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EDITORIAL

HUMAN MICROBIOTA

BY

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Microbes are usually live in communities, and each of these communities has a distinct taxonomical structure. Due to its close relationship with human health and disease, the human microbiome has received great attention and is probably considered to be the most valuable biomarker in preventing and solving human diseases **(Cong and Zhang, 2018).**

Microbiota is an "ecological community of ***commensal***, ***symbiotic*** and ***pathogenic organisms***". It is found in and on all multicellular organisms studied to date from plants to animals. The ***human microbiota*** is the aggregate of ***microorganisms*** on or within any of a number of human tissues and biofluids, including the skin, mammary glands, placenta, seminal fluid, uterus, ovarian follicles, lung, saliva, ***oral mucosa***, ***conjunctiva***, ***biliary*** and gastrointestinal tracts. The ***human microbiome*** refers specifically to the collective genomes of resident microorganism **(Sherwood et al., 2013)**.

They include ***bacteria***, ***archaea***, ***fungi***, ***protists*** and ***viruses***. Bacterial type is present mainly in human mouth, vagina and GIT (**Sommer and B?ckhed, 2013)**. ***Archaea*** are present in the human gut, but, in contrast to the enormous variety of bacteria in this organ, the numbers of archaeal species are much more limited (**Eckburg et al., 2005)**. **Fungi** in particular ***yeasts***, are present in the human gut. The best-studied of these are ***Candida*** species due to their ability to become pathogenic in ***immuno-compromised*** and even in healthy hosts. Yeasts are also present on the skin, such as ***Malassezia*** species, where they consume oils secreted from the ***sebaceous glands*** **(Erdogan and Rao, 2015). Viruses** especially bacterial viruses (***bacteriophages***), colonize various body sites. These colonized sites include the skin, gut, lungs, and oral cavity. Virus communities have been associated with some diseases, and do not simply reflect the bacterial communities (**Abeles et al., 2014)**.

Relative number of microbiota:

In 2014, the American Academy of Microbiology published a FAQ that emphasized that the number of microbial cells and the number of human cells are both estimates, and noted that the human microbiome includes around 100 trillion bacterial cells and that an adult human typically has around 10 trillion human cells.

Gut Flora:

The gut flora has the largest numbers of bacteria and the greatest number of species compared to other areas of the body (**Quigley, 2013)**. In humans, the composition of gut

flora is established during birth. Birth by ***Cesarean section*** or vaginal delivery also influences the gut's microbial composition. Babies born through the vaginal canal have non-pathogenic, beneficial gut microbiota similar to those found in the mother (**Mueller et al., 2015)**. However, the gut microbiota of babies delivered by cesarean section harbors more pathogenic bacteria such as ***Escherichia coli*** and ***Staphylococcus***, and it takes longer to develop non-pathogenic beneficial gut microbiota (**Wall et al., 2009)**.

Bacteria can be transferred from mother to child through direct contact and after ***birth***. The infant microbiome is established, commensal bacteria quickly populate the gut, prompting a range of immune responses, and "programming" the immune system with long-lasting effects **(Cahenzli et al., 2012).**

Skin Flora:

The human skin microbiota play an important role in the generation of human odors **(Verhulst et al., 2010 and Bouslimani et al., 2015)**. Human odor profiles include more than 350 identified compounds **(Bernier et al., 2000),** and it has been shown that bacteria on human skin are involved in the release of approximately 150 volatile organic compounds (hereafter referred to as VOCs) **(Verhulst et al., 2009).** Some of these VOCs released by bacteria are typically found in human odor (**Bouslimani et al., 2015)**.

Importance of gut microbiota:

Some human gut microorganisms benefit the host by fermentating dietary fiber into short-chain fatty acids (SCFAs), such as acetic acid and butyric acid, which are then absorbed by the host. Intestinal bacteria also play a role in synthesizing vitamin B and vitamin K as well as metabolizing bile acids, sterols, and xenobiotics **(Sherwood et al., 2013).**

Changes in the composition of gut microbiota has also been found to be correlated with harmful effects on health, from these effects is cancer. Microorganisms are implicated in about 20% of human cancers. Particularly for potential factors in ***colon cancer***, bacterial density is one million times higher than in the ***small intestine***. Approximately, 12-fold more cancers occur in the colon compared to the small intestine, possibly establishing a pathogenic role for microbiota in colon and ***rectal*** cancers. Microbial density may be used as a ***prognostic*** tool in assessment of colorectal cancers (**Gagnière et al., 2016)**. The microbiota may affect carcinogenesis in three broad ways: **(i)** altering the balance of tumor cell proliferation and death, **(ii)** regulating immune system function, and **(iii)** influencing metabolism of host-produced factors, foods and pharmaceuticals**.** International Agency for Research on Cancer stated that Microbes may secrete proteins or other factors directly drive cell proliferation in the host, or may up- or down-regulate the host immune system including driving acute or chronic inflammation in ways that contribute to carcinogenesis (**Garrett, 2015)**.

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