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Pharmacological Modulation of the Microbiome in the Prevention and Treatment of Infectious Diseases: Current Evidence and Future Directions

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Abstract

Human microbiome is a significant point of contact for immunity building and prevents contagious diseases. If the microbiome is disrupted, especially due to broad-spectrum antibiotics, it will make infections more likely to occur with complex disease outcomes like Clostridium difficile colitis. Pharmacological interventions such as probiotics, prebiotics, and microbiome therapy strategies one to two generations ahead and the transplant method, FMT, are all very promising solutions for infection prevention and treatment through their effects on the microbiome. The purpose of this review is to evaluate the present state of knowledge concerning the relationship between the microbiome and infections and to present some of the new pharmacological microbiome modulation strategies. It gives examples where microbiome-targeted therapy has led to a reduction in the infectious risk, a very welcome situation regarding hospitalized/immunocompromised patients, for instance. Nevertheless, though a lot of people are fascinated by the area, problems such as personalized varieties one by one, institutional prejudices, and regulatory unknowns are still the main issues for clinical translating. The use of microbiome-modulating clinical practices is backed up by the research that goes with infectious disease therapies. These fields' growth will necessarily involve collaboration among scientists from different areas and massive error-free clinical trials to confirm the effectiveness and safety of the treatments in different subcategories of patients and infection strains.

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INTRODUCTION

The microbiome contains trillions of microorganisms, such as bacteria, archaea, viruses, and fungi, and is regarded as the one responsible for the balance between different physiological processes and immune and metabolic functions [1]. Different ecosystems such as the mouth, the nose or the vagina are among the first chosen by the individuals to live in and the gut microbiome, which is the densest, has been the one of them that has been very much studied for its systemic impacts [2]. Metagenomics and multi-omics approaches have proved that shifts in the microbial community structure, or dysbiosis, results in perturbation of the infectious disease response, among others [3]. Comprehensive functions of the microbiome include the right development of an immune system that can produce resistant barriers through different means, pathogens defense, and lastly, mucosal integrity maintenance [4]. It is interesting to note that the stable microbiome can be the source of the body's colonization resistance, i.e., preventing the overgrowth of potential pathogens, changing the immune response, and handling the challenges well [5].

Nonetheless, the microbiome caused by therapy with antibiotics, for example, or by other environmental factors may increase the risk of infection [6]. The aim of pharmacological manipulation of the microbiome is to alter microbial communities and bring them into balance to enhance host defenses [7]. These interventions include probiotics, prebiotics, fecal microbiota transplantation (FMT), and next-generation microbial consortia. They aim to decrease the threat of pathogens, enhance the activity of the immune system, as well as lower the risk of side effects from medications [8]. **Fig. 1** depicts the various locations where microbial communities, or microbiomes, exist in the human body, including the oral, respiratory, skin, stomach, small intestine, large intestine, and urogenital areas.

This review discusses how the microbiome interacts with infectious agents, protective mechanisms, consequences of dysbiosis, as well as proof of concept from animal and human studies. Furthermore, we shed light on the emerging therapeutic opportunities of microbiome modulation for the prevention and treatment of infectious diseases [2].

