

The Microbiota-Medicine Nexus: Exploring the Impact of Gut Microbiota on Pharmacotherapy

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Abstract

Researchers have uncovered in the last few years that as small as capsules of trillions of microscopic organisms in the intestine, called the gut microbiome, can have a large portion of the effects on our medications. It is this complex connection that this review paper attempts to describe between gut microbiota and pharmacotherapy, which in general means using a drug to treat diseases. We'll become aware of what factors form the composition of our gut microbiota, the diet being one of them, and even the influence of antibiotics and how this may affect how drugs enter, pass through, and get used by our body. This further supports the successful implementation of tailored regimens, decreasing levels of drug-induced toxicity, and increasing the efficiency of medications. This paper emphasizes the need to be mindful of gut microbes when you develop and apply medications. It may be a trailblazing step toward individualized and more productive therapeutic approaches.

Key words: Diseases, drug, gut, microbiota

INTRODUCTION

Microbiome is a micro-miniature ecosystem of microorganisms that are usually disclosed to exist within the human body. Microorganisms are classified as either bacteria, viruses, fungi, or even archaea. These microbial communities, a multitude of members that dominate different habitats, including the skin, the mouth, the gastrointestinal tract, and the genital areas, are present among these anatomical locations. Their synergy manifests as different effects complicatedly interweaved, leading nowhere but to overall health improvement of the individuals and the species' genetic fitness. The health repercussions could be possible due to mechanisms as digestion and immunity, or even neurology. Microbiota is not simply a flavor mate but a competent team whose participation is in processes like nutrient metabolism, immune regulation, and defending from microbes, pathogens, and even cancer. Alteration of the homeostasis mediated by diet, drugs (antibiotics), lifestyle, and stress, triggers the appearance of disorder also known as dysbiosis, and this condition combined with a spectrum of disorders made of gastrointestinal diseases, metabolic disorders,

and even neurological conditions. Therefore, awareness of the invaluable microbial role in controlling a person's health emerges. Referring to this, research into having a wide community of microbiota becomes necessary for receiving the healthiest influences.^[1]

The intestinal microbiota is the engine behind human health, and it acts on the host as many systems of human physiology as well as maintains the stability and homeostasis of a host's body. This microbiome is surprisingly complex rather and it is particular to different bodily sites inside us, like the skin, bucking, oral cavity, and urogenital tracts. This host-microbiome mutualism is a basic requirement for preserving health as well as disallowing pathogens from colonizing. Cambridge University Press within the lining of the gastrointestinal tract, you can find a range of microorganisms that absorb some of the food nutrients, synthesize certain vitamins which lead to maturing and

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proper functioning of the immune system. Dysbiosis in the microbial composition (disturbances) is believed to play a part in multiple disorder causes, including inflammatory bowel diseases, metabolic disorders including obesity and diabetes, among others, and mental health illnesses such as depression and anxiety.^[2] Alteration of the normal microbial balance due to factors such as diet, drugs (especially antibiotics), lifestyle, and stress results in a condition known as gut microbiota dysbiosis, which has been associated with several chronic diseases, including liver disease, diabetes, heart disease, and cancer, as illustrated in Figure 1.

Digestive health

The various types of microbiota in the gut play many roles, for example, in the digestion process and nutrient absorption. This includes two of the most essential vitamins that plants can produce in large amounts, like vitamin K and certain B vitamins. They also affect the digestive system during digestion, where they help in the breaking down of large molecules into digestible components.

Immune system regulation

Tiny bacteria that are in your gut help normalize your immune response. The immune system can select the good ones from the bad, either useful or harmful objects or pathogens, so it can also prevent harmful immune responses such as allergies and autoimmune diseases.^[3]

Protection against pathogens

The colonizers are also the controllers of these pathogen populations, so they can stop their takeover by offering them competition for the limited resources. These are species of fellow competitors that actually keep the vulnerability to infections at bay.^[4]

Metabolism and weight regulation

It has just been recently found that this gut microbe composition might be the actual mechanism of control over metabolism and weight, which are the main functions regulating the body's energy balance. Scientists have proved that there is a link between weight gain and certain strains of Gram-negative bacteria, and in addition, it has been demonstrated that lean bacteria are related to a lean body. Discovering how the microbiota in the gut influences the regulation of metabolic function and weight could be an innovative approach to preventing metabolic diseases.^[5]

