An Initial Study on Normal Commensel Flora of Throat

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Abstract:
Introduction: The normal throat flora of humans is complex and consists of several species of bacteria.
Materials & Methods: The study aimed at finding out the normal commensel flora of throat of healthy individual in a tertiary care hospital with 157 selected individuals of different ages and both sexes over a period of three months (January 2015 to March 2015). Diagnosed cases of immunocompromisation were excluded from the study. Aseptically collected throat swabs were processed for microbiological workup as per standard protocols. Speciation and antimicrobial susceptibility testing of the isolates were done by VITEK-2 Advanced Expert System. Data were analyzed as per standard statistical methods.
Results: Amongst study population, Staphylococcus aureus was isolated in 71 cases (45.22%), viridans group of Streptococcus (Streptococcus mitis) was isolated from 93 cases (59.23%) and Diphtheroids were isolated in 29 cases (18.47%). Moraxella spp were isolated in 17 cases (10.82%). Streptococcus pneumoniae was isolated in 13 cases (8.08%) and Candida albicans was isolated in 9 cases (6.17%). Polymicrobial isolations were associated in 139 cases (88.53%). All of the Streptococcus isolates were sensitive to Penicillin and Erythromycin. Amongst 71 isolated Staphylococcus aureus, 19 were Methicillin resistant (26.76%). Candida isolates were sensitive to Fluconazole and Itraconazole.

Conclusion: Viridans group of Streptococcus is the leading microbe to form the commensal flora of throat specially after 10 years.

Keywords: Throat swab, flora, VITEK-2AES, Viridian Streptococcus

I. Introduction

The normal flora of humans is complex and consists of several species of bacteria. The makeup of the normal commensel flora may be influenced by various factors specially chronological age, gender, hormonal change and immune status (1). Developmental changes in humans such as weaning invariably affect the composition of the oral cavity and normal flora in the intestinal tract. However, within the limits of fluctuations, the distribution of bacterial flora of throat and oral cavity is sufficiently constant to chalk out a general description (2).

In utero, the fetus is sterile and first becomes colonized by a normal flora at the moment of birth and passage through the birth canal. Handling and feeding of the infant after birth leads to establishment of a bacterial flora on the skin, oral cavity and intestinal tract within first 48 hours (3). It has been calculated that there are about 10^{12} bacteria on the skin, 10^{10} in the oral cavity and 10^{14} in the gastrointestinal tract (1, 4).

Knowledge of normal commensel flora of throat of healthy individual is important to diagnose the alteration of flora in diseased condition as well as to identify true pathogens isolated from upper gastrointestinal tract and upper respiratory tract.

II. Aim & Objective(s)

The study aimed at finding out the normal commensel flora of throat of healthy individual in a tertiary care hospital with following objectives:
1. Isolation of different microbes from throat swabs collected from healthy individuals.
2. To find out the distribution of normal throat flora amongst different age groups and gender.

III. Materials & Methods

The study was conducted in a tertiary care hospital in Kolkata with 157 selected healthy individuals of different ages and both sexes over a period of three months (January 2015 to March 2015). Diagnosed cases of
imunocompromisation were excluded from the study. Throat swabs were collected aseptically and processed for microbiological workup as per standard protocols (5). Culture was performed at 37°C for overnight at aerobic condition. Gram staining and Albert staining were performed. For bacterial isolation, nutrient agar, blood agar, chocolate agar, Mac-Conkey’s agar and potassium telluride blood agar were used. Speciation and antimicrobial susceptibility testing of the isolates were done by VITEK-2 Advanced Expert System (VITEK-2 AES). Data were analyzed as per standard statistical methods.

IV. Results
Amongst 157 selected cases, Staphylococcus aureus was isolated in 71 cases (45.22%), viridans group of Streptococcus (Streptococcus mitis) was isolated from 93 cases (59.23%) and Diphtheroids were isolated in 29 cases (18.47%). Moraxella spp were isolated in 17 cases (10.82%). Streptococcus pneumoniae was isolated in 13 cases (0.08%) and Candida albicans was isolated in 9 cases (0.057%). Polymicrobial isolations were associated in 139 cases (88.53%) where as in rest 18 cases, only Streptococcus mitis was isolated (11.46%). All of the Streptococcus isolates were sensitive to Penicillin and Erythromycin. All isolated Staphylococcus aureus were sensitive to Vancomycin and Linezolid. Amongst 71 isolated Staphylococcus aureus, 19 were Methicillin resistant (26.76%). Candida isolates were sensitive to Fluconazole and Itraconazole. No significant difference of pattern of commensal flora was noticed amongst different genders of the same age group.

<table>
<thead>
<tr>
<th>Age (years)</th>
<th>Number of cases</th>
<th>Isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;10</td>
<td>31</td>
<td>Streptococcus pneumoniae, Staphylococcus aureus, Candida albicans</td>
</tr>
<tr>
<td>10-20</td>
<td>35</td>
<td>Viridians Streptococcus, Methicillin resistant Staphylococcus aureus, Diphtheroids</td>
</tr>
<tr>
<td>21-40</td>
<td>30</td>
<td>Viridians Streptococcus, Staphylococcus aureus, Diphtheroids, Moraxella spp.</td>
</tr>
<tr>
<td>41-60</td>
<td>31</td>
<td>Viridians Streptococcus, Methicillin resistant Staphylococcus aureus.</td>
</tr>
<tr>
<td>&gt;60</td>
<td>30</td>
<td>Viridians Streptococcus, Methicillin resistant Staphylococcus aureus, Candida albicans</td>
</tr>
</tbody>
</table>

Table 1: Isolated microbes from throat swabs collected from study population varies with age group.

V. Discussion
Streptococcus pneumoniae, Candida albicans, Viridians Streptococcus, Staphylococcus aureus, Diphtheroids and Moraxella spp. were isolated as throat flora of study population. This finding simulates several documentations (1).

In our study, the percentage of Methicillin Resistant Staphylococcus aureus colonization in throat was a bit lower than that of reported by Ringberget al. (6).

In this present study, all Streptococcus isolates were sensitive to Penicillin and Erythromycin whereas in other works, resistance to Erythromycin is reported (7).

Candida albicans was isolated from study group belonging to below 10 years and above 60 years. Moraxella spp. was isolated from the age group of 21 years to 40 years. Viridians Streptococcus and Methicillin Resistant Staphylococcus aureus were isolated from the study population aged ≥10 years. Overall, Viridans group of Streptococcus was the commonest isolate (59.23%). These findings were similar to that of Bista et al. (8).

VI. Conclusion
Throat swabs aseptically taken from 157 healthy individuals of different age groups and gender revealed that Viridans group of Streptococcus is the leading microbe to form the commensal flora of throat specially after 10 years. Colonization of Methicillin Resistant Staphylococcus aureus ≥ 10 years is an alarming sign against injudicious use of antimicrobials.

Limitations of the study
The study should be continued for a prolong period so that seasonal variation can be recorded if any. Anaerobic workup should also to be performed.
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References