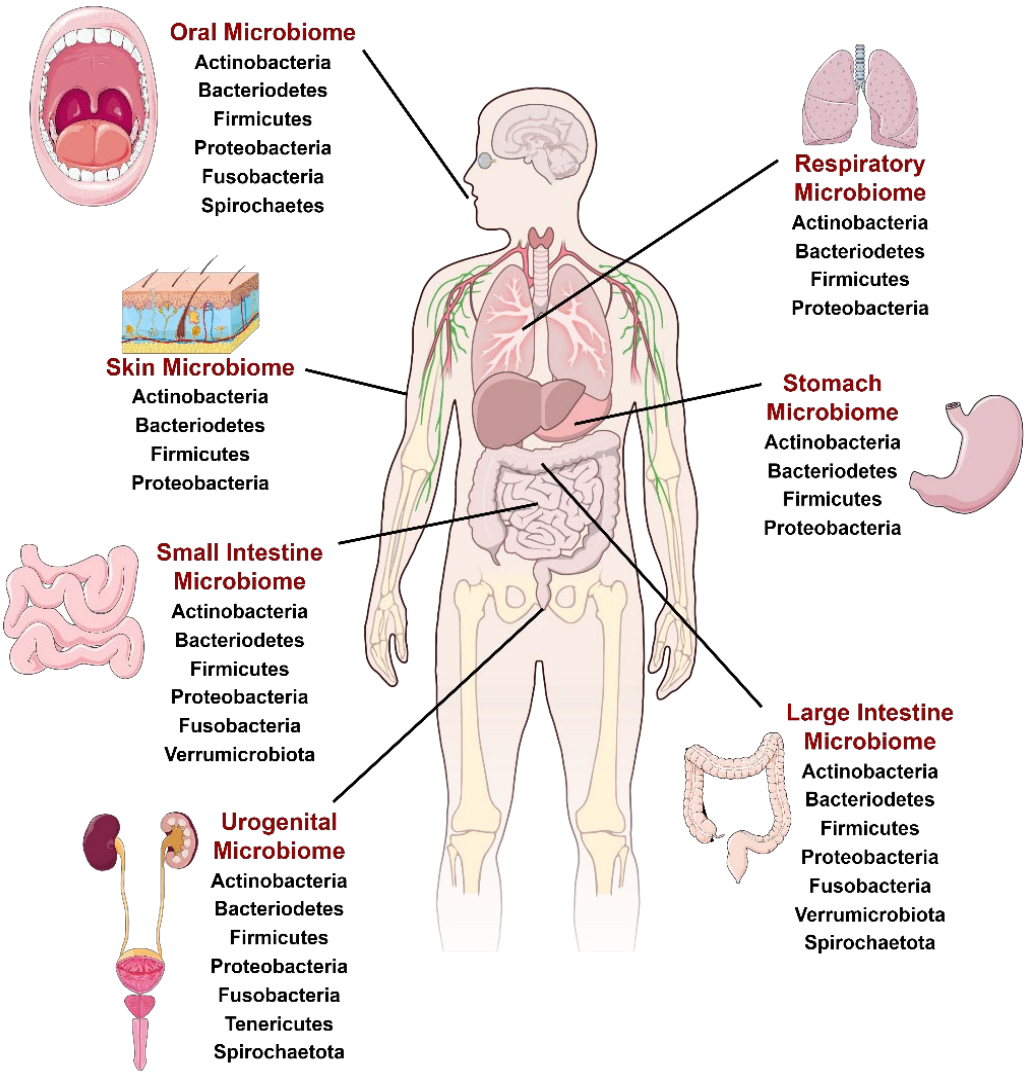

Fig. 1. Composition of the Human Microbiome Across Body Sites (Created by the author)

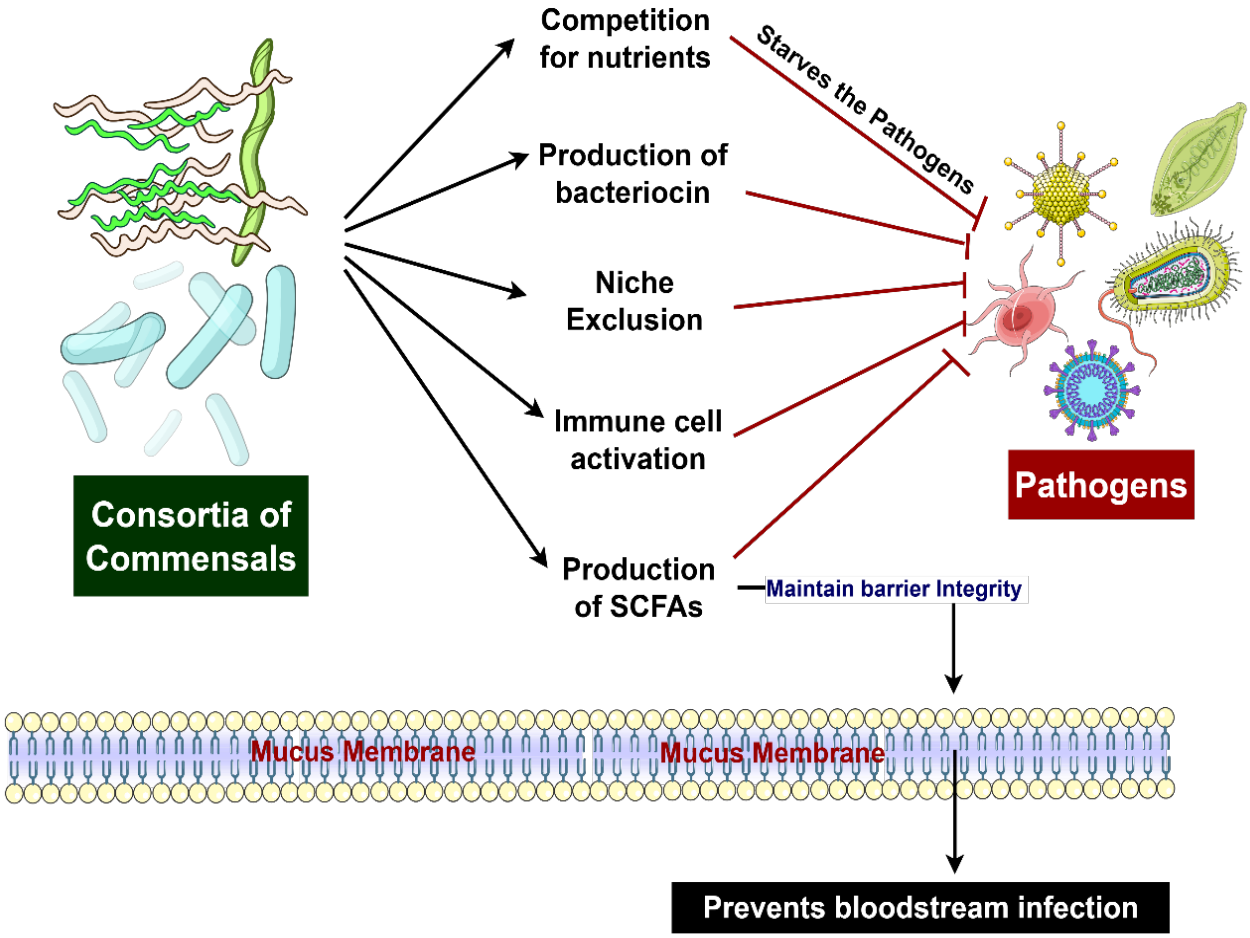

Fig. 2. Mechanisms of Colonization Resistance by Commensals (Created by the author)

