

ORAL MICROBIOTA AND ORAL HEALTH CONNECTION

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ABSTRACT :

Introduction: Oral involuntary changes in total edentulous age often lead to therapeutic difficulties and complications that may interfere with or influence prosthetic iatrogenesis. **Purpose:** The aim of this clinical study was to identify bone complications of denture bearing areas and to establish their frequency in the group of complete edentulous patients. **Material and methods:** The study group consisted of 130 patients, 60 males and 70 females, complete edentulous aged between 30 and > 80 years. All data obtained from study group patients were centralized and statistically analyzed. **Results and discussions:** Of the 130 patients, after clinical examination it was revealed the presence of 86 hyperostotic tuberosities. A total of 49 patients (37.69%) were diagnosed with a maxillary tori and the existence of mandibular torus was found in the case of 26 patients (20%). **Conclusions:** Careful investigation of the general and local condition, is a particularly valuable tool in detecting bone complications
Keywords: dentures, exostosis, tori, osseous complications, etc.

INTRODUCTION.

The microbiome refers to the population of microbial occupants in our bodies. Joshua Lederberg, a Nobel laureate, developed the word "microbiome" to define the ecological community of symbiotic, commensal and pathogenic microorganisms.

These germs literally inhabit our bodies. [1] The number of bacteria in our bodies is nearly equal to, if not more than, the number of cells. [2].

It includes trillions of microorganisms including bacteria, fungi, archaea and viruses inhabiting a particular host. These microorganisms may have beneficial or deleterious effects on their host [3].

Oral microbiome was first identified by the Dutchman Antony van Leeuwenhoek who first identified oral microbiome using a microscope constructed by him [4].

He was named the "father of

Microbiology" and was a pioneer in the discovery of both protists and bacteria. [5] In 1674, he noticed his own tooth plaque and described it as a "very living animalcules prettily moving"[6].

A genome is an organism's genetic material. It refers to the entire set of DNA, including all of its genes. The collective genome of bacteria that live in the oral cavity is referred to as the oral microbiome. [6,7].

The human microbiome is divided into two parts: the core microbiome and the variable microbiome.

The core microbiome is shared by all humans, whereas the variable microbiome is unique to each individual based on lifestyle and physiological variances.

About 700 kinds of microorganisms exist in the human mouth, and these microbes constitute the human oral microbiota. It is one of the most complex

microbial communities in the human body [7].

Bacteria can colonize two types of surfaces in the oral cavity: the hard and soft tissues of teeth, as well as the oral mucosa. [7] Microorganisms thrive in a rich habitat provided by the teeth, tongue, cheeks, gingival sulcus, tonsils, hard palate, and soft palate. [8] The oral cavity's surfaces are covered with a thick layer of germs, known as bacterial biofilm [9,10]

The normal temperature of the oral cavity on an average is 37°C without significant changes, which provide bacteria a stable environment to survive. Saliva also has a stable pH of 6.5–7, the favorable pH for most species of bacteria. It keeps the bacteria hydrated and also serves as a medium for the transportation of nutrients to microorganisms [11].

OVERVIEW

The NIH Human Microbiome Project (HMP), which was launched in 2007, comprised 18 different studies to map and characterize the human microbiome and its role in human health and disease. It is well appreciated that the human microbiome is present in nearly every human body site [5], and the HMP has established, thus far, that there are 48 main microbial habitats in the human body [12].

According to the HMP [6], 34% of all primary microbial habitats were associated with human skin, 25% of all habitats were related to the gastrointestinal tract, and 20% of all habitats were associated with cavities of the head and neck region.

Among these main human habitats, the oral cavity is a challenging environment for microbial survival, since it undergoes high daily fluctuations in nutrient supply, temperature, pH, sheer and mechanical forces from mastication and hygiene practices, and chemical exposure from hygiene, pharmaceutical or toxic/smoking products [13].

Yet it retains a rich and complex ecosystem, harboring different micro-colonizers that thrive in this dynamic environment – the oral microbiome [8]

Healthy people from different countries have similar compositions of oral microbiota. In the human mouth, 85 species of fungi can be found [11].

Among these primary human habitats, the oral cavity is a difficult environment for microbial survival due to daily fluctuations in nutrient supply, temperature, pH, sheer and mechanical forces from mastication and hygiene practices, and chemical exposure from hygiene, pharmaceutical, or toxic/smoking products [14].

