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Research Article

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The Role of Oral Microbiome in the Pathogenesis of Oropharyngeal Cancers. A Comprehensive Review

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Abstract

The microbiome is currently considered to be a unique isolated ecosystem that closely interacts with the host organism. Due to this interaction, the qualitative and quantitative composition of the microbiome might affect many pathologic and physiologic processes, including malignant solid tumors. However, the existence and significance of dysbiosis in oral/oropharyngeal cancer is yet to be clearly established.

According to a variety of literature data, bacteria colonizing the oral mucosa can induce production of inflammatory cytokines, cell proliferation, and inhibition of apoptosis, cellular invasion, and migration thorough host cell genomic alterations. In this regard, the role of the

bacterial factor as one of the main factors in the development of tumors of the oral mucosa is currently being discussed.

Some works that are taking into consideration in this systematic review have also shown that such species as Prevotella sp., Fusobacterium sp., Porphyromonas gingivalis play important role in cancer proliferation and has strong correlation with cancers of oropharyngeal zone.

This review was made according to some studies that are documented and published in PubMed.

In conclusion, all this study has been shown a high percentage of anaerobic bacteria in the direct cancer site in patients with oropharyngeal zone cancers, then in the health parts of cancer patients or healthy control group.

Keywords: Oral Microbiome, Dysbiosis, Dysbiosis and Cancer, Anaerobic Bacteria

Introduction

The microbiome is currently considered to be a unique isolated ecosystem that closely interacts with the host organism. The oral cavity and nasopharyngeal regions maintain an ideal environment for the growth of microbiome. More than 700 bacterial species reside in the oral cavity. Aerobic bacteria create localized niche for the anaerobes. Both pathogenic and mutualistic bacteria coevolve together to maintain homeostasis.

Due to this interaction, the qualitative and quantitative composition of the microbiome might affect many pathologic and physiologic processes, including malignant solid tumors.

In recent years, there has been a lot of evidence that the oral microbiota and its changes may play an indirect role in the development of cancer of the oropharyngeal zone. The right balance between communal microbes and the host is necessary to maintain physiological homeostasis, response to environmental changes, and survival. The omposition of the microbiota in various anatomical sites is controlled by the genetics of the host, especially the polymorphism of genes associated with immunity, as well as environmental factors such as lifestyle and nutrition [1-14].

Analysis of the microbiome of tumor tissues compared with normal buccal mucosa of patients with OSCC using 16S rDNA sequencing revealed an increase in genes associated with cell motility in tumor sites, such as bacterial chemotaxis and flagellar assembly, genes associated with a proinflammatory bacterial component, such as biosynthesis lipopolysaccharides, and genes involved in the metabolism of cofactors and vitamins This systematic review obtained a few researches that has been shown the concept of the question in numbers [3, 15-20].

In which we can see the potential role of our microbiome in cancer pathogenesis. The genera, species, or combinations of bacteria that may be involved in the process have also not been described in detail.

Microbes found in biomaterials from patients with tumors reflected the presence of dysbiosis in the microbiota of the oral cavity. At the same time, the question of whether the isolated microorganisms are one of the biological agents of the development of squamous cell carcinoma of the oral mucosa needs to be studied in more depth [1-14].

Methodology

Literature search and data extraction methods for this review were specified and documented by a few studies that are published in a PubMed. Studies that were making by the Russian Society of Clinical Oncology which is involved 75 people: 45 patients with cancer of the oral mucosa and 30 people who did not have malignant neoplasms of the oral mucosa (control group). The study was conducted in 2018-2019 on the basis of the Department of Head and Neck Tumors of the Blokhin National Research Medical Center of Oncology of the Ministry of Health of the Russian Federation. The study of the microbiota of the oral cavity was conducted in the microbiological laboratory of the Federal State Budgetary Institution "Blokhin National Medical Research Center of Oncology" [2].

The age of 45 cancer patients ranged from 31 to 82 years, of which 57,8% had primary tumors and 42,2% had recurrences. While control group include 30 people in the age range 26 to 59 years.

