



Review Article

The human microbiome and its expanding role in health and pharmacology

Ashvini Arun Kakad^{1*}, Rucha A Ingle¹, Aarti Mahadev Nimse¹,
Rutuja Devidas Giram¹, Shatrughna Uttam Nagrik¹

¹Anuradha College of Pharmacy, Chikhali, Puna, Maharashtra, India



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ABSTRACT

The broad group of bacteria that live in the human body is called the microbiome. This has recently become an important component of pharmacology, and it offers some of the latest insights into drug processing, effectiveness, and safety. Recent investigations have underlined once again the crosstalk between microbiome and pharmacokinetics: gut microorganisms influence how medications are absorbed, distributed, metabolized, and excreted. The consequences of this relationship in terms of personalized treatment are most relevant because the individual profiles of the microbiome of a person might influence their response to medications and their vulnerability to toxicity. In addition, microbiome manipulation could be used to make care more efficient and diminish adverse effects. It discusses the latest advances in microbiome research, their impact on drug development and clinical practice, and potential future ways in which knowledge regarding the microbiome can be integrated into pharmacological research. This rapidly growing field is promising to transform medication therapy and optimize treatment techniques through the linkage of microbiome science to pharmacology.

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1. Introduction

Bacteria, archaea, fungi, and viruses make up the human microbiome. These mainly found in the gastrointestinal tract form an elaborate ecology with a host and are crucial to human health. This is considered the first thorough research on the microbiome. It was discovered that the number of microbial cells exceeded human cells and were home to a large number of genes, which were termed the 'second genome'. The second genome is also known as the microbiome which plays a role in many biological processes and may be quite different from one individual to another. It is influenced by a range of factors such as genetics and food and exposure to the environment around it.¹ Research has also underscored the ever-changing

nature of the microbiome, which has evolved over time and adapted to changes in diet, lifestyle, and medical treatments.² Microbiota plays a very important role in the digestion of complex carbohydrates, fibers, and resistant starches in humans. Consequently, it forms (SCFAs) such as butyrate, acetate, and propionate that provide energy source and to enhance gastrointestinal health.³ The second includes the synthesis of essential vitamins K and B in which the microbiome is vital for metabolism and blood coagulation.³ The microbiome has a deep immunological interaction with the immune system. It facilitates the generation of immunological cells. It supports the production of immune cells, inflammation is regulated, and the invasion of pathogenic microorganisms is prevented by maintaining the gut barrier.⁴ Dysbiosis, or pathological change in this ecosystem, has been linked to a number of disease states including but not restricted to IBD, obesity, diabetes,

* Corresponding author.

E-mail address: ashvinikakad26@gmail.com (A. A. Kakad).

and psychopathology. This points out the vast effect that microbiome has on health in general. Some studies recently alluded to the presence of the microbiome in pharmacology. The GIT microbiome is capable of having direct influence over drug metabolism in the body which could alter how readily drugs are absorbed, their efficacy level, and toxicity. Gut bacteria may help to metabolize some drugs, activating them or deactivating in the process. This is an advantageous effect if it results in increased drug action; however, it may also lead to undesirable consequences.⁵ With tremendous implications for personalized medicine, microbiomes even make it possible to infer theories and prediction of a patient's response to certain treatments on the basis of the microbiome profile of a patient.⁶ Furthermore, the potential for microbiome-based therapeutics in the form of probiotics, prebiotics, and (FMT) development has opened doors to treat diseases ranging from clostridioides difficile infections to improvements in cancer therapy. All these have reinforced the idea that the microbiome should now be considered an additional component in the finding new drug. The human microbiome encompasses the totality of a heterogeneous assemblage of microbes, viruses, fungus, archaea, colonizing distinct bodily parts. The main parts include the gut, skin, mouth cavity, and respiratory system. Bacteria are the dominant members of the microbiome, and in the gut, the most abundant groups are Firmicutes and Bacteroidetes. This composition varies considerably from individual to individual and even within the same individual over time. For example, Firmicutes can compose either 40% or 80% of the total depending on the individual, and Archaea, especially methanogens, also contribute to the digestion system, most notably in the fermentation of complex carbohydrates.⁷ Fungi, although less in number, are involved in immunomodulation and maintaining the overall balance of microbial communities; among them, *Candida* species have been most investigated.⁸ Viruses, including bacteriophages, interact with the bacterial community structure to define the dynamics of microorganisms and the health of their host.⁹ Since all these are determined by genetic, dietary, environmental, and lifestyle variables, the resultant composition and diversity of the microbiome widely vary from one individual to the other. The geographic location and the cultural food habits play a big role in influencing this status; for example, different individuals in different locations possess different microbial communities compared to their counterparts in other places. Age is an important determinant in the colonization of the gut by microbes. Infants are born with a sterile gut that becomes colonized quite rapidly after birth. It is this initial colonization that influences the microbiome, along with other factors such as mode of delivery, nursing, and early life exposures.¹⁰ Besides, variation between individuals in the metabolic activities is also commonly

