



Bacteria to Biomarkers: The Oral Microbiome's Role in Oscc Detection and Treatment

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ABSTRACT:

Oral squamous cell carcinoma (OSCC) represents the most prevalent malignancy of head and neck cancers, accounting for over 90% of oral cancers globally. The incidence of OSCC is particularly high in Asian nations such as Bangladesh, India, and Sri Lanka, where tobacco use, alcohol consumption, and chronic inflammation are prevalent risk factors. Emerging research highlights a strong association between OSCC and specific bacterial species within the oral microbiome, suggesting that microbiota dysbiosis may contribute to cancer progression. Although bacterial species like *Campylobacter* *gingivalis*, *Prevotella melaninogenica*, *S. mitis*, and *F. nucleatum* are found in elevated quantities in OSCC samples, no definitive biomarkers for diagnosis have been established. Recent studies underscore the dynamic role of the microbiome in cancer advancement, with findings from Yang et al. at Chang Gung Memorial Hospital in Taiwan indicating that the prevalence of bacterial species such as *Parvimonas micra* and *Fusobacterium periodonticum* increases in advanced OSCC stages. These results suggest the potential of microbial profiles as non-invasive diagnostic tools for OSCC surveillance. Furthermore, research by Stashenko et al. using germ-free murine models has shown that the presence of an oral microbiome, irrespective of origin, significantly accelerates OSCC progression, driven by metabolic activity within the microbiome rather than its specific composition. These insights support the hypothesis that targeting microbiome function could offer innovative diagnostic and therapeutic strategies for OSCC, highlighting the value of microbiome modulation in cancer prevention and management.

Dear Editor,

Oral squamous cell carcinoma (OSCC) is the most common malignancy of the head and neck cancer. More than 90% of oral cancers are Oral squamous cell carcinomas (OSCCs) ^[1], whereas melanoma, lymphoma and malignancies of the salivary accessory glands are among the other oral cavity malignancies ^[2]. Together with oropharyngeal malignancies, oral malignancies rank sixth globally in terms of incidence ^[1]. A majority of the estimated 400,000 new instances of oral carcinoma were identified worldwide each year and are detected in Asian nations including Bangladesh, India, Pakistan, Indonesia, and Sri Lanka ^[1,3]. Frequent consumption of

tobacco products, including smoking cigarettes, gnawing on betel quid, consuming alcohol, possessing constant inflammation and human microbiome are highly associated with a wide variety of risk factors for oral cancer ^[4-8]. Approximately 30 trillion germs reside are present in each human. That means there is about one bacteria for every human cell ^[9]. Collectively, these microbes are referred to as the microbiome.

Oral squamous cell carcinoma (OSCC) is linked to specific bacterial species in the oral microbiome, which may be possible biomarkers for the malignancy ^[10]. Nevertheless, there are no reliable biomarkers that can be used to definitively diagnose OSCC, even though a



number of species have been found to increase in OSCC samples, including *Capnocytophaga gingivalis*, *Prevotella melaninogenica*, *S. mitis*, and *F. nucleatum*. Although the presence of different bacteria in OSCC patients raises the possibility of a link between oral cancer and the oral microbiome, more investigation is required to develop accurate diagnostic markers for OSCC.

The majority of research on how the human microbiome affects cancer has concentrated on characterizing the microbial communities found in particular samples or the host's immune response to the bacterial onslaught. Several Studies that are conducted globally had proved that the oral microbiome are one of the causative agent for the progression of cancers from one stage to the other.

A study by Yang et al. at Chang Gung Memorial Hospital in Taiwan has revealed that the oral microbiome has shown a significant increase in the cancer progression from the early stage to the late stage and also found a significant increase in effect in oral cancer and the dynamics of the oral microbiota change when oral squamous cell cancer (OSCC) advances. The results show that people with OSCC have a lot of dysbiosis in their oral microbiome. As the disease gets worse, the predominance of certain bacterial taxa changes in a noticeable way. Interestingly, *Parvimonas micra* and *Fusobacterium periodonticum* are more common in higher OSCC stages, which may indicate the presence of microbiological biomarkers for OSCC progression. The study's findings also suggest that microbial profiles could be employed as non-invasive diagnostic tools to support early diagnosis and OSCC surveillance [11].

Another study by Stashenko et al. in animals, specifically in germ-free murine model at Boston University concluded that germ-free mouse model treated with 4-nitroquinoline-1-oxide (4-NQO) found the presence of an oral microbiome, regardless of its origin, significantly increased both the number and size of tumours compared to germ-free controls exposed to 4-NQO alone. Importantly, the study highlighted that specific metabolic activities within the microbiome, rather than its compositional structure, are essential to OSCC progression. This functional redundancy where different microbiome yield similar tumor promoting activities suggests that microbiome function, rather than specific bacterial profiles, may be a crucial target for

understanding and managing OSCC. This study opens avenues for exploring microbiome-modulating therapies as part of cancer prevention and treatment strategies [12].

Conclusion

It's concluded that the relationship between the oral microbiome and OSCC progression is increasingly evident. Studies reveal that dysbiosis and specific bacterial taxa, such as *Parvimonas micra* and *Fusobacterium periodonticum*, are more prevalent in advanced OSCC stages, indicating their potential as biomarkers. Functional activities within the microbiome, rather than specific microbial compositions, are critical for OSCC advancement, as demonstrated in animal models. This suggests that targeting microbiome function might offer new diagnostic and therapeutic approaches for OSCC, emphasizing the role of microbiome modulation in cancer prevention and management.

Conflict of Interest:

All authors declare that they have no competing interests that couldn't have influenced the review, authorship or publication of this article. We confirm that there is no financial or personal relationship with other people or organisation that could inappropriately bias our work.

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