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Mini Review

Oral Flora as a Mirror to Systemic Health and COVID 19 Patients

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Abstract

The oral microbiome comprises of an array of microbes from various taxas. It contains both commensal and pathognomic organisms; they all reside in harmony during health. During an illness, however, the balance shifts toward an upward trend in pathognomic organisms. The impact of flora is not limited to the oral cavity; it also affects the individual's systemic health and overall well-being. Due to the ongoing COVID-19 pandemic, there has been an increase in the negligence of the maintenance of oral health. This article aims to shed light on the normal oral flora and how it influences systemic health and COVID-19 patients.

Keywords: *Oral Flora; Systemic Health; COVID 19 Patients; Pathognomic Organisms*

Oral flora

The term microbiome coined by Joshua Laderberg means microbes residing in our body. They describe the ecological community of symbiotic, commensal and pathogenic microorganism [1]. The number of microbes present in our bodies is almost same or even more than our own cells [2]. Oral cavity has the second largest microbial community following gut. The exhibit a diversity of function and composed of core microbiome and a variable microbiome. The core microbiome is the organisms present in common in almost all the individuals whereas the variable microbiome is unique to different individuals and determined by the lifestyle and physiological differences [3]. Oral cavity has a hard and soft tissue component and these bacteria can colonise both the areas. Soft tissue component consist of oral mucosa, tongue, hard and soft palate whereas the hard tissue component consist of hard non shedding surface of the tooth [4]. Oral cavity provides an ideal environment for the growth of the organism. The temperature of oral cavity is 37^{o}C and favourable pH which provides a stable environment for the bacterias to thrive. Saliva in the oral cavity hydrates the environment and also helps in the transport of nutrition [5].

The Human Oral Microbiome Database (HOMD) is a database of oral bacterial genome sequences as well as a comprehensive resource that includes descriptions of oral bacterial species and a 16S rRNA identification tool [6]. It's a one-of-a-kind database created by the National Institute of Dental and Craniofacial Research in 2010 to keep track of oral-derived cultivable and noncultivable isolates [7]. The goal of the expanded HOMD (eHOMD) is to provide the scientific community with comprehensive curated information on the bacterial species found in the human aerodigestive tract (ADT), which includes the upper digestive and upper respiratory tracts, pharynx, nasal passages, sinuses, and oesophagus, as well as the oral cavity. The eHOMD contains information of approximately 772 prokaryotic species, where 70% is cultivable and 30% belong to the uncultivable class of microorganisms along with whole-genome sequences of 482 taxa. The vari-

ous methods that are employed to study the oral micro flora are culture and microscopy, gel based technique, polymerase chair reaction based methods, DNA microassay, 16srRNA Sequencing and Next generation sequencing to name a few [8]. At about 6 - 9 months of age until the eruption of teeth, the predominant flora present in the oral cavity include 98% of *Streptococcus salivarius*. Eruption of teeth leads to the colonisation by the *S. mutans* and *S. sanguis* as they require a non-desquamating surface for their colonisation. The presence of gingival crevice leads to the increase in the habitat of anaerobic species and the complexicity of the flora keeps increasing with time as *Bacteroides* and *Spirochetes* colonize around puberty [9].

Oral microbiome and systemic diseases

The commensal organisms play an important role in the maintenance of both oral and systemic health. Tilting of this balance results in oral pathological conditions like periodontitis, dental caries and endodontic disease which is also associated with systemic disease like diabetes, cardiovascular disease, respiratory disease and cancer. The association between oral and systemic disease are complicated and bidirectional. Periodontitis is closely associated with cardiovascular disease and diabetes. When periodontitis is left untreated, microbial infection can lead to the loss of periodontal supporting tissue. Oral pathogenic microbiomes may release virulence factors, triggering an inflammatory response, and infiltrating the body through pathogenic lesions, increasing the risk of non-communicable disease (NCD) exacerbation. Various studies have been conducted to find the association between the oral microbiomes and atherosclerosis with molecular biological techniques. Periodontal pathogens were cultured in atheromatous plaque. Fluorescence *in situ* hybridisation, DNA-DNA hybridization and real-time PCR showed the presence of oral pathogens in atheromatous lesion. On the basis of the results obtained from various studies it has been shown that oral bacteria induced atherosclerotic cardiovascular disease phenomenon [10].