Microbiome-Infection Axis

Mechanisms and Evidence

An essential function of the human microbiome is colonization resistance; that is, the action of resident microbes resisting the establishment of potential pathogens by outcompeting pathogenic microbes for nutrients and ecological niches [9]. For instance, gut commensals produce bacteriocins and SCFAs that inhibit the growth of pathogens [10]. Secondly, they also assist in training and regulation of the immune system by interacting with toll-like receptors and by maintaining a balanced response of the immune system between pro- and anti-inflammatory mechanisms [11]. One primary example is the Lactobacillus-dominated vaginal microbiome; it lowers the pH and produces antimicrobial compounds that reduce the risk of sexually transmitted infections [6]. **Fig. 2** illustrates how a healthy community of commensal microbes protects against pathogens. It shows commensal bacteria outcompeting pathogens, maintaining barrier integrity, and preventing bloodstream infections.

Microbiome Disruption and Infection Susceptibility

Imbalance in the ecological ambient, or dysbiosis, has recently been viewed as being considered a predisposing factor for infection. Decreased microbial diversity via broad-spectrum antibiotics, diet changes, or environmental stressors has finally paved the way for the enhancement of these pathogenic chances. The most known examples of dysbiosis disorders connected to antibiotic treatment are those caused by *Clostridioides difficile*, where the removal of the beneficial flora opens up space for toxin-producing microorganisms [12]. The role of oral dysbiosis in periodontal diseases has been theorized, along with the general inflammation of the body [13]. The different microbes found in the respiratory system might distinguish the susceptible from the non-susceptible TB or other respiratory viral infections like SARS-CoV-2 in this new awareness era of the COVID-19 pandemic [14].

Evidence from Germ-Free Animal Models and Humans

The research on germ-free mice, those are rodents reared in germ-free environments with the absence of native microbiota, has largely uncovered different strategies used by microbiota to protect against infection. The organisms display a state of an underdeveloped immune system and at the same time a very high sensitivity to pathogens like Salmonella and *Citrobacter rodentium* [15]. Bringing back commensals restores the function of the immune system and the infection-fighting ability, which means the presence of a causal relationship [16]. The research conducted on humans has exposed the fact that in ICU patients, a lowered bacterial variety is related to a more prominent chance of getting nosocomial infections [7]. On the other hand, microbial balance is already recovered more than 85% after fecal transplant treatment, even though the patients suffer from infection due to *C. difficile*; in this context, it is suggested that a healthy microbiome is a protective factor [17]. Urbanization, diet, and sanitation are among the factors that are linked with the microbiome diversity and the infections occurring among the population [18].

Pharmacological Methods of the Modulation of the Microbiome

Variations in the microbiome profile have been considered as factors influencing the severity of the disease in an infectious process. Pharmaceuticals are a huge field-it ranges from the usual antibiotics; still, new synthetic biology tools could give the sheep and the goats of microbiota through impacting eubiosis, colonization resistance, and host immunity [19]. Pharmacological strategies for manipulating the microbiome consist of a range of microbiome manipulation interventions extending from the established ones like probiotics and FMT to the emerging ones like engineered microbial consortia. The goal of these therapies is to restore the balance of the microbes, increase the immune resistance of the host, and decrease the probability of infection.

Table 1 gives the summary of pharmacological approaches which put effects on the change of microbiome along with their target infections, mechanism of action, and stage in clinical development. The table outlines the therapeutic spectrum, from established probiotics and FMT to experimental approaches such as engineered microbiota. While probiotics and FMT have entered clinical evaluation, most next-generation interventions remain preclinical, highlighting the translational gap. **Table 2** illustrates specific clinical studies that investigated microbiome interventions for infectious disease across different diseases. It outlines the therapeutic spectrum, from established probiotics and FMT to experimental approaches such as engineered microbiota. While probiotics and FMT have entered clinical evaluation, most next-generation interventions remain preclinical, highlighting the translational gap. **Table 3** connects mechanistic insights to therapeutic outcomes. While mechanisms are increasingly defined, only probiotics and FMT are supported by substantive clinical data; synthetic approaches (postbiotics and engineered strains) remain experimental. **Fig. 3** illustrates how different microbiome-modulating interventions exert their therapeutic effects through distinct but complementary mechanisms.

Table 1. Summary of microbiome-modulating therapeutics.

Strategy	Example Agents	Target Infection	Mechanism	Clinical Stage	Ref.
Probiotics	*Lactobacillus rhamnosus GG*	AAD, VAP	Competitive exclusion, immune modulation	Phase III	[20]
Prebiotics	Inulin, FOS	Traveler's diarrhea	Substrate for beneficial bacteria	Phase II	[21]
FMT	Donor stool	*C. difficile*, GVHD	Microbiota restoration	Approved / Ongoing	[22]
Postbiotics	SCFAs (e.g., butyrate)	Inflammatory infections	Anti-inflammatory signaling	Preclinical	[23]
Engineered Microbiota	Synthetic *E. coli Nissle*	Cancer, IBD	Drug delivery, immune tuning	Preclinical	[24]

Table 2. Selected clinical trials on microbiome interventions.

Intervention	Condition	Population	Outcome	Ref.
Synbiotic mixture	Ventilator-associated pneumonia (VAP)	ICU patients	Reduced VAP incidence	[25]
SER-109	*C. difficile* recurrence	Adults	Decreased recurrence risk	[26]
FMT	GVHD prevention	HSCT patients	Improved gut diversity	[27]
Probiotic lozenges	Recurrent candidiasis	Women	Reduced fungal colonization	[28]

Table 3. Mechanisms of Action of Microbiome-Modulating Interventions.

