

Role of Microbes in Human Health

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Abstract

A variety of microbes exists throughout the human body and have fundamental role in human health. Studies have revealed that human microbiome of every healthy individual differs remarkably in the matter of different varieties of microbes. In the body, these microbes are present in different parts such as skin, nasal cavity, oral cavity, gut and vagina and therefore stay in different habitats. Some microbes that colonize humans are commensal, whereas others have a mutualistic relationship with the host. These interactions are important for human to grow and stay healthy. This mini-review describes about the microbes present in different human habitats and their roles in keeping the person healthy.

Keywords: Microbes; Microbiome; Microbiota; Nasal cavity; Vagina; Gut; Oral cavity; Skin

Introduction

It has been considered that there are about 100 trillion cells in a human body. However, even one tenth are hardly real human cells. The human body is home of trillions of bacteria, viruses, fungi, and other tiny organisms. These organisms are known as microbes. These

microbes belonging to different communities collectively are called as microbiome. The human microbiome is a source of genetic diversity and no two human microbiomes are considered to be the same. Microbiome is an essential component of immunity and a functional entity that influences metabolism and modulates drug interactions. It has been known since long time that microorganisms in the human body play an important role in maintaining human health. Microorganisms inhabit various sites of the human body, including the skin, nose, mouth and digestive gut (Figure 1) [1].

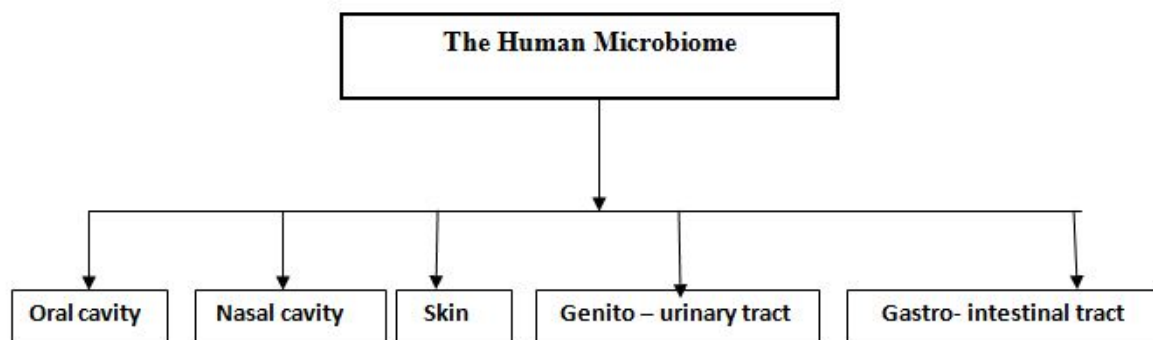


Figure 1: A line diagram indicating various locations of human microbiome.

These microbes make the oldest form of life on earth. These have been around for more than 3.5 billion years. From the past six million years, these microbes are evolving together with humans. As these have changed over time, microbes and humans have formed complex relationships with each other. To stay healthy, humans need microbes and many microbes need specific environment provided by the human body to survive. Humans and microbes rely on these interactions to grow and stay healthy. Different species of microbes live at different places in and on human body and these are adapted to the conditions

in these places [2]. The human host and its microbial flora constitute a complex ecosystem whose equilibrium serves as a remarkable example of reciprocal adaptation. Normally, microbe is responsible for resistance to colonization by exogenous pathogenic microorganisms. However, sometimes potential pathogenic bacteria come in close contact with the host and are responsible for opportunistic infections in immune-compromised hosts [3].

Some microbes that colonize in human are commensal that is they co-exist without harming human, whereas others have a mutualistic relationship with their human host that is both are beneficial to each other (symbiotic approach). Conversely, some non-pathogenic microbes can harm human host *via* the metabolites produced by them viz. trimethylamine, indole sulphate, trimethylamine-N-oxide. Certain microbes perform specific tasks known to be useful to the human host. However, role of most resident microorganisms is not well understood. Moreover, based on evidences, now scientists are convinced that modern trends of diet, excessive use of antibiotics, obsession with cleanliness, caesarean deliveries etc. are disrupting the delicate balance contributing to some of the most perplexing ailments including asthma, allergies, obesity, diabetes, autoimmune diseases, cancer and perhaps even autism. This mini-review briefly describes about the microbes that are present in the human body under normal circumstances and do not cause any disease and are helpful to human in spending a healthy life.

