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# COMPARATIVE ANALYSIS OF ORAL MICROBIAL FLORA OF PATIENTS WITH PERIODONTITS AND HEALTHY INDIVIDUAL.

**Running Title:** Comparative analysis of oral microbial flora of patients with periodontitis and healthy individual

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#### **Abstract:**

Aim: This study aims to determine the changes caused by microbes in patients with periodontitis

**Background**: Periodontitis is one of the most common bacterial infections in humans. The disease is a consequence of destructive host immune responses to pathogenic bacterial species resulting from the dysbiosis of oral microbiota

**Objective:** To comparatively analyze the oral microbial flora of healthy individual and patients with periodontitis

**Materials & Method:** Salivary samples of healthy individual and patients with periodontitis will be collected and will be analyzed in the Microbiology Laboratory for presence of any microorganisms. The findings will be compared to arrive at a conclusion on the diversity of the microbial profile between the two groups.

**Results**: The oral microbes included Streptococcus, Staphylococcus, Candida Albicans, Enterococcus and Lactobacillus.

**Conclusion**: Knowledge of the difference in the microbial flora of healthy individual and patients with periodontitis can help aid in more specific treatment options and prevent recurrence of the disease.

**Keywords:** Saliva, Microbes, Periodontitis

## INTRODUCTION:

One of the most prevalent bacterial illnesses in people is periodontitis. The dysbiosis of the oral microbiota leads to damaging host immunological responses to pathogenic bacterial species, which in turn cause the illness [1,2,3]. Assessment of the subgingival microbiota's composition and assemblage in relation to health and illness has thus continued to be of interest.

Over the course of more than a century, a number of generations of knowledgeable scientists and clinicians have conducted extensive research on the microbiota connected to periodontal health and disease. [4,5] According to research, poor dental hygiene and dietary changes might modify the makeup of the oral bacteria (6,7). The oral microbiota is an incredibly dynamic and complex organism that is significantly impacted by host-mediated selection pressures and constantly changing local surroundings. The appropriate development of mucosal immunity depends on the existence of a commensal microbiota, which includes potential pathogens. (8)

The typical oral flora is therefore in a balance between pathogens and commensals, which needs routine cleaning to be maintained. The oral cavity may contain up to 19 000 bacterial phylotypes. When oral hygiene suffers, oral biofilms quickly accumulate on tooth surfaces and, if addressed, develop into gingival inflammation, periodontitis, alveolar bone loss, and tooth loss.

If bacterial colonisation leads to overt illness, it is likely that variations in the host's defensive systems, especially antimicrobial protein profiles, are to blame. (9)

Effective approach and monitoring methods for periodontal treatment might be created using knowledge of the components and assembly procedures of the oral microbiota. This study looked at the salivary microbiome before and after the first round of treatment in people with chronic periodontitis and people with healthy gums. The appropriate development of mucosal immunity depends on the existence of a commensal microbiota, which includes potential pathogens. (10,11).

#### MATERIALS AND METHOD:

the spittle of twenty Five male people were chosen, of which 15 had chronic periodontitis while the remaining 10 appeared to be in good condition. The Saveetha Dental College gathered saliva samples, which were then forwarded to the Microbiology Department for cultivation. The materials were infected using the spread plate method into nutrient agar. At 37°C for 24 hours, the culture plates were injected, and microbial growth was monitored. The following information was manually calculated for the colony forming units. Both Gram staining and colony morphology were used to identify the species.



Fig shows the saliva samples cultured on nutrient agar.

# **RESULTS & DISCUSSION:**

There were 25 participants in the research, 15 of them had chronic periodontitis, and the other 10, who were generally in good health. A completely new oral flora develops as a result of periodontitis, which significantly alters the mucous membranes of the mouth and worsens the environment for the growth of beneficial bacteria. Table 1 shows the differences in the micro flora between healthy persons and those with periodontitis.

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The study demonstrates that staphylococcus and streptococcus mutants were the two most common bacteria discovered in the oral cavities of individuals with periodontally damaged teeth (548). (498)

Despite not often being harmful, Staphylococcus is a Gram-positive bacteria that poses an increased risk of infection in immunocompromised people.

Dental caries are brought on by S. mutans, which is most frequently present in the oral cavity. Almost 19 different kinds of streptococci have their natural home in the human oral cavity. When S. mutans is growing in a biofilm, its rate of transformation is 10- to 600-fold greater than when it is developing as a single cell in an open environment. S. mutans is not now the subject of a vaccine. [16]

There were several candida albicans found (265) An opportunistic infection of the mouth cavity is oral candidiasis. It is prevalent and underdiagnosed among the elderly, especially in those who wear dentures, and is frequently preventable with appropriate oral hygiene practises.

