The Human Microbiome Evaluated from an Ecological Perspective

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Abstract

The human microbiome is incredibly diverse and plays an important role in human health. As more studies are done, more diseases are becoming increasingly linked to microbiome health. In this review, we discuss the microbiome from an ecological perspective, to help understand the processes of the microbiome and how we can apply ecological principles to further the advancement of medicine in this relatively new field of study. First, we go over the establishment of the microbiome and how it is influenced by environmental factors. Then we discuss the spatial dynamics of the gut microbiome and the implications if it is disturbed. Finally, we discuss current treatments for microbial related diseases, and look to how we can improve them in the future with a better understanding of the microbiome.

Introduction

Bacteria are all around us, on our skin, in our mouths, and in our stomachs. As more and more studies are done, many aspects of our health are being connected to these microbes. For example, the microbiome has been linked to depression and anxiety (Xiong et al., 2023), IBD and Crohn's disease (Shan et al., 2022). Fundamental principles from the field of ecology and evolution can help us better understand how microbes are established, how they interact with the host and with each other, and how different compositions of the microbiome can occur after a disturbance, such as with antibiotic treatment. Therefore, a deeper understanding of the microbiome through an ecological perspective is crucial to help us harness these kinds of interactions to create better treatments for various health issues.

In this review, we discuss how we can use ecological principles and theories to deepen our understanding of the microbiome and its relation to human health. First, we go over how the microbiome is initially established and how initial establishment is influenced by people’s geographical location and diet. Then, we go over the spatial dynamics and keystone taxa of the microbiome and the possible health implications when it is disrupted. Next, we go over the theory of the evolution of microbes in response to disturbances like antibiotics and antidepressants. Finally, we go over current treatments for microbiome-related diseases, their benefits and drawbacks, and future implications of medicine in the microbiome. Using ecology as a lens to view the microbiome, we may be able to gain deeper insights into the future of medicine.

Establishment

One of the most defining times for a person’s microbiome is the first few years, when the microbiome is initially established (Ma et al., 2024). Studies suggest that it takes roughly 3 years for the microbiome to stabilize and transition to a more diverse microbiome from the initial pioneer organisms from the mother’s birth canal (Ma et al., 2024). But studies have also shown that babies born via caesarean section do not have the initial pioneer population on their skin

(Gonzalez et al., 2011). When infants are born, gut microbiomes are generally dominated by *Bifidobacterium spp.* before diversifying to include *Firmicutes* and *Bacteroidetes* (Ma et al., 2024).

From an ecological perspective, the initial colonization would be categorized as the *primary succession*, or in other words, the initial colonization (Gonzalez et al., 2011). From here, the infant's diet and environment begin to diversify the few initial pioneer species into microbiomes resembling those of an adult (Perez-Muñoz et al., 2017). This period can last for a few years before the microbiome reaches "climax community" or peak diversity during adolescence (Ma et al., 2024, Gonzalez et al., 2011). Taking antibiotics or other medications that might disturb the microbiome would lead to *secondary succession*, or essentially restarting the microbiome from the little resources left after being wiped out (Ma et al., 2024). As our microbiome ages, it reaches its final succession, where diversity decreases, ultimately opening the door for intestinal, skin, and liver disorders (Kadyan et al., 2025). But this destruction and rebuilding isn't always a bad thing, and it's actually happening more often than you think! Daily activities like taking a shower, brushing your teeth, or even just washing your hands kill the microbes on your skin and in your mouth, including the potentially harmful ones, prompting a secondary succession (Macklis et al., 2020).

The types of microbes available to colonize an infant are highly dependent on many factors, such as diet or even physical location. As an infant develops, its diet and exposure to certain microbes dictate the changes within its microbiome (Rampelli et al., 2025). Studies have shown that individuals with a traditional diet (more nuts, some meat, greens, berries) had increased amounts of *Streptococcaceae, Erysipela Clostridiaceae, Butyricicoccaceae, and Eggerthellaceae* compared to more *Bifidobacteriaceae, Rikenellaceae, Oscillospiraceae, and Ruminococcaceae* typically found in "western" diets (Ma et al., 2024).