Microbes on Skin

Skin is the largest human organ which is the point of contact with the world. The most diverse populations of microbes present in human live on the skin. There are at least 1,000 different species of bacteria, fungi, viruses and other microbes which live on the skin. Most of which are harmless or even beneficial to human host. Colonization on skin is highly variable depending on endogenous host factors, topographical location and exogenous environmental factors. Symbiotic microorganisms occupy a wide range of skin niches and protect against invasion by more pathogenic or harmful organisms. One example of bacteria that protects the skin is *Bacillus subtilis*. It produces bacitracin on the skin, a toxin that helps it in fighting with other microbes. The property of bacitracin to act as an anti-bacterial agent has been exploited to use it as antibiotics. Skin microflora may also have a role in educating the billions of T cells, priming them to respond to similarly marked pathogen [4].

Primary bacterial colonizers are *Staphylococcus epidermidis* and other coagulase-negative Staphylococci. Other microorganisms that are generally regarded as skin colonizers are species of *Corynebacterium*, *Propionibacterium* and *Brevibacterium*. The most commonly isolated fungal species is *Malassezia sp.* which is especially prevalent in areas of the skin enriched in sebaceous glands. The *Demodex mites* viz. *Demodex folliculorum* and *Demodex brevis* are microscopic arthropods and these are also regarded as part of the normal skin flora [5].

Microbes in Nasal Cavity

A little is known about the microbes in nasal cavity. However, evidences suggested that microbiota of the nasal cavity plays a crucial role in determining the reaction patterns of the mucosal and systemic immune system. Different microbiota are found in different parts of the nasal cavity. Many studies are conducted to know about the microbiota of nasal cavity. The studies suggested absence of Gram-negative bacteria in nasal passage that are regularly present in pharynx. However, viridans type *Streptococci* are sparsely present in the nasal cavity. On the other hand, species of *Corynebacterium*, *Aureobacterium*, *Rhodococcus* and *Staphylococcus* have been found to be present dominantly. These data suggested that microbiota present in the nasal cavity of adult humans are strikingly different from that of the pharynx [6].

Savolainen et al. [7] examined 194 nasal cavities of 97 young healthy persons and showed that all had aerobic bacteria. However, only 76.5% cavities had anaerobic bacteria. They showed that most common aerobic bacteria found was *Staphylococcus epidermidis* in 79% cases, whereas diphtheroids were on second number (in 41% cases) and *Staphylococcus aureus* on third number (in 34% cases). They also found *Haemophilus influenzae* in 5% cases and *Streptococcus pneumoniae* in 0.5% case. The anaerobic bacteria found were *Propionibacterium acnes* in 74.5% cases and *Peptococcus magnus* in 3.5% cases.

Microbes in Mouth/Oral Cavity

The oral cavity or mouth includes several distinct microbial habitats such as teeth, gingival sulcus, gingiva, tongue, cheek, lip, gingival sulcus hard palate, and soft palate. The microorganisms found in the human oral cavity are called as the oral microflora, oral microbiota or oral microbiome. This microflora comprises over 600 species with distinct combination at different habitats. Most organisms that are colonizing are beneficial to human health but some microbes transit from a commensal relationship to pathogenicity. The reasons for the transition are not understood, however it is believed that it may be because of changes in the environment or personal hygiene [8].

The oral microbiome includes the species of *Actinobacteria*, *Bacteroidetes*, *Chlamydiae*, *Chloroflexi*, *Euryarchaeota*, *Firmicutes*, *Fusobacteria*, *Proteobacteria*, *Spirochaetes*, *Streptococcus*, *Synergistetes* and *Tenericutes*. Scientists have found the agonist as well as antagonist interactions between these microbes. For example, interaction between *Streptococcus gordonii* and *Actinomyces naeslundii* are both agonist and antagonist in nature. Both these microbes are involved in biofilm production. The *A. naeslundii* allowed *S. gordonii* to grow in the absence of arginine and removes hydrogen peroxide from co-aggregate cultures resulting decrease in protein oxidation in *S. gordonii*. Conversely, hydrogen peroxide produced by *S. gordonii* inhibits growth of *A. naeslundii* [9]. Another example of antagonist relationship is of *Streptococcus mutans*, which is a leading cause of dental caries. It uses quorum sensing and releases bacteriocin when introduced to other bacteria while *Streptococcus*, *Actinomyces*, and *Lactobacillus* generate an acidic pH, which results in inhibition of growth of a variety of bacterial species [10,11].

