

Investigating The Role of The Microbiome in Health and Disease

Arifa MEHREEN

Quratulane GILLANI

Ayesha Bintay FAROOQ

Rumaisa NAWAL

Maria NAZIR

Minal HUSSAIN

Shafeeq ur REHMAN

Muhammad SAFDAR

Introduction

The human body harbors a vast and vital community of microorganisms known as the microbiome, comprising bacteria, viruses, fungi, and other organisms. Recent advances in sequencing technology have unequivocally demonstrated the crucial role of the microbiome in human health (Gebrayel et al., 2022). This chapter will deliver a comprehensive overview of the microbiome, encompassing its definition, composition, impact on health, and potential treatment applications. The microbiome encompasses all microorganisms (as shown in Table 1) residing in different body parts, with the highest concentration found in the gastrointestinal tract and other mucosal surfaces. The complex ecosystem of bacteria in the human body is predominantly composed of the phyla Bacteroidetes and Firmicutes (Rinninella, Raoul, et al., 2019). The microbiome is influenced by various factors, making it a multifaceted process. Genetics, birth methods, antibiotic use, and environmental influences are significant, but the role of a healthy diet is particularly emphasized (Fletcher, 2015).

Table 1: The Human Microbiome: A Quantitative Overview

Microbiome Marvel	Astonis- hing Value	Explanation	References
Total Micro- bial Cells	~38 trillion	The microbiome's vast influence is emphasized by outnumbering human cells.	(Bolan, 2019)
Diversity of Species	Thousands	This category comprises diverse microorganisms such as bacteria, viruses, fungi, and other organisms with distinct functions.	(Coleman & Whitman, 2005)
Weight of Microbes in Gut	2-5 pounds (0.9-2.3 kg)	Of equal weight to the human brain, highlighting its significance towards digestion, immunity, and general well-being.	(Mocanu, 2021)
Microbial to Human Cell Ratio	~1.3:1	Shows the important function that microorganisms have in human biology and physiology.	(Salvucci, 2019)

Numerous studies have highlighted the strong influence of diet on the gut microbiome. The composition and diversity of the gut microbiome have a mutually beneficial relationship with the host. Gut bacteria break down complex carbohydrates, produce essential vitamins, and contribute to the production of short-chain fatty acids (SCFAs), which significantly impact health (Portincasa

et al., 2022). Additionally, the gut microbiome goes beyond nutrient production and digestion. It plays a crucial role in training and regulating the immune system, safeguarding the body against excessive activation (which can lead to inflammation) and insufficient activation (due to reduced pathogen defense) (Shao et al., 2021). An effective microbiome function acts as a defense against potential invasion by harmful pathogens (McLaren & Callahan, 2020). Increasing evidence suggests that an imbalance in gut bacteria, known as dysbiosis, is connected to chronic conditions such as inflammatory bowel disease (IBD), as well as non-digestive conditions like type II diabetes, obesity, and contact allergies.

2. Understanding the Human Microbiome

The human microbiome is an intricate and dynamic ecosystem that hosts a myriad of microorganisms, including bacteria, viruses, fungi, archaea, and other unicellular life forms that are too small to be seen with the naked eye. These microorganisms, collectively known as microbiota, are distributed throughout various body regions, such as the skin, oral cavity, and urogenital track (as shown in Figure 1). However, the largest microbial population that can be found in the human body is represented by the gastrointestinal microbiota, with the largest part of it residing in the large intestine (Hillman et al., 2017). Microorganisms present and living inside of the stomach are known as the ‘gut microbiome’. These microbes are therefore among this diverse community that plays various roles in the physiological functions of the body including digestion, absorption of nutrients, and Immune regulation (as shown in Table 2). The complex interplay between the human body and the gut microbiota has become the focus of attention in scientific research due to the growing understanding of their significance in human health and pathology (Afzaal et al., 2022).

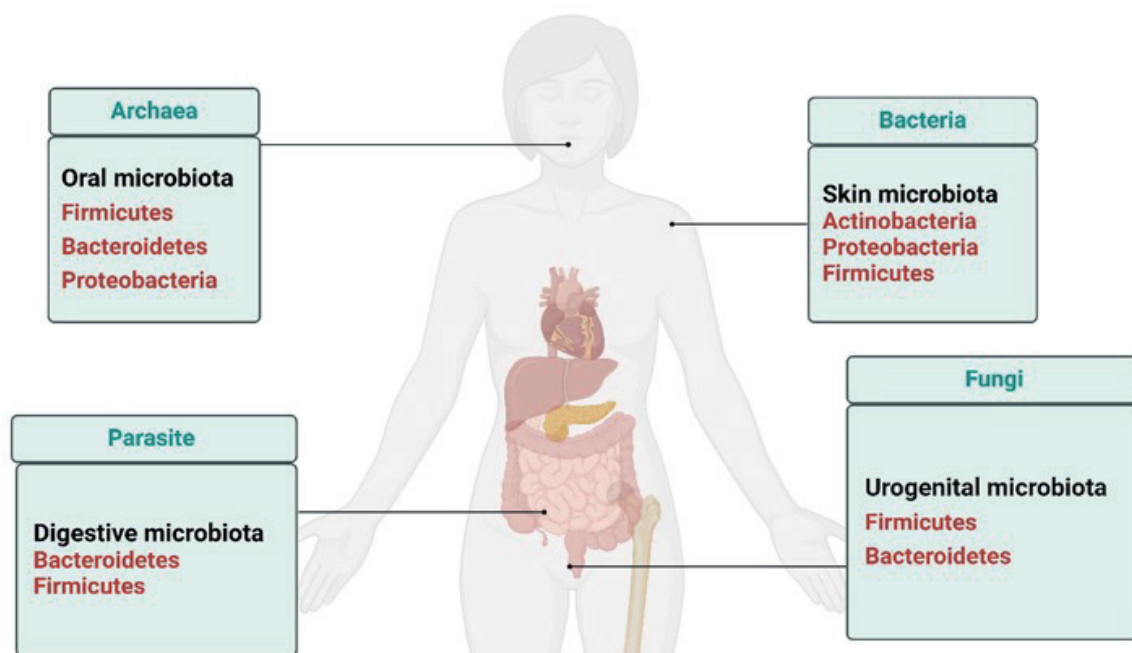


Figure 1. Composition of the Human Microbiome

The gut microbiome is defined as a complex community of microbial specimens that can inhabit the human intestine. Over 1,000 bacterial species have been discovered with two of the most abundant being phyla Bacteroidetes and Firmicutes (Zafar & Saier Jr, 2021). Furthermore, smaller species of Prokaryotes, Actinobacteria, Proteobacteria, and Verrucomicrobiaia have also been present in the environment (Fujimoto, 2012). It is critical to comprehend the complex interactions between these biotic structures and the numerous factors affecting the populations, to enhance and improve the knowledge of microbiome functionality. Every anatomical site of the human body has

its niche with specific conditions to which the microbial community occupying it has to adapt to perform specific physiological functions. That's because it is the gut microbiome that is involved in the digestive process and therefore, it is capable of deriving those nutrients from foods, even from those intricate dietary compounds without which we would be lacking. Not only does it produce vitamins and SCFAs, but these products are also vital for energy metabolism and the gut environment, respectively (Blaak et al., 2020). Another function of the gut microflora is related to the immune system, with both playing significant roles in protecting the body against diseases.