The microbial ecology of the mouth cavity is varied and rich biologically, with various niches that provide a unique environment for bacterial colonization [15].

Due to changes in shear forces, nutrient/energy supply, temperature, pH, and oxygen content in different environments, bacteria have evolved by leveraging specific survival strategies, including co-aggregation of different cells into communities embedded in extracellular matrices – biofilms [10].

Despite the existence of planktonic bacteria in the oral cavity, most of the oral microbiome exists in a biofilm state, known as the oral biofilm [16].

Biofilms are defined as an organized community of aggregated bacterial cells (of the same or different species) embedded and encased in a self-produced extracellular polymeric matrix (EPM) and adhering to an inert or alive surface [17].

Specifically, for oral bacterial biofilms (commonly referred to as “oral biofilms”), features of the oral cavity have shaped bacterial communities to adapt to high cell density, which, in turn create a micro-environment capable of modulating the pH, redox, and oxygen levels in its core [7,16,18]

Oral biofilms are formed by an initial adhesion of planktonic bacteria, known as “early colonizers” [19].

Typically, these early colonizers are saccharolytic aerobes and facultative anaerobes that primarily feed on oral glycoproteins and salivary mucins, with 80%

of the early colonizers being represented by *Streptococcus* species [7,17,18].

Different surfaces in the mouth are colonized preferentially by the oral bacteria due to specific adhesins on their surface which bind to complementary receptors on an oral surface [20].

After the initial colonization, the surface-attached bacteria change their metabolic and gene expression profiles to produce and secrete EPMs, which, for oral biofilms, is made up of polysaccharides, proteins, lipids and extracellular DNA (eDNA) [7,21-24].

The most common commensal fungi and members of the basal oral mycobiome are the *Candida* genera [55], which are found in 70% of healthy patients [13] as confirmed by Ghannoum et al. [26] and Peters et al [27].

The most abundant species in this genera is *C. albicans*, which is found in 40–80% of healthy individuals, followed by *C. glabrata*, *C. parapsilosis*, *C. tropicalis*, *C. krusei*, *C. stellatoidea*, *C. kefyr*, *C. khmerensis* and *C. metapsilosis* [26,27].

Among these fungi, the most important one is *Candida* [17].

Candida is neutral when the oral microbiota is normal; however, when the oral microbiota balance is broken, *Candida* will seek the opportunity to attack oral tissue. *Candida* forms a biofilm with *Streptococcus* to play a pathogenic role [18].

Oral bacteria are the main components of the oral microbiota. Common oral bacteria include *Streptococcus mutans*, *Porphyromonas gingivalis*, *Staphylococcus*, and *Lactobacillus* [23].

S. mutans is the main component of the oral microbiota, and it is one of the main components of dental plaque [24].

It is also the main pathogen of caries, which is a bacterial infectious disease that occurs in hard tissues of the teeth and has the highest incidence among oral diseases

[25].

The oral microbiome can undergo massive and rapid changes in composition and activity, both geographically and temporally, and it is developmentally dynamic with the host.

These multiplex, nonequilibrium dynamics are caused by a variety of factors, including the temporal frequency of host and diet, the response to pH variations, interactions among bacteria, and, on a larger scale, gene mutations and horizontal gene transfer, which confer new features on the strain.

The bacteria in our oral cavity have a mutually beneficial symbiotic connection. The commensal populations do not cause harm and keep harmful species at bay by preventing them from adhering to the mucosa. Only once the bacteria cross the barrier of the commensals do they become harmful, producing infection and sickness [24].

The microbial communities found in the human body have a role in essential, physiological, metabolic, and immunological activities such as food digestion and nutrition, energy generation, differentiation and maturation of the host mucosa, and immune system development; control of fat storage and metabolic regulation; processing and detoxification of environmental chemicals; skin and mucosal barrier function; immune system maintenance and the balance of proinflammatory and antiinflammatory processes; promotion of microorganisms (colonization resistance); and prevention of disease invasion and growth [1].

Nine sites from the oral cavity were sampled from healthy volunteers in the HMP. These sites were the tongue, dorsum, hard palate, buccal mucosa, keratinized gingiva or gums, palatine tonsils, throat and supra- and subgingival plaque and saliva.

K Li Bihan and Methe (2013) studied the HMP database and detected a relatively stable and a small core oral microbiome present in a majority of samples but in low abundance [24].