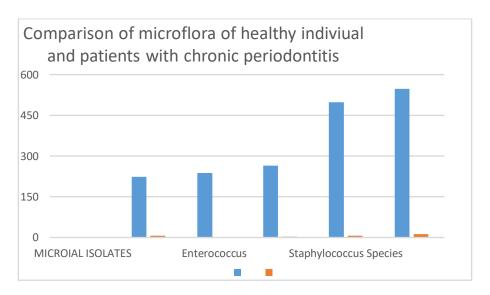
It can also be a symptom of a systemic illness, such as diabetes mellitus, and it is a prevalent issue in those with impaired immune systems.

The number of enterococci found was (237), however the number of lactobacilli was rather low (223) High salt concentrations and harsh temperatures are both something that Enterococcus can tolerate. [7] The degree of inherent antibiotic resistance is considerable. It is an uncommon neurosurgical complication that frequently has to be treated with intravenous vancomycin. [9] They have the potential to spread illnesses including meningitis, bacteremia, and bacterial endocarditis. [7,10] Although there are more than 17 species of Enterococcus, only a small number of them are known to cause clinical infections in people. Although there are more than 17 species of Enterococcus, only a small number of them are known to cause clinical infections in Antibiotic resistance in Enterococcus can be either inherent or acquired, which can lead to nosocomial infections. Beta-lactamases, chloramphenicol, tetracyclines, rifampin, fluoroquinolones, aminoglycosides, and vancomycin were other drugs that helped them develop resistance to penicillin. Vancomycin resistance comes in six phenotypes: VanA, VanB, VanC, VanD, VanE, and VanG. The most prevalent strain, VanA, has significant levels of teicoplanin and vancomycin resistance, whereas VanB isolates have varying levels of teicoplanin and vancomycin resistance. The VanC1 and VanC2 chromosomal genes mediate the VanC phenotype. Only a few Enterococci strains have VanD, VanE, and VanG phenotypic descriptions. Newer antibiotics with higher action against Enterococcus include quinupristindalfopristin, linezolid, daptomycin, and tigecycline.

Lactobacilli are rods or coccobacilli that are Gram-positive, do not produce spores, and typically have DNA with a G+C concentration of less than 50% mol%. They have complicated dietary needs and are only strictly fermentative, aero-tolerant or anaerobic, aciduric or acidophilic (e.g. for carbohydrates, amino acids, peptides, fatty acid esters, salts, nucleic acid derivatives, and vitamins). Since they don't produce porphyrinoids, they lack heme-dependent functions. Some

species' strains may utilise porphorinoids from the environment and display catalase, nitrite reduction, or even cytochrome activities (Meisel, 1991). In Lb strains, pseudo-catalase is produced. mali. If glucose is used as a carbon source, lactobacillus can either be homofermentative, which results in the production of more than 85% lactic acid, or heterofermentative, which results in the equimolar production of lactic acid, CO2, ethanol (and/or acetic acid), and CO2. Increased levels of acetate may be created in the presence of oxygen or other oxidants at the expense of lactate or ethanol, resulting in the production of an extra mole of ATP thanks to the acetate kinase process. As a result, changes in the metabolic end products might happen. Numerous substances, including as citrate, malate, tartrate, quinolate, nitrate, and nitrite, among others, may be metabolised and employed as an energy source or an electron acceptor.

Due to their capacity for producing bacteriocin and resistance to a variety of antibiotics, Streptococcus and Enterococcus are significant. Due to the underlying cause of periodontitis, it is increasingly common practise to combine antimicrobial therapy with scaling and root planing. The aim of the current study was to isolate, identify, and characterise oral bacteria. Understanding the differences between the microbial flora of healthy people and those with periodontitis can help with more targeted treatment choices and prevent the disease from returning.



MICROIAL ISOLATES	MICROBES IN INDIVIDUALS WITH CHRONIC PERIODONTITIS	MICROBES IN HEALTY INDIVIDUALS
Lactobacillus	223	6
Enterococcus	237	2
Candida Albicans	265	3
Staphylococcus Species	498	6
Streptococcus Mutants	548	12

# (Table 1)

# **Conclusion:**

Because of the underlying microbial basis of periodontitis, it is more conventional to use antimicrobial therapy adjunctively with scaling and root planing. Knowledge of the difference in the microbial flora of healthy individual and patients with periodontitis can help aid in more specific treatment options and prevent recurrence of the disease.

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