Biomaterial was taken from the tumor surface in all patients and from the "visually healthy" oral mucosa in 10 of them in parallel. In the control group (healthy individuals), biomaterial sampling was performed only from the oral mucosa.

Whereas 50 patients with SCC (squamous cell-carcinoma) of the oral buccal mucosa (median age: 61 years; 63% men and 37% women) were recruited from the Department of Oral and Maxillofacial-Head and Neck Oncology of the Ninth People's Hospital (Shanghai, China), from January 2018 to July 2018.

All patients were first diagnosed with OSCC and they had no history of cancer. For this study, the center collected bilateral cheek mucosa tissues from the same patient with OSCC, in this case 100 oral tissue samples (50 paired samples) were obtained from non-tumor (50) and tumor sites (50). By the way, the patients didn't take antibiotics for 1 week before taking the sample and had no history of other diseases of the oral mucosa or severe systemic disorders [9-17].

At the University of Chicago Medical Center 35 patients with oral cancer and 31 control patients were recruited for similar study. 21 out of 35 (60.0%) cancer patients and 17 out of 31 (54.8%) control patients were males. The median age was 66 for the cancer subgroup and 63 for the control subgroup [10].

Results

According to the data obtained during the study by the Oncology Center in Moscow, it was revealed that in patients with tumors of the oropharyngeal zone, in which the total number of anaerobic bacteria directly isolated from the surface of the tumor and oral mucosa was significantly higher than aerobic bacteria and fungi (58% vs. 42%).

Due to the data which was obtained by the center of oncology in Russia, the most common microorganism in the group of patients with tumors of the oropharyngeal region was Prevotella spp. which was sown significantly more often than in healthy individuals (35.9% vs. 4.0%, respectively). Moreover, such bacteria as Porphyromonas spp. (5.9% vs. 0%). and Fusobacterium spp. (14.7% vs. 0%) were also sown more often in the group of patients with tumors than in healthy individuals. Veillonella spp., on the contrary, was sown more often in the control group than in the group of patients with tumors (42% vs. 16.5%, respectively).

In the study group, in 45 patients (including 10 patients who were simultaneously sampled biomaterial from a visually unchanged oral mucosa) a total of 293 microorganisms were isolated from the tumor surface, while 123 microorganisms were isolated from the oral mucosa in the control group (30 people) [2].

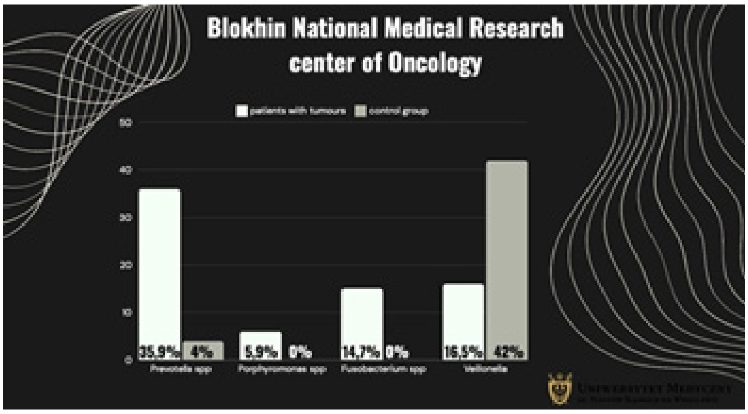

Figure: 1

While in the data that was obtained by the Department of Oral and Maxillofacial-Head and Neck Oncology of the Ninth People's Hospital the percent of Prevotella spp. was 17,85% in cancer patients and 11,99% in control group. Porphyromonas spp. (3,47% vs 2,47%) and Fusobacterium spp. (11.03% vs 3,29%), while Veillonella (3,05% vs 5,33%). So, in this study we can see correlation between health part of the buccal mucosa and from non-tumor buccal mucosa in the same person [9-18].

