Microbiota and You: An Unlikely Friendship

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Although often considered the forgotten organ, microbiota play an essential role in human health and disease. With over 100 trillion cells living in or on us this symbiotic relationship provides us with a wide array of benefits ranging from protection from pathogens to aiding in digestion. This microbiome contains taxa including archaea, bacteria, viruses, and eukaryotic microbes (Clemente, Ursell, Parfrey, & Knight, 2012). With over 1000 species of bacteria alone. 90% of our microbes are characterized by six phyla: *Verrucomicrobiota, Proteobacteria, Fuseobacteria, Actinobacteria, Bacteroides,* and *Firmicutes* (Lizumi et al., 2017). Irregular balances of microbiota can be associated with a plethora of diseases such as inflammatory bowel disease, obesity, autoimmunity, and metabolic syndrome (Marchesi, et al., 2015).

**Introduction**

Although we would like to consider ourselves independent entities, we in fact are a host of millions of microorganisms referred to as microbes (Lizumi et al., 2017). The symbiotic relationship is essential for both parties (Luca, Kupfer, Knights, Khoruts, & Blekhman, 2018). Co-evolution between microbes and the human body has led to a cooperative rather than an incompatible association (Palm, Zoete, & Flavell, 2015).

**Recent Progress**

With the recent boom in technology, research of microbiota and their influences has greatly increased opening up a new realm of discovery in the human microbiome.

While we would like to think, we are independent entities we are in fact not (Palm, Zoete, & Flavell, 2015). We rely on microbiota for essential roles in our wellbeing (Luca, Kupfer, Knights, Khoruts, & Blekhman, 2018). Some of these roles include but are not excluded to energy and nutrient extraction, appetite signaling, and enzyme production. The majority of our microbiota inhabit our gut with smaller factions existing in the oral, respiratory tract, vaginal, and epithelial regions of the body (Marchesi, et al., 2015). Microbiota and their wide-ranging genome (over 150 times more genes than the human genome) have great influence over our digestive tract (Qin, Junjie, et al). This assistance helps us break down food such as carbohydrates and absorb the nutrients (Clemente, Ursell, Parfrey, & Knight, 2012). Another role the microbiota play is providing a barrier of protection against pathogens. This happens through competitive exclusion and synthesis of antimicrobial constituents. The microbes already present in our gut compete with other pathogens for residence This competition helps keep unwanted microorganisms out (Palm, Zoete, & Flavell, 2015). One of the most crucial roles of our microbiome is the induction of maturation in immune cells and their functions (Lizumi et al., 2017). The gut microbiota play a crucial role in immune maturation and development. Studies have shown microbiota to be immunologically important. This has been shown by studies on germ free mice. The mice raised without any microbial influence have a severely immature intestinal immune system. There are two factors separating the immune influencing microorganisms from the non-influencing ones. The first being that they are native members of the microbiome. While the second is that they interrelate with the host in a manner that leads to their recognition by the intestinal immune system. This leads to specific responses by the immune system. These essential microbes can then be split into another two commensals: inflammatory and immunoregulatory. As expected the inflammatory symbionts induce an inflammation effector response by the immune system. The immunoregulatory includes everything but the inflammatory microbes. The immune system also plays a role in the regulation of microbes (Palm, Zoete, & Flavell, 2015). This symbiotic relationship helps maintain homeostasis and prevents intestinal disorders (Lizumi et al., 2017) .

Though the relationship seems to be more beneficial than incompatible some irregularities in the microbiome can lead to a plethora of ailments. Majority of gut microbiota is made up by affiliates of the divisions *Firmicutes* and *Bacteroidetes* (Lizumi et al., 2017). Microbial presence has a significant influence human health and disease. For instance, early colonization of *lactobacillus* can be associated with a reduced presence of allergies. Another effect is the correlation between decreased presence of *Bacteroidetes, Firmicutes, and Methanobrevibacter smithii* with increased chances obesity.In contrast, they can influence anorexia as well with the elevated presence of *Methanobrevibacter smithii.* In patients with Crohn’s there have been shown to be less diversity in the *Bacteroides: Ovatus, Vulgatus, and Uniformis* (Clemente, Ursell, Parfrey, & Knight, 2012)*.* One key element in building our microbiome is our mothers initial contribution. This can have significant influence over potential health of the individual.

While most people associate microbes with our gut they exist everywhere on and in us including our reproductive organs. Recent studies have found to suggest that microbes play a significant role in reproductive health for both sexes. Microbiota also play an essential role in healthy pregnancies. While in the womb the fetus is considered to be. Once born the infant has almost no microorganisms in its this can be shown by an analysis of the infants’ earliest stool deposit known as the meconium. Studies have shown this sample is void of any detectable viral elements and harbors very low levels of bacteria (Younes, et al., 2018). Once birthed through the vaginal tract the infant is exposed to a plethora of microbes ranging from oral, fecal, vaginal, and epithelial (Clemente, Ursell, Parfrey, & Knight, 2012). Most of the microbes being vaginal resembling those of their mothers’ respective community. In contrast infants’ microbes delivered through caesarean section resemble those of the epithelial communities (*Staphylococcus* and *Propionibacterium*). These contrasting forms of delivery have a great influence on the infants’ microbiota development. Initially after birth whether it be vaginally or through caesarean section the infants’ have relatively low diversity of both viruses and bacteria (Younes, et al., 2018). Over time the diversity exponentially climbs creating a personalized microbiome (Palm, Zoete, & Flavell, 2015). It takes about 11 months for the child’s microbial community to differ from the mother’s. This development can be stunted or slowed down with the introduction of antibiotics (Younes, et al., 2018).

**Discussion**

Thanks to Alexander Flemings discovery of penicillin in 1928 we have modern day antibiotics. The impact of antibiotics has been undeniably beneficial to us. Although in the last 20 years some adverse effects of using antibiotics as treatment have become apparent. Overtime exposure to antibiotics can produce antibiotic resistant bacteria. Leading to illnesses like MRSA, *Clostridium difficile,* and VRE (Lizumi et al., 2017). The use of antibiotics at a young age has been correlated with the development of autoimmune and allergic diseases. Many reports indicate early exposure to antibiotics can lead to both risk of obesity and weight gain in babies (Younes, et al., 2018). Use of antibiotics reduces the gut microbiome diversity but there are ways to help compensate for the loss (Marchesi, et al., 2015).

In closing microbiota have a significant influence in relation to our overall wellbeing. Irregularities can lead to a plethora of health complications. With the aid of recent advancements in technology we can now study in depth the effects of microbes and their symbiotic relationship with our body. With this knowledge, we could potentially elucidate the influence of our microbiome composition and its influence over disease predisposition and development (Palm, Zoete, & Flavell, 2015).

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