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### **The Critical Function of the Gut Microbiota**

Have you ever heard that there are millions of bacteria on virtually every surface that we touch? Did you know that there are also millions of bacteria inside of us? Often, bacteria is associated with sickness and has a negative connotation associated with it. However, this is simply inaccurate for many of the bacterial species that live in the human gut.

Scientists have studied mutualism, where two organisms of different species benefit from the activity of each other, for years (Mutualism, 2015). One specific case of mutualism that is incredibly important to modern humans is the relationship between humans, the host, and their gut bacteria. In this relationship, the gut microbiota live in the digestive tract of humans (Tannock, 2017). This benefits the bacteria by giving them a place to live and eat, while humans are benefited through numerous health functions of the bacteria (Mueller, et al., 2012).

In our modern society, ironically, our gut bacteria communities have actually deteriorated, and there is now a lack of diversity. This is a real problem that needs to be addressed (Moeller, et al., 2016). In this paper, I will dive into the significance and the variety of health benefits that these gut microbiota provide, including that of disease prevention (Hall, Tolonen, & Xavier, 2017). Additionally, I will speak to the state of the gut microbiota in the current state of our humans, and how the specific bacteria that our entire microbiota is composed of, has changed (Moeller, 2014; Moeller, 2016). Finally, I will detail the stakes of the gut microbiota, and how our knowledge of the microbiota, along with future research and

technologies, can enable us to increase health of individuals. (West, et al., 2015)

### **Basic Functions of the Gut Microbiota**

Deep in our gut, we have a large community of diverse bacterial species. These gut bacteria as a whole are called the gut microbiota, the entire population of bacteria living in a gut. The gut microbiome refers to the genetic scale and is about the genomes present in the gut microbiota.

Gut bacteria live in large communities in our gut, where they are able to block space that pathogens would potentially use. This therefore inhibits pathogen accumulation (Tannock, 2017). At the start of our lives, we have no gut microbiota; it starts forming upon our birth. The full microbiota that we usually fully develop by the age of two years old is shaped by both environmental and genetic factors (Moeller, et al., 2016; Mueller, et al., 2012). The gut microbiota also aids in the production of several vitamins, B and K, important to our health (Tannock, 2017). A negatively impacted gut microbiota can have severe impacts to different aspects of an individual's health. Microbiota development, through a study done, was shown to affect, “maturation of the gut mucosal immune system, metabolic function in multiple host tissues, plus musculoskeletal and brain development.” (Blanton, et al., 2016, p.3) This is critical because it shows that having just one insufficient item, an unhealthy or undernourished gut microbiota, can have lifelong effects on the affected hosts. Additionally, studies show the role of gut bacteria in reducing the chance of health impeding diseases, like obesity (West, et al., 2015), and studies have shown that there is a correlation between a healthy gut microbiota in individuals and healthy growth (Blanton, 2016). More generally, besides specifically deterring pathogens and preventing disease, others have simply cited that, “gut bacteria are critical for normal

development” (West, et al., 2015, p4), which shows a more general role of the gut microbiota.

### **Genetic and Environmental Interactions**

Each individual has a unique gut bacterial makeup, which could be detrimental or beneficial based on the health of this microbiota. This is because the gut microbiota, besides its many obvious functions, such as pathogen reduction and vitamin production, has many residual benefits as well that are connected to genetic structures (Hall, Tolonen, & Xavier, 2017).

Although the entire gut microbiota of an individual is based off environmental factors, there is a large part of the gut microbiota, including strain and species diversity, that is based on host genetics. Studies showed that the gut microbiota of monozygotic twins are much more similar than that of dizygotic twins, which exemplifies this genetic impact (Hall, Tolonen, & Xavier, 2017). The impact that genes have on our gut microbiota is huge. Some genetic variants, such as an intolerance to lactose or gluten, could shift or influence what we eat, and therefore indirectly manipulate our internal bacterial community. Individuals diagnosed with such variances would have a more limited bacterial community and have less diversity than those exposed to a wider variety of foods. Other genetic variants are more direct, and could potentially bring about a microbiota that increases susceptibility to or even induces certain disease. This happens when an individual is, “predispose[d]...towards microbiome dysbiosis,” which negatively affects the body in diseases that target metabolism (Hall, Tolonen, & Xavier, 2017, p.2). The main point, however, is that the gut microbiota is highly based on genetic interactions that cannot be controlled for.

In modern humans, even with our current push towards medical innovation, one thing that may be overlooked or underemphasized is the health of our gut microbiota. Due in part to

unhealthy practices, such as overuse of antibiotics, there has been a loss of microbacterial diversity in many of the world. Antibiotics, when used often, deteriorate the diversity of the gut microbiota by killing healthy gut microbiota as a byproduct of removing detrimental bacteria in the body (Mosca, et al., 2017). Compared to people living in Malawi, Africa, humans in the USA have a much less diverse set of microbiota (Moeller, 2016). While the Malawi people have many of the descended bacterial lineages and strains, most people living in the USA sampled lack these, leading to lower total diversity.

### **Cospeciation of Gut Bacteria with Hosts**

All species change in time in response to environmental changes. At this point, it is clear that ancestors of humans in the past, dating millions of years ago in hominin ancestors possessed gut microbiota communities, similar to the way that modern humans do now. However, there is also evidence that the communities of gut bacteria, and specific species of bacteria, have changed significantly as time has gone on (Moeller, 2016).