Table 2: Relative Abundance of Major Bacterial Phyla in Different Body Sites.

Body Site	Dominant Bacterial Phyla	Functions	References
Gut	Bacteroidetes, Firmicutes	Breaking down food, absorbing nutrients, producing vitamins, regulating the immune system, and shielding against pathogens.	(Zhang et al., 2015)
Skin	Actinobacteria, Proteobacteria, Firmicutes	Defense against harmful microorganisms, upkeep of skin's protective barrier, control of inflammatory responses	(Dou et al., 2019)
Oral Cavity	Firmicutes, Bacteroidetes, Proteobacteria	Maintaining oral health and preventing dental illnesses.	(Wade, 2013)
Respiratory Tract	Firmicutes, Bacteroidetes, Proteobacteria	Respiratory infections, possible involvement in lung health	(Shima et al., 2016)

It is also important to state that the human microbiome is not a stable community of microorganisms but rather a dynamic community shaped by genetic and environmental factors (as shown in Table 2). An intake of a healthy diet can go down and even change the human metabolism, the working of the vital organs, and even the behavior patterns. Immunomodulation Prescribing extended periods of dietary pattern changes affects the microbial community residing in the intestines (Leeming et al., 2019). Some factors include mode of birth, where the child was born by either vaginal, CS, antimicrobial use, age, and exposure to animals, particularly pets or farms among others (Renz & Skevaki, 2021).

3. The Gut Microbiome and Health

The human body thus has a populace of diverse microorganisms that make up a huge network that is referred to as the human microbiota. This system includes bacteria, viruses, fungi, archaea, and many other microorganisms that are minute to the naked eye. Although bacteria of different types are divided based on their specialization in the skin, mouth, and urogenital tract, the largest colony and variety are found in the large intestine known as the 'gut microbiota (Matter, 2019).

Table 3: Factors Influencing Gut Microbiome Composition (Kumbhare et al., 2019)

Factor	Impact on the Gut Microbiota	Examples
Diet	Diet plays a significant role in determining the composition of microbial communities that are influenced by extended dietary habits.	Diets rich in fiber enhance diversity, while Western diets (high in fat and low in fiber) reduce diversity.
Lifestyle	Physical activity, amount of rest, and stress levels affect the types of microorganisms living in the body.	Engaging in more physical activity can result in positive changes dysbiosis can be caused by chronic stress.
Medications	Antibiotics can disturb the balance of bacteria in the gut, which may result in dysbiosis.	Prolonged antibiotic usage leads to lower variety and higher likelihood of <i>Clostridium difficile</i> infection.

Factor	Impact on the Gut Microbiota	Examples
Genetics	Genes of the host have an impact on the environment and mold the microbiome.	Inherited genes can impact the makeup of the gut microbiome for specific illnesses.
Environment	Early-life experiences and continuing environmental elements can impact the development of the microbiome.	The way a baby is born (vaginal or C-section), contact with pets or farm animals, and where someone lives can impact the makeup of their microbiome.

The gut microbiome exhibits a remarkably high level of diversity, encompassing an estimated 10,000 to 50,000 strains within the average human. Recent research by (DE GIANI, 2022) has revealed that the preponderance of bacterial species in this milieu exceeds 1000, predominantly comprising the Phyla of Bacteroidetes and Firmicutes. Additionally, Actinobacteria, Proteobacteria, and Verrucomicrobia, while present in lower quantities, play ancillary roles. A comprehensive understanding of the intricate interplay between fiber diet interactions and microflora, along with their abundance elements, is imperative for gaining insights into the dynamic nature of the microbiome (as shown in Table 3).

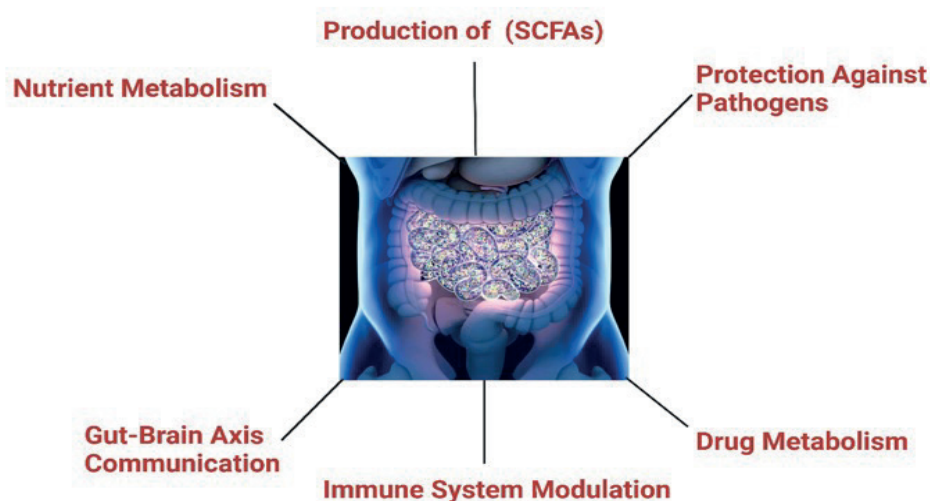


Figure 2. Gut Microbiomes and their functions

The human body encompasses a diverse resident microbial community within each specific niche, demonstrating distinct diversity by specific ecological and physiological functions (as shown in Figure 2). Notably, the gut microbiome, comprising the microbial population in the gastrointestinal tract, holds profound significance in facilitating the digestion process by enabling the extraction of nutrients from complex dietary components that would otherwise remain indigestible. In addition, the microbiome is involved in the production of various vital vitamins comprising certain B-group vitamins and SCFAs for energy requirements and intestinal barrier integrity (LeBlanc et al., 2017). Furthermore, through the integration of signaling pathways, the gut microbiome helps in the regulation of known immune cells to determine between pathogenic and helpful organisms. The human microbiome is not static but rather dynamic, influenced by a complex interplay of genetics and environment. Diet and daily habits play a significant role in determining an individual's health. Long-term dietary patterns, particularly the intake of protein and carbohydrates, are major contributors to the composition of the gut microbiota (Rinninella, Cintoni, et al., 2019). Lifestyle factors such as exercise, sleep, and stress also leave an imprint on the microbiome (Gültekin et al., 2021). Early

environmental exposures, such as the mode of delivery at birth (vaginal birth or Cesarean section), as well as maternal factors like pet ownership and farm exposure, have substantial effects on the developing immune system and the diversity of microbes (García-Serna et al., 2021).