Neurological function

The messages of gut microflora interact with the brain via the gut–brain axis in two different ways. Such communication

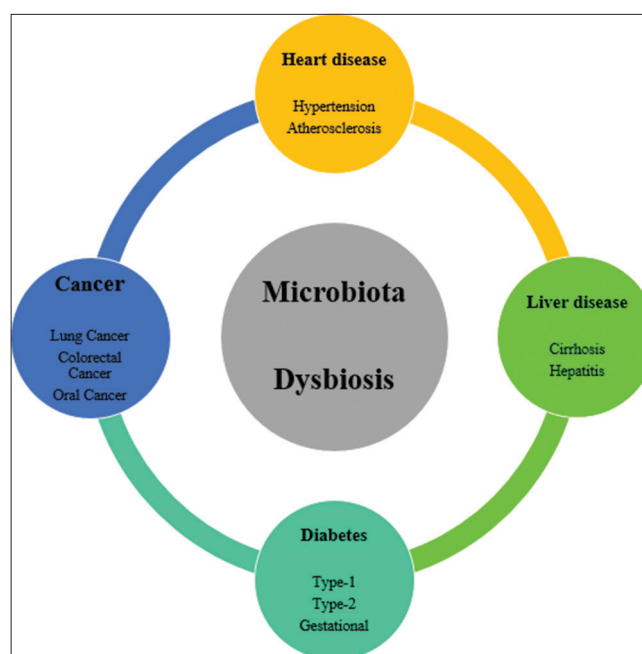


Figure 1: Gut microbiota dysbiosis

leads to alterations in neurobiological activities such as the regulation of emotions, the understanding of psychological pressure, and cognitive function.^[6]

PHARMCOTHERAPY

Pharmacology which is the narrow area of medical science that deals with the subjects of imitating of sicknesses by supplying pharmaceuticals as well as other medical preparations is found to be very helpful for diagnostics. The treatment comprises an array of therapeutic techniques: The treatment (a peck of treatments of this sort): Pharmaceuticals, biologics, and other genres of medicine delivery for the signs and symptoms or even the disease as systemic progression.^[7]

The proper functioning and safety of therapeutic drugs are mainly dependent on their drug metabolism, which is the process of altering the drugs chemically to facilitate their elimination. The metabolism of most drugs is in the liver, where enzymes change the medications into metabolites that can be easily removed by the kidneys or intestine. This biotransformation is responsible for drug metabolism into more or less active forms via either drug activation, inactivation, or conversion of drugs. The end result is altered drug effectiveness and safety. Many drug metabolism factors exist, e.g., there are different genetic variations in drug-metabolizing enzymes, other prescribed medications that interfere with enzyme activity, age, gender, as well as existing health issues. A comprehension of these factors becomes crucial for achieving the desired therapeutic effects and ensuring safety against adverse events. Absorption, distribution, metabolism, and excretion (ADME) (which includes drug absorption, distribution, metabolism, and

removal) is the key pharmacokinetic principle contributing to drug efficacy. Even minute alterations in any of the intra-body systems may hinder the circulation of a drug to its target site, rendering the drug ineffective. It is an illustration whereby poor absorption may lead to disproportionate levels of drugs in the blood, whereas rapid metabolism may cause inadequate exposure to the drug and consequently failure of treatment.

The term pharmacodynamics deals with how the body and its biochemical processes respond to drug effects and the drug concentration at the site of action. The pharmacodynamics and pharmacokinetics of drugs cannot be underestimated too; when it comes to treatment regimens from these drugs, the from will always be there. The prescribing of drugs in the clinical setting is quite magnanimous when it comes to the pharmacokinetics of drugs beyond the metabolism to give a specific drug regimen that will be the optimum choice just to give maximum response and minimum side effects that are caused by the treatment. Coming from the research advancements in using the genetic information for designing new therapies with molecular targets that are specific to individual drugs and the disease conditions, pharmacogenomics teams up with the whole phenomena of personalized medicine, and bringing success and hope to the drug treatments, given the fact that it takes into consideration the individual differences in drug metabolism and response and their link to genetic variations that influence the expression of the protein coding. Taking medications metabolism and pharmacokinetics into account would be critical to optimal treatment in clinical situations; all healthcare professionals should be well versed in this area since the responsible use of drugs is the prerogative and determinant factor of high health outcomes for patients.^[8]