observed; that is to say, the way in which each one's microbiome does the processing of nutrients, medicines, and toxins differs. This variation explains the differences in individualized health outcomes and susceptibility to diseases.¹¹ Microbiome communicates with the host through various vital mechanisms such as the GBA, immune modulation, and metabolic interaction. The gut-brain axis explains how the gut microbiota communicates with the central neurological system that influences mood, cognition, and behavior. Studies have indicated that alterations in gut microbial composition could not only modulate neurotransmitter synthesis but also blood-brain barrier permeability, which in turn impacts mental health illnesses like anxiety and depression.¹² The immune system depends on the microbiome for development and regulation. In this case, the microbiota also contributes to immune cell maturation and the development of tolerance to harmless antigens, which consequently protects against pathogens through the maintenance of MBI.¹³ The microbiome participates in the fermentative breakdown of indigestible fibers, producing (SCFAs) as an energy source and anti-inflammatory molecules. In other words, the microbiome is engaged in food metabolism and homeostatic immunity, as stated by Flint et al.¹⁴

2. Microbiome and Drug Metabolism

2.1. Influence of microbiome on drug absorption

"Gut bacteria change physical and chemical characteristics of drugs in the gastrointestinal system, resulting in a great impact on drug absorption. The microbiome can manipulate the solubility, stability, and permeability of drugs, and this eventually manipulates bioavailability. For example, certain microorganisms produce the enzyme that degrades bile acids and thus affects the solubility of lipid-soluble drugs and their absorption occurs. Moreover, the microbial metabolism of fibers during digestion forms (SCFAs), which reduce the pH in the large intestines; the value for the physiological dissolution and absorption rate of the drug could be altered through this pathway.¹⁵ The bacterial efflux pumps act by actively moving drug molecules out, hence reducing the concentration of drugs in the stomach and restricting their absorption into the bloodstream.¹⁶

2.2. Microbiome's role in drug metabolism

The human microbiome is involved in drug transformation with microbial enzymes for the activity of activating, deactivating, or detoxifying/toxinizing pharmaceuticals. These processes, in general, are called xenobiotic metabolism and can take place not only before substances are converted into medicines but also after their administration and have entered the body, which at first pass is the liver. As an example, the metabolism of the digoxin by gut bacteria, such as *Eggerthella lenta*, changes

its absorption into the bloodstream and its activity in treating the heart. It contribute to the metabolism of prodrugs that require microbial activation to be pharmacologically active. Sulfasalazine, which is used in the treatment of IBD, is metabolized to its therapeutically active forms in the intestine by bacterial azoreductases.¹⁷

2.3. Microbiome-mediated drug efficacy and toxicity

"Microbiota-mediated metabolism also has an influence on the pharmacokinetics of drugs, with a possible enhanced or deteriorative outcome of treatment. The intestinal flora metabolizes nonsteroidal anti-inflammatory drugs (NSAIDs), such as aspirin, resulting in lowered efficacy and increased gastrointestinal toxicity due to the formation of toxic metabolites.¹⁸ Similarly, the microbial activity in the bowel that converts chemotherapy medication irinotecan into toxic metabolites may cause severe gastrointestinal toxicity.¹⁹ At the same time, certain anti-cancer immunotherapies have been found to increase efficacy where the redirection of immune reactions by the microbes increases therapeutic outcome; therefore, the microbiome serves two roles in the efficacy of an intervention.²⁰ Personalized medicine, taking into account the specificity in composition of the individual microbiome, is an emergent priority toward optimal treatment response and minimization of side effects.²¹

