Oral Health Status: The Level of Oral Microbial Flora in Healthy Girls

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ABSTRACT

The normal oral flora comprises a diverse group of micro-organisms and then 300 species inhabit the oral cavity of which about 50 are found routinely and account for the majority of the cultivable strains, these factors, together with the fact that the indigenous microbiota plays an important role in health and disease of a human and animals. It contribute to the development of the immune system and provide resistance to colonization by allochthonous or pathogenic micro-organisms. The aim of our study is to determine the most frequent micro-organisms as normal flora in healthy individuals. A total of 30 healthy students, all belongs to Jinnah University for Women of same age group were studied. Throat swabs were plated with human-blood agar, chocolate agar and apply bacitracin disk on both plates, SDA agar were incubating for 24 hours for isolation of Candida species. Organisms were cultured on Blood agar, SDA agar, Mannitol salt agar to observe the colonies. Different spot test like catalase and coagulase test were performed for identification of Staphylococcus species. Identification was also done by microscopic examination by gram stain. Catalase-positive, gram-positive rods were found to be as most frequent micro-organisms as normal flora of healthy students and were only micro-organisms detected 46.6% and total Staphylococcus species were (30%); Staphylococcus aureus (13%) and other Staphylococcus species (17 %) where as Streptococcus species (catalase-negative gram positive cocci) isolated from oral specimen of healthy individuals.

Key words: Microbiota, Oral flora, Staphylococcus sp., Throat swab.

INTRODUCTION

The microbial flora of the oral cavity are rich and extremely diverse. This reflects the abundant nutrients and moisture and hospitable temperature, and the availability of surface on which bacterial populations can develop. The presence of a myriad of micro-organisms is a natural part of proper oral health. However, a imbalance in the microbial flora can lead to the production of acidic compounds by some micro-organisms that can damage the teeth and gums. Damage to the teeth is referred to a dental caries. It has been estimated that at least 35% of denate U.S adult s aged 30 to 90 years have Peridontitis (Yamamoto et al., 1994). In addition specific oral bacterial species have been implicated several systemic disease, such as bacterial endocarditis (Michalek et al., 1990) aspiration pneumonia (Childers et al., 1989), osteomyelitis in children (Farnaud et al., 2003) preterm low birth weight (Corthesy et al., 1999) and cardiovascular disease (Tenovuo et al., 1994). Surprisingly, little known about the microflora of the healthy oral cavity. These include the tougue, epithelial cells lining the roof of the mouth and the cheeks, the hard enamel of the teeth. In particular, the microbial communities that exist on the surface of the teeth are known as dental plaque. The adherent communities also represent a biofilm. Oral biofilm develop over it time into...
exceedingly complex communities. Hundreds of species of bacteria have been identified in such biofilm. Examples of some bacteria that are typically present as primary colonizers include Streptococcus, Actinomyces, Neisseria and Veillonella. Examples of secondary colonizers include Fusobacterium nucleatum, Prevotella intermedia and Capnocytophaga species. With further time, another group of bacteria can become associated with the adherent community. Examples of these bacteria include Campylobacter rectus, Eikenella corrodens, Actinobacillus Actinomycetem comitans, and the oral spirochetes of the genus Treponema. The mouth is the largest natural opening in the human body, and is a major component in the mucosal barrier system. It has its own immune barriers, which we call the oral immune system. The primary function of the immune system of the mouth is to protect the teeth, jaws, gingivae and the rest of the oral mucosa against infection (Yamamoto et al., 1994). The flow of saliva has a mechanical effect, flushing microorganism from mucosal and tooth surfaces. Saliva also contains important antimicrobial agents (Tenovuo et al., 1994). The intact stratified squamous epithelium supported by the lamina propria presents a mechanical barrier to oral microorganism. The continuous shedding by exfoliation of epithelial squamous limits microbial colonization of the surface. Intra-epithelial dendritic langerhans cells are peripheral antigen-presenting cells which can process antigen in their MHC-class II abundant intracellular compartments. They migrate to the regional lymph nodes to present antigenic peptides complexed to MHC-class II molecules to prime naive helper T cells. The oral epithelium also forms part of an intercommunicating network of the immune system, in which signals are regularly exchanged in dynamic interactions (Yamamoto et al., 1994) as the nonspecific defense factors include mucins, nonimmune salivary glycoproteins, lactoferrin, lysozyme, peroxidase, histatins, and cystatins. SIgA is considered the first line of defense against pathogens which colonize and invade surfaces bathed by secretions (Mcnabb et al., 1981). SIgA antibodies may play an important role in the homeostasis of oral resident microbiota and in the prevention against caries and periodontal diseases (Michalek et al., 1990). The normal oral flora comprises a diverse group of micro-organism, including bacteria, fungi, protozoa and possibly even viruses (Marsh et al., 1999). More than 300 species inhabit the oral cavity of which about 30 are found routinely and account for the majority of the cultivable strains, these factors, together with the fact that the oral cavity has a wide range of sites with different environment condition, make the study of oral microbiology complex and difficult. The indigenous microbiota plays an important role in health and disease of humans and animals. It contributes to the development of the immune system and provides resistance to colonization by allochthonous or pathogenic microorganisms (Crabbe’ et al., 1968).