KNOWLEDGE OF THE GUT MICROBIOTA

The digestive tract is considered the place where exists various microorganisms in a state known as gut microbiota flora that is helpful for human health and supports the diseases in their development. What is unique about this microbiome is that a combination of different strains and species of microbes is affected by different factors which include taking different types of food, antibiotics, lifestyle, and genes of the host.^[9]

Diversity and composition of gut microbiota

The gut microbiota chiefly includes bacteria, but other microbes such as viruses, fungi, and archaea also exist. The bacterial component is dominated by a few phyla, where the Firmicutes and Bacteroidetes genera are the most abundant. Among these phyla, there are a vast number of genera and species existing; constructing an intricate ecosystem comprises complex interactions. Diversity of gut microbiota means the degree of variety and even distribution of all species present in the environment, which contributes to ecosystem stability and functional resilience.^[10] A representative classification of

the dominant, rare, and transient microbial species present in the gut microbiota is shown in Table 1.

Factors affecting gut microbiota composition

Diet

It appears that eating habits are the primary modulators of the bacterial composition of the gut, with some Lactobacilli and Bifidobacteria being able to proliferate when fed a high-fiber diet. On the other hand, eating sweets and fats may affect the amount of unfriendly bacteria in the population.^[11]

Antibiotics

The use of antibiotics may have an effect on the makeup of the intestinal microbiota by eliminating bacteria that are susceptible to them as a result of a decline in microbial diversity. This may also foster an environment that is conducive to the growth of pathogens.^[12]

Lifestyle

While factors such as stress, physical activity, and sleep patterns can influence the gut microbiota composition indirectly via diet modification and the immune pathways they control.^[13]

Host genetics

Genetic factors play a part in the fact that human beings have differences in the composition of bacteria in their guts, but the exact degree of this influence is yet to be understood.^[14]

The gut microbiota's dynamic nature and pharmacotherapy relevance

The digestive microbiota is a variable one, showing a cyclic pattern under the influence of different factors, for example, changes in diet, medication use, and exposure to the environment.^[14]

Drug metabolism

The gut microbiota may be able to degrade certain drugs (either directly or indirectly) by means of their enzymatic

Table 1: Compositions of gut microbiota

Sr. No.	Composition		
	Dominant species	Rare species	Transient species
1	<i>Clostridium</i>	<i>Streptococcus</i>	Yeasts, Lactic acid bacteria
2	<i>Bifidobacterium</i>	<i>Enterobacteriaceae</i>	
3	<i>Bacteroides</i>	<i>Escherichia coli</i>	
4	<i>Eubacterium</i>		
5	<i>Faecalibacterium</i>		

activity; consequently, this may foster changes in the drugs' pharmacokinetic characteristics and effectiveness.^[15]

Drug interactions

The gut microbiota can interact with pharmacologic agents, modifying their ADME by mechanisms that include drug-bacteria interactions or the alteration of the gut barrier.

In fact, the reason behind comprehending the structure, diversity, and dynamic nature of the gut microbiota is to achieve optimum pharmacotherapy outcomes. Utilizing information on host-microbe interactions in drug creation as well as in clinical application is an amazing possibility for creating more effective treatments and reducing negative side effects.^[16]

DRUG INTERACTIONS WITH THE GUT MICROBIOTA

The role of the gut microbiota in drugs and their therapeutic effects is becoming evident with drugs impinging on the landscape of modern pharmacotherapy. The gut microbiota, a complex ecological system of microorganisms within the gastrointestinal tract, is responsible for driving metabolism through several mechanisms. Certain compounds, especially those with complicated structures or low bioavailability, may be transformed by the action of gut bacteria into metabolites with altered properties. The impact of microbial metabolic activities on drugs' efficacy, bioavailability, and toxicity status is huge. The metabolic capabilities of the gut microbiome include a variety of enzyme-contained chemical reactions, such as hydrolysis, reduction, oxidation, and conjugation, which may turn the drugs into more or less active forms. For instance, a gut bacterial process known as the prodrug conversion of sulfasalazine, a common treatment, increases its therapeutic efficacy in inflammatory bowel disease. However, microbial metabolism can also result in the deactivation of drugs, an occurrence that lowers the drugs' effectiveness and could require more doses for the same therapeutic effect.^[17]

Similarly, the gut microbiota can exert an indirect modulation over the systemic effects of drugs via a few different mechanisms. The microbial metabolism of the dietary components and the endogenous compounds may change gut permeability, and so the absorption of orally administered drugs can be affected. Besides, gut flora may compete with medicines for binding sites on transport proteins, which uptake drugs from the gut and make them accessible for systemic circulation. On the other hand, drugs could trigger gut microbiota selection, driving changes in microbial composition as well as function. Antibiotics are a well-known culprit for destroying diversity across the gut microbiome and strengthening antibiotic-resistant bacteria, consequently emphasizing the complexity of relationships between bacterial ecology and drug therapy.