3. Pharmacomicrobiomics: Personalized Medicine and Microbiome

3.1. Personalized drug therapy based on microbiome composition

Pharmacomicrobiomics is an emergent field concerned with tailored pharmacological therapy depending on the microbiome composition of a person. This field realizes the great power that gut bacteria have in the metabolism of drugs, their efficacy, and expression of their side effects. Variations in the gut flora can result in differences in absorption and metabolism of drugs between people. Individuals with elevated amounts of *Escherichia coli* experience diminished cardiac action of the medication digoxin because there occurs inactivation of the bacteria, as demonstrated by Haiser et al.²² Personalized pharmacotherapy can comprise microbiome profiling to determine the most effective drug or dose, consequently reducing side effects and enhancing therapeutic activity. This is particularly valuable for drugs with low therapeutic indices, because even small variations in metabolism may lead to overdosing or underdosing.²³

3.2. Predicting drug response through microbiome analysis

"Microbiome profiling can predict patient response to a certain drug based on specific microbe patterns in relation with the metabolism of clinically used drugs. By analyzing the microbial composition, it is even possible to predict how efficient certain drugs will be metabolized or whether they could adversely affect us. These include the efficiency of immune checkpoint inhibitors administered to treat cancer and associated with some variation in gut microbial population state. Such inhibitors work well with patients who contain certain bacteria in their gut.²⁴ Predictive modeling of the microbiome offers opportunities to inform chemotherapy, antibiotics or anti-depressant efficacy. Ultimately, this permits up-front personalized treatments for single patients to prevent adverse events and improve outcomes.²⁵

3.3. Microbiome as a biomarker in disease and treatment

"The role of the microbiome as a potential biomarker for developing disease and predicting therapeutic responses continues to gain attention. An adverse disruption of the microbial composition, termed dysbiosis, has been correlated with a host of chronic diseases such as IBD, obesity, and cancer.²⁶ Knowing about shifts in the microbiome can help researchers track disease progression and evaluate whether a therapy has any chance of working. For example, in colorectal cancer, a distinct gut microbial composition can also function as a predictive biomarker, guiding clinicians to select the most suitable treatments.²⁷ Moreover, it allows the identification of microbiome-based biomarkers permitting clinicians to predict drug-induced toxicity, enabling them to adjust dosages and/or therapies in advance to avoid adverse events.²⁸

4. Microbiome-Targeted Therapies

4.1. Probiotics and prebiotics in pharmacology

Probiotics can be described as live microbial feed supplements that when administered in appropriate quantities will beneficially affect the host organism through control of the microbiota. Some of the probiotics that are in the live form and commonly used to enhance gastrointestinal (GI) comfort, guard against infections and also used to cure conditions like irritable bowel syndrome include *Lactobacillus* and *Bifidobacterium*.²⁹ Prebiotics are non-digestible food ingredients, which selectively stimulate the growth and activity of lignifying bacteria including *Bifidobacteria* and *Akkermansia muciniphila*.³⁰ Members of this category include inulin and fructooligosaccharides; they alter the composition of the microbiota and produce short-chain fatty acids that support gut health and the

immune system. The growing recognition of the importance of probiotics and prebiotics in modulating the microbiome to enhance drug efficacy, improve immunity, and reduce side effects has been noted."

4.2. Fecal microbiota transplantation (FMT)

"Fecal microbiota transplantation is a process that involves removing stool from a healthy donor and putting it into the gastrointestinal tract of a patient so as to replenish the variety of organisms. Fecal transplantation has been proven to be very effective in the treatment of recurrent infections caused by *Clostridium difficile*, which often occur with antibiotic therapies. The procedure works via the restoration of a balanced microbiome and prevention of overgrowth of pathogenic bacteria, such as *C. difficile*, which causes CDI.³¹ In addition to CDI, the effectiveness of FMT has further been researched in the treatment of inflammatory bowel disease, obesity, and diseases even in the brain, such as autism spectrum disorder. The implication in studies that exhibited a major association between gut dysbiosis and these diseases has been shown: even though FMT is promising, it still needs to be studied for further uses, and there are still regulatory hurdles that need to be taken down regarding the standardization and safety of the method.

