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Antibiotic Susceptibility Patterns of Staphylococcus Aureus and Coagulase-Negative Staphylococci in Dental Professionals

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KEYWORDS
Methicillin resistant S aureus, MR-CoNS, VITEK 2 SYSTEM

ABSTRACT:

Introduction: The occurrence of multidrug-resistant S.aureus strains is a substantial problem in healthcare sector across the globe. The World Health Organization (WHO) highlights the widespread prevalence of MRSA, resistant to multiple antibiotics, across various healthcare settings globally. According to WHO and CDC to over 100,000 deaths in 2019. The objective of this study was to determine the frequency of methicillin-resistant *S. aureus* (MRSA) and methicillin-resistant Coagulase-negative Staphylococci (MRCoNS) among dental students and healthcare workers, as well as their patterns of drug resistance.

Materials and Methods: The present study involved 36 healthcare workers from Sree Balaji Dental College & Hospital, located in Chennai, India. Nasal swabs were collected from the participants for microbiological examination. identification and antimicrobial susceptibility testing done by the standard procedures.

Results: Out of all the patients, 25% were found to have *S. aureus* contaminants with a prevalence of MRSA at 22.2%. Inaddition36.1% of the participants were identified with CoNS, including 19.4% with MRCoNS. Compared to Male workers a higher incidence observed among females. The analysis of antibiotic resistance profiles observed different susceptibility patterns among the isolates, following Resistant was observed significantly against cefoxitin, gentamicin, and erythromycin.

Conclusion: This study emphasises the significance of monitoring and implementing steps to reduce the spread of antibiotic-resistant staphylococcal infections in healthcare facilities.

Introduction

S. aureus, a Gram-positive bacterium, is a leading cause of infections in both healthcare and community settings due to its resistance to multiple antibiotics. Methicillin-resistant S. *aureus* (MRSA) strains present a significant clinical challenge with limited treatment options, resulting in higher morbidity and mortality compared to methicillin-susceptible strains [(1)]. In 2019, MRSA alone caused over 100,000 deaths, according to Murray et al [(2)]. Recognized by the WHO and CDC, MRSA is a key target

Journal of Chemical Health Risks
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for combating bacterial virulence. The term "hospital-acquired" or "healthcare-associated MRSA" (HA-MRSA) is used to denote this strain, initially identified in healthcare settings [3].

In hospital settings, MRSA infections have become a major world health problem around the globe, it increases healthcare costs, prolonged hospital stays, and higher rates of treatment failure [4]. The percentage of incidence and prevalence of MRSA vary in different countries and healthcare facilities. In developed countries, such as the United States and European countries, MRSA is a significant cause of healthcare-associated infections, including surgical site infections, bloodstream infections, and pneumonia [5]. However, the burden of MRSA infections in developing countries, including India, is also on the rise last two decades, posing additional challenges to healthcare systems with limited resources [6].

In India, MRSA has been identified as a major cause of nosocomial infections, particularly in tertiary care hospitals and healthcare facilities with high patient turnover rates [7]. MRSA has been reported to have a prevalence ranging from 20% to 50% among clinical isolates in Indian hospitals. This underscores the imperative for robust infection control measures and surveillance programs to curb its dissemination [8].

Challenges associated with MRSA include its ability to colonize asymptomatically in the anterior nares of individuals, facilitating its transmission within healthcare settings and the community [9]. In addition, the emergence of multidrug-resistant MRSA strains further complicates treatment options, necessitating the use of alternative antibiotics and combination therapies [10]. The lack of rapid diagnostic methods for identifying MRSA strains in clinical laboratories delays appropriate treatment initiation and contributes to the spread of infections [11].

The clinical significance and public health implications of MRSA infections, there is a need for continuous surveillance and research efforts to understand the epidemiology, antimicrobial resistance patterns, and risk factors associated with MRSA colonization and infection. Based on the above rational data, the present study objective was designed to investigate the prevalence of MRSA colonization among dental students and healthcare workers in a tertiary care dental hospital in Chennai, India.

Our goal is to assess the prevalence of MRSA carriage in this population, intending to aid in the formulation of targeted infection control strategies and antimicrobial stewardship programs. This initiative aims to mitigate the spread of MRSA within healthcare settings.