4. Microbiome Dysbiosis and Disease

The complicated and one-sided equilibrium in our microbial community determines whether our health status is intact. Taxa disorders or dysbiosis is a condition of the disproportion in the levels of the bacteria within the microbiome as a transient state of insufficient number of beneficial bacteria and sometimes the appearance of potentially harmful microbes (Ceballos et al., 2021). Gut dysbiosis, these types of fluctuations in the gut microbiota, may indeed bring major health risks to the human system (as shown in Figure 3). Dysbiosis interferes with the mission-critical microbial processes that a healthy commensal community can carry out. It results in the ability of body functions to integrate foods, generate vitamins and SCFAs, regulate immunity, and resist pathogenic bacteria. In addition to that, dysbiosis brings about a situation where there is a smaller degree of inflammation, which is the origin of various chronic diseases (Potrykus et al., 2021).

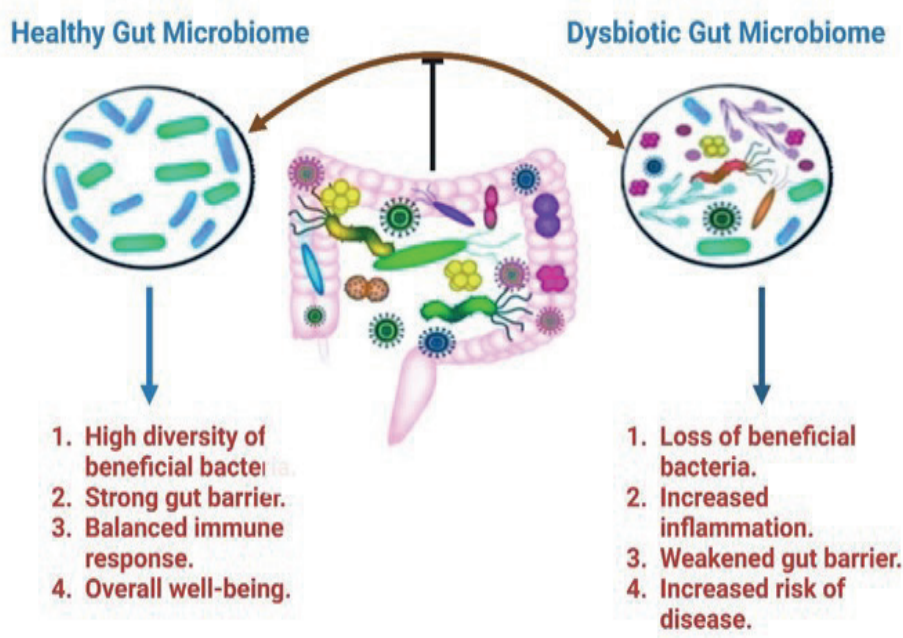


Figure 3. Microbiome Dysbiosis and Disease

Inflammation, genetics, and environment could play a role in the development of several, local, and systemic diseases that, research suggests, have a firm link to dysbiosis. Here's a look at how microbiome disruptions may factor into disease development and progression (as shown in Table 4).

4.1. Inflammatory bowel diseases (IBD): The fermentation imbalance is the nascent phenomenon of IBD, containing diseases such as Crohn's or ulcerative colitis. A consequence of interruption in the microbiome balance of the gut is the appearance of abnormal immune responses, which lead to the appearance of chronic intestinal inflammations (Pullaiah, 2016). The Imbalance in the gut microorganisms, if severe, may be among the causes of IBD and is believed to promote it.

4.2. Metabolic syndrome and Type 2 diabetes: Dysbiosis can handle energy control, insulin sensitivity, and fat handling through this mechanism, giving a reason for insulin resistance and metabolic disorders. Hosting gut microbes, in turn, affects host metabolism, reducing processed

food intake and lowering the host's body fat. The elevated probability of developing obesity and type 2 diabetes due to the emergence of these factors is one of the risks (Wu et al., 2014).

4.3. Irritable bowel syndrome (IBS): However, it is not as straightforward as in an IBD case, because dysbiosis is present but not strongly diagnosed in IBS patients. The specific gut microbial pattern that is connected to IBS has influences on abdominal pain, bloating, and changes in bowel habits symptoms (Duan et al., 2019).

4.4. Atopic diseases (Eczema, Asthma, Allergies): There are now studies that link a dysbiosis of children's baby's stomach flora in infancy with an increased risk of allergy, a pruritus called atopic dermatitis, and asthma. Disruption of the microbiome during the fetal period and infancy interferes with the formation of the immune system's regulatory system and leads to hyperactivity and allergies (Donald & Finlay, 2023).

4.5. Neurological and Neuropsychiatric conditions: The gut-brain axis is an active research area analyzing the complex dialogue between our gut microbiota and the brain. Disruption or imbalance in the microbiome has been demonstrated to be associated with illnesses such as Parkinson's disease and multiple sclerosis. Researchers are researching the possible influence of social networking on mental health conditions including anxiety, depression, and autism spectrum disorders (Donald & Finlay, 2023).

5. The Microbiome as a Therapeutic Target

Microbiome is more and more being respected as those microorganisms do not participate in your wellbeing only but also have a considerable influence on the development of diseases along with a wide array of other phenomena. During the last decade, microbiome research has become one of the dominating issues among scientists, which has led to its increasing popularity (Cullen et al., 2020).

Table 4: Microbiome-Associated Diseases and Potential Therapeutic Interventions

Disease	Potential Microbiome Changes	Therapeutic Interventions	References
Obesity	Reduced variety, higher ratio of Firmicutes to Bacteroidetes.	Diet changes, prebiotics, probiotics, FMT	(Sankararaman et al., 2023)
Inflammatory Bowel Disease (IBD)	Reduced variety, decline in helpful bacteria, rise in inflammatory microbes	Diet adjustments, prebiotics, probiotics, fecal microbiota transplantation (as studied), particular medications	(Durchschein et al., 2016)
Type 2 Diabetes	Changed biochemical routes, and decreased levels of bacteria that generate butyrate.	Dietary measures, prebiotics, probiotics (limited evidence)	(Bordalo Tonucci et al., 2017)
Irritable Bowel Syndrome (IBS)	Altered microbial composition and function	Dietary changes, probiotics	(Staudacher & Whelan, 2016)

Some of the core strategies under development and clinical investigation include: When it comes to cancer, arising from different biological origins is one of the reasons why it's incurred. Besides environmental and behavioral factors, each type of cancer is particularly caused by different gene mutations (Sankpal et al., 2012). Hence, the core strategies in development and clinical investigation in which:

5.1. Dietary interventions: It is well known that diet is more salient to the microbiome, impacting both composition and function. Although dietary modulation is thought to be a controversial

technique (as shown in Table 3) for structuring the microbiota, it is widely recommended by health professionals and nutritionists (y Abreu et al., 2021). The same diets will need to emphasize the role of fiber in plants which is meant for improving the quality of microorganisms needed for good digestion. Notwithstanding, the brew drinkers, the grains community as well and the vegetable community may find themselves fortunate to be alive as it will be possible to preserve their population, which is a healthy habit. The bad fats and excessive sugar in the blatantly processed and purified food varieties are the major contributors to weight gain and obesity (Kwan & Graves, 2013). Switching to traditional Mediterranean eating is to be seen among the most important principles of food combination with high nutritional content. Besides, this might be just a starting phase which may result in significantly improved chronic disease management longer-term.