4.3. Development of microbiome-modulating drugs

"Recent advances in the study of the microbiome have now fueled the development of microbiome-targeted therapeutics intended for disease treatment. These drugs, known variably as 'live biotherapeutics,' are rationally designed to help re-establish homeostasis within the microbial ecosystem or to introduce beneficial bacteria with a view to resolving diseases linked to dysbiosis. An example is SER-109, composed of purified bacterial spores designed to address recurrent *C. Aggressive* infections.³² A final emerging area is the development of synthetic prebiotics and postbiotics, under which are understood materials that can modulate microbial activity and enhance health outcomes. Microbiome modulators are currently being studied for use in cancer patients to increase the likelihood of success with immunotherapies. They work by modulating the composition of gut microbiota and through this modulate the host immune response. These developments are paving the way for the next generation of personalized medicine in which microbiome regulation will become a part of comprehensive treatments for illnesses.

5. Discussion

5.1. Challenges and ethical considerations

5.1.1. Complexity of the microbiome, variability, and difficulties in standardization

"The human microbiome is characterized by its intricate and extensive makeup, containing trillions of bacteria showing variability not only in different individuals but even within different regions of the same body. The factors responsible for this heterogeneity include nutrition, environment, genetics, and lifestyle. This makes it hard to be able to put together a uniform reference microbiome.³³ Besides, the dynamic nature of the microbiome itself, changed over time and under the influence of medical interventions, is a real stumbling block for researchers in their strive to get replicable results among studies. Furthermore, a lack of standard methodologies of sample collection, sequencing, and analysis creates such issues and reduces the possibility of study replication and comparison.³⁴ The microbial biocommunity research field will only advance properly if there are standardized research methodologies that are cross-verified with several data types, such as metagenomics, metabolomics, and transcriptomics."

5.1.2. Safety and regulatory concerns

Major safety concerns apply to all microbiome-targeted medicines, including probiotics, prebiotics, and FMT. Although therapeutically these interventions are promising, just as they provide new microbes to the host, there might be unexpected issues like infections or deleterious metabolic effects. For example, while FMT has been proven to help cure recurrent *Clostridium difficile* infections, in some cases, it led to severe infections of several patients.³⁵ At present, the regulatory systems for microbiome therapeutics are not well set up, and there is a need for the precise regulations or standard in order to maintain safety as well as efficacy. This requires the development of strict quality standards of products and with therapies based on microbiome. It also includes decision making on the right clinical end points that should be used to assess the effectiveness in trials.³⁶

5.2. Ethical issues

Besides the scientific objectives, there are ethical discussions all along the advancement in the science of microbiome. Especially disconcerting are the needs to get informed consent because samples may contain highly sensitive genetic information about both the subject and close contacts; this raises worries about privacy.³⁷ Managing and owning the rights to the data of the microbiome, say for use in developing a particular treatment plan based on the explicitly stated microbiome of a particular individual, only serves to exacerbate these questions of permission. It also raises concerns in terms

of ethics, as this type of manipulation may change the microbial population, producing unknown consequences for health with potential transgenerational impact.³⁸ It is thus important that ethical guidelines be set forth, which first and foremost respect the principles of patient privacy and at the same time regard the broader implications for society in moving forward through responsible microbiome research.

6. Future Directions in Microbiome Research and Pharmacology

6.1. Innovations in sequencing, data analysis, and bioinformatics

"Recent developments in tools for microbiome analysis have revolutionized studies of microbial communities. Next-generation sequencing technologies, especially the high-throughput sequencing of the 16S rRNA gene and whole-genome shotgun metagenomics, have greatly advanced the detection and quantification of species with increased precision and accuracy in complex ecosystems, including the human gut. These methods allow insight into microbial diversity and function that cannot be achieved with traditional culture-based methods.³⁹ Advances in bioinformatics, which includes analysis tools, have provided a computational framework for the analysis and interpretation of large datasets produced with these sequencing technologies. Machine learning techniques and metagenomic assembly processes are on the rise in applicability to discovery for novel microorganisms and microbial functions, along with forecasting microbial interactions and responses to environmental change. These advances will enable researchers to explore the dynamics of the microbiome in health and disease states and allow for an accurate assessment of the evolutionary changes in microbial communities in response to diet, drugs, and disease.