The bidirectional intertwining between microbiota-gut interactions and medications has profound effects on personalized medicine and therapeutic optimization. The appreciation of gut microbiome peculiarities at every individual level can be helpful in predicting drug responses and thus allowing treatment adjustment to minimize adverse effects while achieving the best possible therapeutic effect. Furthermore, treatments that aim to alter gut microbiota, such as probiotics, prebiotics, and fecal microbiota transplantation, show potential for improving the response and reducing the side effects of certain medications in certain patient types.

While we continually gain new knowledge about gut microbiota-drug relationships, there are still many uncertainties about the mechanisms by which these interactions occur and the clinical importance of these connections. The research remains poorly understood at present in terms of gut microbiota and drug therapy differences across different diseases and populations. Notwithstanding this, the use of host microbiota knowledge to influence the process of drug development and the practice of healthcare presents an excellent opportunity to tailor drug effects and enhance patient care that fits the era of precision medicine.

The intestinal microflora has a powerful effect on the uptake, metabolism, and excretion of various drugs alternating the bioavailability of drugs and their pharmacokinetic profile. The gut microorganisms conduct a variety of metabolic processes, among them degrading the drug molecules and changing their chemical structure, thus producing the drug effects which are different from those that they could exhibit in the absence of these bacteria. One of the significant endorsements of the gut flora to the drug's bioavailability is biotransformation. Taking high levels of drugs which have complicated chemical structure or whose bioavailability is low, a gut bacteria enzyme may be able to debrminate them. This can be done by using different forms of raw materials and varying the degradation process, leading to the generation of metabolites having different pharmacokinetic profiles. The whole intestinal metabolism of microorganisms might be either increased or decreased in health-effectiveness through the effects of their metabolites. A further case is nucleoside absorption from the gut microbes of the prodrug, sulfasalazine, to sulfapyridine and 5-aminosalicylic acid to treat inflammatory bowel disease.^[18]

CASE STUDIES OF CERTAIN MEDICATIONS INFLUENCED BY INTESTINAL FLORA

Statins

Statins are from a group of meds that are specifically used to lower cholesterol to high levels so that the occurrence of cardiac events will favorably follow. New findings suggest

that the cause of statin synthesis could be almost connected to the gut microbiota composition. An illustration of this effect is when gut bacteria like *Eggerthella lenta* are shown, through research, to break down statins. As a result, the effectiveness of the chemotherapeutic plan may diminish.^[19]

Proton pump inhibitors (PPIs)

PPIs make wide use in blocking stomach acid secretion in heartburn and peptic ulcers by inhibiting pumps that secrete hydrogen ions into the stomach. However, PPIs may well have repercussions for other enteric microbiota composition and diversity that could ultimately result in dysbiosis. The intestinal microbial changes after PPIs are relevant, together with a higher risk of gastrointestinal infections, including *Clostridium difficile* and many others.

Anticancer drugs

The gut microbiota possesses the ability of endogenous antibacterial activity; therefore, it may use the bacterial members of it to degrade drugs with medication-metabolizing enzymes. As an instance, irinotecan, which is the prodrug for SN-38, consistently fulfils its role as an end product after the biotransformation by the intestinal bacterial cells. However, at best, the intestinal microbes can turn these SN-38s into the harmless forms that eventually can be described as a lessened drug effect. One of the biggest issues in the therapy of cancer through drug metabolism is the local microflora of the gut which is going to be a key factor in the results of treatment.^[20]

Metformin

Monotherapy with metformin is most often a choice of first-line treatment with minimal risk and a very good efficacy for type 2 diabetes patients. Study results of the recent time have proven that the gut microbiota strongly influences the way the medication functions and affects the patient. The so-called protective role of these bacteria was unveiled, as experiments showed that one of these bacteria, namely *Akkermansia muciniphila*, was able to improve metformin bearing the glucose levels, either in their production or their intake/consumption, as it can stimulate glucose metabolism in the host of short-chain fatty acids.^[21]

Antibiotics

These antibiotics have the properties of drugs and also evoke a specific bacteria-to-inhibit state as well as act as regulators and controllers of gut microbiota. The problems of using microbiological drugs include upsetting the balance between the microbes, altering the normal condition, and cannot take the relationship between the gut microbiota with other drugs.