5.2. Probiotics: Correctly processed probiotics involve the living microorganisms that are supposed to be a part of obligatory nutrition for the human body (Awaisheh, 2012). Also, if a necessary amount is not received by the human body due to improper diet, then, it affects the health in a very negative way. The following foods contain these species of *Lactobacillus* and *Bifidobacterium* of the *deltaccaecithe* genera of bacteria. The aim is to eliminate the microbes that cause seals and enhance the ones that support health at the same time (seen in Figure 5). In addition, a significant milestone is the use of probiotics in managing intestinal bowel syndrome (IBS) and antibiotic-associated diarrhea, (as shown in Table 4) a factor that has made such products so popular nowadays (Reque & Brandelli, 2022). Nevertheless, researchers at the same time are more and more thinking that if allergens strictly mean a particular kind of group, then people of this kind group are probably born with no ventilated disease or at all sinuses.

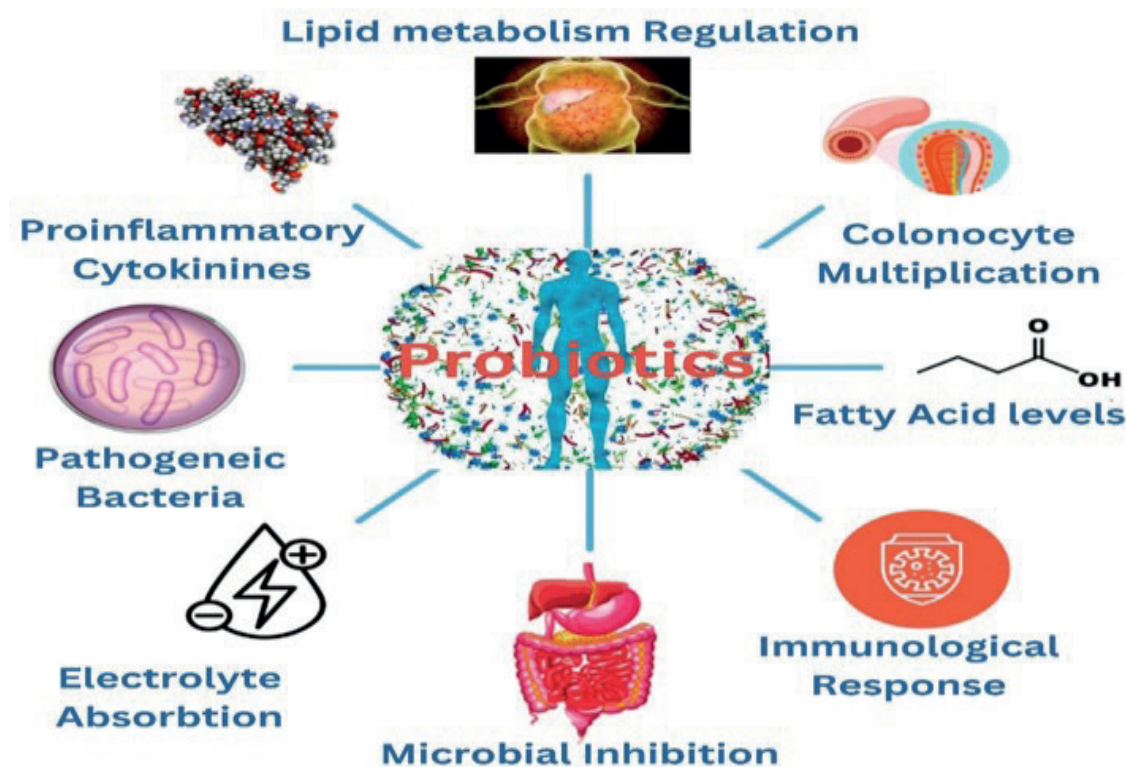


Figure 5. Probiotics

5.3. Prebiotics: These are examples of unfermentable dietary fibers (mostly resistant starches, fructans, and galactooligosaccharides) and they nourish the gut where there are good micro-organisms for the beneficial bacteria to thrive. The increase in the count of health-promoting bacteria in the intestines due to prebiotics (Lordan et al., 2020) is the main thing and with it there is an increase in their capability to carry out their objective. The dietary supplement is usually filled with inulin and Fos due to the presence of GOS (galactooligosaccharides) in daily routine (Mutanda et al., 2014). Attention will be paid precisely to the prebiotic efficacy of the co-treatment, along with

other factors. The investigators may well establish there will be a decreased incidence of diseases such as, for instance, inflammatory bowel disease or metabolic diseases.

5.4. Fecal microbiota transplantation (FMT): This technique is done by seeding the recipient with a healthy microbiome of the donor's dysbiotic gut and there are some methods through which this is done by the researcher. The objective is to gradually add some of the bacteria back and the microbial environment to get their balance back and digestion intact is what Goal is aiming for. This once-a-year Follow the Money (FMT) trial was the core evidence that the appearance of this issue cannot be underestimated and it is one of such ways to cure recurrent *C. difficile*. (1) The first weakness in antibiotics is (2) rising concern because of antibiotic resistance, MDR bacteria then (3) are a threat because of the emergence of multi-drug resistant bacteria. To illustrate, the antibiotic-resistant probability (MDR) is higher than the point made by the traditional drug (Tarín-Pelló et al., 2022). The other approach, as well as the Humanized Microbiota Transplantation (seen in Figure 7), is also considered to be applied to deal with diseases that are complex just as IBD, metabolic disorders, and psychological conditions subject to a lot of risk assessment and long-term safety studies.

