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Review

Microbiota in the oral cavity, Review

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Abstract: Microbiota are present everywhere in human existence and have an impact on every facet of it. Many species can be found within the human mouth. The human oral cavity is home to a variety of habitats. The combination and cooperation of the modified oral microbes protect the human body from the intrusion of external stimuli. On the other hand, systemic and oral illnesses are linked to an imbalance in the microbial flora. The human microbial community is significantly influenced by oral microbiomes. The use of recently noticed molecular tools has significantly improved our understanding of the makeup and roles of the oral microbiome in both wellness and sickness. Research on oral microbiomes and their relationships to microbiomes in different body locations and health conditions is essential to understanding our bodies and understanding how to improve human health. The purpose of this review is to go over the most recent information that explains the possible mechanisms underlying the relationships between oral and overall systemic health. The theory is that the influence of oral diseases on overall health may be partially explained by the oral microbiota. We will discuss the basic principles, the primary techniques in microbiology for describing oral organisms, and the most important information pointing to a biologically tenable connection between systemic illnesses and the oral microbiota.

Keywords: Oral cavity, microbiota biofilms, normal flora, Bacteria.

1. Introduction

The term "microbiota" originated in the early 1900s. It has been found that a wide variety of microorganisms live in every one of the organs of the human body. Furthermore, the human microbiota—also referred to as "the hidden organ"—contributes more than 150 times as much genetic material as the entire human genome [1]. Despite the fact that the terms "microbiota" and "microbiome" are frequently used synonymously, they have some distinctions [2]. A defined environment's population of living microorganisms, such as the oral and gut microbiota, is referred to as its microbiota. The term "microbiome" refers to the gathering of genomes from all environmental microorganisms, including metabolites, structural components, and environmental factors, in addition to the microbial community. Microbiome is a more comprehensive term than microbiota in this sense [3]. The oral cavity can be further subdivided into various habitats of microbiota, such as the tongue, saliva, buccal mucosa, palate, tooth surfaces, gums, and subgingival/supragingival plaque.

Due to a variety of reasons, including pH fluctuations, gene mutations, and bacterial interactions, these habitats can exhibit notable and rapid shifts in composition and activity. Although there are a few small differences, the microbial composition of all seven sites is comparable. *Actinobacteria*, *Fusobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* are generally the main types of bacteria found in the oral microbiota [4]. In recent decades, important studies have focused on the connection between the microbiota and diseases like cancer, diabetes, and neurological problems. Furthermore, altering the microbiota of the human body might be essential to the treatment of several diseases [5]. We present a summary and discussion of the current understanding of the human microbiota in the oral

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cavity, how it mediates health conditions, and how it may be used clinically to treat diseases.

2. An overview of the characteristics of the oral microbiota

In the environment and other parts of the human body, mouth bacteria are not as common as they are elsewhere [6]. More than 1000 species that support health can be found in the oral community [7, 8]. But each individual harbors between 100 and 200 species on average [9]. Because of the oral cavity's continuous interaction with the outside world, the mouth microbiota may have a dynamic composition [7]. According to some research [10, 11, 12], oral bacterial communities are arranged into biofilms.

It is possible to study the composition of the oral microbiota at various taxonomic resolutions, just like with any other microbiome. Starting from the phylum and going down through the levels of family, genus, or species, the strain is the most specific and has the highest level of generality. In recent decades, important studies have focused on the connection between the microbiota and diseases like cancer, diabetes, and neurological problems. Furthermore, altering the microbiota of the human body might be essential to the treatment of several diseases [5,13].

Just six phyla constitute (80–99,9%) of the taxa that inhabit oral bacteria [14, 15, 16]. Less than 16 genera represent around 88% of all bacteria found in the oral cavity; furthermore, less prevalent genera are present, but in much smaller amounts [17]. *Actinobacteria, Bacteroidetes, Chlamydia, Euryarchaeota, Fusobacteria, Firmicutes, Proteobacteria, Spirochaetes,* and *Tenericutes* comprised the majority of the oral microbiota [18]. Oral members of the proposed phylum radiation (CPR) are linked to oral disorders such as periodontitis and halitosis. It is believed that they alter the structural hierarchy and functions of the oral microbiome. The oral microbial ecology is impacted by this [19]. However, it is challenging to culture CPR pure; only TM7 had been cultivated in the human oral cavity [20].

The oral cavity contains about 100 different species of fungi. The common genera include *Rhodotorula, Fusarium, Gibberella, Aureobasidium, Candida, Cladosporium, Cryptococcus, Saccharomycetales, and Schizophyllum* [21]. Fungi have been found to make up 0.004% of all oral microorganisms and have only been found in specimens from supragingival plaque, hard palate, and mouth rinses [22]. Recent research, however, found a wide variety of fungi in saliva samples and distinguished between two distinct genus-level community types *(Candida* and *Malassezia*). Notably, oral rinse samples from healthy individuals exhibit high inter individual variability in fungal species [23].

3. The oral microbiota biofilms

The numerous and diverse oral microorganisms found in oral microbial biofilms, which are linked to a range of oral diseases, form complex ecological environments. Based on the acquired pellicle created by salivary proteins, first-time colonizing bacteria, such as *Streptococcus gordonii, Streptococcus mitis, Streptococcus oralis, and Streptococcus sanguinis,* bind specifically to their complementary salivary receptors using their surface adhesions [24]. Extracellular polymeric substances (EPS) are made up of structural proteins, nucleic acids, extracellular polysaccharides, and cell fragments. In the end, a three-dimensional ecosystem is created, which is made up of a range of microorganisms, EPS, proteins, and lipids from food and saliva, in addition to conduit and voiding systems [25].