Methods

Study Design:

The present study is designed as a cross-sectional study assessed the prevalence of S. aureus, including MRSA, MSSA, as well as coagulase-negative staphylococci (CoNS), among dental students and healthcare workers in a tertiary care dental hospital in Chennai, India.

Ethical Approval

The study protocol was reviewed and approved by the Institutional Ethical Committee of Sree Balaji Dental College & Hospital, Bharath Institute of Higher Education & Research, Chennai, India (Ref No: SBDCH/IEC/06/2021/1). Informed consent was obtained from all participants before sample collection.

Participant Selection

This study encompassed 36 dental students (17 males, 19 females) pursuing Bachelor of Dental Surgery (BDS)/CRRIs at Sree Balaji Dental College & Hospital. Selection criteria included the absence of respiratory tract infection, nasal surgery, skin and soft tissue infections, or rhinitis in the last 3 months, as well as no history of nasal medications or antimicrobial therapy within 2 months prior to sample collection. Immunocompromised individuals were excluded from the study.

Sample Collection: Anterior Nasal swabs were collected from volunteers using sterile cotton swabs. The swabs were then transported to the microbiology laboratory in nutrient broth supplemented with NaCl for further processing [12].

In the Laboratory nasal swabs were sub-cultured in to blood agar plates (5% sheep blood) and MacConkey agar [13]. Gram staining and standard biochemical tests, including O-F fermentation, catalase, oxidase, and coagulase production (slide & tube method), were performed to identify Staphylococcus species. Presumptive identification of *S. aureus* was done phenotypically by selective medium, mannitol salt agar (HiMedia laboratories Pvt Ltd, India). Yellow colonies on mannitol salt agar were scored as S. aureus, while pink

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colonies were scored as Staphylococcus species other than S. aureus.

Antibiotic Susceptibility Testing:

Antibiotic susceptibility testing was performed based on the Clinical and Laboratory Standards Institute (CLSI) standard guidelines [14]. The VITEK-2 automated system (bioMe´rieux) was used for further identification of staphylococcus species and determination of antibiotic sensitivity patterns. The prevalence data for S. aureus, encompassing MRSA and MSSA, along with CoNS, were analyzed following CLSI guidelines. The antibiotic resistance profiles of the isolates were reported as percentages of resistant (R), intermediate (I), and susceptible (S) strains.

Results

Among the 36 participants included in the study, Male Participants: Among the 20 male participants, 6 individuals (30%) were colonized with S. aureus, including 2 cases (10%) of MRSA and 4 cases (20%) of MSSA. Additionally, 2 male participants (10%) were colonized with MRCoNS, and 2 individuals (10%) with MSCoNS.Female Participants: Out of the 16 female participants, 3 individuals (18.75%) were colonized with MRSA, while 5 participants (31.25%) were colonized with MSSA. MRCoNS were found in 5 female participants (31.25%), and MSCoNS were detected in 4 individuals (25%).

A total of 9 participants (25%) were colonized with S. aureus, with 2 individuals (22.2%) harboring MRSA strains and 7 individuals (77.7%) carrying MSSA strains.Coagulase-negative Staphylococci (CoNS): CoNS were isolated from 13 participants (36.1%), with 7 individuals (19.4%) showing colonization with methicillin-resistant CoNS (MRCoNS) and 6 individuals (16.7%) harbouring methicillin-susceptible CoNS (MSCoNS) (Table-1).

Table 1: Gender-Based Distribution of Staphylococcus Colonization and Methicillin Resistance in Study Participants

Gender n=20	MRSA n=2	MSSA n=7	MR CoNS n=6	MS CoNS n=5
Male n=6	0	2	2	2
Female n=14	2	5	4	3