Intervention	Mechanism of Action	Evidence Type	Ref.
Probiotics	Competitive exclusion, antimicrobial production, immune modulation	Clinical /Preclinical	[29]
Prebiotics	Substrate for beneficial microbes, SCFA production	Preclinical /Clinical	[21]
FMT	Restoration of diverse microbial communities	Clinical	[27]
Postbiotics	Immunomodulatory metabolites (e.g., butyrate)	Preclinical	[23]
Engineered Microbiota	Targeted drug delivery, immune tuning	Preclinical	[24]

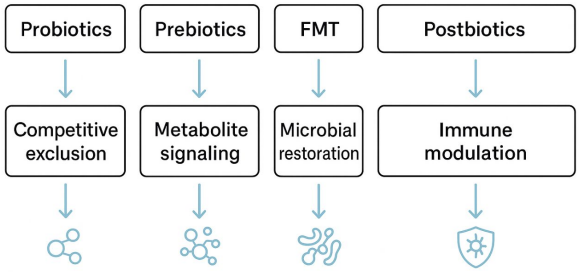

Fig. 3. Mechanisms of Action of Microbiome Modulating Interventions (Created by the author).

Antibiotics

Antibiotics are still considered a cornerstone of treatment for infections, but oftentimes, they cause unwanted, broad-spectrum disruption to the gut microbiota. Such interference could lead to a reduction in microbial diversity, a loss of beneficial commensals, and increased susceptibility of the host to opportunistic pathogens such as *Clostridioides difficile* [23]. Dysbiosis has been implicated as an aggravating factor in graft-versus-host disease and sepsis [30].

Narrow-Spectrum and Microbiome-Sparing Alternatives

Narrow-spectrum antimicrobials are under extensive development in an attempt to minimize collateral damage. Lysins are enzymes of phage origin, produced to parasitize bacterial hosts. They act only on pathogenic bacteria and leave commensals untouched. Engineered lysins present an opportunity for mediating the reshaping of microbial communities without inducing dysbiosis [31]. Precision antibiotics and quorum-sensing inhibitors are two other approaches to microbial control [24]. **Fig. 4** shows how antibiotics can lead to dysbiosis, which in turn causes a reduction in gut microbial diversity, an altered abundance of the gut microbiome, increased antibiotic resistance, and changes in host metabolism.

Probiotics and Prebiotics

Mechanisms of Action: Competitive Exclusion and Immune Signalling

Probiotics (*Lactobacillus, Bifidobacterium*, for example) may help enhance gut health, competing with pathogens, producing antimicrobial compounds, and mediating immune responses [29]. Prebiotics, such as inulin, serve as substrates facilitating the selective growth of beneficial bacteria. These mechanisms ensure mucosal barrier integrity and diminution of systemic inflammation [21].

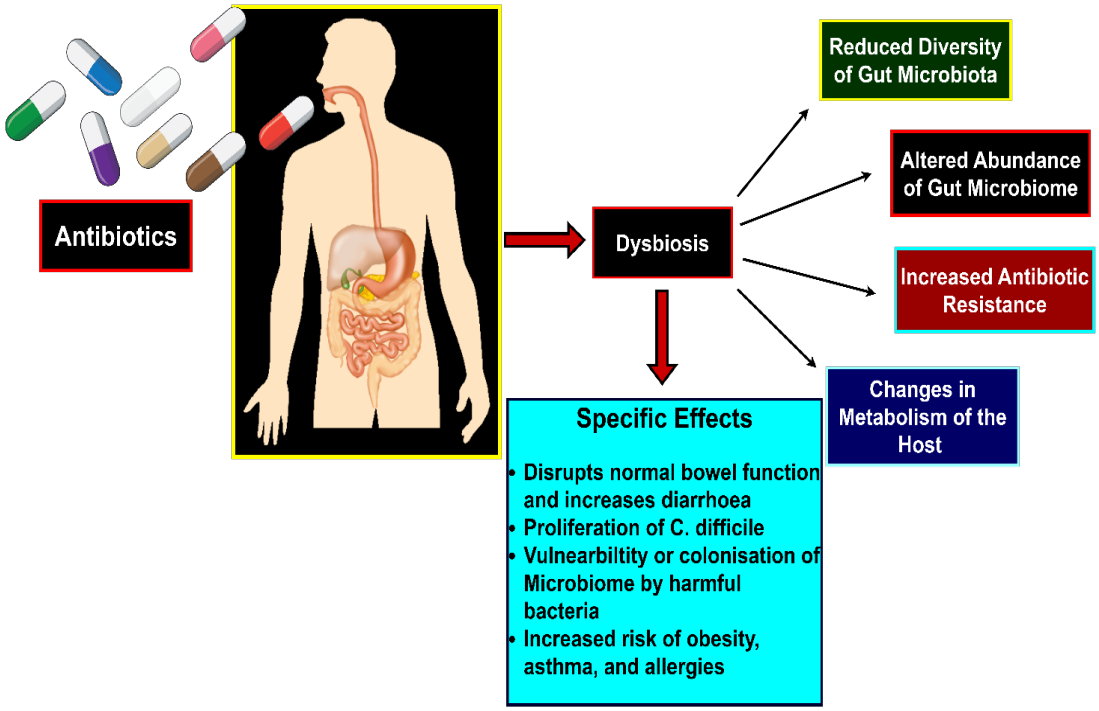

Fig. 4. Effects of Antibiotics on Microbiome Composition (Created by the author)