**MATERIALS AND METHODS**

**Specimen:** A sterile cotton swab specimen, vigorously rub on both tonsillar surface and the posterior pharynx. Remove swab from mouth and insert tip down into wrapper.

**Requirements:** Petri plates, sterile cotton swabs, test tubes, pipettes.

**Media and Reagents:** Catalase reagent, Blood base, Mannitol salt agar, bacitracin disk, gram staining reagents.

**Procedure:** Throat swabs were plated with human-blood agar, and SDA agar. Place bacitracin disk on blood agar plates. Both plates were incubated at 37 °C for 24 hours. Gram staining was performed to observe the gram reaction and morphology of microorganism. The organisms were streaked in order to check haemolysis. Catalase test and coagulase test were also performed.

**RESULTS**

Catalase-positive, Gram-positive rods were found to be as most frequent micro-organisms as normal
flora of healthy students and were only micro-
organisms detected 46.6% and total gram positive
cocci were found 53% in which total Staphylococcus
species were 30%; Staphylococcus aureus 13% while
other Staphylococcus species were 17 % where as
catalase-negative Gram-positive cocci were also
isolated from oral specimen of healthy individuals
(Table I).

**Table I.** Frequency rate of isolated micro-organisms from
oral cavity.

<table>
<thead>
<tr>
<th>Microorganisms</th>
<th>No. of Individuals</th>
<th>Percentage (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Staphylococcus aureus</strong></td>
<td>4</td>
<td>13</td>
</tr>
<tr>
<td>Other Staphylococcus species</td>
<td>5</td>
<td>17</td>
</tr>
<tr>
<td>Catalase positive, gram-positive rods</td>
<td>14</td>
<td>47</td>
</tr>
<tr>
<td>Catalase-negative gram-positive cocci</td>
<td>7</td>
<td>23</td>
</tr>
<tr>
<td>Candida</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSION**

There is a distinctive bacterial flora in the healthy
oral cavity which is different from that of oral disease
for example, many species specifically associated
with periodontal disease, such as Porphyromonas
gingivalis, Tannerella forsythia, and Treponema
denticola, were not detected in any sites tested. In
addition, the bacterial flora commonly thought to
be involved in dental caries and deep - dental cavities,
represented by Streptococcus mutans, Lactobacillus
species, Bifidobacterium species and Atopobium
species, were not detected in supra and sub gingival
plaques from clinically healthy teeth. The bacterial
species associated with sore throat such as lancifield
group A  β-haemolytic Streptococcus pyogenes were
also not detected. It is necessary to first define the
bacterial flora of the healthy oral cavity before we
can determine the role of oral bacteria n disease.

**REFERENCES**