6.2. Potential for new drug discovery

Study of the microbiome presents great opportunities for identification of new medicinal treatment. Such a relation can unfold different pharmacological targets and their pathways which have not been explored till date. Microbial enzymes involved in xenobiotic metabolism may even affect the manner in which pharmaceutical products are metabolized inside the host body, thus assisting in the detection of microbial metabolites with potential drug-like properties.⁴⁰ The identification of bacterial strains with anti-inflammatory or immunomodulatory properties offers new possibilities for probiotic treatments, as seen in the development of live biotherapeutic products (LBPs). These LBPs, which contain specific bacterial strains, are currently being studied for their potential use in treating conditions like inflammatory bowel

disease (IBD), metabolic disorders, and cancer therapy.⁴¹ Additionally, high-throughput screening methods have enabled the discovery of bioactive molecules from microbial metabolites. These compounds have shown antibacterial, antiviral, and anticancer effects, creating new opportunities for drug discovery based on the microbiome.

6.3. Integration of microbiome science into clinical practice

However, with the increasing knowledge of the microbiome there has been a shift to want the incorporation of microbiome studies in the regular practice of medicine. Currently, microbiome profiling is employed in some points of the healthcare system and a approaches to gastrointestinal problems such as *Clostridioides difficile*-associated disease. In such conditions, fecal microbiota transplantation (FMT), has now emerged as an approved therapy.⁴² Further, the data from the microbiome is applied in the development of methods of treatment as well. For this reason, the composition of the microbiome is still being analyzed to determine how it may influence patients' response to immune checkpoint inhibitors in cancer treatment. This present research helps oncologists to target immunotherapies according to the type of microbiome for each patient.⁴³ Thus, in consideration of studies on the Microbiome in pharmacology today it is established that of the factors that affect effectiveness and safety of medications and dosages it is an important point and provides for better decision making on the medications and treatment plans. The use of the microbiome data as a component of the personalized medicine may bring the next level of success in treating diverse diseases such as metabolic syndromes, autoimmune, and mental illnesses.

7. Conclusion

The concept of microbiota plays a crucial role in pharmacology because microbiota influence drug metabolism and absorption as well as the efficacy of some medications. Microbiome effects on mediations through complex adaptors in the host physiology impacts therapeutic benefits and propensity to develop unfavorable side effects. The understanding of the microbiome has resulted in the creation of novel therapeutic approaches, such as: living medicines, bioactive drugs, prebiotics and probiotics that can affect someone microbial profile and therefore the type of therapy to administer to him or her. These onward developments are altering the drug discovery processes and it is clearly pointing to the fact that microbiome should be taken into account while delivering any therapy. Microbiome-based therapeutics can be a game-changer in the world of treatment by using microbiome profiles of a patient. Both probiotics and prebiotics as well as Fecal microbiota transplantation (FMT) showed

effectiveness in the management of the inflammation of the bowel and *C. difficile*. Besides, live biotherapeutic products are being developed to treat such diseases as metabolic diseases and cancer. These treatments demonstrate one of the trends toward using precision health care where drugs are chosen based on the patient's microbiome for better efficacy with minimal side effects. Microbiome research is progressing well and has lots of prospect as a promising and promising field of pharmacology. Promoting the technological development of microbiome analysis methods, improving safety requirements, and addressing the related ethical issues are critical steps toward realising the above potentials of microbiome science. Biomedical decision makers have been adopting microbiome data into clinical practice and drug development and are predicted to further increase, giving new ways to understanding and addressing diseases. Investigation of the microbiome will not only improve the historical knowledge of human health but also revolutionize diagnosis, treatment, and customer-oriented medicine to form the future of healthcare.

8. Author Contribution

All authors have contributed equally to the design, data collection, manuscript composition, revisions, and editing of the review article in the realm of scientific writing.

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10. Conflict of Interest

None.