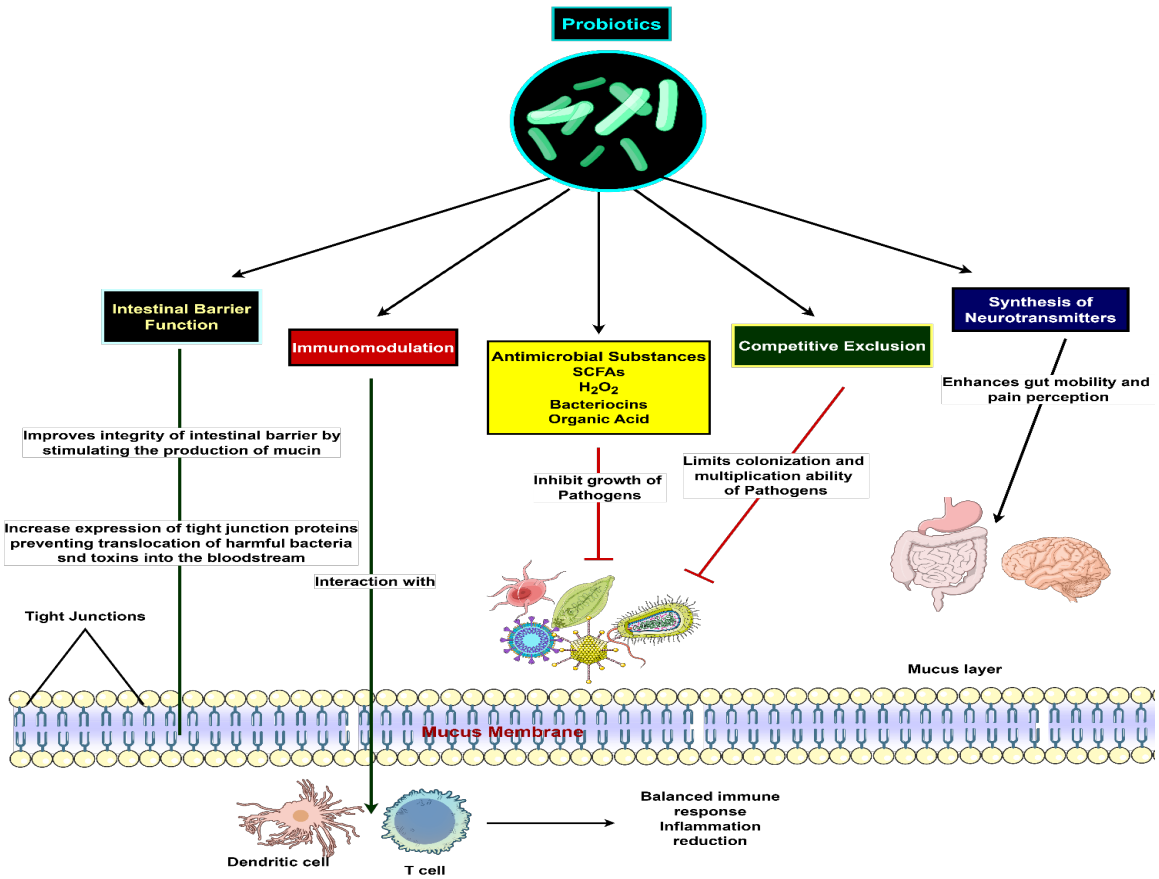

Fig. 5. Mechanisms of Action: Probiotics and Prebiotics (Created by the author)

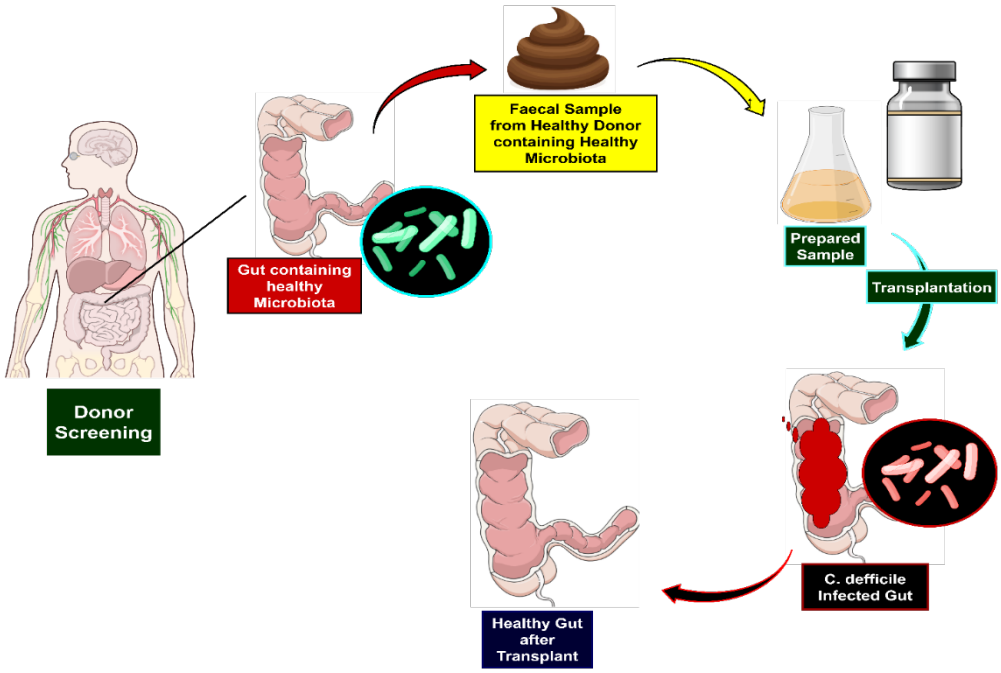

Fig. 6. Process of Fecal Microbiota Transplantation (FMT) (Created by the author).