Antibiotic-resistant pattern

The antibiotic resistance profiles of the isolated Staphylococcus strains were comprehensively assessed across various antibiotics. In terms of beta-lactamase resistance, 44.4% of *S. aureus* strains demonstrated resistance, while all S. epidermidis isolates remained susceptible. Conversely, resistance to cefoxitin was evident in 22.2% of *S. aureus* strains, whereas all S. epidermidis isolates displayed resistance to this antibiotic. Notably, all *S. aureus* and S. epidermidis isolates exhibited susceptibility to benzylpenicillin. However, resistance to oxacillin was identified in 22.2% of *S. aureus* strains, while all S. epidermidis isolates remained susceptible. Concerningly, 33.3% of both *S. aureus* and S. epidermidis strains were resistant to gentamicin. Similarly, resistance to ciprofloxacin was prevalent among 55.5% of *S. aureus* strains and 66.6% of S. epidermidis isolates. Strikingly, none of the *S. aureus* strains were resistant to levofloxacin, whereas 66.6% of S. epidermidis isolates exhibited resistance. Furthermore, 44.4% of *S. aureus* strains were resistant to erythromycin, while 66.6% of S. epidermidis isolates displayed resistance. Intriguingly, none of the *S. aureus* strains exhibited resistance to clindamycin, whereas all S. epidermidis isolates remained susceptible. These findings underscore the variability in antibiotic susceptibility profiles among Staphylococcus strains and emphasize the importance of ongoing surveillance and antimicrobial stewardship efforts.

Journal of Chemical Health Risks
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Table-2: Antibiotic Resistance Profiles of Staphylococcus Species												
Antibiotics	***S. aureus n*=9 (%)**			**S. epidermidis n=9 (%)**			**S.warneri n=1 (%)**			**S. lentus n=1 (%)**		
	R	**I**	**S**	**R**	**I**	**S**	**R**	**I**	**S**	**R**	**I**	**S**
Beta-lactamase	4 (44.4)	0(0)	5 (55.5)	6 (66.6)	0(0)	3 (33.3)	1 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)
Cefoxitin	2 (22.2)	0(0)	7 (77.7)	4 (44.4)	0(0)	5 (55.5)	1(100)	0(0)	0(0)	1 (100)	0(0)	0(0)
Benzylpenicillin	9 (100)	0(0)	0(0)	9 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)
Oxacillin	2 (22.2)	0(0)	7 (77.7)	5 (55.5)	0(0)	4 (44.4)	1 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)
Gentamycin	3 (33.3)	0(0)	6 (66.6)	3 (33.3)	0(0)	6 (66.6)	0(0)	0(0)	1 (100)	1 (100)	0(0)	0(0)
Ciprofloxacin	5 (55.5)	0(0)	4 (44.4)	6 (66.6)	0(0)	3 (33.3)	0(0)	0(0)	1 (100)	1 (100)	0(0)	0(0)
Levofloxacin	0(0)	6 (66.6)	3 (33.3)	1 (11.1)	6 (66.6)	2 (22.2)	0(0)	0(0)	1 (100)	1 (100)	0(0)	0(0)
Erythromycin	4 (44.4)	0(0)	5 (55.5)	3 (33.3)	0(0)	6 (66.6)	0(0)	0(0)	1 (100)	1 (100)	0(0)	0(0)
Clindamycin	0(0)	0(0)	9 (100)	0(0)	0(0)	9 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)
Linezolid	0(0)	0(0)	9 (100)	1 (11.1)	0(0)	8 (88.8)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)
Teicoplanin	0(0)	0(0)	9 (100)	0(0)	0(0)	9 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)
Vancomycin	0(0)	0(0)	9 (100)	0(0)	0(0)	9 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)
Tetracycline	2 (22.2)	0(0)	7 (77.7)	2 (22.2)	0(0)	7 (77.7)	1 (100)	0(0)	0(0)	0(0)	0(0)	1 (100)
Tigecycline	0(0)	0(0)	9 (100)	0(0)	0(0)	9 (100)	0(0)	0(0)	1 (100)	0(0)	0(0)	1 (100)
Nitrofurantoin	0(0)	0(0)	9 (100)	0(0)	1 (11.1)	8 (88.8)	1 (100)	0(0)	0(0)	0(0)	0(0)	1 (100)
Rifampicin	0(0)	2(22.2)	7(77.7)	0(0)	2(22.2)	7(77.7)	0(0)	1 (100)	0(0)	0(0)	0(0)	1 (100)
Trimethoprim/ Sulfamethoxazole	7(77.7)	0(0)	2 (22.2)	5 (55.5)	0(0)	4 (44.4)	0(0)	0(0)	1(100)	1 (100)	0(0)	0(0)
R- Resistance; I-intermediate resistance; S-Sensitivity; N- number of isolates;												

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Table-3: Methicillin Resistance Profiles of Staphylococcus Species