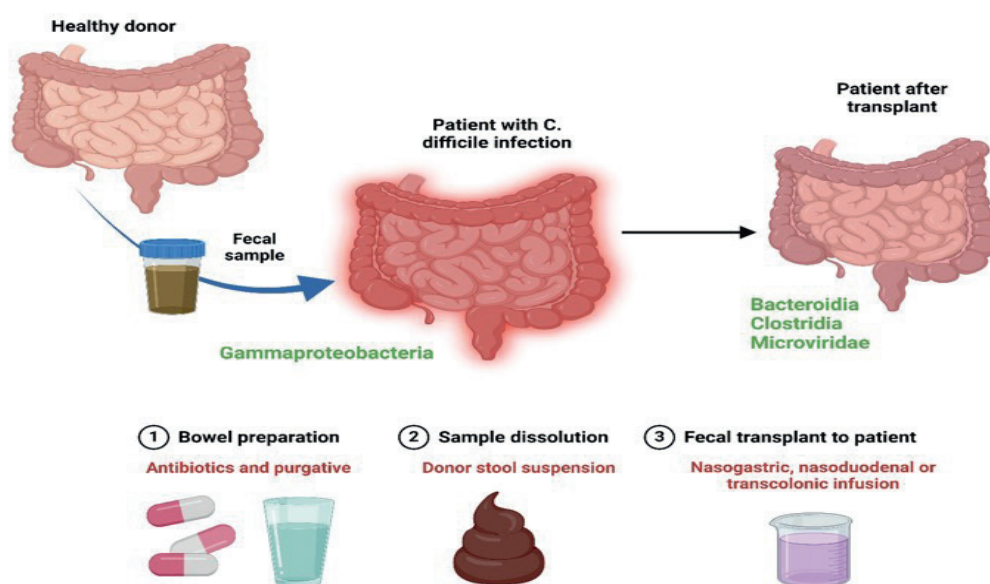


Figure 6. Fecal Microbiota Transplantation (FMT)

To boost the efficacy of our therapy, we intend to integrate dietary interventions based on prebiotics, probiotics, and fecal microbiota transplantation (FMT), as tools that are capable of dealing with this deficiency (Perillo et al., 2020). The level of the microbiome-targeted therapy is however at the initial stage of development and more research is required. A department with clinical evidence as a base should be observed as a possible route for the cure of many diseases. Still, there are some key considerations in which a certain selection of people can be quite special in some situations:

5.4.1 Specificity: Investigators cannot depend on low-grade kind of probiotics and prebiotics. They are of no effective good outcome! The microbes in some cases may carry out some tasks other than acting as antagonists. This is particularly notable when a patient already has other problematic conditions. Specifically, that is, the treatment and everyday supplementations most probably will not have an effect as required (Nieuwenhuizen et al., 2010).

5.4.2 Regulation: The governance leans toward the sovereign or national institutions, yet each country decides whether there will be governing for folic acids, prebiotics, and fecal microbial transplantation. The boundary between drugs and medication now is becoming a grey area as both

a type of medication fall into the group of supplements while the other may be used as a drug (Herzberg, 2010). In the course of this theme, it is important to ensure the tighter implementation of laws going with the advancement of these inventions from funding some market gaps to uniform medical use.

5.4.3 Individual variability: The specificity of the microbial population in the human microbial context varies thereby; the effect of the therapy on the microbial communities may vary widely from one patient to another (Mira et al., 2017). Apart from the genetic factors, eating habits and a way of life also matter much as regards determining which treatment method should be applied to the patients, who in the long run can have the outcome of becoming either well or worse. Detecting these parameters is fundamental, so it may be possible, to be accurately specialized in personalized treatments for these people.

5.4.4. Potential risks: Probiotics comprise live microorganisms, so as a general rule, they are free from side effects. However, some populations like those with reduced immunity natural or immune-suppressed due to an underlying condition can be adversely affected by probiotics. FMT has a chance of contamination and spreading unknown pathogens or microbes, which may not be beneficial and acceptable. The members of such a microbe might be harmful to the ill person (Manges et al., 2016). It can indicate the screening of donors to further prevent this situation. The unanswered questions regarding the FMT after prolonged use trials are the most dreading issue for clinicians.

6. Advancements in Microbiome Research

The microbiome research has dramatically undergone a revolution that is the outcome of improved new technologies and instruments used for diagnosis. Some key developments expanding our understanding of the microbiome include Some noteworthy findings, shedding light on the complexity of the microbiome in particular, as follows:

6.1. Large-scale cohort studies and biobanks: As of right now, a massive number of projects as the Human Microbiome Project exist that are responsible for amassing huge amounts of information about microbial diversity. This targeting of the relationship between microbiome's modifications and diseases gives mushrooms for study (Jayachandran et al., 2017). The biobanks, as tissues linked to health records, are used for the longitudinal studies which are focused on establishing exact long-term communication between microbiome and health. Big data, it is now, tells a story that is shaping the factors or identifying any possible biomarkers with a much higher outcome.

6.2. Refinement of culturomics: A thing that was a common view in this field was that not many small gut microbes were able to turn into laboratory research, and hence the prior learnings were greatly based on 'easily grown species. The emergent technologies of complex growth media and conditions as well as isolation and studying proposals of more diverse microorganisms deliver quite profound scientific knowledge reinforcement beyond one 'culturable' microbiome (Iqbal et al., 2024). This handover lets us fill in the distance separating the level of detail that can be now well provided in the sequence proceeding and the extent of experimental exploration.

6.3. Animal models: For mice studies, researchers are the ones who set the ideal conditions that will set the condition where they get to notice the effect of the changes in the microbiome, their mechanisms, and also the effects of new medications targeting the microbiome. The sterile mice (without natural microbiota) and also have low or absent microbiome are used to uncover the effect of introducing selected bacterial species only or communities as well as to observe the effect on health and disease in a very well-controlled situation (Kostic et al., 2013). The groups noted the metagenome, metatranscriptome, and metabolomes were the new-generation techniques and technologies for microbiome research (Anandaraj et al., 2021). The field of microbiome has become more polished and with the steady evolution of an accurate and precise set of research

tools a great tool for future research is created. Here's a look at some key techniques in which:

6.3.1. Metagenomics: The process of obtaining DNA from microbial populations is based on addressing the microbiome and then using direct sequencing. This viable strategy is not similar to just all the bacteria, viruses, and microbes, but forms a complete picture of the microbes forming into communities and containing their diversity. The researchers investigate whether there is a certain species or simply provide the data to know the number and their genes as they may be antibiotic resistant or the generation of vital metabolic functions (Crofts et al., 2017). The snapshot of genetic talents is preserved among different organisms that make up the metagenome.

6.4.2. Metatranscriptomics: In contrast, synchronous instruction, especially for massively open online courses (MOOCs), has increasingly become necessary to keep student engagement. The collection of the gene expression profiles and then the presence of certain microbes is ensured in addition to their genes that are active at a given period as well as what their function and activity are concerned (Franzosa et al., 2014).

6.4.3. Metabolomics: Gut microbial activity analyzing the small molecules that are produced by the microbes will be the direct evidence of the microbial species' capability functional activities as well the indication of how the microbes interact with each other. Metabolome can be used to determine the effective molecules and these are either supportive of breeding farm animal health or they have elevated susceptibility to the animals getting the disease (Sun et al., 2019). One as a caveat, the translation the metabolites can reach and the creation of the chemical language and to assess how it affects physiology is possible.