Clinical Trial Evaluations for Infectious Disease Prevention

Clinical evidence is availably supporting the use of probiotics in lowering ventilator-associated pneumonia, side effects of *Helicobacter pylori* eradication, and *C. difficile* recurrence [26]. Synbiotics are undergoing trials for cardiometabolic and dermal conditions associated with microbial imbalance [32]. **Fig. 5** illustrates the key mechanisms through which probiotics and prebiotics work. They function via competitive exclusion, immunomodulation, the production of antimicrobial substances, and the synthesis of neurotransmitters.

Fecal Microbiota Transplantation (FMT)

FMT remains the most successful microbiome-based intervention we have, with more than 85% efficacy for recurrent *C. difficile* infection [22]. It restores a diverse microbial ecosystem that limits pathogenic overgrowth [32].

Emerging Applications in Resistant Infection and Immune Modulation

The other conditions being studied for FMT are graft-versus-host disease, sepsis, opioid withdrawal, and skin disorders [27,29,33]. It is also being considered in veterinary medicine and agriculture for chronic gastrointestinal disorders in animals [26]. **Fig. 6** outlines the process of FMT, beginning with the screening of a healthy donor, preparing a fecal sample, and transplanting it into a patient with a *C. difficile* infection to restore a healthy gut microbiota.

Postbiotics and Next-Generation Microbiome-Based Drugs

Next-gen microbiome therapeutics target precise blends of bacteria possessing immunomodulatory skills. They have much better reproducibility and safety compared to traditional FMT. Uses range from IBD and cancer to liver disorders [34].

Bacterial Metabolites

Postbiotics, which include various non-viable microbial products such as SCFAs and bile acids, are evidenced in promoting immune signaling and controlling intestinal permeability and inflammation [23]. And butyrate, in particular, promotes regulatory T cell differentiation and mucosal repair [30].

Synthetic biology and engineered microbiota

As of now, scientists are developing quorum-sensing genetic circuits to release medications when the signals associated with the disease are detected and thus improve treatment accuracy and decrease the side effects occurrence [24]. Thus, these technologies will serve as microbiome precision medicine tools for cancer, IBD, and infection.

Clinical Applications and Current Evidence

Pharmacological modifications in the microbiome were found to have great potential for the treatment and prevention of infectious diseases, especially in vulnerable individuals like those in hospitals and the immunocompromised. Evidence from preclinical models and clinical trials suggests that the composition of the microbiome largely affects vulnerability to infections, therapeutic response in the patient, and hence the end result [35]. While evidence supports FMT's >85% efficacy in recurrent *C. difficile*, broader application is constrained by donor variability and safety concerns. Probiotics demonstrate benefits in VAP and recurrent candidiasis, but heterogeneity and small sample sizes temper conclusions. Moreover, as [36] emphasized, case–control microbiome studies often suffer from inadequate power, detection bias in rare taxa, and sequencing artifacts: "differences in sampling depth, library size, and normalization methods can bias results" Thus, interpreting apparent associations requires caution.

Hospital-Acquired Infections (HAIs)
Hospital-acquired infections, such as *C. difficile*, ventilator-associated pneumonia, or bloodstream infection, are major threats in the clinical setting. Dysbiosis due to antibiotics and critical illness predisposes patients to colonization by multidrug-resistant organisms [37]. Restoring the microbiome through FMT or probiotics has reduced multidrug-resistant organism colonization rates and subsequent infections in ICU patients [38]. The other two approaches that have been proposed include administration of microbiota-sparing antibiotics and targeted bacteriophage therapies to help prevent dysbiosis-associated HAIs [24].

Antibiotic-Associated Infections
Disruption of microbial diversity after broad-spectrum antibiotic therapy is one of the main pathogeneses of infections like relapsing *C. difficile* colitis. FMT is still considered the gold standard for restoration of the microbiota in this setting, with cure rates above 85% [27]. Synbiotic therapeutics and postbiotics are also being considered for similar indications. Consideration has also been given to emerging evidence regarding use of defined bacterial consortia (e.g., SER-109) for treatment of antibiotic-associated dysbiosis as standardized microbiota-based drugs [39].

Viral Infections and Microbiome Status
The microbiome is a crucial basis in shaping the antiviral immune response [40]. Altered profiles of gut microbiota have been shown to be associated with infections such as COVID-19 and influenza, wherein decreased levels of *Faecalibacterium prausnitzii* and *Bifidobacterium spp.* correlate with severity [41]. Prebiotic or probiotic supplementation has been discussed in the attempt to enhance vaccine efficacy or to modulate inflammatory processes. Several studies document that gut microbial metabolites, including SCFAs, regulate antiviral immunity through inducing T-cell differentiation and interferon production [42].