Because of its strong and broad adhesive capacity, *Fusobacterium nucleatum* forms interdependent interactions with other elements of the microbiota, bridging the gap between the early and later bacterial invaders of the oral microbiota [26].The primary determinant of *F. nucleatum's* adhesion capacity is its outer membrane proteins, which are classified into two categories: those that inhibit lactose (like Fap2) and those that inhibit amino acids (like RadD and FomA) [27]. Gram-positive bacteria like *Staphylococcus aureus, Streptococcus gordonii, S. mutans,* and even *Candida albicans* typically colonize an area through the mediation of RadD [28]. A strain of *F. nucleatum* with the radD gene deleted exhibited decreased coadhesion with *S. gordonii*. Lack of fad-I, a gene that is expressed directly upstream from radD, causes radD to be expressed more, which in turn causes *F. nucleatum* and *S. gordonii* to coaggregate more frequently and form biofilms as a result. These results imply that a significant function of the lipoprotein Fad-I is to regulate RadD adhesion [29].

4: Biofilm Formation: Bacterial Interactions

In the planktonic phase, coaggregation happens when two paired individual bacteria are suspended. But "coadhesion" typically describes a state in which a coadhering microorganism is suspended and one microorganism is adhered to a surface [30].The binding

process, which is essential for the formation of multispecies biofilms, depends on the adhesion molecules expressed on one species' surface and the complementary polysaccharide-containing receptor expressed by another [31].

Oral microbial biofilms frequently contain *S. gordonii*, which may coaggregate with *Actinomyces , Fusobacterium, Streptococcus , and Veillonella* [32]. *S. gordonii* is significant in the biofilm formation process. The surfaces of all Streptococcus in the human oral cavity are coated in proteins related to the antigen I/II (AgI/II) family, which have highly conserved basic sequences and structures [33].

A polysaccharide of *Actinomyces oryzae* T14V that contains glucose, mannose, and galactose is recognized by the AgI/II family member SspA protein of *S. gordonii*. This recognition aids in the coaggregation of the two bacteria. It's noteworthy that this combination has some specificity. For example, according to [34], This polysaccharide does not bind to other proteins in the Lactis AgI/II family; it solely binds to SspB, particularly is expressed by *Lactococcus lactis*. A recent study discovered that the unique intrageneric coadhesion between *S. agalactiae* and *S. mutans* is facilitated by glucoside transferases B (GtfB) and GtfC [35].

Another study showed that not a single strain of Lactobacillus, including isolates taken from children with dental caries, was capable of creating biofilms in vitro out of the six strains tested. Nevertheless, all Lactobacillus exhibited a marked increase in biofilm formation when grown with *S. mutans*. This phenomenon was linked to the GtfB transfer from *S. mutans* to the Lactobacillus species [36].

5: Interactions of Fungi and Bacteria in the Formation of Biofilms

The most prevalent fungus in the oral cavity, *Candida albicans*, has been the subject of numerous studies [37]. Mycelia's development and transformation from yeast to mycelia are considered to be its main virulence factors [38].The presence of *Candida albicans* in the oral cavity of children suffering from severe early childhood caries is known to significantly increase the activity of gut flora (Gtfs) in the dental plaque as well as the abundance of highly acidogenic and acid-tolerant bacteria, including *S. mutans, Lactobacillus*, and *Scardovia* species. As a result, there may be a greater number of caries-active *S. mutans* due to the corresponding increase in EPS production [39]. *C. albicans*'s genes and proteins related to carbohydrate metabolism are greatly increased when the two strains are combined and cultured, according to an analysis of their interaction with *S. mutans*. Additional substances like mannan and glucan also saw an increase in concentration. These findings suggest that mixed incubation may increase fungal activity [37].

More research also revealed that the mechanism by which the GtfB secreted by S. mutans primarily binds to the mannan layer of *C. albicans* significantly facilitates the formation of the extracellular matrix and the growth of mixed-species biofilms [40]. In recent years, the focus of oral microbial biofilm investigations has switched from characterizing and assessing the microorganisms to looking at extracellular proteins, extracellular matrix components, and other matrix elements. The matrix is necessary for meshing microbial cells, provides three-dimensional scaffolding to limit cell dispersion, and preserves microenvironmental heterogeneity in addition to helping cells survive in their assigned niches. Particularly, pathogenic *S. mutans* produces dental plaque with a highly organized matrix that other microorganisms can attach to [41]. Recently, the development of matrix inhibitors has gained a lot of attention as a result of a better understanding of the roles and effects of various matrix components [42].

6. Conclusion

We have gradually identified a new role for bacteria in health and illness after decades of investigation. It is now shown that microbiota can impact nearly every element of the host, whereas its numerous disorders are linked to dysbiosis. We are able to closely examine how bacteria contribute to pathogenesis and preserve human health because of improved research technologies. But the majority of research on microbiota focuses on the bacterial component; less is known about the roles played by fungi, viruses, and other microorganisms in health and illness. Furthermore, even though dysbiosis of the microbiota is frequently seen in disease states, the microbiota's causal function in these conditions is yet unknown.

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Author's Contributions

All authors have contributed equally and read and approved the final paper.

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