

Abstract

The human body hosts many mutualistic microorganisms living inside and out, known as the microbiome. The microbiota of specific locations in the body can vary, both from person to person, and even within the same individual. Past research has shown a link between certain aspects of health and the concentration and diversity of an individual's microbiome. The vast catalog of microorganisms within the human body has been studied for centuries; however, only recently has research begun to peer into the origination of a person's microbiome as well as their similarities and differences to that of others. While there currently exists extensive knowledge surrounding the general taxa contained within the the human body, there has been much less research corresponding to the procurement and development of these taxa. Further exploring the provenance of these microorganisms can help facilitate more information regarding the transference of microbes on a person-to-person basis with those around them and their significance in the immune system and the transmission of diseases. More recent studies, like the one discussed in this microreview, have provided notable insight into the communicability of microorganisms between individuals in contact with each other, namely those in the same household, and how the similarities and discrepancies in microbiota are affected by environmental changes. Despite these important findings, many holes still exist in the research surrounding the genetic and phenotypic relationship relative to the transferability of these microbes and difficulties in identifying and isolating all microorganisms fixed at specific sites in the body. New information on this topic could help provide insight into the transference methods of certain forms of bacteria namely pathogens, and what role repeated proximity to others plays in this process.

Introduction

The microbiome is an important and functional component of an individual's health. Everything from the mouth to the gut is affected by this interrelationship of mutuality. The earliest recorded discoveries regarding the variability of the body's microbiome can be traced back to the 1600s. Experiments performed by the founding father of microbiology, Antonie Van Leeuwenhoek, in which he noted the dissimilarities in the characteristics of microorganisms collected from various parts of the body widely accepted as the beginning of research concerning the human microbiome[2]. Notable functions of symbiotic microorganisms include aiding food digestion, occupation of the body, thereby preventing colonization of pathogens, and even bolstering the body's immune functions to prepare it for foreign invasion [3]. One of the most widely accepted and scientifically backed theories behind the initial colonization and development of the human microbiome is its derivation from the bacteria involved in the host's birthing method [1]. Studies have shown strong similarities in the microbiome of infants born naturally with the microorganisms in their mother's birth canal and those born via C-section with a microbiome resembling that of human skin [2]. However, as individuals age, their microbiome begins to diversify, and little research exists in this realm of study. Theories suggest that this diversity is obtained through transference from the mother at birth and those in their everyday environment [1]. Previously, studies have provided little insight into the significance of person-to-person transmission of both oral and gut bacteria; however, this review discusses a series of experiments that were performed to find a noteworthy link between similarities within the microbiomes of individuals with types of interpersonal relationships. In this series of

experiments, data were collected from various metagenomes across 20 countries to ensure a diverse collection of microbiomes to sample from a wide selection of backgrounds to attain a global representation of data [1]. The basis of testing in this experiment centered around examining strains of certain bacteria within the microbiomes of individuals since they are the most specific form of genetic diversity within each organism and therefore, more easily compared.

Recent Progress

Results showed that mothers and their infants displayed the most similarity in their microbial strains at a rate of 34%, however, it also showed that individuals also had similarities in their microbiome from living in the same village at a rate of 8%[1]. Conversely, the study also clearly showed a lack of strains in common between individuals within the same populace at a rate of 82% and almost no similarities between those from different metagenomes [1]. Another group of nearly 900 individuals had their microbiomes mapped and compared to their household members resulting in similarities ranging from 11% to 77% when compared to people in the same populace not living together [1]. To test the viability and longevity of strains obtained by cohabitation, an experiment was also performed involving identical and non-identical twins that moved out of the same household at various points in life [1]. The results showed a clear distinction between the preservation of shared strains in identical twins and non-identical twins in that in the identical samples the strains were detected much longer than in the others, but also a moderate decline in the number of strains as time was spent apart between them [1]. Despite the indication of a genetic component, this could also hint at the lack of cohabitation resulting in a gradual diversification of their microbiomes. The potential for strain transmission between individuals solely in the same community and not necessarily with any direct contact was also tested. Data showed the presence of identical strains among individuals that lived in the same community but not the same household in approximately two-thirds of the villages that were surveyed [1]. Out of the strains detected, some of the most prominent and widely spread were members of the genus *Streptococcus* and are potential human pathogens [1]. This finding displays the possibility that not only mutualistic bacteria but also pathogens could effectively spread through the community via person-to-person contact. In contrast to the gut microbiome, the oral microbiome is much more easily diversified due to microorganisms' ability to be spread through saliva. As a part of the study, a sample collection of approximately 2,000 metagenomes of saliva was collected. Results indicated the similarity between house members' oral bacteria strains was 32% displaying a clear correlation to the proximity-based transmission of oral bacteria [1].

Discussion

These results seem valid, as the studies provide a connection between cohabiting individuals regardless of relationship and a percentage of shared bacteria strains in both their oral and gut microbiota. This evidence is further supported by the lack of similarities between individuals within the same metagenome sample who had a low likelihood of contact and those from differing metagenome samples who display almost no commonalities. The statistics provide grounds for the theory that the developing microbiome can be diversified by the acquisition of microbes from those around us, and not just through diet and colonization at birth. Despite the evidence supporting these theories, there was also room for error in the study. Namely, the potential for genetic factors such as the experiment

involving twins in which the identical twins retained strain similarities much longer than the non-identical twins who had also lived apart [1]. Another discrepancy lies in the inability to test for a directional pattern between the more transmissible strains of bacteria [1]. Lastly, the sample size was too small to be applied to a global scale despite its diverse sample groups. In summation, the experiments performed provided insight into the probability of person-to-person contact and transmission within the household as a factor in developing the microbiome as we age.

References

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