7. Future Directions

The narrow Transition that the microbiome research field is facing is however very purposeful because it holds a huge promise. Here are some key areas likely to see significant advancements in the coming years. The following are the prominent fields in which:

7.1. Precision Medicine: Integrating microbiome analysis into the person's health tracker, genetic weaknesses, and lifestyle factors is a main element that may be employed to implement microbiome-concentrated adjustments. It can be the case that not only do the dietary recommendations need tailoring but also the choice of such probiotics or even the FMT is the treatment key to enhancing results while reducing side effects (Scott et al., 2015).

7.2. Expanding beyond the gut: The attention is on the gut microbiome which has been widely explored. Nonetheless, the field is increasingly diversifying to the other domains of the body such as the skin, the airways, and the mouth. These microbial options may well be identified through tamponade therapy, skin disorders including eczema and prostatitis, and even lung diseases, which could help in the future developments of newer medical standards (EDITION, 2013).

7.3. Novel therapeutic targets: Highlighting the mysterious ways microbiota converses with our human body in an interconnected system, hope may arise to improve the therapeutic prospects of future medicine. This approach could involve the substantially complex production of probiotics or prebiotics which are intelligently designed to work with metabolic pathways, reducing inflammation or strengthening the immune system, which is necessary for multiple health issues (Kouhounde et al., 2022).

7.4. Bioengineered microbes: Synthetic biology as an entirely new space allows one to create these microorganisms which may be purely designed following the specific needs of the environment. Such genetically modified microbes could be administered to a patient's body directly to allow them to produce an intragastrical medication that could carry the medication, neutralize any potential metabolic products, or even improve the potency of the current medication.

7.5. Addressing regulatory challenges: The hyper-accumulative dynamics of immunotherapies development require the governmental and scientific communities to hold a conversation on the governing rules and regulations to ensure the patient safety and effectiveness of these novel treatments (Garg et al., 2022). Consequently, the standards, which protect patients from being victimized and, in addition, guarantee the proper and ethically sound application of microbiology in practice will be developed.

8. Conclusion

The human Microbiome, the microorganisms that inhabit our bodies are sometimes less known, is a very huge, quite still unknown ecosystem, with a large number of them firmly connected to our health and well-being. Microbiome research is a place of the child of a new exploration on the creating agency are recruiting significance of microbes in the general physiological procedures and their susceptibility to various diseases. Making future drugs of the top-notch kind by reprogramming the bacterial gut for health-benefiting purposes is an excellent prospect for medicine development. Rather than facing up to the problem with such a narrow array of weapons, the opening of microbiome-based interventions to the public is a continuous process at the early stage. Such therapy is a type of very promising treatment with an extensive patient population who otherwise will have to take the old-style therapies which are very conservative.

References

- Afzaal, M., Saeed, F., Shah, Y. A., Hussain, M., Rabail, R., Socol, C. T., Hassoun, A., Pateiro, M., Lorenzo, J. M., & Rusu, A. V. (2022). Human gut microbiota in health and disease: Unveiling the relationship. *Frontiers in microbiology*, 13, 999001.
- Anandaraj, M., Manivannan, S., & Umadevi, P. (2021). Rhizosphere Microbiome: The Next-Generation Crop Improvement Strategy. *Environmental and Agricultural Microbiology: Applications for Sustainability*, 243-256.
- Awaisheh, S. S. (2012). Probiotic food products classes, types, and processing. In *Probiotics*. Intechopen.
- Blaak, E., Canfora, E., Theis, S., Frost, G., Groen, A., Mithieux, G., Nauta, A., Scott, K., Stahl, B., & Van Harselaar, J. (2020). Short chain fatty acids in human gut and metabolic health. *Beneficial microbes*, 11(5), 411-455.
- Bolan, S. S. (2019). GUT MICROBES–HEAVY METAL (LOID) INTERACTIONS.
- Bordalo Tonucci, L., Dos Santos, K. M. O., De Lucas Fortes Ferreira, C. L., Ribeiro, S. M. R., De Oliveira, L. L., & Martino, H. S. D. (2017). Gut microbiota and probiotics: Focus on diabetes mellitus. *Critical reviews in food science and nutrition*, 57(11), 2296-2309.
- Ceballos, D., Hernández-Camba, A., & Ramos, L. (2021). Diet and microbiome in the beginning of the sequence of gut inflammation. *World Journal of Clinical Cases*, 9(36), 11122.
- Coleman, D. C., & Whitman, W. B. (2005). Linking species richness, biodiversity and ecosystem function in soil systems. *Pedobiologia*, 49(6), 479-497.
- Crofts, T. S., Gasparrini, A. J., & Dantas, G. (2017). Next-generation approaches to understand and combat the antibiotic resistome. *Nature Reviews Microbiology*, 15(7), 422-434.
- Cullen, C. M., Aneja, K. K., Beyhan, S., Cho, C. E., Woloszynek, S., Convertino, M., McCoy, S. J., Zhang, Y., Anderson, M. Z., & Alvarez-Ponce, D. (2020). Emerging priorities for microbiome research. *Frontiers in microbiology*, 11, 491374.
- DE GIANI, A. (2022). Impact of prebiotics and probiotics on gut microbiota and human health.

Donald, K., & Finlay, B. B. (2023). Early-life interactions between the microbiota and immune system: impact on immune system development and atopic disease. *Nature Reviews Immunology*, 23(11), 735-748.

Dou, J., Zeng, J., Wu, K., Tan, W., Gao, L., & Lu, J. (2019). Microbiosis in pathogenesis and intervention of atopic dermatitis. *International Immunopharmacology*, 69, 263-269.

Durchschein, F., Petritsch, W., & Hammer, H. F. (2016). Diet therapy for inflammatory bowel diseases: The established and the new. *World Journal of Gastroenterology*, 22(7), 2179.

EDITION, F. (2013). *Standard Treatment Guidelines and Essential Medicines List*.

Fletcher, S. (2015). Understanding the contribution of environmental factors in the spread of antimicrobial resistance. *Environmental health and preventive medicine*, 20, 243-252.

Franzosa, E. A., Morgan, X. C., Segata, N., Waldron, L., Reyes, J., Earl, A. M., Giannoukos, G., Boylan, M. R., Ciulla, D., & Gevers, D. (2014). Relating the metatranscriptome and metagenome of the human gut. *Proceedings of the National Academy of Sciences*, 111(22), E2329-E2338.

Fujimoto, M. (2012). *Microbial succession on the lake sturgeon egg surface: Mechanisms shaping the microbial community assembly during succession and the effect of microbial successional processes on host life history traits*. Michigan State University. *Microbiology and Molecular Genetics Ecology*

García-Serna, A. M., Martín-Orozco, E., Hernández-Caselles, T., & Morales, E. (2021). Prenatal and perinatal environmental influences shaping the neonatal immune system: a focus on asthma and allergy origins. *International Journal of Environmental Research and Public Health*, 18(8), 3962.

