Role of Gut Microbiota in Host Health and Disease

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**Abstract**

A microbiome is any specific environment that a microorganism lives in; this can include in nature, on a host’s epithelial layer, or inside a host. When referring to the microbiome of a host the most common thought is the collection of bacteria, archaea, and eukaryotes inside the gastrointestinal tract. The gut microbiota deals with not only the microorganisms in this niche, but also how they interact with the host and their mutualistic relationship that has developed. Recent discoveries by scientists find that this complex and dynamic microbiome has a significant effect on how the rest of the body functions, not just the gastrointestinal tract. One of the most crucial roles these microorganisms have is “maintaining immune and metabolic homeostasis and protecting against pathogens” (Thursby & Juge, 2017). The effects of the gut microbiota on host health and disease are still being uncovered and studied, however, it is known that variations in bacterial composition of the host has been linked to pathogenesis. It is only in the last decade that scientists have been able to extensively study the mechanisms of the gut microbiota. This research is possible due to a move from culture-based methods in a laboratory to culture-independent studies (Thursby & Juge, 2017). More efficient research techniques are still being tested and discovered. Attempting to cultivate bacteria, archaea, and eukaryotes outside their natural environment poses the greatest problem against furthering the knowledge of the gut microbiota because of its difficulty to accomplish.

**Introduction**

 A host’s gastrointestinal tract is one of the largest interfaces in most organisms, creating the most extensive entrance and exit through the body. The gastrointestinal tract consists of the mouth, esophagus, stomach, intestines, and anus. In humans alone, 60 tons of food passes through this system along with an abundance of microorganisms. This passage of food creates an estimated ratio of 1:1, human to bacterial cells within a given hosts gastrointestinal tract (Thursby & Juge, 2017). The microbiota usually has a mutualistic relationship with the host that have an essential role in nutrient uptake, the production of hormones, and support of the gut microbial homeostasis (Feng, Chen, & Wang, 2018). Along with the regular upkeep of the hosts microbial health, the gut microbiota can also specifically strengthen gut epithelial integrity, protect against pathogens that pass through the digestive tract, and help with host immunity to these pathogens (Thursby & Juge, 2017). Since it is such an essential part to the functioning of host gut microbiota it has the possibility to be disrupted from a modified microbial gut composition and ratio. Individual hosts’ gut microbiota development is currently considered to begin at birth, with significant colonization throughout the first two years of life due to the health of the host such as fevers and infections, medication taken by them, and any changes made in diet (Thursby & Juge, 2017). After roughly two years of life, an infant’s gut microbiota contains a configuration and function similar to those of an adult. There are six phyla present in host microbiota consisting of: Firmicutes, Bacteroidetes, Protobacteria, Actinobacteria, Verrucomicrobia, and Fusobacteria. Within a healthy host’s gut composition the majority of the phyla are Firmicutes and Bacteroidetes, with only a small percentage of the four other phyla. A key sign of a microbiota in dysbiosis is a larger ratio of Protobacteria, Actinobacteria, Verrucomicrobia, and Fusobacteria gut composition than Firmicutes and Bacteroidetes. The environment of the gut affects these compositions through “chemical, nutritional and immunological gradients” that either enhance or inhibit specific bacterial growth (Thursby & Juge, 2017). The environment of the gut microbiota is specifically linked to either a negative or positive affect on host health throughout their life as shown through these studies.

**Recent Progress**

The majority of recent information discovered about gut microbiota comes from the studying of bacterial 16s ribosomal RNA. This is a particularly beneficial way to survey the gut microbiota due to this gene being present in all bacteria, as well as containing highly variable regions. The variable regions allow researchers to specifically identify individual bacterial genus. To identify the composition of bacteria in the gut without harming the host, scientists will often collect the 16s ribosomal RNA from fecal samples. Though using this method of collecting information is the best to date, there are still weaknesses to this method. The main problems are that it does not distinguish between live and dead cells, and it does not inform about the functions of the species that are present. There is a recent push to make the process cheaper and quicker, by focusing on shorter sub regions of the 16s genes in greater depth. This focus is being pushed even though it can lead to more errors in the reading of the genome. A more reliable estimate of microbiota composition would be provided from sequencing the whole genome because of a “higher resolution and sensitivity” from these techniques (Thursby & Juge, 2017). Processing the whole genome, however, is still under development to completely understand the cost efficiency and if it is worth it to proceed. Most of the recent progress in research branches from the effort to collect cultures from their natural environment, due to the inability for a large majority of bacteria to be grown in a laboratory setting.

Specific research has been studied depicting that a hosts’ diet has one of the largest effects on gut microbiota. Diet is so important due to the “availability of microbiota-accessible carbohydrates (MACs)”, which is found in dietary fibers of a hosts gut (Thursby & Juge, 2017). Studies comparing the effects of fiber through extreme diets, such as mostly animal based or mostly plant based have resulted in wide-ranges in the composition of the gut microbiota in a host (Thursby & Juge, 2017). This thesis was further exemplified by other studies, where nearly matching diets with high resistant starch or non-starch polysaccharide fibers resulted in different bacterial species being enriched in the host gut that thrived under these specific conditions (Thursby & Juge, 2017). The environment a host creates within their gut microbiota is directly related to which bacteria, archaea, or eukaryotic cells thrive within this niche. Besides the bacteria, archaea, and eukaryotes, benefiting from living within a host microbiota, there are also benefits for the host, creating this mutualistic relationship. There are many key vitamins that cannot be synthesized without the help of the microorganisms in the gut. One example of these benefits for the host is the production of vitamin B-12, which an important organism to its production are lactic acid bacteria in the gut because the human body cannot synthesize them on its own (Thursby & Juge, 2017). This relationship is key to the health and development of a host body along with its bacteria counterparts in the gut.

**Discussion**

Research is still being developed to discover the best way to study the gut microbiota. From what scientists have learned just within the last decade changes much of the “understanding of the mechanisms linking the gut microbiota composition and its activity to health and disease phenotypes” in the host (Thursby & Juge, 2017). Everything that has been learned so far has increased the knowledge on how to enhance the health of a host through the use of the mutualistic relationship between a host and microorganisms. Dysbiosis and altered gut composition has been connected to multiple diseases, however, specific affects on the gut microbiota are still not known enough to make broad scientific judgments on diet and health efforts (Feng, Chen, & Wang, 2018). With further knowledge of the specific causes and affects of the gut microbiota on host health many diseases in the future can be diagnosed quicker, understood better, or maybe even prevented just based on diet and intake of chemicals into the body. The need to be able to study the gut microbiota in whole is what would help with this uncertainty, but the requirement to culture bacteria, archaea, and eukaryotes outside of their natural growth environment is the greatest dependent on if this is possible.

**Resources**

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