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References

1. Consortium HMP. Structure, function, and diversity of the healthy human microbiome. *Nature*. 2012;486(7402):207–14.
2. Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI, et al. The human microbiome project. *Nature*. 2007;7164:804–10.
3. Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, et al. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*. 2010;464(7285):59–65.
4. Flint HJ, Scott KP, Louis P, Duncan SH. The role of the gut microbiota in nutrition and health. *Nat Rev Gastroenterol Hepatol*. 2012;9(10):577–89.
5. Leblanc JG, Milani C, De Giori G, Sesma F, Sinderen DV, Ventura M. Bacteria as vitamin suppliers to their host: a gut microbiota perspective. *Curr Opin Biotechnol*. 2013;24(2):160–8.
6. Hooper LV, Littman DR, Macpherson AJ. Interactions between the microbiota and the immune system. *Science*. 2012;336(6086):1268–73.
7. Clemente JC, Ursell LK, Parfrey LW, Knight R. The impact of the gut microbiota on human health: An integrative view. *Cell*. 2012;148(6):1258–70.
8. Schulz MD, Atay C, Heringer J, Romrig FK, Schwitalla S, Aydin B, et al. High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. *Nature*. 2014;514(7523):508–12.
9. Wilson ID, Nicholson JK. Gut microbiome interactions with drug metabolism: A missing link in personalized medicine. *Pharmacol Therap*. 2017;172:30–42.
10. Jiang C, Li G, Huang P, Liu Z, Zhao B. The gut microbiota and Alzheimer's disease. *J Alzheimer's Dis*. 2020;73(4):1239–52.
11. Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI, et al. The human microbiome project. *Nature*. 2007;7164:804–10.
12. Samuel BS, Hansen EE, Manchester JK, Coutinho PM, Henrissat B, Gordon JI, et al. Genomic and metabolic adaptations of *Methanobrevibacter smithii* to the human gut. *Proceed Na Acad Sci*. 2007;104(25):10643–8.
13. Underhill DM, Iliev ID. The mycobiota: Interactions between commensal fungi and the host immune system. *Nat Rev Immunol*. 2014;14(6):405–16.
14. Reyes A, Haynes M, Hanson N, Angly FE, Heath AC, Rohwer F, et al. Viruses in the faecal microbiota of monozygotic twins and their mothers. *Nature*. 2010;466(7304):334–8.
15. Yatsunenko T, Rey FE, Manary MJ, Trehan I, Dominguez-Bello MG, Contreras M, et al. Human gut microbiome viewed across age and geography. *Nature*. 2012;486(7402):222–7.
16. Dominguez-Bello MG, Costello EK, Contreras M, Magris M, Hidalgo G, Fierer N. Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. *Proceed Nat Acad Sci*. 2010;107(26):11971–5.
17. Zhu B, Wang X, Li L. Human gut microbiome: The second genome of human body. *Protein Cell*. 2010;1(8):718–25.
18. Cryan JF, Dinan TG. Mind-altering microorganisms: The impact of the gut microbiota on brain and behaviour. *Nat Rev Neurosci*. 2012;13(10):701–12.
19. Hooper LV, Littman DR, Macpherson AJ. Interactions between the microbiota and the immune system. *Science*. 2012;336(6086):1268–73.
20. Flint HJ, Scott KP, Louis P, Duncan SH. The role of the gut microbiota in nutrition and health. *Nat Rev Gastroenterol Hepatol*. 2012;9(10):577–89.
21. Swann JR, Want EJ, Geier FM, Spagou K, Wilson ID, Sidaway JE, et al. Systemic gut microbial modulation of bile acid metabolism in host tissue compartments. *Proceed Nat Acad Sci*. 2011;108(1):4523–30.
22. Enright EF, Gahan CG, Joyce SA. The impact of the gut microbiota on drug metabolism and clinical outcome. *Yale J Biol Med*. 2016;89(3):375–82.
23. Clarke G, Sandhu KV, Griffin BT, Dinan TG, Cryan JF, Hyland NP, et al. Gut reactions: Breaking down xenobiotic-microbiome interactions. *Pharma Rev*. 2019;71(2):198–224.
24. Haiser HJ, Gootenberg DB, Chatman K, Sirasani G, Balskus EP, Turnbaugh PJ, et al. Predicting and manipulating cardiac drug inactivation by the human gut bacterium *Escherichia coli*. *Science*. 2013;341(6143):295–8.
25. Peppercorn MA, Goldman P. The role of intestinal bacteria in the metabolism of salicylazosulfapyridine. *J Pharma Exp Therap*. 1972;181(3):555–62.
26. Gonzalez A, Vazquez-Baeza Y, Inlay MA, Stumpf S, Escapa IF, Walters WA, et al. The mind-body-microbial continuum: Evolving views on the gut-brain axis. *Microbiome*. 2016;4(1):1–10.
27. Wallace BD, Wang H, Lane KT, Scott JE, Orans J, Koo JS. Alleviating cancer drug toxicity by inhibiting a bacterial enzyme. *Science*. 2010;330(6005):831–5.
28. Viaud S, Saccheri F, Mignot G, Yamazaki T, Daillère R, Hannani D, et al. The intestinal microbiota modulates the anticancer immune effects of cyclophosphamide. *Science*. 2013;342(6161):971–6.