Garg, R., Garg, R., & Eddy, N. O. (2022). *Handbook of research on green synthesis and applications of nanomaterials*. IGI Global.

Gebrayel, P., Nicco, C., Al Khodor, S., Bilinski, J., Caselli, E., Comelli, E. M., Egert, M., Giaroni, C., Karpinski, T. M., & Loniewski, I. (2022). Microbiota medicine: towards clinical revolution. *Journal of translational medicine*, 20(1), 111.

Gültekin, F., Akın, S., İzler, K., & Kalkanlı, S. (2021). The Key to Strong Immunity: Lifestyle. *Academic Platform Journal of Halal Lifestyle*, 3(2), 90-107.

Herzberg, D. (2010). *Happy pills in America: from Miltown to Prozac*. JHU Press.

Hillman, E. T., Lu, H., Yao, T., & Nakatsu, C. H. (2017). Microbial ecology along the gastrointestinal tract. *Microbes and environments*, 32(4), 300-313.

Iqbal, S., Begum, F., Ullah, I., Jalal, N., & Shaw, P. (2024). Peeling off the layers from microbial dark matter (MDM): recent advances, future challenges, and opportunities. *Critical Reviews in Microbiology*, 1-21.

Jayachandran, M., Xiao, J., & Xu, B. (2017). A critical review on health promoting benefits of edible mushrooms through gut microbiota. *International journal of molecular sciences*, 18(9), 1934.

Kostic, A. D., Howitt, M. R., & Garrett, W. S. (2013). Exploring host–microbiota interactions in animal models and humans. *Genes & development*, 27(7), 701-718.

Kouhounde, S., Adéoti, K., Mounir, M., Giusti, A., Refinetti, P., Otu, A., Effa, E., Ebenso, B., Adetimirin, V. O., & Barceló, J. M. (2022). Applications of probiotic-based multi-components to human, animal and ecosystem health: concepts, methodologies, and action mechanisms. *Microorganisms*, 10(9), 1700.

Kumbhare, S. V., Patangia, D. V., Patil, R. H., Shouche, Y. S., & Patil, N. P. (2019). Factors influencing the gut microbiome in children: from infancy to childhood. *Journal of biosciences*, 44, 1-19.

Kwan, S., & Graves, J. (2013). *Framing fat: Competing constructions in contemporary culture*. Rutgers University Press.

LeBlanc, J. G., Chain, F., Martín, R., Bermúdez-Humarán, L. G., Courau, S., & Langella, P. (2017). Beneficial effects on host energy metabolism of short-chain fatty acids and vitamins produced by commensal and probiotic bacteria. *Microbial cell factories*, 16, 1-10.

Leeming, E. R., Johnson, A. J., Spector, T. D., & Le Roy, C. I. (2019). Effect of diet on the gut microbiota: rethinking intervention duration. *Nutrients*, 11(12), 2862.

Lordan, C., Thapa, D., Ross, R. P., & Cotter, P. D. (2020). Potential for enriching next-generation health-promoting gut bacteria through prebiotics and other dietary components. *Gut microbes*, 11(1), 1-20.

Manges, A. R., Steiner, T. S., & Wright, A. J. (2016). Fecal microbiota transplantation for the intestinal decolonization of extensively antimicrobial-resistant opportunistic pathogens: a review. *Infectious Diseases*, 48(8), 587-592.

Matter, W. M. (2019). *The Development of the Human Microbiome. The microbiome: Interactions with organ systems, diet, and genetics*, An Issue of *Gastroenterology Clinics of North America*, Ebook, 357.

McLaren, M. R., & Callahan, B. J. (2020). Pathogen resistance may be the principal evolutionary advantage provided by the microbiome. *Philosophical Transactions of the Royal Society B*, 375(1808), 20190592.

Mira, A., Simon-Soro, A., & Curtis, M. (2017). Role of microbial communities in the pathogenesis of periodontal diseases and caries. *Journal of clinical periodontology*, 44, S23-S38.

Mocanu, V. (2021). *Harnessing Gut Microbial Modulation in Chronic Inflammatory Gastrointestinal Disease*.

Mutanda, T., Mokoena, M., Olaniran, A., Wilhelmi, B., & Whiteley, C. (2014). Microbial enzymatic production and applications of short-chain fructooligosaccharides and inulooligosaccharides: recent advances and current perspectives. *Journal of Industrial Microbiology and Biotechnology*, 41(6), 893-906.

Nieuwenhuizen, W. F., Weenen, H., Rigby, P., & Hetherington, M. M. (2010). Older adults and patients in need of nutritional support: review of current treatment options and factors influencing nutritional intake. *Clinical nutrition*, 29(2), 160-169.

Perillo, F., Amoroso, C., Strati, F., Giuffrè, M. R., Díaz-Basabe, A., Lattanzi, G., & Facciotti, F. (2020). Gut microbiota manipulation as a tool for colorectal cancer management: recent advances in its use for therapeutic purposes. *International journal of molecular sciences*, 21(15), 5389.

Portincasa, P., Bonfrate, L., Vacca, M., De Angelis, M., Farella, I., Lanza, E., Khalil, M., Wang, D. Q.-H., Sperandio, M., & Di Ciaula, A. (2022). Gut microbiota and short chain fatty acids: implications in glucose homeostasis. *International journal of molecular sciences*, 23(3), 1105.

Potrykus, M., Czaja-Stolc, S., Stankiewicz, M., Kaska, Ł., & Małgorzewicz, S. (2021). Intestinal microbiota as a contributor to chronic inflammation and its potential modifications. *Nutrients*, 13(11), 3839.

Pullaiah, T. (2016). *Biotechnological approaches for sustainable development*. Regency

Publications, New Delhi.

Renz, H., & Skevaki, C. (2021). Early life microbial exposures and allergy risks: opportunities for prevention. *Nature Reviews Immunology*, 21(3), 177-191.

Reque, P. M., & Brandelli, A. (2022). An introduction to probiotics. In *Probiotics* (pp. 1-17). Elsevier.

Rinninella, E., Cintoni, M., Raoul, P., Lopetuso, L. R., Scaldaferri, F., Pulcini, G., Miggiano, G. A. D., Gasbarrini, A., & Mele, M. C. (2019). Food components and dietary habits: keys for a healthy gut microbiota composition. *Nutrients*, 11(10), 2393.

Rinninella, E., Raoul, P., Cintoni, M., Franceschi, F., Miggiano, G. A. D., Gasbarrini, A., & Mele, M. C. (2019). What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms*, 7(1), 14.

Salvucci, E. (2019). The human-microbiome superorganism and its modulation to restore health. *International journal of food sciences and nutrition*, 70(7), 781-795.

Sankararaman, S., Noriega, K., Velayuthan, S., Sferra, T., & Martindale, R. (2023). Gut microbiome and its impact on obesity and obesity-related disorders. *Current gastroenterology reports*, 25(2), 31-44.

