

# [The bacteria, fungi, protozoans, viruses or some other](https://assignbuster.com/the-bacteria-fungi-protozoans-viruses-or-some-other/)

The collection of gene and their products from all the microbesliving within and on the human body are referred to as the human microbiome. Thesemicrobes 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 phylumthat primarily includes Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria1. Based upon the anatomical area of human body the microbiomediffers in composition as:-Skin:- Skin being our interface with environment acts as both abarrier as well as a habitat to microbes, thus contains the most flexiblemicrobiota composition.

As our skin shows physiochemical variations with variousanatomical sites thus it can be concluded as a hub of habitats harboring a vastdiversity of microbes. Also the composition of our skin microbiota differs considerablywith various physiological areas of the skin like moist areas includingunderarms and dry area including forearms skin. Propionibacteria and Staphylococci species are the main bacterial speciesfound in sebaceousarea while Corynebacteria and Staphylococci are major species in moist places of theskin. In dry areas of the skin a mixture of species is observed dominated by b-Proteobacteriaand Flavobacteriales 2. Such as the phylumFirmicutes comprise the major phylum in the vagina while Malassezia is abundant in atopicdermatitis 3. Skinmicrobiota also includes some fungi like Candida species and Penicillium species.

4Gut:-Gut is the largesthabitat for commensals inside the human body. It can be divided into upper(stomach and duodenum) and lower gastro intestinal tracts (jejunum, ileum, caecum, colon, and rectum). The majorly colonizing phyla’s are Firmicutes, Bacteroidetes, and Proteobacteria 5, 6. Gut microbiota is established after the birthdepending upon various factors and there are compositional changes related todiet, age and diseased conditions 7.

Gut microbiota also varies incomposition according to various anatomical areas of GI tract. Like in stomachmajor microbial colonies are of Proteobacteria, Firmicutes, Bacteroidetes andActinobacteria 8. Major generaobserved in human stomach are Helicobacter, Streptococcus, and Prevotella 9. Similarly in small intestine majorly there are facultative and obligateanaerobes (Streptococcus sp., enterobacteria, Clostridium sp., Bacteroidetes). Oral cavity:-Our oral cavity alsoacts as a habitat for microbes, thus a distinct type of oral flora occursthere.

Firmicutes has the major populationin 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 muchavailability of habitats on a human body facilitates the microbial species togrow up in count as well as diversity. Thus there is generated a complexecosystem containing a blend of genomes and their expressions. Microbiomeestablishment and early colonizationBeforebirth, we have no microbes on or inside our body.

With increasing time after birthdifferent species of microbes start to colonize in every possible habitat on ourbody. With age we acquire large sized different populations of various microbesin the habitats around our bodies. With our age, our microbiota continues tochange in composition and diversity.

With time ourmicrobiome increase in count and adapt according to the changes in environmentof their habitat. For example, the foods we eat, theamount of microbes we’re exposed to on a daily basis and the level of stress welive with, all these factors alters the state and structure of our microbiome. Microbialintroduction and persistence is a random process influenced by many factors thatleads to formation a much complex microbiome. Majorfactors influencing the establishment and development of human microbiome areas follows:-Ø Mode Of DeliveryØ Host’s Age Ø Host  Lifestyleo  Dietary factorso  Sanitation and otherso  Day routine activities and interactionso  Visited places (Hospitals etc.). Ø Host’s Genetic make up Ø Environmental FactorsØ Geography Ø DemographyØ Health Fluctuationso  Medical conditions( Diseased, Pregnancy)o  Antibacterial courseso  Medicinal courses with various drugso  Septic conditions (injuries)o  Operations. Modeof Birth (delivery)                                                                                       Species diversity is found to be low in infants but it isobserved to be increased with time and exposure to environment. It is obvious thatthis exposure differs by mode of delivery and place of birth.

Massive bacterialcolonization occurs at birth upon exposure of the newborn to vaginal, fecal, and skin microbiota. Deliverymode can affect this early-life establishment of microbiota and its composition12. Babies delivered vaginally are covered by a film of microbialcolonies as they pass through the birth canal. Thus their primary microbiotacontains 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 14During caesarian delivery, the direct contact withmaternal vaginal and intestinal flora is absent, and non-maternally derivedenvironmental microbes play an important role in primary colonization. Thus babiesdelivered by cesarean section are colonized mainly by skin microbes (e. g., Staphylococcus, Corynebacterium, Propionibacterium spp.) composing of a verydifferent set of species than the babies born vaginally.

Caesarean section introduces opportunisticmicrobial species, including Enterobacter cancerogenus/E. hormaechei, Haemophilus spp. and Staphylococcus15.  AgeAge is a major factors effecting microbial composition ofour microbiome. From birth, as the age increases the microbial diversity alsoincreases and converges toward an adult like microbiota by 3 to 5 years ofbirth, with a quite differing set of microbial colonies in comparison to those foundin an infant’s microbiota.

Various factors like mode of delivery, diet, genetics etc. play a role in primary establishment of the microbiota, onceestablished the adult microbiota is comparatively stable in compositionthroughout the life. After birth, gut microbiota closely resembles that of themother within the first year of life 16. Primary colonizers of infant gut arethe facultative anaerobes that create an environment that promotes the growth ofstrict anaerobes like Clostridium, and Bifidobacterium spp. The gut microbiotaof infants is of low diversity and majority of the phyla Proteobacteria andActinobacteria are observed. The microbiota increases in diversity with theintroduction 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. changesconsiderably with aging, which naturally affects the microenvironments on skinhabitats supporting different microbes.  In teenagers, puberty associated changes in the skinphysiology, are the reasons behind changes in the skin microbial communitycomposition and diversity.  Overall there is an increase in diversity of skinmicrobiota during the first eight years of life along with a reduction inabundance of the Order Lactobacillales (mainly Streptococcus) and relativelyincrease in other taxa also takes place. In puberty there is reduction indiversity due to increase in population of Actinobacteria species (such asPropionibacterium acnes) 19.

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