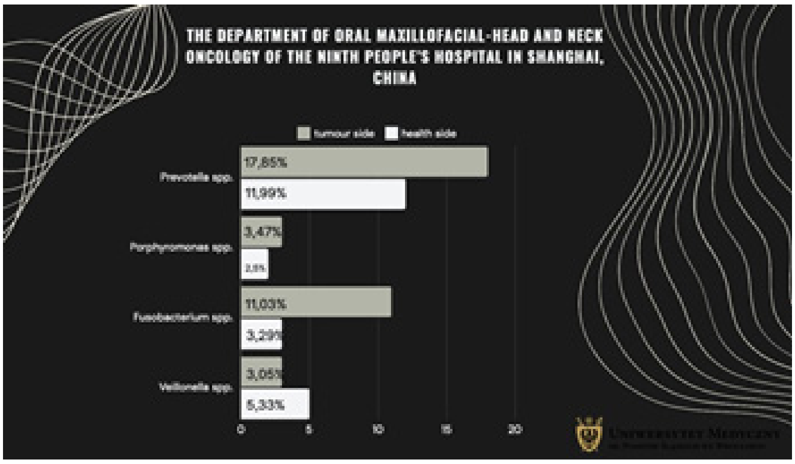

Figure: 2

The percentage of Prevotella spp. in similar studies, that has been performed by the University of Chicago Medical Center is 7,14% in patients with oral cancer and 5,83 in a healthy group. Porphyromonas spp (2,07% vs 0,81%, respectively) and Fusobacterium (7,67% vs 3,04%, respectively), while Veillonella (4,93% vs 7,11%) [10].

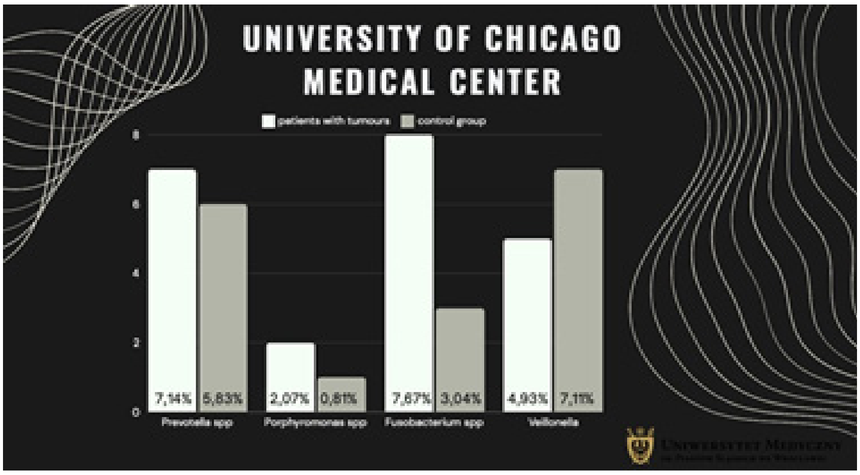

Figure: 3

Conclusion

Currently, it is believed that the oral microbiota may be associated with mutational changes that can lead to cancer. The composition of the oral microbiota includes a high number of bacteria and the negative ratio of bacterial flora can lead to dysbiosis. Oral pathogenic bacteria can have indirect or direct effects on the human immune response and affect to normal cell signalling pathways preceding carcinoma development [8].

Most studies identify this factor and even focus special attention on bacteria found in a higher percentage of cancer patients than in healthy people (for example, anaerobic bacteria such as Prevotella spp., Fusobacterium spp., Porphyromonas spp.) During the study, it was revealed at the microbiological level that there are pronounced changes in the microbiome of the oral cavity in patients with cancer of the oropharyngeal zone towards anaerobic bacteria.

This review confirms the association of oral microbiota with oncogenesis in oral squamous cell carcinoma (OSCC) and shows which bacteria can be used as biomarkers for early diagnosis of OSCC. Microbial dysbiosis is evident in patients with OSCC. Several types of bacteria appear to influence the progression of oral cancer. All in all, the human microbiota may lead to essential screening tools and treatment options that would be valuable in improving clinical outcomes.

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