Microbiomes in Human Health: The Future of Biomedical Science

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When many people think of bacteria, they consider the negative effects from infections, and the headlines about antibiotic resistant bacteria becoming a problem for treating those infections. Few people really consider the good aspects of bacteria and the positive benefits gained from certain bacterial communities in the world around us. Unfortunately, the fear of microorganisms has caused some people to lose sight of the evolutionary advantage that commensal microbiota have provided for the human body. Microbiomes are the genetic material from communities of microscopic organisms that work together in a specific environment, and one such environment that has been receiving attention lately would be the human body (Martín, Miquel, Langella, & Bermúdez-Humarán, 2014). As Ravel et al. (2013) phrased it best, "understanding the microbial side of ourselves may therefore be critically important for understanding human biology, including drug responses, susceptibility to infectious and chronic disease, and perhaps even behavior," (p. 1).

Although certain parts of the body are considered sterile sites without any other genetic material besides the individual, there are plenty of important areas within the human body that harbor a variety of microorganisms. Advertisements for probiotics have touted the importance of certain bacteria for digestion, and obstetric and gynecology providers understand how a shift in normal vaginal microbiota can lead to certain health problems among women and newborns (Solt, 2014). Even oral microbiomes have complex interactions that scientists are only recently coming to understand (Wade, 2013). Sometimes these microbial communities are beneficial to human health, but they can also work together for the detriment of the human host as well.

Realizing that the field of medical microbiology needs to shift its attention from singling out specific pathogenic organisms, scientists now believe a better approach to human health would be established through altering the entire communities of microbiota for the benefit of the individual (Martín et al., 2014). Even though the study of microbiomes would not have seemed possible a few decades ago, recent technological advances in science have given microbiologists a chance to inexpensively acquire data on microbiota through molecular diagnostics and genomics practices (Methé, Nelson, Pop, Creasy, Giglio, Huttenhower, & ... Mitreva, 2012). With this new technology, the analysis of microbial communities is not only possible but feasible, opening the field of microbiome research to new areas of biomedical science. In this research paper, an analysis of microbiome studies and the resulting implications will be detailed to prove the importance of understanding human microbiomes in relation to disease states and applying information obtained from microbiome research.

While microbiota have been elusive in the past, with many strains difficult to culture in the laboratory setting, recent developments in molecular and genetic techniques have improved the ability of researchers to identify and catalog more microbial species than ever before (Methé et al., 2012). The Human Microbiome Project Consortium (HMP) has developed an extensive framework of microbial communities in the human body from which researchers may pull information pertaining to specific microbiomes when performing studies (Methé et al., 2012). With this data, scientists can set up more detailed studies on different aspects of the human microbiome and utilize the framework for quality control measures and methodologies (Methé et al., 2012). According to Methé et al. (2012), “this resource may promote the development of novel prophylactic strategies such as the application of prebiotics and probiotics to foster human health," (p. 5). Now that a framework has been set for microbiome research, scientists can utilize various methodologies for collecting and analyzing microbiome data.

Greenblum et al. (2013) have begun to establish a systems-level model of the human microbiome that can be used in conjunction with the human microbiome framework developed by the HMP. Since microbiomes can vary widely from person to person among healthy individuals, creating a model can lead to a better understanding of which variations in the microbiome are helpful and also which ones are harmful (Greenblum et al., 2013). This is accomplished by combining integrated multi-species interaction models with individual organismal models, and then creating human host with microbiome interaction models (Greenblum et al., 2013, p. 812). These data models and microbiome framework models can be applied through the field of metagenomics to many aspects of microbial biomedicine for the improvement of human health.

