

Alteration In The Oral Microflora Of Patients With Oral Cancer In East Indian Population

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I. INTRODUCTION: -

As per NCPR, India houses 1/3 rd. of the total oral cancer cases worldwide. In India, oral cancer accounts for 30% of total cancer burden. [1]

The etiopathology of oral carcinoma has always been an enigma to the pathologists. Several etiological factor in the name of carcinogen, co-carcinogen, promoters have found their association in etiogenesis of oral carcinoma.

We are trying to detect the alteration in oral microbiota because microbial culture is a much simpler and cheaper process than any other diagnostic tools used to detect oral cancer.

In this study we want to identify whether there is any alteration in the oral flora or there any other pathogenic microbe which can be identified when a person is suffering from oral cancer by performing microbiological study of the swab sample collected from the patients. This alteration in the microorganisms if any can be used as an early detection marker for the diagnosis of oral cancer.

II. Review of Literature: -

- In a study made by Zixuan et al ,2021 on Chinese population suggest that oral microbiota plays a vital role in oral cancer. Here in this study, Metagenomic sequencing was found useful to compare the microbial composition of three groups of samples from Chinese patients with oral cancer, patients with precancerous lesion, and normal individuals. The microorganisms found in the oral cavity of the patients with precancerous lesions was found to be richer than that of oral cancer patients and healthy controls, whereas in terms of microbiota diversity, there was no difference as such between the three groups. The three groups of samples tested showed statistically significant differences in microbiota composition and metabolic function at the family, genus, and species levels. Bacteroidetes was found to be the most differentially enriched phylum. At the genus level, the main differentially enriched taxa were Prevotellaintermedia, Peptostreptococcus stomatis, Carnobacterium, and Diastella.[2] The prediction of microbiota function showed that oral cancer is mainly associated with coenzyme A biosynthesis, phosphopantothenic acid biosynthesis, inosine 5'-phosphate degradation, and riboflavin biosynthesis.[4] Furthermore, the increase in C-reactive protein level in oral cancer patients was found to be closely related to P. intermedia. Significant differences between the oral cancer group and normal group were seen in this study. Hence, from this study it can be concluded that microbes can be employed as diagnostic markers and treatment targets for oral cancer.[5]
- In another study made by Ling Zhang et al,2020, suggest that the microbiota compositions between tumor sites and opposite normal tissues in buccal mucosal of 50 patients with oral cancer using the 16S rDNA sequencing. Diversity of bacteria was found to be significantly higher in tumor sites than in the control tissues and it included six families (Prevotellaceae, Fusobacteriaceae, Flavobacteriaceae, Lachnospiraceae, Peptostreptococcaceae, and Campylobacteraceae) and 13 genera, including Fusobacterium, Alloprevotella and Porphyromonas. At the species level, the abundances of Fusobacterium nucleatum, Prevotella intermedia, Aggregatibactersegnis, Capnocytophagaleadbetteri, Peptostreptococcus stomatis, and another five species were significantly seen to increase, suggesting a potential association between these bacteria and Oral squamous cell carcinoma.[6] The families Streptococcaceae, Micrococcaceae Actinomycetaceae and Carnobacteriaceae were decreased in the Oral squamous cell carcinoma group.[7] Overall, oral bacterial profiles showed significant difference between cancer sites and normal tissue of OSCC patients, which might be considered diagnostic markers and treatment targets.[3]

III. OBJECTIVE: -

- 1) To find out whether there is dysbiosis in the oral flora in people affected by squamous cell carcinoma

- 2) To find whether this dysbiosis can be used as an early detection marker for the same in Indian Population.
- 3) To find if any other pathogenic microbe is associated with oral cancer which is normally not present.
- 4) To find if count of Streptococcus sp decreases or increases with the progression of the disease.

IV. RESEARCH METHODOLOGY: -

After taking the informed consent from the patient we will collect swab from the oral cavity of clinically diagnosed four categories of patients: -normal, pre malignant, malignant and patients with periodontal problems.

These swabs will be sent to laboratory to identify the presence of the species of microorganisms where they will be plated on microbial culture media and incubated.

After the growth of the colonies, they will be picked up and placed under the microscope in a slide for identification.

After getting the report from the laboratory, we will analyze the data and correlate to see if there is dysbiosis seen in the normal oral flora in the case of pre malignant and malignant cases.

V. STATISTICAL ANALYSIS

- 1) Correlation between oral cancer with dysbiosis of oral flora
- 2) Alteration in the microflora seen with normal, pre malignant, malignant and periodontitis cases.

Software used: SPSS version 19.0

AS per the statistical analysis final report will be prepared.

VI. CONCLUSION: -

From the data obtained from the laboratory, it can be concluded whether or not there is change in the normal oral flora in patients suffering from oral cancer or whether any specific microbe is associated with it. If something comes to conclusion then we could be able to use that as an early detection marker for oral cancer.

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