Study conducted by Matsha., *et al*. showed that there was an alteration in the composition of the oral microbiome across different glycemic status as well as at different stages of periodontal disease with the use of 16S rDNA sequencing of dental plaque [11]. High-throughput metagenomic sequencing (16S rDNA or rRNA) of oral microbiomes also demonstrated the role of the oral microbiome in the development of DM [12]. Recently Peshaw., *et al*. showed that treatment of periodontitis could reduce the inflammation in diabetic patient indicating that periodontitis and diabetes increasing the systemic inflammation [13]. Systematic review on this topic also showed procedure like scaling and root planning helped patient with better glycemic control [14].

Oral microbiome in COVID-19 patients

Corona Virus Disease 2019 (COVID 19) caused by severe acute respiratory syndrome coronavirus 2(SARS CoV 2) has spread over the world to cause [15]. SARS-CoV-2 positive patients frequently report pain in the tongue and gustatory dysfunction, including loss of smell and taste [16], which could be linked to greater expression of ACE2 in the epithelial cells of the tongue or the potential of direct SARS-CoV-2 infection of neurons or glia [17]. However, more research is needed into how initial infection of non-neural cells affects chemical sensing. Oral mucosal lesions have also been reported in SARS-CoV-2 positive patients [18]. Furthermore, increased membrane fusion activity of the virus was indicated by elevated expression of ACE2 sheddases (ADAM17 and ADAM10) and endopeptidases (CAPN1 and CAPNS1) in distinct regions of the oral mucosa [19], suggesting it could be a virus reservoir.

The gingival sulcus, a well-established microbial niche where enzymes and inflammatory chemicals are produced, encouraging the colonisation of bacteria, is another possible home for SARS-CoV-2. Both clinically healthy gingival sulci and periodontal pockets have been found to contain herpes simplex virus, Epstein-Barr virus, human papillomavirus, and human cytomegalovirus [20]. This increased viral growth in the gingival sulci could be owing to a symbiotic interaction between the virus and the bacteria that live in these crevices [21]. Furthermore, gingival crevicular fluid (GCF) is thought to contain SARS-CoV-2, which is discharged by infected periodontal cells or terminal capillary complexes in periodontal tissues and can then reach the oropharynx. Validation of this option, however, is difficult due to technical difficulties in isolating GCF for reliable measurements [22].

The introduction of the metagenomic next-generation sequencing (mNGS) technique has made it possible to investigate novel or mixed pathogens (i.e. RNA viruses, DNA viruses, bacteria, and fungus) directly from original clinical samples, particularly those from emergent patients [23]. The presence of higher numbers of oral and upper respiratory commensal bacteria was discovered in the bronchoalveolar lavage fluid (BALF) of 8 COVID-19 patients after metatranscriptome sequencing [24]. In COVID-19 patients, bacterial diversity is dramatically reduced, with higher relative abundance of opportunistic pathogens and lower relative abundance of beneficial symbionts [25]. An oral-lung aspiration axis is well-known as a crucial component in the development of many infectious illnesses [26]. Saliva looked to be an acceptable clinical specimen in the early stages of the disease, with SARS-CoV-2 found in 91.7 percent (11/12) of patients' initial saliva [27], however the sample size was modest in that investigation. In another study by To., *et al.* viral load of SARS-Cov-2 was highest in the posterior oropharyngeal saliva during the first week of symptom [28]. Current guideline for the management of COVID-19 does not emphasize enough on the oral care practice. It has been shown that poor oral hygiene leads to accumulation of pathogens in the oral cavity and immune disorders caused by the viral infection can promote additional bacterial/fungal infection increasing the risk of secondary pneumonia. So it is necessary to undertake good oral hygiene measures in COVID-19 patients. Povidine Iodine (PV-I), Cetylpyridinium Chloride (CPC) and hydrogen peroxide (H_2O_2) are effective in reducing the number of oral microbiota [29]. Studies have also shown SARS-CoV and MERS-CoV can be inactivated by the use of the above mentioned components within 1 minute. Chlorhexidine (CHX) have the ability to impair the biofilm formation of Viridans streptococci and proinflammatory effects of *Candida albicans* [30].

Conclusion

Oral microbiome is complex and dynamic at the same time. It exerts its influence in systemic conditions and with the ongoing COVID-19 pandemic it is important not to neglect the oral care measures.

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Conflict of Interest

None.

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