The field of metagenomics studies microbial ecosystems as dynamic communities of organisms in their environments that can establish an equilibrium which would represent the healthiest scenario for both the microorganisms and the host (Martín et al., 2014). As many people are beginning to understand the importance of probiotics for a healthy gut, realizing that probiotics can work for human health in other ways seems to be the next logical step in the progression of biomedical science. According to Martín et al. (2014), an imbalance in one of the microbial communities of the human body can result in many health problems, and this condition has been phrased as a dysbiosis (p. 413). Many environmental factors play a role in altering the human microbiomes, resulting in different pathophysiological conditions of the human body, which can be improved with the administration of probiotics (Martín et al., 2014). The only problem is in understanding the complex relationship of these communities and providing the right microorganisms to balance out the apparent dysbiosis.

Documented studies have uncovered a correlation between alterations of microbiomes and the onset of disease states using metagenomic analysis (Li, 2011). By analyzing the distribution of microbiota in healthy individuals and comparing that data to the distribution of microbiota in individuals with specific pathophysiological conditions, the shift in an individual's microbiome can be documented for further analysis (Li, 2011). There are numerous applications for microbiome research in the field of medicine that could lead to better patient care, but the most studied microbiomes thus far have come from the gastrointestinal tract, vaginal biota, and oral biota.

The gastrointestinal tract has been the main focus of many microbiome projects, and it was one of the first microbial system that scientists focused on when studying microbes of the human body. Although previous indications of gut microbiota being related to gastrointestinal diseases states were only correlative, recent studies have given causal evidence to shifting gut microbial flora and diseases. In an interesting article on the subject of the gut microbiome, Bradlow (2014) described an evidentiary link between obesity and gut microbes with studies that have shown specific communities of bacteria involved in the regulation of fat and proper digestion. Numerous studies have detected a shift away from the bacteriodes class of bacteria to the firmacutes class in individuals that struggle with obesity (Bradlow, 2014). One bacterial strain that keeps popping up in gut microbiome research has been *Akkermansia muciniphila*, which appears in the gut of all healthy individuals and is present in much lower numbers for obese individuals (Bradlow, 2014).

These studies may have found a keystone species *in A. muciniphila*, as it appears to also encourage the growth of other beneficial bacteria in the gut microbiome (Van den Abbeele et al., 2011). This discovery was further analyzed by Van den Abbeele et al. (2011) by studying the shift in gut microbiota after administering prebiotics to encourage the growth of beneficial bacterial communities. When obese mice were give supplements containing nutrients that feed the bacteriodes class of bacteria and *A. muciniphila*, the mice showed signs of improved health, with less weight gain and less obesity-induced inflammation (Van den Abbeele et al., 2011). Although a great deal of evidence has linked the importance of microbiome studies to a healthy gut, recent studies have branched out to other microbiomes of the human body.

One such microbiome that has been studied extensively in recent years has been that of the vaginal microbial flora. With many healthcare providers struggling to treat recurrent cases of bacterial vaginosis and newborn health issues, studying the vaginal microbiome has proven to bring valuable insight in obstetric and gynecological cases (Solt, 2014). Molecular technology has improved the ability to diagnose bacterial vaginosis and watch out for potential preterm deliveries with low birth weight newborns (Solt, 2014). Molecular studies have implicated bacterial infections of amniotic fluid as a major cause of premature membrane rupture and preterm delivery, and this was not noticed before molecular diagnostics became available because of the difficulty in obtaining viable specimens by routine culture techniques (Solt, 2014). Another issues that has come to light concerning gynecology is the positive correlation between vaginal delivery and the newborn’s lifetime health (Solt, 2014). Vaginal delivery has been associated with better overall health, and this is believed to be related to the colonization of microbes that occurs during delivery, although more studies are being performed to determine the exact causality (Solt, 2014). Upon researching the vaginal microbiome, scientists have discovered a link between shifts in the vaginal microbiome and microbiomes from other areas of the body. Certain bacterial infections of amniotic fluid have been found in pregnant women whose oral microbiome has shown a shift in bacterial flora representing the same bacterial strains (Solt, 2014).