Microbiome Modulation in Immunocompromised Patients
In immunocompromised patients, during and after HSCT and other treatments for the malignance, discordance of microbiota increases the risk of systemic infections and immunological complications [30]. FMT and engineered probiotics are tested as methods for preventing GVHD and enhancing mucosal immunity. Specific microbial signatures are present in cancer concerning tumors and are understandably involved in modulating response to immunotherapy [43]. Hence, microbial modulation might lead to improved response to treatment and lesser side effects.

Challenges and Limitations
Making the necessary advancements involves a high degree of complexity in the translation of microbiome-targeted pharmacology into clinical applications. Microbiome science is prone to systemic biases. Nearing et al., [44] said one potential reason for inconsistent results across studies is due to the inability of random and systematic bias to be eliminated from sequenced-based human microbiome studies- from collection through storage, sequencing, and analysis. These biases extend from collection to storage, sequencing, and analysis. For example, they postulated that biopsy specimen collection induces strong biases toward mucosa-associated microbes and that microbiome data are compositional and do not represent actual counts of microbes. Such pipeline sensitivity further amplifies the variability across studies.

Causal inference is another major challenge. Walter *et al*. [45] showed that 95% of human microbiota–associated rodent studies reported phenotype transfer, an "implausibly high rate" that risks overstating causality. They cautiously advocated for a more rigorous and critical approach for inferring causality to avoid false concepts and prevent unrealistic expectations that may undermine the credibility of microbiome science. Analytical heterogeneity also undermines reproducibility. Kleine Bardenhorst *et al*. [46] reviewed 419 studies and found considerable heterogeneity in analysis strategies, with many failing to account for clustered structures or compositionality. This explains contradictory outcomes across seemingly similar studies. Beyond methodology, ecological resilience limits intervention durability. For example, [47] observed that even when microbiotas are manipulated, ecological forces drive them back toward baseline states. He proposed introducing controlled randomness or perturbation protocols to overcome adaptive rebound. Finally, [48] addressed the need for bias assessment tools in microbiome meta-analysis. Their risk-of-bias rubric, adapted from ROBINS-I, highlights domain-specific confounders such as sequencing batch effects and metadata limitations. Applying such frameworks would clarify which findings deserve greater weight.

Inter-Individual Variability in Microbiome Response
Variance exists in microbiome composition due to genetics, diet, geography, age, and antibiotic exposure in the putative target population. Microbiome differences modulate microbiome-based treatment efficacy and safety. Uncontrolled clinical trials yield contradictory results while standardization remains a difficult issue [49].
In turn, patient stratification may actually aid in the storage and eventual commercialization of existing microbiome modulation approaches.

Safety and Standardization Issues
While FMT undoubtedly works, issues concerning pathogen transmission, immune reactions, and other long-term concerns remain. As a matter of urgency, donor screening processes, modes of delivery, and microbial composition require standardization [38]. However, engineered microbes pose their own dangers-they may engage in genetically unforeseen interactions or trigger immune responses [50].

Regulatory and Ethical Issues
No regulations are universally accepted for bacteriotherapy. Some geographic areas regulate FMT as a biological product, in others, it is considered a drug, and say in some others, it is considered to be a tissue transplant. The presence of synthetic consortia and GMOs defies clarification of the regulatory path [34].

Ethical issues including informed consent, patient safety, and donor privacy are raised by the transfer of microbiota.
Gaps in Mechanistic Understanding
It is presently known that associations exist between the microbiome state and the disease state, but those that are causative mechanisms have been largely left unexplained. This creates all sorts of difficulties for drug discovery and clinical translation. Most microbial metabolites have yet to be identified, and microbiome-host interactions have yet to be mapped [51]. Systems biology and high-resolution modelling are being pursued in order to overcome these deficiencies in unravelling microbiome-host-drug networks. In **Table 4**, the major roadblocks in microbiome therapeutics have been listed, with suggestions to overcome them.

Table 4. Challenges and opportunities in microbiome therapeutics.

Challenge	Cause	Solution Pathway	Ref
Inter-individual variability	Diet, antibiotics, genetics	Personalized therapies	[49]
FMT standardization	Donor diversity	Defined microbial consortia	[38]
Regulatory ambiguity	No unified classification	International regulatory reform	[50]
Safety concerns (FMT/GMOs)	Risk of pathogen transfer	Long-term safety trials	[27]

Future Directions

Microbiome-targeted pharmacology is an ever-changing field with multiple forefront directions promoting precision therapeutics. Caminero *et al*. [52] argue that microbiome science must transition from correlative regimes toward rigorous, reproducible, and clinically relevant designs, emphasizing AI-assisted integration, multi-omics, and mechanistic validation. Combining standardized bias assessments [48], best-practice workflows [44], ecological insights [47], and rigorous causal frameworks [45] will be key to progress.

Personalized Microbiome Therapeutics

Due to the enormous inter-individual variability in microbiome constitution, an approach customized for each patient may better optimize treatment. Microbiome sequencing realizes patient stratification of those most likely to respond to a given probiotic, postbiotic, or FMT preparation [53]. Microbial therapies, which rely on host genetic profiles as well as functional microbiome signatures, are now coming into being [54]. Microbiome-informed diagnostics are also used to identify risk groups and predict responses, primarily in cancer and transplantation [43].