Geographical location can also have an effect on the microbiome, with individuals at higher latitudes tending to have increased levels of the phylum Bacillota and lower latitudes tending to have greater levels of Bacteroidetes (Suzuki & Worobey, 2014). While this only highlights two phyla, it could be a potential explanation for microbiome diversity across different geographical locations around the world.

Spatial Dynamics

The spatial organization of the microbiome is maintained by both the physical environment and the interactions between communities, and their locations in the body, which have vast impacts on health. Microbes that are displaced within the body (eg, stomach bacteria in the colon) have been linked to obesity, cancer, and other intestinal diseases (Cao et al., 2022). The location of the community and its interaction with surrounding communities can greatly affect the role and function of a microbe within the microbiome (Yang et al., 2025).

Microbes and their physical environment

One of the most well-known examples of microbes affected by their physical environment is the gut microbiome. The gut microbiome is divided into 5 sections: the duodenum, jejunum, ileum, cecum, and the colon, and each section is composed of a distinct microbial composition due to the physical constraints of the host environment. The duodenum is the highest part of the intestine, directly after the stomach, and its primary purpose is to reestablish pH balance directly after the extreme acidity in the stomach. Because of its still slightly acidic pH (6-6.5), there are only about 10^3 colony-forming units (CFUs) per milliliter, the lowest of any section in the gut microbiome (Yang et al., 2025). The Duodenum is dominated by *Firmicutes* and *Proteobacteria*. Most of the bacteria in this section mainly serve to continue digesting food and extracting nutrients (Yang et al., 2025).

The jejunum is directly after the duodenum and is the longest part of the intestine. The primary function of the jejunum is to absorb lipids and fats. Oxygen levels, pH, and bile concentrations limit the number of CFUs in the jejunum, though the jejunum is slightly higher than the duodenum, at roughly between 10^4 and 10^7 CFU/ml (Kuang et al., 2024). The jejunum is also dominated by *Firmicutes* and *Proteobacteria.*

The ileum is the primary site for amino acid and vitamin absorption and comes after the jejunum. The ileum also contains microbes responsible for the immune system combating colon cancer (Yang et al., 2025). The proximal ileum is very similar to the jejunum in terms of composition, with mostly *Firmicutes* and *Proteobacteria.* However, towards the distal end, the ileum contains mostly *Firmicutes* and *Bacteroidetes*. Following the general trend, this section tends to have a higher concentration of colony-forming units, between 10^7 and 10^8 CFUs/ml.

The cecum functions mostly to absorb water and contribute to stool formation (Yang et al., 2025). In the cecum, since oxygen levels are relatively low, the main microbes are facultative anaerobes, meaning they can produce ATP via aerobic respiration, but can switch to anaerobic respiration in the absence of oxygen. Among these, *Escherichia coli*, *Lactobacillus*, and *Enterococcus* make up the largest percentage of the cecum. The cecum contains roughly 10^8 CFUs/ml. As seen, these microbes are well-suited for this section of the intestine and its conditions.

The colon plays a similar role to the cecum, participating mainly in stool formation and water absorption. However, thicker layers of mucus within the colon allow for a greater concentration of microbes to survive (Kuang et al., 2024). Within the colon, there are estimates to be between 10^11 and 10^12 CFUs/ml, significantly higher than the rest of the intestinal tract (Yang et al., 2025). The colon contains mostly *Bacteroides*, *Faecalibacterium*, and *Escherichia*.

Microbes and their interactions with other microbes

Beyond the physical environmental constraints of the different parts of the human body, interactions between communities can also have an enormous impact on the composition of a microbiome, and thus have an impact on the function of the microbiome (source 3). For example, commensalistic relationships within the microbiome, like biofilms, increase the tolerance to stressors for all microbes involved. With increased chances of survival from external factors like phages and environmental pressures, these microbes can continue to perform in their niche and maintain their role in the ecosystem. The relationships between communities of microbes can be separated into four major categories. Neutral, antagonistic, commensalistic, and competitive. Neutral interactions, generally the most common, provide neither harm nor benefit to both parties involved (Ma et al., 2024). The next most common are antagonistic relationships. This is where one benefits at the expense of another; for example, some vaginal bacteria like *Lactobacillus reuteri* have shown the ability to secrete chemicals inhibiting the growth of some pathogenic bacteria like *Staphylococcus aureus* (Voravuthikunchai et al., 2006). Next is competitive relationships. This is where neither side benefits from the interaction, but both continue to compete for resources to survive. For example, *Intestinimonas butyriciproducens* and *Shigella flexneri* have shown reduced growth when in proximity to each other (Ma et al., 2024).