The expanded HOMD (eHOMD) is created with a goal of providing the scientific community with comprehensive curated information on the bacterial species present in the human aerodigestive tract (ADT), which includes the upper digestive and upper respiratory tracts, pharynx, nasal passages, sinuses and esophagus and the oral cavity.

Although the oral microbiome has resilience (i.e. capacity of an ecosystem to deal with perturbations without shifting its state of symbiosis [16]), insults or changes, such as tobacco use, can shift the eubiotic balance from mutualism/commensalism to a unbalanced parasitic/pathogenic state, thus, promoting disease in the host [25,26].

This specific parasitic/pathogenic state wherein microbials promote disease in the host is known as “dysbiosis” [27].

This is also known as an “unbalanced microbiome” [28,29].

According to Peterson et al [21], dysbiosis can be characterized by three different scenarios that are not mutually exclusive and may occur simultaneously. i) the overall loss of microbial diversity; ii) losing the beneficial microbes; and iii) expansion of the pathogenic microbes.

Computational techniques, such as in silico models, can be used to understand biological systems as well as to select, complement, and inspire laboratory experiments [29,30]. For example, certain computational approaches can be used to estimate the immunogenic response of an antibody to a particular virulence factor [31] or evaluate the competition between two different bacterial species [32].

Despite the harmful effects that can be

mediated by a dysbiotic oralome within the host, a complete elimination of the oralome is not the answer, since a eubiotic oralome provides health benefits to the host.

Rather, techniques to modulate the dysbiotic oralome to re-establish a eubiotic state would be preferred. Among the current and novel techniques being studied, we discuss the use of traditional oral hygiene techniques, antimicrobial peptides (AMPs), nano-sized drug delivery systems, prebiotics, probiotics, EPM disruption techniques, and modifiers of the inflammatory response.

Oral biofilm dysbiosis can be modulated through the use of antibiotics, however, antibiotics eliminate both pathogenic and commensal bacteria [33].

Also, due to their incomplete absorption by humans and animals, a large amount of ingested antibiotics are excreted into the environment via the feces or urine, contributing to environmental and multi-drug resistance concerns [34].

Therefore, new antimicrobial molecules are needed to effectively modulate microbial dysbiosis to address these concerns. In this regard, antimicrobial peptides (AMP) have shown promise in modulating oral biofilm dysbiosis.

Due to their broad-spectrum antimicrobial activity, some AMP have the potential of becoming the next generation of antibiotics, and they may be useful in dealing with the crisis of multi antibiotic-resistant bacteria [35].

Oral microbiota can influence body health through digesting certain types of food. Other factors include food patterns (vegetarian or not) and food extracts (like red wine). Here, we show how diet patterns and food extracts can affect body health.

Oral microbiota can produce metabolites in the mouth, which can affect the development of a range of oral diseases.

Since Antony van Leeuwenhoek

discovered bacteria in tooth plaque in the early 1670s, the role of oral microbes has developed from being considered simply "passengers" on the human host to one of benefiting and causing diseases in their human hosts.

The eubiosis-dysbiosis theory, which proposes that the oralome can move from a healthy to a sick state through harmful host-pathogen interactions, has been proposed to explain the balance between health and disease.

Although the reasons for this shift remain unknown, *in silico* studies have thrown light on this, revealing that tiny changes, such as pH shifts in certain oral locations, may be

CONCLUSIONS

1. The oral microbiota is a fascinating and rapidly increasing subject of study. Because it can cause both oral and systemic disorders, the oral microbiome is critical to health. It lives within biofilms throughout the oral cavity, forming an ecosystem that keeps health in balance.
2. Careful investigation of the general and local condition, is a particularly valuable tool in detecting bone complications
3. Certain aberrations in this state of

driving this imbalance.

Diabetes, atherosclerosis, Alzheimer's disease, and head and neck cancer have all been associated to oral dysbiosis. These studies show the presence of oral microorganisms in various sections of the human body, linking systemic disorders to oral dysbiosis and, as a result, providing fresh insights into such diseases.

equilibrium, however, allow infections to develop and cause disease.

4. Dybiosis is caused by disruption of the oral microbiome. The first stage in human microbiome research is to identify the microbiome in health, followed by understanding the role of the microbiome in the change of functional and metabolic pathways associated with sick states.
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