

The bacteria, fungi,
protozoans, viruses
or some other



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The collection of genes and their products from all the microbes living within and on the human body are referred to as the human microbiome.

These microbes can be commensals or opportunistic ones. They can be bacteria, fungi, protozoans, viruses or some other microscopic organisms.

The major contributor of human microbiome is the bacterial phylum that primarily includes Actinobacteria, Bacteroidetes, Firmicutes and

Proteobacteria¹. Based upon the anatomical area of human body the microbiome differs in composition as:-**Skin:-** Skin being our interface with environment acts as both a barrier as well as a habitat to microbes, thus contains the most flexible microbiota composition.

As our skin shows physiochemical variations with various anatomical sites thus it can be concluded as a hub of habitats harboring a vast diversity of microbes. Also the composition of our skin microbiota differs considerably with various physiological areas of the skin like moist areas including underarms and dry areas including forearms skin. Propionibacteria and Staphylococci species are the main bacterial species found in sebaceous areas while Corynebacteria and Staphylococci are major species in moist places of the skin. In dry areas of the skin a mixture of species is observed dominated by β -Proteobacteria and Flavobacteriales². Such as the phylum Firmicutes comprise the major phylum in the vagina while Malassezia is abundant in atopic dermatitis³. Skin microbiota also includes some fungi like Candida species and Penicillium species.

4Gut:- Gut is the largest habitat for commensals inside the human body. It can be divided into upper (stomach and duodenum) and lower gastrointestinal tracts (jejunum, ileum, caecum, colon, and rectum). The majorly colonizing

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phyla's are Firmicutes, Bacteroidetes, and Proteobacteria 5, 6. Gut microbiota is established after the birth depending upon various factors and there are compositional changes related to diet, age and diseased conditions 7.

Gut microbiota also varies in composition according to various anatomical areas of GI tract. Like in stomach major microbial colonies are of Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria 8. Major genera observed in human stomach are Helicobacter, Streptococcus, and Prevotella 9. Similarly in small intestine majorly there are facultative and obligate anaerobes (Streptococcus sp., enterobacteria, Clostridium sp., Bacteroidetes). Oral cavity:-Our oral cavity also acts as a habitat for microbes, thus a distinct type of oral flora occurs there.

Firmicutes has the major population in the oral cavity along with proteobacteria, bacteroidetes, actinobacteria, fusobacteria and spirochaetes 10. Other Body surfaces:-There are also some other body surfaces other than the above mentioned, that act as a habitat for the microbes. They include vagina, lungs, uterus etc. Like in lungs some Prevotella, Sphingomonas, Pseudomonas species are observed 11. That much availability of habitats on a human body facilitates the microbial species to grow up in count as well as diversity. Thus there is generated a complex ecosystem containing a blend of genomes and their expressions. Microbiome establishment and early colonization Before birth, we have no microbes on or inside our body.

With increasing time after birth different species of microbes start to colonize in every possible habitat on our body. With age we acquire large sized

different populations of various microbes in the habitats around our bodies. With our age, our microbiota continues to change in composition and diversity.

With time our microbiome increases in count and adapts according to the changes in environment of their habitat. For example, the foods we eat, the amount of microbes we're exposed to on a daily basis and the level of stress we live with, all these factors alter the state and structure of our microbiome. Microbial introduction and persistence is a random process influenced by many factors that leads to formation of a much complex microbiome. Major factors influencing the establishment and development of human microbiome areas follows: -

- Ø Mode Of Delivery
- Ø Host's Age
- Ø Host Lifestyle
- Ø Dietary factors
- Ø Sanitation and others
- Ø Day routine activities and interactions
- Ø Visited places (Hospitals etc.).
- Ø Host's Genetic make up
- Ø Environmental Factors
- Ø Geography
- Ø Demography
- Ø Health Fluctuations
- Ø Medical conditions (Diseases, Pregnancy)
- Ø Antibacterial courses
- Ø Medicinal courses with various drugs
- Ø Septic conditions (injuries)
- Ø Operations.
- Mode of Birth

(delivery)

Species

diversity is found to be low in infants but it is observed to be increased with time and exposure to environment. It is obvious that this exposure differs by mode of delivery and place of birth.

Massive bacterial colonization occurs at birth upon exposure of the newborn to vaginal, fecal, and skin microbiota. Delivery mode can affect this early-life establishment of microbiota and its composition¹². Babies delivered

vaginally are covered by a film of microbial colonies as they pass through the

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birth canal. Thus their primary microbiota contains microbial species from the vaginal and intestinal flora of the mother. They are colonized primarily by *Lactobacillus* sp., *Prevotella* and *Sneathia* spp.

13. During vaginal delivery, facultative anaerobic species such as *E. coli*, *Staphylococcus*, and *Streptococcus* also colonize the infant gut. 14. During caesarian delivery, the direct contact with maternal vaginal and intestinal flora is absent, and non-maternally derived environmental microbes play an important role in primary colonization. Thus babies delivered by cesarean section are colonized mainly by skin microbes (e. g., *Staphylococcus*, *Corynebacterium*, *Propionibacterium* spp.) composing of a very different set of species than the babies born vaginally.

Caesarean section introduces opportunistic microbial species, including *Enterobacter cancerogenus*/*E. hormaechei*, *Haemophilus* spp. and *Staphylococcus*. 15. Age is a major factor effecting microbial composition of our microbiome. From birth, as the age increases the microbial diversity also increases and converges toward an adult like microbiota by 3 to 5 years of birth, with a quite differing set of microbial colonies in comparison to those found in an infant's microbiota.

Various factors like mode of delivery, diet, genetics etc. play a role in primary establishment of the microbiota, once established the adult microbiota is comparatively stable in composition throughout the life. After birth, gut microbiota closely resembles that of the mother within the first year of life. 16. Primary colonizers of infant gut are the facultative anaerobes that create an environment that promotes the growth of strict anaerobes like

Clostridium, and Bifidobacterium spp. The gut microbiota of infants is of low diversity and majority of the phyla Proteobacteria and Actinobacteria are observed. The microbiota increases in diversity with the introduction of Firmicutes and Bacteroidetes as the time after birth increases 17, 18.

Various characteristics of the skin like thickness, capability to hold moisture and to produce sebum, oiliness, hair cover, etc. changes considerably with aging, which naturally affects the microenvironments on skin habitats supporting different microbes. In teenagers, puberty associated changes in the skin physiology, are the reasons behind changes in the skin microbial community composition and diversity. Overall there is an increase in diversity of skin microbiota during the first eight years of life along with a reduction in abundance of the Order Lactobacillales (mainly Streptococcus) and relatively increase in other taxa also takes place. In puberty there is reduction in diversity due to increase in population of Actinobacteria species (such as Propionibacterium acnes) 19.

Lipophilic bacteria like Propionibacterium tend to increase in abundance between the ages of 25-30 years due high production of sebum by the skin 20.