However, there is only a fixed number of resources for all the communities of microbes, leading to many different interactions between communities of microbes. The most prevalent non-neutral interaction is commensalism (Ma et al., 2024). The most common example is cross-feeding, where one microbe produces nutrients that can be used by another and vice versa. Some examples of this are *Bacteroidetes* breaking down polysaccharides for use by other organisms (S. Wang et al., 2024) and the relationship between *Acetobacter pomorum* and *Lactobacillus plantarum,* supplying each other with essential nutrients for growth (Ma et al., 2024). There are also mutualistic relationships where both parties benefit from the interaction. For example, communities can make biofilms, with common participants being *Bacteroides*, *Lactobacillus*, and *Bifidobacterium* (Ma et al., 2024). These microbes benefit from such biofilms because they increase the efficiency of nutrient breakdown, and they also increase the group's overall tolerance to environmental stressors found in the extreme conditions of the intestine (Ma et al., 2024).

Species that have a disproportionate impact on the microbiome relative to their concentration are *keystone taxa* (Weiss et al., 2023). These species can have both a positive or negative effect on the ecosystem. For example, lab tests showed that *B. caecimuris* significantly impacted the abundance of 4 species in a polysaccharide medium. But these impacts can go beyond just nutrient decomposition. Media without *E. faecalis* showed a higher level of acidity, and thus also a lower concentration of certain microbes (Weiss et al., 2023). Further analysis of individual species and their impacts on the microbiome is needed to truly identify relevant keystone taxa.

Another common interaction in the microbiome is antagonistic/competitive relationships. This is where one organism benefits by harming another, or both harm each other, trying to gain control of resources. An example of this is the competition between *Roseburia intestinalis* and *Bacteroides ovatus*. Since both are efficient at breaking down xylan, they are forced to compete for resources (S. Wang et al., 2024). When scenarios like this occur, it can increase diversity by forcing one species out of a niche and into a new one. This theory is called niche filling or niche differentiation (Pereira & Berry, 2017). This slight change in niche increases the diversity in the microbiome, creating slightly different niches to be filled (Pereira & Berry, 2017). Competition for resources is always happening in the microbiome, and this can lead to the small-scale evolution of some microbes called coevolution.

Theory of evolution of microbes

The theory for microbial evolution is very similar to that of larger organisms in that environmental pressures can cause changes in the taxonomic composition of the ecosystem, and the genes expressed by the organisms in it (Dapa et al., 2023). For example, if a host is consistently exposed to certain pathogens, natural selection for microbes that are resistant to that pathogen will happen, causing slight changes in the expressed genes within the microbiome (Hulse et al., 2023). In the case of microbes, researchers have observed the evolution of certain microbes along with the evolution of mammals, expressing different genes and adjusting to the diet of the host organism (Davenport et al., 2017). This co-evolution becomes co-speciation when the host organism diverges into a new species, and the microbiome follows suit. For example, as chimpanzees and gorillas evolved into humans, so did our gut microbiota (Moeller et al., 2016). Genome analysis showed that *Bacteroidaceae* and *Bifidobacteriaceae* showed increased diversification around the same time that humans began evolving from our ape predecessors (Moeller et al., 2016).

Constant competitive interactions and coevolution between organisms can push organisms towards two different evolutionary strategies. Some become more specialists, and some become more generalists. *Specialists* are very strong competitors in a limited range of niches, while *generalists* are considered weaker competitors, though in a wider range of niches (Xu et al., 2022). Both have evolutionary advantages and disadvantages, but which path a community goes down is entirely random and up to genetic mutations.