Incorporating Microbiome Data in Antimicrobial Stewardship

In an attempt to prevent unwarranted patients' exposure to such broad-spectrum agents, antibiotic stewardship programs have started integrating microbiome data. This calls for the rational use of narrow-spectrum or microbiome-sparing antibiotics in accordance with microbial ecology principles [37]. Real-time microbiome surveillance may soon become a practice in guiding individualized prophylaxis in ICU and oncology units, to reduce dysbiosis and opportunistic infections.

Microbiome-based Vaccine Adjuvants

The microbiome stands as one of the most common factors that may affect vaccine efficacy through innate and adaptive immunity modulation [55]. Probiotic- and postbiotic-based substances are being explored as vaccine adjuvants, especially in poor immunogenic settings such as the elderly and immunocompromised [35]. It has been shown in some studies that SCFAs, bacterial outer membrane vesicles, and microbial DNA fragments promote T cell responses and seroconversion [41].

Multi-Omics Approach to Pharmacological Interventions

Multi-omics combine metagenomics, transcriptomics, metabolomics, and proteomics, lending themselves to unveil deep insight into host-microbe-drug interactions [34]. These approaches aid in the detection of novel microbial biomarkers, therapeutic targets, and drug metabolites to guide drug design and delivery. Multi-omics is now being used to further refine vaccine adjuvants and predict immune responses in viral infections such as COVID-19 [56].

Author's Perspective

The authors argue for microbiome modulation to become the core of infectious disease treatment, instead of being considered as complementary or exploratory tools. However, an early integration may affect the credibility. Caminero et al. [53] argued that the lack of rigor, reproducibility, and mechanistic validation may lead to an overpromise of the microbiome science. The upcoming research must be so that it includes domain-specific bias assessments and make use of the top-quality pipelines, reduce causal claims and focus more on the ecological rebound. It is only by doing these steps that the microbiome-based therapeutics will get beyond the hypothesis stage and become a clinical standard. Evidence has been piling up to support the claim that indeed, the microbial communities play a very significant role in the immune system of the host, resistance to pathogens, and outcomes of treatments. It is suggested that microbiome interventions such as probiotics, postbiotics, fecal microbiota transplantation, or synthetic microbial consortia and not only antibiotics and antivirals should be the preferred treatments at hospitals, among immunocompromised populations, and in the infection-prone areas.

Only a continuous interdisciplinary cooperation within the field can be the key for the real breakthrough. The host-microbiome-pathogen interplay is so advanced that it requires a wide range in the kind of study undertaken, microbiology, pharmacology, immunology, bioinformatics, and even systems biology all have a place in it. Microbiome-based therapeutics that will make it into the market should not only be the consequence of the biological background but they will also be enabled by the use of computation to model interactions, optimize the formulation, and individualize the treatment according to the patient's microbiome profile.

Table 5 provides a comparative advantage of the traditional infectious disease models, which are centering on pathogens, as against the new microbiome-centered approaches. The shift from promise to reality consequently requires bigger, faster, well-controlled multi-center clinical trials that are far superior to the very limited and exploratory clinical studies that are being carried out at the moment. Given in **Table 5** is a comparative vantage of the conventional infectious disease models focusing on pathogens vis-a-vis the emerging microbiome-centered approaches. At the same time, there must be regulatory frameworks that are easy to understand but also adaptive enough to learn from the unique aspects of microbiome-based interventions' nature, most obviously apparent in the intervention at the same time being a biological product and a living drug. Such regulations are a starting point for new therapeutic types to get through the clinical acceptance process, even if there is a clear mechanism of action for the therapy and even if the therapy is truly innovative.

Table 5. Comparison of traditional vs microbiome-focused infectious diseases approaches.

Approach	Focus	Example Treatment	Limitation	Ecosystem Benefit	Ref.
Conventional	Pathogen elimination	Broad-spectrum antibiotics	Resistance, microbiome damage	Low	[57]
Microbiome-centered	Microbial restoration	FMT, probiotics	Variability, regulatory gaps	High	[30]

The researchers are imagining a time coming when the control and treatment of infectious diseases go through a drastic shift from being pathogen-centric to the ecosystem-centric model. The interventions will not only be about getting rid of some specific microorganisms but also to improve and protect a naturally occurring microbial community that would act as a barrier against infection, with the immune response being the main factor that guides the community behaviour by promoting the beneficial health outcomes throughout individual's lifetime.

CONCLUSION

The human microbiome plays a significant role in changing the risk of infections, the immune response, and drug alteration. A disruption in the balance of the microbiota leads to an escalation of the infection risk that affects the immune defense mechanisms of the host and makes the vaccination processes useless. Conversely, if these microbial communities are controlled, improved, or revitalized by drugs, they may contribute to the infection rate reduction in hospital setups and facilitate better vaccine results like those in the reduction of the occurrences of antibiotic-related diseases, etc. Intervening with the microbiome using a pharmacological approach like probiotics, prebiotics, FMT, or engineered microbes may not be the first thing that comes to one's mind but it is a feasible method and a potentially powerful treatment for infectious diseases. The rapid advancements in the field over the last ten years are indeed very promising and at the same time, it is no less than a matter of regret that there is not much of a measure for coping with the situation in clinics, when the implementation of microbiome manipulations is concerned, for infectious diseases, mainly due to safety issues and other factors like the ecosystem adaptability, the regulatory system biases, and the variation in the methodological approaches. Given the accumulating evidence, microbiome-based therapeutics hold potential to become integral to clinical practice, but this transition requires validation through robust Phase III trials and standardized protocols.

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