In cospeciation, two species that interact evolve in response to each other. For example, if human's developed a new form of nutrients in their gut that could be captured by gut microbiota, the gut bacteria might evolve specialized food gathering tools in response. These small changes accumulate eventually into large changes, as these species are constantly responding and evolving to both environmental and opposite species changes. Cospeciation occurs when two species are in close proximity to each other, and thus it is expected from gut microbiota and humans, as they have a mutualistic relationship where the gut bacteria live inside of the human (Jones, 2016).

In two different studies done in 2014 and 2016, by many of the same people, and with a

similar target question, corroborating results were found that showed that there is indeed cospeciation between bacteria and their respective hominin hosts. (Moeller, et al., 2014, 2016). In specific gut bacterial families of *Bifidobacteriaceae*, *Bacteroidaceae* and *Lachnospiraceae*, researchers examined the DNA sequencing of the different families from different animal fecal samples to see if changes existed on a strain level. Most of the strain level changes in the *Bifidobacteriaceae* and *Bacteroidaceae* corresponded to existing phylogenetic trees that have been constructed that detail hominin history; that is, the bacteria changed as species diverged or separated from common ancestors, as humans eventually evolved (Moeller, et al., 2016). However, for the *Lachnospiraceae*, it did not show as many changes. This is hypothesized to be due to the nature of its reproductive methods: “Lachnospiraceae...are spore-forming and can survive outside the gut, which may enhance their ability to disperse and transfer among host species” (Moeller, et al., 2016, p.5). This observation demonstrates how the bacteria that reside in our gut can in some ways manipulate the extent of their own evolution via different reproductive methods.

The significance of the differential microbiota communities is that it shows that although gut microbiota change within individuals over the span of a lifetime, these changes are not just individual based. These changes in gut microbiota makeup are eventually homogenized into a population to the point that different species have different strains of DNA for the same species of bacteria. This proves the ability of the gut microbiota to evolve and for these evolved changes to stick over the course of many years (Moeller, et al., 2014).

### **Potential Applications of Gut Microbiota for Diagnostics and Therapy**

The gut microbiota has been proven to have a critical and unique role to humans' health

without any of the hosts consciously doing anything. Besides this quiet mutualism, the gut bacteria could potentially help us even more.

Individuals' health can be gauged by examining compositions of their microbiota via fecal samples. This allows easy access to show both current and potential health problems. Scientists examine the bacteria and look for healthy levels of diversity, as well as specific susceptibilities to diseases, as gut bacteria is also linked with resistance in disease. This is done on a strain level, where different DNA sequences are searched for, as well as on a species richness level, where the scientists look for specific families of gut bacteria (West, et al., 2015). Different sequencing approaches such as quantitative PCR and DNA microarrays are implemented to examine the DNA and diversity of these microbiota communities (West, et al., 2015). Once health conditions are assessed, therapies that already exist can be prescribed to prevent the advancement of these diseases.

In some cases, the therapeutic uses of gut microbiota are as simple as examining gut microbiota samples of individuals in different individuals, but it can also be more complex than that. Gut microbiota affects healthy maturation of the gut mucosal immune system; one study showed that IgA, the main antibody secreted by this immune system, respond to up to 30 bacterial taxa. This means that if there is a lack of diversity of gut bacteria in a host's body, the host will be unable to fight diseases as well (Blanton, et al., 2016). Researchers showed that manipulating food can affect microbiotic communities in individuals, as some ingredients would be linked to different health benefits in the gut bacteria community. (Blanton, et al., 2016).

Finally, in a study published in 2016, researchers found and stated the potential for transplanting microbiota into different individuals to increase health. In the experiment, gut

bacteria from both healthy and malnourished Malawian child donors were transplanted into young mice. Overall, the mice with the healthy gut microbiota had a statistically significant health advantage: “Mice harboring donor microbiota from healthy infants gained significantly more weight and lean body mass” (Blanton, et al., 2016, p.3). This shows that there is a causal relation between gut microbiota and undernutrition, and displays the feedback loop taking place: in order to have an inadequate microbiota, one must be undernourished. When one does obtain this limited microbiota that lacks diversity, they become malnourished as a result. This direct effect of the gut microbiota even in a different host combined with transplantation potential means there may be some more therapeutic potential beyond simply examining people’s gut microbiota. In the future, healthy samples of gut microbiota could potentially be transplanted into sick or malnourished individuals (Blanton, et al., 2016). However, most of this work is preliminary, so the extent to which this can work in the future is still unclear and should be ethically considered before advancing to human trials.

## **Conclusion**

We know how critical the entire gut microbiota is to the health of its human hosts; the gut microbiota in humans is an important factor in health regulation through functions of pathogen inhibition, vitamin supplementation, and more. However, this has not prevented modern humans from having malnourished gut microbiotas.

The state and health of each individual’s microbiota heavily influences their fitness; an individual with an underdeveloped or not diverse bacterial community will be more susceptible to diseases and may not have as diverse of a set of functions (West, et al., 2015). Due to changes within bacterial species over time, there are many individuals in modern day that lack diversity

in their microbiome, which could lead to many potential health risks (Moeller, et al., 2016). This lack of genetic diversity is a widespread issue in a lot of the population, and should be targeted.

To fix modern humans and their gut microbiota, there are some things we can consider, such as the reduction of antibiotic use. More drastic measures would include raw transplantations of healthy gut microbiota from humans into malnourished people. There are obvious limitations to this however; there have been limited experiments done outside of transplanting gut bacteria to mice (Blanton, et al., 2016), but there is real potential, due to the widespread impact of gut bacteria.

Overall, the modernization of humans and the quest towards medical advancements may have hurt us. Many humans lack the genetic diversity of bacteria that their ancestors once had, and this will continue to hurt their health. This issue cannot be overlooked and must be looked in to.



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