PHARMACOKINETICS AND GUT MICROBIOTA

The community of microorganisms, the gut microbiota that lies in the gastrointestinal tract, is one of the major mechanisms of drug action and concerns the effectiveness and metabolism. This may be either exacerbating or enhancing drug efficacy and has complicated health policy-making. Your gut microbiome, after several antibiotic treatments, may be depleted by some dying species of bacteria capable of converting drugs into compounds that are less active by way of special enzymes. For this reason, antibiotic therapies will not be as effective. However, microbiota can also contribute to drug function by providing biocatalysis as well as the performance of prodrugs. This is particularly obvious when we consider the fate of sulfasalazine (a drug for the oral administration of diseases such as colitis, ulcerative colitis, and rheumatoid arthritis), which is metabolized by gut bacteria into two of its main components, namely, sulfapyridine and, most recently, 5-aminosalicylic acid, thereby increasing its therapeutic effect. Apart from the multi-aspect overview, it gives on the diversity of drug efficacy among different individuals depending on the specific makeup of their gastrointestinal flora, the cross-linguistic cooperative nature of this union even implies inner conversations across the body.^[22]

Since microbiota are invoked in the activation of prodrugs, the microbial implications in pharmacokinetics are of paramount importance, and being able to utilize this knowledge during drug design and drug delivery technology has become an essential tool. Prodrugs, drugs that are inactive until they are converted into their active form by the human body, take a substantial part in this process, which is highly assisted by the gut microbiota through its participation in enzyme-substitution activities that cannot be carried out by the human digestive enzymes. For example, as the prodrug irinotecan is degraded by intestinal beta-glucuronidase into its active metabolite, it can cause a severe tumor response in the digestive tract. This means that this has to be done by going through the drug design and by concurrent use of the different classes of antibiotic adjuvants or low-concentrating mode inhibitors to control the activity of the microbiota, with eventual inhibition in tincture.

In addition, the role of the microbial communities in the gut with regard to drug safety outcomes is manifested in their ability to either suppress or enhance the immune response of the host, metabolic activity, and even susceptibility to drug-induced side effects. Different proportions of bacteria (microbiota composition) among individuals will bring about various metabolisms of a drug, effectiveness, and adverse reactions. This could be a case of *E. lenta* metabolizing digoxin, a cardiac glycoside, to some extent, resulting in a range of patients' varying efficacy and eventually a need to consider some individual gut microbiota profiles in the context of personalized medicine. Furthermore, microbiota alterations, especially after administration of antibiotics,

dietary changes, or diseases, modify dramatically the drug metabolism pathways, which can result in decreased therapeutic effectiveness or an increased risk of adverse effects. An emerging field of research demonstrates the significance of the attitude of the microbiome in drug development and personalized treatment, which will enhance their effectiveness and safety and make them successful.

VARIABILITY IN THE MICROBIOTA PRESENTS DIFFICULTIES FOR PHARMACOTHERAPY

The intracluster individual differences in composition of the gut microbiota raise great difficulties in deciphering pharmacotherapy, which becomes most pronounced in cases of determining the predictable drug effects across a number of patients. The complexity is a result of a number of factors, some of them genetic differentials, diet, age, and antibiotic exposure, that all come together to make each person's gut microbial ecosystem different from others. This diversity leads to differences in the metabolism of drugs, not limiting it to only their absorption, distribution, and elimination, which can result in the treatments becoming ineffective or unsafe. On the one hand, being persiripan untuk enzymes in particular could lead either to hastened drug metabolism and consequently ineffective involution or to a very slow elimination of drugs that, on the other hand, may result in toxicity.

