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Oral Microbiome in Head and Neck Cancers: An Insight Are We Looking at a Step Beyond in Unraveling the Challenge?

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Dear Editor

Head and Neck Cancers (HNCs) contribute to one of the global health concerns and have been a challenge to oncologists for decades. Breakthroughs in research with evidence-based reports based on diagnostic and therapeutic approaches in clinical practice have been published to address patient concerns. Risk factors, namely age, sex, diet, habits, and geographical variations, pose an established link with the prevalence of HNCs. Despite ongoing studies in cancer, the 5-year survival rate of the patients remains <50% to date. This has encouraged the scientists to research other possible novel risk factors and prognosis transformers that could present as targets for preventive or therapeutic interventions.

"Oral Microbiome" refers to collective genomes of microorganisms that reside in the oral cavity (1). Microbiome in oral health may be taken as a reliable tumor biomarker in comparison to regional microbiome variation of the human body due to its low intra/inter microbial variations and effective growth due to comparatively stable and favorable oral environmental conditions. In March 2020, Human Oral Microbiome Database (HOMD) using Next Generation Sequencing Technology (HOMINGS) proposed 784 bacterial species with 1,567 genomes in the mouth (2). Firmicutes phylum (266 taxa and 588 genomes) and a subset of this, the *Streptococcaceae* family (38 taxa and 200 genomes), have been considered to be of functional significance in oral diseases. A balanced state of the oral microbiome with systemic health, diet, and oral environmental factors (pH variability, saliva, and gingival crevicular fluid) contribute to the maintenance of the human oral ecosystem (3). Dysbiosis in this mechanism of host-microbial interactions is a proposed key factor in the occurrence of oral diseases. The relative importance of this in HNCs still needs to be explored.

Oral swab/ rinse and saliva samples are chair-side collection methods that are used routinely for microbial examination. Due to wide microbial variants and environmental influence, an accurate analysis method that has gained importance is *'Metagenomic studies'* via 16s rRNA technology (4). This method categorizes and analyzes the microbial community, proteins, metabolites, and genetic material associated with these species. Altered microbial profiling in HNCs is shown in Table 1 (5-6). Pictorial representation in Figure 1 has been put forward to understand the role of oral microbiomes in HNCs based on the existing literature (7-8).

Table 1. Possible Oral Microbiome Involvement in HNCs (5-6)

Microbial species	Taxonomical classification
Bacteria	HIGH - Porphyromonas, Fusobacterium, Prevotella, Veillonella, Peptosteptococcus, Clostridium, Gemellaceae, Enterobacteriaceae, Leptotrichia, Lactobacillus, Corynebacterium, Actinomyces LOW - Haemophilus, Neisseria, Aggregatibacter, Firmicutes Haemophilus & Streptococcus (Altered levels based on species variation)
Viruses	HIGH - Herpes simplex virus (HHV 1&2), Epstein-Barr virus (EBV) Cytomegalovirus; Human papillomavirus (HPV); Hepatitis C Virus
Fungi	HIGH – Candida species – C.albicans, C. tropicalis, C. krusei, C. glabrata, C. parapsilosis

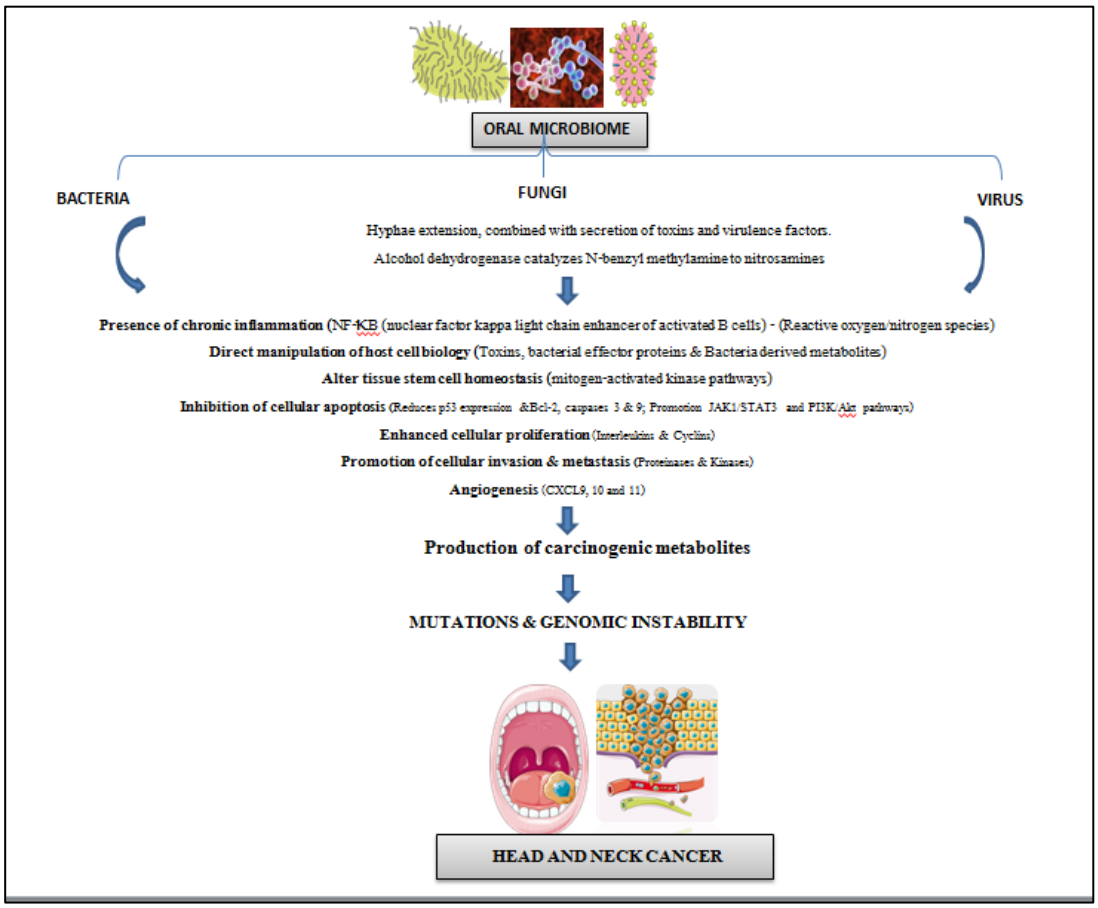

Fig. 1. Possible and Proposed Pathophysiology of oral microbiomes in HNCs (7-8)

We would like to hypothesize that 'dysbiosis in oral microbiomes also should be considered as a possible risk factor for HNCs'. Further research must be carried out to understand the mechanisms by which the tumor's microbial community influences the behavior of the oral neoplasm. Despite the advances in salivary tumor biomarker diagnostics, the paradigm shift in oral microbiomes may offer new tumor biomarkers (proteins, metabolites, or genomes) that may reduce human biological variation for HNCs in the future. Over the regular radiotherapy and chemotherapy, adjuvant therapy using antimicrobial peptides, probiotics, and epidrugs may show substantial improvement for cancer treatment, as they may intervene in cancer pathology, boosting the immune system, and lastly, alter the dysbiosis of oral microbiomes related to HNCs (9).

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Nil.

Conflict of Interest

The authors declared no conflict of interest.

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