Sankpal, U. T., Pius, H., Khan, M., Shukoor, M. I., Maliakal, P., Lee, C. M., Abdelrahim, M., Connelly, S. F., & Basha, R. (2012). Environmental factors in causing human cancers: emphasis on tumorigenesis. *Tumor Biology*, 33, 1265-1274.

Scott, K. P., Jean-Michel, A., Midtvedt, T., & van Hemert, S. (2015). Manipulating the gut microbiota to maintain health and treat disease. *Microbial ecology in health and disease*, 26(1), 25877.

Shao, T., Verma, H. K., Pande, B., Costanzo, V., Ye, W., Cai, Y., & Bhaskar, L. (2021). Physical activity and nutritional influence on immune function: an important strategy to improve immunity and health status. *Frontiers in physiology*, 12, 751374.

Shima, K., Coopmeiners, J., Graspeuntner, S., Dalhoff, K., & Rupp, J. (2016). Impact of micro-environmental changes on respiratory tract infections with intracellular bacteria. *FEBS letters*, 590(21), 3887-3904.

Staudacher, H. M., & Whelan, K. (2016). Altered gastrointestinal microbiota in irritable bowel syndrome and its modification by diet: probiotics, prebiotics and the low FODMAP diet. *Proceedings of the Nutrition Society*, 75(3), 306-318.

Sun, H., Plastow, G., & Guan, L. (2019). Invited review: Advances and challenges in application of feedomics to improve dairy cow production and health. *Journal of Dairy Science*, 102(7), 5853-5870.

Tarín-Pelló, A., Suay-García, B., & Pérez-Gracia, M.-T. (2022). Antibiotic resistant bacteria: current situation and treatment options to accelerate the development of a new antimicrobial arsenal. *Expert Review of Anti-infective Therapy*, 20(8), 1095-1108.

Wade, W. G. (2013). The oral microbiome in health and disease. *Pharmacological research*, 69(1), 137-143.

Wu, Y., Ding, Y., Tanaka, Y., & Zhang, W. (2014). Risk factors contributing to type 2 diabetes and recent advances in the treatment and prevention. *International journal of medical sciences*, 11(11), 1185.

y Abreu, A. A., Milke-García, M., Argüello-Arévalo, G., Calderón-de la Barca, A., Carmona-Sánchez, R., Consuelo-Sánchez, A., Coss-Adame, E., García-Cedillo, M., Hernández-Rosiles, V., & Icaza-Chávez, M. (2021). Dietary fiber and the microbiota: A narrative review by a group of experts from the Asociación Mexicana de Gastroenterología. *Revista de Gastroenterología de México (English Edition)*, 86(3), 287-304.

Zafar, H., & Saier Jr, M. H. (2021). Gut Bacteroides species in health and disease. *Gut microbes*, 13(1), 1848158.

Zhang, Y.-J., Li, S., Gan, R.-Y., Zhou, T., Xu, D.-P., & Li, H.-B. (2015). Impacts of gut bacteria on human health and diseases. *International journal of molecular sciences*, 16(4), 7493-7519.

About The Authors

Arifa Mehreen is an Assistant Professor of Zoology at the University of Agriculture Faisalabad (UAF). Her research focuses on the antimicrobial properties of natural products, drug formulation and pharmacokinetics, and characterization of bacterial pathogens. She has studied the antimicrobial and toxicological effects of *Origanum vulgare*, developed a fixed-dose combination drug for cardiovascular disease, and investigated the characteristics of *Staphylococcus aureus* strains.

E-mail: arifa.mehreen@uaf.edu.pk

ORCID: 0000-0001-5899-8027

Dr Qurat-ul-Ane Gillani is an Assistant Professor of Zoology at Women's University Multan. Her research primarily focuses on the effects of various substances on animal physiology and behavior, particularly in mice. She has investigated the impact of nickel chloride on fish, plant extracts on mice, and the neurological mechanisms of COVID-19. Additionally, her work has explored the role of GABAB receptor antagonists on behavior, hematology, and biochemistry in mice models, sometimes with a focus on neonatal brain damage. She has also researched detecting blood parasites in cattle.

E-mail: anneegillani@wum.edu.pk

ORCID: 0000-0002-1068-4472

Ayesha Bintay Farooq is a researcher in the Department of Physiology, Life Sciences, at Government College University Faisalabad, Pakistan. Her primary research interests lie in the field of neuroscience, with a particular focus on neuroimaging. Ayesha is dedicated to exploring the intricacies of brain function and structure through advanced imaging techniques. Her work aims to enhance the understanding of neural processes and contribute valuable insights to the field of neuroscience.

Email: ayeshabintyfarooq@gcuf.edu.pk

ORCID: 0009-0003-7009-222X

Maria Nazir is an MPhil Scholar of Microbiology at the Cholistan University of Veterinary and Animal Sciences (CUVAS) in Bahawalpur, Pakistan. She is involved in a National Research Program for Universities (NRPU) Project, with research interests in Molecular Characterization. She has submitted abstracts to various conferences and authored and coauthored of several book chapters. Her research focuses on the isolation and Molecular characterization of *Corynebacterium pseudotuberculosis* and their applications in promoting animal health. Her interested research criteria are based on genetics, molecular biology, and bioinformatics.

Email: nazirmaria545@gmail.com

ORCID 0009-0004-6714-6212

Dr. Rumaisa Nawal received her MBBS degree in 2024 from Multan Medical and dental college. She is a house officer in Bhawal Victoria Hospital, Pakistan. She has done internship program at District Headquarters Lodhran.

Email: rumaisanawal9@gmail.com

ORCID:0009-0000-1903-8365

Minal Hussain graduated from Cholistan University of Veterinary and Animal Sciences in Bahawalpur Pakistan. He continues his postgraduate study in Microbiology from Cholistan University of Veterinary and Animal Sciences Bahawalpur. Her research interest is in Bacteriophages, Bacteriology, Molecular cell biology, and Microbial genetics etc. She has published few book chapters in international journals.

Email: 2019-cu-bios-023@cuvas.edu.pk

ORCID: 0009-0004-0143-5644

Shafeeq Ur Rehman earned his Bachelor in Applied microbiology from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. Currently he is pursuing M. phil in Microbiology from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. He is also working as research assistant in a project titled as “Robust Molecular Detection of Silent Circulation of FMD and PPR Viruses in Cholistan as a Model for Disease-Free Zone”. His research interest is in FMD and PPR Viruses, Mucosal Immunity, Virology, Molecular cell biology, Cell culture, Microbial genetics and CRISPR case tools for combating viral diseases. He has published 7 articles and many book chapters in national and international journals.

Email: shafeequrrehmanbhutta@gmail.com

ORCID: 0000-0003-3571-8226

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk

ORCID: 0000 0002 3720 2090

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