This rapid evolution is already observed in healthcare and drug therapeutics today. For example, even in indirect ways, microbes are becoming more resistant to antibiotics. With increased mental health awareness, the amount of antidepressants being taken by patients has also increased, almost to the amount of antibiotics taken each year in the US (Y. Wang et al., 2023). But some common antidepressants could have negative impacts on gut microbiota. Researchers have discovered that exposure to common antidepressants can actually increase antibiotic resistance among communities. Researchers have hypothesized that constant exposure to antidepressants stimulates the stress response of bacteria and increases the expression of efflux pumps, which enable a microbe to pump out antimicrobial substances (Y. Wang et al., 2023). By stimulating the stress response, bacteria can also form biofilms, providing them protection from some antibiotics (Y. Wang et al., 2023). Researchers exposed an E. coli strain to common antidepressants, and results showed increased resistance to common antibiotics like tetracycline and amoxicillin (Y. Wang et al., 2023). As researchers have seen, changes inthe prescription of certain medications are indirectly or even directly driving the evolution of microbes within humans.

In addition to antidepressants, continual use of antibiotics can decrease microbial diversity and promote the growth of drug-resistant bacteria. Antibiotics can induce evolution of microbes through natural selection, where microbes that have favorable genes are resistant to antibiotics.

Microbes can also go through coevolution. Changing dynamics for one microbe can trigger a co-evolution scenario for other microbes. For example, by eliminating competition for mutated bacteria, those populations have the space and resources to grow to unhealthy levels (Ma et al., 2024). However, studies have shown that with time, commensal bacterial communities can provide enough competition to eventually re-establish a healthy microbiome (Bhattarai et al., 2024). Antibiotic use can also promote resistant commensal strains, which could have a major impact on the future of medicinal treatments for diseases caused by pathogenic bacteria like *E. coli* and *Klebsiella* (Bhattarai et al., 2024). Heavy antibiotic use has also shown to lead to increased risk of health conditions like gout and diarrhea due to damaged kidney cells (Wallace et al., 2010, Liu et al., 2023).

Overview of current microbiome medicine and treatments

Given the impacts the microbiome can have on health, medical treatments are being extensively researched for all kinds of microbial issues. Currently, the most common methods to repair a disrupted microbiome are through probiotics, prebiotics, and fecal transplants. All are meant to either directly re-establish healthy colonies of bacteria or to promote their growth over other potentially harmful competition. Many of the current microbiome treatments are centered around ecological principles of competition and succession.

The first of these methods is probiotics. Probiotics are bacteria that can be inserted into a microbiome to promote healthy microbiomes, leading to health benefits for the host (Latif et al., 2023). Probiotics work to limit the populations of pathogenic bacteria primarily in competitive ways. Some bacteria in the gastrointestinal tract outcompete pathogenic bacteria for receptor sites (Bermudez-Brito et al., 2012), some compete for nutrient resources, and some can secrete antimicrobial peptides to kill off harmful bacteria (Plaza-Diaz et al., 2019). This kind of competition, where one species can outcompete another and nearly eliminate the other species from competition, is called *competitive exclusion* (Plaza-Diaz et al., 2019).

The next treatment is prebiotics. Prebiotics are nutrients that feed specific bacterial species, promoting their growth over others (Davani-Davari et al., 2019). Prebiotics can also have increased health benefits for the host through the production of short chain fatty-acids (SCFAs). When some species of bacteria break down prebiotics, they produce SCFAs, which are then released into the bloodstream. These compounds can boost parts of the immune system and improve colon health (Clarke et al., 2010, Zhou et al., 2013). However, prebiotics can have adverse side effects as cross-feeding can promote the growth of potentially unwanted levels of certain bacteria (Davani-Davari et al., 2019). Though prebiotics continue to be extensively researched to create more selectivity among bacteria that are promoted.

The last common treatment is fecal transplants. This treatment is most common for treating *C. difficile* infections (Khoruts & Sadowsky, 2016). This method primarily attempts to quickly restore a healthy microbiome in order to create competition for *C. diff* strains (Khoruts & Sadowsky, 2016). Many bacteria already present in a healthy gut can fend off *C. diff* through competitive exclusion for space and resources, secreting inhibitory compounds, or by stimulating the host immune system (Khoruts & Sadowsky, 2016). Current research is being done to determine if fecal transplants could be useful against other harmful bacteria and whether they could cause diversity problems due to potentially increasing homogenized gut compositions.

Conclusion paragraph

Many ecological principles that can be applied to animals can also be applied to microbes in our own microbiomes. Ecological theories about organism interactions, succession, and establishment are all crucial to understanding the current research and treatment for the microbiome. Microbiome research is a relatively new field, and conducting research from an ecological perspective can help jumpstart the field and its potential to greatly improve human health.

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