The oral microbiome is one of the most diverse microbial environments, with many species coming and going, but there are also many strains of microbiota that remain as constants, providing important functions to the human host (Wade, 2013). Just by their presence, oral microbes prevent infections from pathogenic bacteria, which the oral system is being bombarded with every day (Wade, 2013). Some oral bacteria even help break down enzymes for the human body to use in maintaining cardiovascular health, which has been shown in recent scientific studies to be disrupted with overuse of antimicrobial mouth rinses (Wade, 2013). The disruption of this community by antibiotics has also been proven to cause infections by opportunistic pathogens (Wade, 2013). When the oral microbiome shifts towards less healthy constituents, disease states such as dental caries and gingivitis can occur, which may be reversed by reestablishing a healthy oral microbiome (Wade, 2013). As mentioned previously, the oral microbiome has also been implicated in other disease states in the human body, and future scientific studies may provide data for other relationships between the oral microbiome and various diseases.

With all of this evidence accumulating on the importance of microbiomes, the study of pathophysiology needs to take a closer look at microbiomes of the human body and integrate these findings with treatment of diseases. By prescribing to the use of probiotics to increase the colonization of beneficial bacteria in the gastrointestinal tract and the use of prebiotics to encourage the growth of those beneficial bacteria, healthcare providers may be able to slow the obesity epidemic decrease obesity related diseases (Bradlow, 2013). Certain dietary alterations may be considered to encourage the growth of good gut microbiomes, as well (Bradlow, 2013). When the gut microbiome is altered to a healthy arrangement of microbiota, overall inflammation was shown to decrease, risk of numerous types of cancers was also decreased, the host immune system operates better, and there has even been correlations between behavior and a healthy gut microbiome (Bradlow, 2013).

Although there has been less research on changes to the vaginal microbiome, some significant research has shown that certain treatments can also be implemented to improve this microbiome as well (White, Creedon, Nelson, & Wilson, 2011). Currently, the best method for dealing with abnormalities of the vaginal microbiome include proper diet and probiotics, just as this benefits the gut. Knowing that there has been a shift in the normal vaginal microbiome can be an important diagnostic tool for gynecologists in determining prenatal risk and the possibility of preterm delivery (White et al., 2011). Since routine culture has not been successful at providing this important diagnostic assessment, molecular diagnostics would be a better method for determining this important risk factor (White et al., 2011). Although the healthcare provider may not be able to definitively return the vaginal microbiome to a healthy state, dietary changes could help and encouraging the health of other microbiomes may lead to a better outcome for the pregnancy (Solt, 2014). Even a change in the oral microbiome may improve the health of the newborn, as well as many other areas in the human body.

Currently, oral microbiomics is being studied in relation to other disease states in the body, as it has already been linked to fetal-maternal health in amniotic fluid (Wade, 2013). Instead of pushing more oral hygiene, it may be better for some change their oral hygiene routine since the overuse of antimicrobial mouthwash causing a decrease of beneficial bacteria in the mouth (Wade, 2013). Instead of attempting to prevent oral diseases by overusing mouthwash, dentists may suggest alterations in an individual's diet to encourage beneficial bacteria and reduce the amount of pathogenic bacteria that cause oral diseases (Wade, 2013). Specific, certain cheeses and fermented meat have been shown to increase the amount of enterococci which may lead to endodontic infections in individuals who are predisposed to these types of diseases (Wade, 2013).

With all of these studies, the common theme for a healthy microbiome has been linked to dietary changes and reduced use of antimicrobial agents. Further studies may provide more insight for healthcare provides, but there is plenty of evidence to justify the need for implementing microbiome analysis in routine health assessments. Before the field of molecular diagnostics became common and molecular testing inexpensive, microbiomics would have only been a dream. Now that microbial genomes can be quickly and easily sequenced, scientists have built extensive research databases. From these databases of microbial communities, researchers have the opportunity to study the effects of different microbiomes in the human body and correlate them with diseases and health. Since researchers have provided this much needed knowledge, it is now the responsibility of the medical community to utilize it for the benefit of patients.

The future of microbiome research has many opportunities available, and this analysis of microbiome studies and the resulting implications prove the importance of understanding human microbiomes in relation to disease states and applying information obtained from microbiome research.

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