Genetic diversity affecting the microbiome also has a major influence on personalized medicine, urging the need for a switch in medication dosage at times for ideal results. Among others, personalized medicine aims to design medical treatment based on specific features of clinical situations, for which microbiota composition has been voted as one of the most important factors. Nevertheless, just like the microbiome, which varies according to lifestyle, dietary habits, or disease development, the whole process of drug development gets more difficult because adjusting the dosing regimen is required. This, in a way, drives the need for a robust and feasible drug administration strategy that may allow for periodic microbiome testing to decide eventual dosages. In addition, probiotics or prebiotics may be used as an additional intervention with the target of modulating the microbiome for improved drug action. Hence, even though the microbiome acquires the status of a known factor that drives drug metabolism, the exploitation of the microbiome profiles for the predictive purpose of drug responses still represents a formidable challenge. The complexity and variability of the microbiome, as well as the fact that we still have to understand the interrelationships of the microbiome with the drug, limit the ability to predict only the outcomes of therapeutics based on microbiome analysis. Research now concentrates on accurately identifying the colonies of microbes interacting with medications and discovering the molecular processes involved in these effects. Nevertheless, translating this newly gained knowledge into clinical practice

is a problem that can be solved by using advanced, and at the same time, user-friendly, tools that are able to carry out microbiome data analyses quickly and accurately and then integrate them into the clinical decision-making process. This has indicated that the microbiome has more to bring to the field of refinement of pharmaceutical therapy, and so we need more science and advanced technology to enable us to achieve the full potential of personalized medicine.^[23]

RESEARCH ON MICROBIOTA-PHARMACOTHERAPY'S FUTURE DIRECTIONS

As pharmacomicrobiomics gains momentum, a disruptive frontier in biomedical research will be established, allowing for the development of further microbiota-targeted strategies that will improve therapy outcomes and reduce patient exposure to potentially harmful medications. The expanding horizons within this field are turning their attention to gut microbiome modifications that can affect pharmacokinetics and pharmacodynamics, with the aim of using this information to devise novel therapy methods. Such a purpose can be served by deploying drugs that additionally modulate the microbiome in order to maximize the benefits of therapy. For instance, the production of non-antibiotic substances that are involved in the inhibition of pathological bacterial enzymes but do not affect the normal microbiome in general will neutralize the drug side effects and improve the drug efficiency.^[24]

The gut microbiota, because of its ability to influence the design and pharmacokinetics of drugs, can be targeted with prebiotics and probiotics to regulate drug metabolism. These microbiota-directed therapies could be utilized not only for the activation of prodrugs but also to protect microflora from the side reactions leading to dysbiosis, which may ultimately reduce the effectiveness of the drugs. Besides this, the use of synthetic biology exhibits potential to build gut microbial strains, which can directly produce therapeutic agents in the gut or can be programmed to fight disease and respond on time, thereby offering personalized treatment targets. For the bioactive compounds to take shape in the medicines, a strategy integrating microbiology, pharmacology, and genomics is indispensable.^[25]

Such an approach should involve cutting-edge molecular diagnostics to reveal the intricate connections between the microbiome and drugs, with computational simulation for what-if scenario simulations when using drugs. Finally, though, studies that involve microbiome analysis during therapy will be critical in proving the role of microbiota in drug response in assorted patient populations. Combining this sort of integrated system will tabulate and direct our understanding of microbiota-pharmacotherapy departments and promote the transition of these gains into pediatric treatment, which will ultimately be superior, more efficient, and more effective.

CONCLUSION

Summing up, the perspective of microbiome research relating to pharmacotherapy proves to be an interesting and relevant subject in medicine today. We know now that the trillions of bacteria residing in our gut can be a dominant factor in what affects the way medications work in our bodies. Among them, knowing and wanting these responses and drug interactions is accompanied by the fact that health practitioners can enhance the efficiency and safety of medications for the patients.

Contributing factors, for example, diet, antibiotics as well as lifestyle choices have an influence on the structure and the way our gut microbiota functions. Consequently, the process of drug absorption, as well as metabolism and use by our bodies, is affected. This emphasizes the importance of targeted therapies in the treatment of drug targets, which consider the variations in gut microbiota in each individual. To move on, research in this area will be a key factor in the success of developing drugs which can be used more accurately and differentiated from one another. The path that the gut microbiome can be used in pharmacotherapy is highly promising. In the long turn, we expect that this will help in improving treatment results, minimizing side effects, and of course, in personalizing the approach which will contribute to better health outcomes.

