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**INDO AMERICAN JOURNAL OF
PHARMACEUTICAL SCIENCES**<http://doi.org/10.5281/zenodo.1481985>Available online at: <http://www.iajps.com>**Research Article****A STUDY ON THE ROLE OF ORAL MICROBIOME IN
HEALTH AND DISEASE**¹Dr. Syed Imran Abbas Shah, ²Dr. Iqra Rehman Alvi, ³Dr. Syed Siraj Ahmad¹Sheikh Zayed Medical College, Rahim Yar Khan²Dental Surgeon at RHC110/TDA, Layyah³De'Montmorency College of Dentistry, Lahore**Abstract:**

Every human body contains a personalized set of foreign inhabitants essential to maintaining health, yet also capable of eliciting disease. The totality of these microorganisms, their genomes and ecosystems encompasses the microbiome. The basic aim of the study is to find the role of oral microbiome in health and disease. As the correlation between the human microbiome and health becomes more evident, microbiome research is becoming central to the advancement of disease diagnostics and therapeutics as well as the development of personalized medicine. There are several ways to sequence a metagenome or segments of a metagenome, each technique serving a unique purpose. The most common techniques include 16S ribosomal RNA sequencing, pyrosequencing, and shotgun sequencing. The bacterial flora in a healthy oral cavity vs a diseased one is distinctly different, suggesting there may be a profile for a core oral microbiome of health. According to various studies, identical bacterial sequences have been discovered in the oral cavities of unrelated healthy individuals.

Corresponding author:

Dr. Syed Imran Abbas Shah,
Sheikh Zayed Medical College,
Rahim Yar Khan

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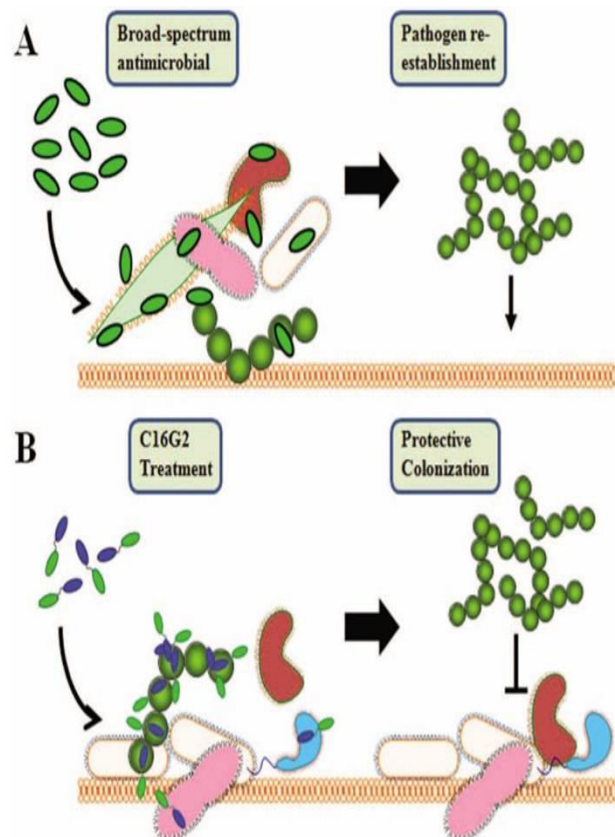
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INTRODUCTION:

Every human body contains a personalized set of foreign inhabitants essential to maintaining health, yet also capable of eliciting disease. The totality of these microorganisms, their genomes and ecosystems encompasses the microbiome. The number of microbial cells within a human body exceeds the total number of human cells in the body by nearly 10 times. These microorganisms contribute their genome, known as the metagenome, to the human body, multiplying human genes by approximately 100 times. The activity of the microbiome and, specifically, the expression of its metagenome provide the human with resources and traits that did not originally evolve with the body. For example, the microbiome contains genes that allow humans to digest certain plant polysaccharide [1].

The last few decades have witnessed an increasing interest in studying the human microbiome and its role in health and disease. The focus of those studies was mainly the characterization of changes in the composition of the microbial communities under

different conditions [2]. As a result of those studies, we now know that imbalance in the composition of the microbiome; also referred to as *microbial dysbiosis* is directly linked to developing certain conditions. Dysbiosis of the oral microbiome is a prime example of how this imbalance leads to disease in the case of periodontal disease. However, there is considerable overlap in the phylogenetic profiles of microbial communities associated with active and inactive lesions, suggesting that the difference in periodontal status of those sites may not be explained solely by differences in the sub-gingival microbial composition [3]. These findings suggest that differences in functional activities may be the essential elements that define the dysbiotic process. Researchers have recently begun to study gene expression of the oral microbiome in situ with the goal of identifying changes in functional activities that could explain the transition from health to disease. These initial results suggest that, rather than a specific composition, a better understanding of oral dysbiosis can be obtained from the study of functional activities of the microbial community [4].