Microbes in Human Gut

The human gut serves two major functions: nutrition and defense. It digests food, absorbs nutrients, and assists with waste excretion. At the same time, intestine serves as house for enormous population of microbes that help in digestion and guard against pathogenic microbes. The intestinal microbiota of newborns is characterized by low diversity and a relative dominance of the phyla *Proteobacteria* and *Actinobacteria*. Initial microbial colonization of the gut in infants appears to be dependent on delivery mode that is vaginally delivered babies acquire microbiota similar to those of their mother's vagina (dominated by *Lactobacillus* and *Prevotella*) and babies delivered *via* caesarian section acquire microbiota similar to those typically associated with the skin which has *Staphylococcus*, *Propionibacterium* and *Corynebacterium* [12]. There are also differences between the gut microbiota of formula-fed and breast-fed infants. By the end of the first year of life, the microbial profile is distinct for each infant. It is found that by the age of 2.5 years, the microbiota fully resemble the microbiota of an adult in terms of composition. The microbiota becomes more diverse with the emergence of the dominance of

Firmicutes (predominantly *Clostridia* and *Bacilli*) and Bacteroidetes (predominantly *Bacteroides fragilis* and *B. thetaiotaomicron*) which resemble the adult microbiota [13].

The composition of the flora is influenced not only by age but also by diet and socio-economic conditions. Microbial population is influenced by the interactions between diet, the microbiota and health status. Interactions between host and microbes are well studied. For example, ability of bacterial disaccharidases to salvage unabsorbed dietary sugars such as lactose, alcohols and convert them into short-chain fatty acids (SCFAs) that are then used as an energy source by the colonic mucosa [14,15]. The microbiota can also be seen to play a critical role in protecting the host from colonization by pathogenic species. Some intestinal bacteria produce a variety of substances, ranging from relatively non-specific fatty acids and peroxides to highly specific bacteriocins which can inhibit or kill other potentially pathogenic bacteria. Certain strains also produce proteases capable of denaturing bacterial toxins [16].

Microbes in Reproductive Tract

Successful human reproduction is possible by the existence of healthy microbial community in the reproductive tract. Microbial communities exist throughout the entire length of the female reproductive tract at variable composition and density and play a role in reproductive cyclicality, gametogenesis, pregnancy and successful delivery of newborns. The vaginal microbiota play a key role in the prevention of multiple diseases including bacterial vaginosis (BV), yeast infections, sexually transmitted diseases, urinary tract infections, and human immunodeficiency virus [17]. Lactic acid producing bacteria viz. *Lactobacillus sp.* in vagina are thought to play key protective role by lowering the environmental pH through lactic acid production and/or by producing various bacteriostatic and bacteriocidal compounds, and/or through competitive exclusion. The levels of lactobacilli fluctuate with menses with a notable increase in *Gardnerella vaginalis* during menstruation. This is due to increased iron availability because of the presence of vaginal blood during menses. A healthy vaginal microflora does not contain high numbers of many different species of *Lactobacillus*. Rather, one or two lactobacilli from a range of three or four species (mainly *L. crispatus*, *L. iners*, *L. jensenii* and *L. gasseri*) are dominant. The microflora composition depends on the racial variation and geographical area. However, different racial groups within the same geographical region have significant differences in the dominant vaginal organism [18-20].

The male genital tract microbiota has important role in the health of the person and his partner. It has been found that microbiota exists in urethra and coronal sulcus which are parts of male lower genital tract. In most of the cases, upper genital tract has been reported to be germ-free. However, there are reports of the presence of coryneform bacteria which have been shown to have ambivalent role in male urogenital tract. The interactions between the microbiota of male and female genital tract may exist, however, much lesser studies have been carried out on the genital tract microbiota from the couples [21].

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