REFERENCES

- Dekaboruah E, Suryavanshi MV, Chettri D, Verma AK. Human microbiome: An academic update on human body site specific surveillance and its possible role. *Arch Microbiol* 2020;202:2147-67.
- Thursby E, Juge N. Introduction to the human gut microbiota. *Biochem J* 2017;474:1823-36.
- Yoo JY, Groer M, Dutra SV, Sarkar A, McSkimming DI. Gut microbiota and immune system interactions. *Microorganisms* 2020;8:1587.
- Caballero-flores G, Pickard JM, Núñez G. Microbiota-mediated colonization resistance: Mechanisms and regulation. *Nat Rev Microbiol* 2023;21:347-60.
- Shrestha RT, Malabanan A, Haugen BR, Levy EG, Hennessey JV. Adverse event reporting in patients treated with thyroid hormone extract. *Endocr Pract* 2017;23:566-75.
- Gwak MG, Chang SY. Gut-brain connection: Microbiome, gut barrier, and environmental sensors. *Immune Netw* 2021;21:e20.
- Mazayen ZM, Ghoneim AM, Elbatany RS, Basalious EB, Bendas ER. Pharmaceutical nanotechnology: From the bench to the market. *Futur J Pharm Sci* 2022;8:12.
- Maxwell SR. Pharmacodynamics and pharmacokinetics for the prescriber. *Medicine*. 2024;52:1-0.
- Rinninella E, Raoul P, Cintoni M, Franceschi F, Miggiano GA, Gasbarrini A, *et al.* What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms* 2019;7:14.
- Narayan Biswal B, Narayan Das S, Kumar Das B, Rath R. Alteration of cellular metabolism in cancer cells and its therapeutic prospects. *J Oral Maxillofac Pathol* 2017;21:244-51.
- Fu J, Zheng Y, Gao Y, Xu W. Dietary fiber intake and gut microbiota in human Health. *Microorganisms* 2022;10:2507.
- Konstantinidis T, Tsigalou C, Karvelas A, Stavropoulou E, Voidarou C, Bezirtzoglou E. Effects of antibiotics upon the gut microbiome: A review of the literature. *Biomedicines* 2020;8:502.
- Dzierzewski JM, Sabet SM, Ghose SM, Perez E, Soto P, Ravyts SG, *et al.* Lifestyle factors and sleep health across the lifespan. *Int J Environ Res Public Health* 2021;18:6626.
- Tabrett A, Horton MW. The influence of host genetics on the microbiome. *F1000 Res* 2020;9:1-9.
- Pant A, Maiti TK, Mahajan D, Das B. Human gut microbiota and drug metabolism. *Microb Ecol* 2023;86:97-111.
- Weersma RK, Zhernakova A, Fu J. Interaction between drugs and the gut microbiome. *Gut* 2020;69:1510-9.
- Steiner HE, Gee K, Giles J, Knight H, Hurwitz BL, Karnes JH. Role of the gut microbiome in cardiovascular drug response: The potential for clinical application. *Pharmacotherapy* 2022;42:165-76.
- Sun C, Chen L, Shen Z. Mechanisms of gastrointestinal microflora on drug metabolism in clinical practice. *Saudi Pharm J* 2019;27:1146-56.
- Hussain A, Kaler J, Ray SD. The benefits outweigh the risks of treating hypercholesterolemia: The statin dilemma. *Cureus* 2023;15:e33648.
- Fu C, Yang Z, Yu J, Wei M. The interaction between gut microbiome and anti-tumor drug therapy. *Am J Cancer Res* 2021;11:5812-32.
- Soiza RL, Donaldson AI, Myint PK. Vaccine against arteriosclerosis: An update. *Ther Adv Vaccines* 2018;9:259-61.
- Hammerhøj A, Gubatan JM, Nielsen OH. Gut microbiome and disorders of the gastrointestinal tract. *Microorganisms* 2024;12:576.
- Hasan N, Yang H. Factors affecting the composition of the gut microbiota, and its modulation. *PeerJ* 2019;7:e7502.
- Wallenborn JT, Vonaesch P. Intestinal microbiota research from a global perspective. *Gastroenterol Rep* 2022;10:goac010.
- Rowland I, Gibson G, Heinken A, Scott K, Swann J, Thiele I, *et al.* Gut microbiota functions: Metabolism of nutrients and other food components. *Eur J Nutr* 2018;57:1-24.

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