Credit: Eckert R, et al. / Adv. Dent. Res. 2012

Figure: Targeted antimicrobials in the oral microbiome

Objectives of the study

The basic aim of the study is to find the role of oral microbiome in health and disease.

Correlation of human microbiome and health

As the correlation between the human microbiome and health becomes more evident, microbiome research is becoming central to the advancement of disease diagnostics and therapeutics as well as the development of personalized medicine. Because each individual harbors a unique microbiome that plays a key role in the etiology of disease within the body, disease may manifest and progress differently among different individuals, making personalized medicine imperative for optimal health care [5].

However, microbiome research must develop a deeper understanding of the fundamentals and specifics of microbial activity within the body during health and disease before it can contribute to personalized care. First, there should be a clear picture of which microorganisms exist in the body and how they affect the host's physiology and health condition. Then, microbial characteristics of specific diseases should be studied to recognize microbiome patterns that distinguish one disease from another. Finally, proper diagnostic methods and technologies

should be developed to enable professionals to identify individual microbial profiles and treat specific microbes responsible for disease [6].

Methodologies for the detection of microbiome

There are several ways to sequence a metagenome or segments of a metagenome, each technique serving a unique purpose. The most common techniques include 16S ribosomal RNA sequencing, pyrosequencing, and shotgun sequencing. As certain metagenomes have already been synthesized and the species identified, researchers can also use more conventional techniques to determine the presence of a microorganism [7]. These techniques include culture-based identification, microscopy, enzyme analysis, and immunological assays. Although less advanced, these procedures complement the sequencing processes by providing information on the physical characteristics and additional behavioral and metabolic properties of microbes. It may be beneficial or even necessary for the future dentist to be familiar with sequencing and the other identification techniques in case these laboratory procedures arrive in the clinical setting for an on-the-spot microbial identification and personalized care [8].

Table 1. Methodologies for the detection of microbes and microbiomes

| | Technique | Procedure | Purpose | Pros | Cons |
|--------------|---------------------|---|--|---|--|
| Metagenomics | 16S rRNA sequencing | Amplification and cloning sequencing of DNA segments using PCR | DNA sequences analyzed to identify species | 1. Rapid 2. Accurate 3. Detects viral DNA | 1. PCR subject to bias 2. PCR sensitive to contamination |
| | Pyrosequencing | Sequencing of small DNA segments. Pyrophosphates are emitted as nucleotides come together and synthesis DNA | DNA sequences analyzed to identify species and also biodiversity | 1. Successfully determines biodiversity 2. Subject to less bias because does not require cloning 3. Produces many sequences | 1. Expensive 2. Does not produce full-length 16S rDNA sequences necessary for taxonomic studies |

| | | | | | |
|---------------------------|--------------------|--|--|---|--|
| | Shotgun Sequencing | Long DNA is randomly fragmented and sequenced. Several rounds of this are performed for multiple overlapping reads for the target DNA. Computer programs use the overlapping ends of different reads to assemble them into a continuous sequence | DNA sequences analyzed to identify which organisms are present and also to suggest the metabolic processes they are responsible for in the microbial community | <ol style="list-style-type: none"> 1. Less expensive 2. Rapid 3. Forms long stands of continuous DNA 4. Less need for human intervention 5. Suggests information on metabolic activity | <ol style="list-style-type: none"> 1. High error rate in constructing the continuous set of overlapping sequences 2. Computationally intensive |
| Conventional microbiology | Culture analysis | Growth of bacteria on specific medium | <ol style="list-style-type: none"> 1. Physical, behavioral, and chemical properties 2. Metabolic requirements | <ol style="list-style-type: none"> 1. Highly accurate 2. Resistance testing is possible | <ol style="list-style-type: none"> 1. Time-consuming 2. Many periodontal pathogens anaerobic and/or fastidious, many species are uncultivable |

Oral cavity and its microbiome

To understand the role of the oral microbiome within the oral cavity, it is important to analyze its fundamental characteristics and dynamics. The oral cavity harbors over 700 species of bacteria that contribute to the health and physiological status of the oral cavity. Within the oral cavity, there are two types of surfaces for which bacteria can colonize: the hard surfaces of teeth and the soft tissue of the oral mucosa [9]. The teeth, gingival sulcus, tongue, cheeks, hard and soft palates, and tonsils each provide enriching environments in which microbial communities can flourish. Different types of microorganisms prefer distinct niches according to varying surface structures and functions. Each niche provides the optimal conditions and nutrients for its populating microbes. In fact, research has shown the

maxilla, hard palate, soft palate, and even the tongue's lateral sides and dorsal side each to have a different bacterial profile [10].

CONCLUSION:

The bacterial flora in a healthy oral cavity *vs* a diseased one is distinctly different, suggesting there may be a profile for a core oral microbiome of health. According to various studies, identical bacterial sequences have been discovered in the oral cavities of unrelated healthy individuals. The analysis identified 10 variables shared between 11 bacterial species. However, the same study also showed that significant inter individual differences exist, supporting the concept of both a core and variable microbiome within the oral cavity.

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