

## An Initial Study on Normal Commensal Flora of Throat

Dr. Jayashree Konar<sup>1</sup>, Dr. Sanjeev Das<sup>2</sup>, Major Dr. Inam Danish Khan<sup>3</sup>

<sup>1</sup>Demonstrator, Department of microbiology, Nilratansircar medical college & Hospital, Kolkata

<sup>2</sup>Assistant Professor, Department Of Microbiology, R.G.Kar Medical College & Hospital, Kolkata

<sup>3</sup>Clinical Microbiologist, Command Hospital, Kolkata

### 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 commensal 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 (0.08%) and *Candida albicans* was isolated in 9 cases (0.057%). Polymicrobial isolations were associated in 139 cases (88.53%). 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.

*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. Viridans *Streptococcus* and Methicillin Resistant *Staphylococcus aureus* were isolated from the study population aged  $\geq 10$  years.

**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 commensal flora may be influenced by various factors especially 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 commensal 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 commensal 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

immunocompromisation 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.

**Age wise distribution of microbial flora of human throat was as follows :**

Age (years)	Number of cases	Isolates
<10	31	<i>Streptococcus pneumoniae</i> , <i>Staphylococcus aureus</i> , <i>Candida albicans</i>
10-20	35	Viridians <i>Streptococcus</i> , Methicillin resistant <i>Staphylococcus aureus</i> , Diphtheroids
21-40	30	Viridians <i>Streptococcus</i> , <i>Staphylococcus aureus</i> , Diphtheroids, <i>Moraxella</i> spp.
41-60	31	Viridians <i>Streptococcus</i> , Methicillin resistant <i>Staphylococcus aureus</i> .
>60	30	Viridians <i>Streptococcus</i> , Methicillin resistant <i>Staphylococcus aureus</i> , <i>Candida albicans</i>

**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  $\geq 10$  years. Overall, Viridians 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 Viridians group of *Streptococcus* is the leading microbe to form the commensal flora of throat specially after 10 years. Colonization of Methicillin Resistant *Staphylococcus aureus*  $\geq 10$  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 be performed.

### References

- [1]. Sherwood, Linda; Willey, Joanne; Woolverton, Christopher (2013). Prescott's Microbiology (9th ed.). New York: McGraw Hill. pp. 713–721.
- [2]. Cui L, Morris A, Ghedin E (July 2013). "The human mycobiome in health and disease". *Genome Med* **5** (7): 63.
- [3]. Rogers A H (editor). (2008). *Molecular Oral Microbiology*. Caister Academic Press.
- [4]. Guarner F (2006) enteric flora in health and disease. *Digestion* 73: Suppl 15–12.
- [5]. CLSI. Performance Standards for Antimicrobial Susceptibility Testing; Twenty fourth Informational Supplement. CLSI document M100-S24. Wayne, PA: Clinical and Laboratory Standards Institute.
- [6]. Ringberg H, CathrinePetterssonA, Walder M, Hugo Johansson PJ. The throat: an important site for MRSA colonization. *Scand J Infect Dis.* 2006;38(10):888-93.
- [7]. NysS,Tjhie JH, Bartelds AI, Heijnen ML, Peeters MF, StobberinghEE. Erythromycin resistance in the commensal throat flora of patients visiting the general practitioner: a reservoir for resistance genes for potential pathogenic bacteria. *IntJAntimicrob Agents.*2005 Aug;26(2):133-7
- [8]. Bista M, Amatya RCM, Basnet P. Tonsillar microbial flora: A comparison of infected and noninfected tonsils. *Kathmandu University Medical Journal*(2006). Vol4; no.1: Issue13. 18-23.