects for Soil Regeneration and Its Impact on Environmental Protection (pp. 159-172). Cham: Springer Nature Switzerland.
45. Scher, J. U., Nayak, R. R., Ubeda, C., Turnbaugh, P. J., & Abramson, S. B. (2020). Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. Nature Reviews Rheumatology, 16(5), 282-292.
46. Kok, C. R., Rose, D., & Hutkins, R. (2023). Predicting personalized responses to dietary fiber interventions: opportunities for modulation of the gut microbiome to improve health. Annual Review of Food Science and Technology, 14(1), 157-182.
47. Zhang, Y., Thompson, K. N., Branck, T., Yan, Y., Nguyen, L. H., Franzosa, E. A., & Huttenhower, C. (2021). Metatranscriptomics for the human microbiome and microbial community functional profiling. Annual Review of Biomedical Data Science, 4(1), 279-311.
48. Abdulsalam, M., Innocent, M. O., Livinus, M. U., Elelu, S. A., Ibrahim, G. O., Lateefat, S. O., ... & Muhammad, A. S. (2024). Future Research of Soil Microbiomes and Green Technology Innovation for a Better Tomorrow. In Soil Microbiome in Green Technology Sustainability (pp. 569-585). Cham: Springer Nature Switzerland.
49. Musa, I. O., Auwal, A. I., Abdulsalam, M., Livinus, M. U., Abdulhakeem, A. I., Muhammed, A., & Muhammad, A. S. (2024). Microbial Bioprospecting Products of Marine Economy. In Marine Bioprospecting for Sustainable Blue-bioeconomy (pp. 181-204). Cham: Springer Nature Switzerland.
50. Gudivada, V., Apon, A., & Ding, J. (2017). Data quality considerations for big data and machine learning: Going beyond data cleaning and transformations. International Journal on Advances in Software, 10(1), 1-20.

51. Subramanian, I., Verma, S., Kumar, S., Jere, A., & Anamika, K. (2020). Multi-omics data integration, interpretation, and its application. Bioinformatics and biology insights, 14, 1177932219899051.
52. Livinus, M. U., Bala, S. Z., Abdulsalam, M., Innocent, M. O., Hassan, M., & Kini, P. (2024). Natural Occurrences of Soil Dilapidation. In Prospects for Soil Regeneration and Its Impact on Environmental Protection (pp. 205-223). Cham: Springer Nature Switzerland.
53. Abdulsalam, M., Musa, I. O., Livinus, M. U., Elelu, S. A., Ibrahim, G. O., Salami, O. L., & Pal, S. K. (2024). Blue Bioeconomy and Biomedical Innovation. In Marine Bioprospecting for Sustainable Blue-bioeconomy (pp. 143-157). Cham: Springer Nature Switzerland.
54. Muhammed, A., Aminu, B. M., Musa, I. O., Abdulsalam, M., Isma'il, R., Gimba, Y. M., & Moses, E. O. (2024). Blue Economy in Nigeria and the African Continent. In Marine Bioprospecting for Sustainable Blue-bioeconomy (pp. 355-370). Cham: Springer Nature Switzerland.
55. Mogielnicki, M., Swieczkowski, D., Bachorski, W., Zuk, G., Gilis-Malinowska, N., Zarzeka, A., & Jaguszewski, M. (2016). The Food and Drug Administration (FDA) and the European Medicines Agency (EMA) perspective on cardiovascular Polypill: A multidimensional concept. Cardiology Journal, 23(5), 515-517.