29. Elrakaiby M, Dutilh BE, Rizkallah MR, Boleij A, Cole JR, Boleij A, et al. Pharmacomicrobiomics: The impact of human microbiome variations on systems pharmacology and personalized therapeutics. *OMICS: A J Integrat Biol*. 2014;18(7):402–14.
30. Haiser HJ, Gootenberg DB, Chatman K, Sirasani G, Balskus EP, Turnbaugh PJ, et al. Predicting and manipulating cardiac drug inactivation by the human gut bacterium *Eggerthella lenta*. *Science*. 2013;341(6143):295–8.
31. Wilson ID, Nicholson JK. Gut microbiome interactions with drug metabolism: A missing link in personalized medicine. *Pharmacol Therap*. 2017;172:30–42.
32. Gopalakrishnan V, Spencer CN, Nezi L, Reuben A, Andrews MC, Karpins TV, et al. Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. *Science*. 2018;359(6371):97–103.
33. Zimmermann M, Kogadeeva MZ, Wegmann R, Goodman AL. Mapping human microbiome drug metabolism by gut bacteria and their genes. *Nature*. 2019;570(7762):462–7.
34. Clemente JC, Ursell LK, Parfrey LW, Knight R. The impact of the gut microbiota on human health: An integrative view. *Cell*. 2012;148(6):1258–70.
35. Yu J, Feng Q, Wong SH, Zhang D, Liang QY, Qin Y. Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. *Gut*. 2017;66(1):70–8.
36. Spanogiannopoulos P, Bess EN, Carmody RN, Turnbaugh PJ. The microbial pharmacists within us: A metagenomic view of xenobiotic metabolism. *Nat Rev Microbiol*. 2016;14(5):273–87.
37. Hill C, Guarner F, Reid G, Gibson GR, Merenstein DJ, Pot B, et al. Expert consensus document: The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. *Nat Rev Gastroenterol Hepatol*. 2014;11(8):506–14.
38. Slavin J. Fiber and prebiotics: Mechanisms and health benefits. *Nutrients*. 2013;5(4):1417–35.
39. Zhang N, Ju Z, Zuo T. Time for food: The impact of diet on gut microbiota and human health. *Nutrition*. 2015;31(3):365–70.
40. Nood EV, Vrieze A, Nieuwdorp M, Fuentes S, Zoetendal EG, De Vos W, et al. Duodenal infusion of donor feces for recurrent *Clostridium difficile*. *New Eng J Med*. 2013;368(5):407–15.
41. Kelly CR, Khoruts A, Staley C, Sadowsky MJ, Abd M, Alani M, et al. Effect of fecal microbiota transplantation on recurrent *Clostridium difficile* infection in patients with inflammatory bowel disease: A double-blind, placebo-controlled randomized trial. *Gut Microbes*. 2015;6(3):234–42.
42. Kao D, Hotte N, Gillevet P, Madsen K, Faure H. SER-109, a rationally designed microbiome therapeutic, to reduce recurrent *Clostridium difficile* infection in patients with CDI. *J Gastroenterol Hepatol*. 2017;32(2):53–9.
43. Roy S, Trinchieri G. Microbiota: A key orchestrator of cancer therapy. *Nat Rev Cancer*. 2017;17(5):271–85.


Author's biography

Ashvini Arun Kakad, Students

Rucha A Ingle, Associate Professor

Aarti Mahadev Nimse, Students

Rutuja Devidas Giram, Students

Shatrughna Uttam Nagrik, Associate professor  <https://orcid.org/0009-0006-5988-4199>

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