

The Oral Microbiome in Children

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Abstract

The oral cavity is a storehouse of various bacteria and fungi. They are mostly commensals and can sometimes cause various diseases and other conditions. Hence the oral microbiome should be studied well, especially in children.

Keywords: Oral health; children; microbiome

Introduction

The oral cavity and other sites of the body are full of many harmless or commensal bacteria and yeasts, as studied by the Human Microbiome project [1]. The oral microbiome is influenced by food and also determines other things like growth and quality of sleep. Hence study of the oral microbial community in children is of utmost importance and is stressed now.

Inception of the Oral Microbiome

The oral cavity of man is not sterile. It gets colonized right since birth. In fact, now it has been shown that bacterial genera like Streptococcus, Fusobacterium, Neisseria, Prevotella, and Porphyromonas, can be found in the human placenta and in amniotic fluid in up to 70% of pregnant females [2]. In adults the microbiome is linked with good health and alterations have been causally linked with diseases like atherosclerosis. Prevotella spp. and Porphyromonas spp. have been linked with atherosclerosis [2]. Alteration of microbiome at other sites is also linked with good or deranged health. Therefore the microbiome is now becoming an important part and determinant of health in all locations of the human body.

Determinants of the Oral Microbiome in Children

The factors responsible for shaping composition of oral microbiome are genetics, type of labour, delivery mode, antibiotics

use during birth and early infancy, the feeding method, and also maternal oral microbiome characters [2].

Genetic Factors

The high burden of the cariogenic *S. mutans* and its specific pathogenic attributes like acid production in dental plaque and saliva have a close genetic association and link [2]. The high bioload of Gram negative rods like Prevotella, Pasteurellaceae, and Leptotrichia have also been previously found to be associated with SNPs (Single nucleotide polymorphisms) in the host genes that code for ATP-binding cassettes, protein synthesis, cell division, and also tumour suppression [2]. It has been seen that individuals with defects in STAT3 gene (a protein coding gene) are prone to develop dysbiosis of oral fungal and bacterial community and are also susceptible to recurrent oral fungal infections [2]. During and after birth, the newborn child gets exposed to a wide range of microorganisms, like bacteria, fungi, parasites, and virus, under the influence of routes of contact and the infant's immune tolerance [2]. Remarkably, the oral microbial colonization shows a temporal and spatial sequence. Only a subgroup of microorganisms later become permanent residents of the oral cavity [2].

The most frequently detected early colonizers in the oral cavity of the child are the genera Streptococcus (Streptococcus epidermidis and Streptococcus salivarius), Staphylococcus spp.,

and *Fusobacterium* spp. *Streptococcus* is such a good colonizer because, firstly it has good adherence potential, and secondly, it is the dominant bacterial strain present in mother's breast milk [2]. *S. salivarius* is the dominant species in this genus, peaking at 3 months of age, and then decreasing on tooth eruption [3]. In addition to these early colonizers, bacterial genera like *Gemella*, *Granulicatella*, *Haemophilus*, and *Rothia* are common during 3 to 6 months of age with more than 1% of abundance. Their abundance furthermore increases with age [2,3]. A lower count of Gram-positive facultative and a higher level of Gram-negative facultative are found during transition from the preeruptive period to primary dentition [2]. For example, in the first several months of an infant's life, before tooth eruption, *Escherichia coli*, *Pseudomonas*, *Staphylococcus*, along with the lactic acid-producing bacteria such as *Lactobacillus gasseri*, *Lactobacillus crispatus*, and *Streptococcus* spp are very common. *Streptococcus mutans* hastens its own oral colonization at this stage of life in the child, due to the emergence of teeth, their preferred adhesion surface. At the genus level, the two most abundant genera in children's saliva are *Streptococcus* and *Veillonella*, whereas, in dental plaque, the most abundant genera are *Veillonella*, *Actinomyces*, *Streptococcus*, *Selenomonas* and *Leptotrichia* spp [3,4].

Oral mycobiome and its importance

According to culture findings and genomics-based studies, *Candida albicans* is the commonest component of the oral mycobiome. This fungus has been shown to cause *Candida*-induced oropharyngeal thrush in newborns [5]. In addition to *Candida*, more than 100 fungal species have been isolated in the oral cavity of healthy adults, like *Malassezia globosa* and *Rhodotorula mucilaginosa*, using methods like Next Generation Sequencing (NGS) of the primary fungal DNA barcode, the internal transcribed spacer (ITS) region [5,6]. *Saccharomyces* spp. can also be found as a harmless flora of the oral cavity in children. *M. globosa* can be seen more in oral cavity in children with caries than those without caries.

Oral viral community

The commonest viruses found in the human mouth cavity are Rotavirus, Norovirus, HIV, hepatitis C virus, Herpes simplex viruses 1 (HSV1) and HSV2, Epstein-Barr virus and influenza viruses [2].

Effect of oral microflora on infection or inflammation at distant sites

Bacteroidetes and Porphyromonas spp. have been discovered as dominant phyla and genera in the oral cavity in cases of pediatric appendicitis. Firmicutes and *Streptococcus* have also been found in high load in many cases. So the oral microbiota has got a bearing on infection or inflammation at distant sites [3].

Discussion

Thus the oral microbiome in children as well as adults is a diverse conglomeration of various microorganisms and play an important role in health and disease. They are affected by genetics, diet and medication. This topic should be studied more and also taught in curricula.

Conclusion

Oral microbiome is an interesting topic and should be researched more.

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