ANTIBIOTIC RESISTANCE (n=20)	MRSA (n=2)			MSSA (n=7)			MRCONS (n=6)			MSCONS (n=5)		
Antibiotics	**R**	**I**	**S**	**R**	**I**	**S**	**R**	**I**	**S**	**R**	**I**	**S**
Beta-lactamase	**1**	**0**	**1**	**3**	0	**4**	**5**	0	**1**	**3**	0	**2**
Cefoxitin	**2**	0	0	0	0	**7**	**6**	0	0	0	0	**5**
Benzylpenicillin	**2**	0	0	**7**	0	0	**6**	0	0	**5**	0	
Oxacillin	**2**	0	0	**7**	0	0	**6**	0	0	**1**	0	**4**
Gentamycin	**2**	0	0	**1**	0	**6**	**4**	0	**2**	0	0	**5**
Ciprofloxacin	**1**	0	**1**	**4**	0	**3**	**4**	0	**2**	**3**	0	**2**
Levofloxacin		**1**	**1**	0	**5**	**2**	**1**	**3**	**2**	0	**4**	**1**
Erythromycin	**2**	0	0	**2**	0	**5**	**4**	0	**2**	0	0	**5**
Clindamycin	**2**	0	0	0	0	**7**	0	0	**6**	0	0	**5**
Linezolid	0	0	**2**	0	0	**7**	**1**	0	**5**	0	0	**5**
Teicoplanin	0	0	**2**	0	0	**7**	0	0	**6**	0	0	**5**
Vancomycin	0	0	**2**	0	0	**7**	0	0	**6**	0	0	**5**
Tetracycline	0	0	**2**	**2**	0	**5**	**2**	0	**4**	**1**	0	**4**
Tigecycline	0	0	**2**	0	0	**7**	0	0	**6**	0	0	**5**
Nitrofurantoin	0	0	**2**	0	0	**7**	0	**1**	**5**	0	0	**5**
Rifampicin	0	0	**2**	0	**2**	**5**	0	**2**	**4**	0	**1**	**4**
Trimethoprim/ Sulfamethoxazole	**2**	0	0	**5**	0	**2**	**4**	0	**2**	**2**	0	**3**

R- Resistance; I-intermediate resistance; S-Sensitivity; N- number of isolates;

The resistance profiles of other antibiotics, including linezolid, teicoplanin, vancomycin, tetracycline, tigecycline, nitrofurantoin, rifampicin, and trimethoprim/sulfamethoxazole, were also analyzed and will be presented in detail in the manuscript.

Discussion

Gender-based distribution notable differences in colonisation rates among male and female participants were noted, Among the male participants, there was a higher rate of colonisation by S. aureus, with 3% of persons being colonised. This includes both MRSA and MSSA strains. Furthermore, MRCoNS and MSCoNS were identified in 1% of male subjects individually. Among females, while the total rate of colonisation was slightly lower, a greater percentage of individuals were colonised with MRSA (18.75%) compared to males. MSSA, MRCoNS, and MSCoNS were also found in female participants, with various percentage of prevalence, The findings indicate possible gender-specific variations in Staphylococcus colonisation patterns, which could not impact infection management provide significant results for antimicrobial treatment.

The resistance patterns of Staphylococcus strains to various antimicrobials underscore the presence of antimicrobial resistance in Staphylococcus infections. Therefore, a comprehensive evaluation is necessary, revealing varying levels of resistance to multiple categories of antibiotics among both S. aureus and CoNS strains. Significantly, a considerable number of *S. aureus*

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strains exhibited resistance to beta-lactamase and cefoxitin, underscoring the difficulty in treating infections caused by these germs. All the S. epidermidis isolates were remained sensitive to tested drugs. Nevertheless, a significant prevalence of resistance to gentamicin and ciprofloxacin was observed in both S. aureus and S. epidermidis strains, indicating a widespread resistance pattern across various Staphylococcus species. Significantly, all of the *S. aureus* strains exhibited susceptibility to levofloxacin, indicating potential variations in resistance profiles among fluoroquinolones. In the same vein, whereas a significant percentage of *S. aureus* bacteria displayed resistance to erythromycin, none demonstrated resistance to clindamycin. The results emphasise the differences in antibiotic sensitivity patterns among different types of Staphylococcus bacteria. These findings emphasize the importance of ongoing surveillance and prudent utilization of antimicrobial drugs to curb the dissemination of antimicrobial resistance.

The results of our investigation are consistent with the worldwide pattern of rising antimicrobial resistance in Staphylococcus strains, as demonstrated by prior research. Alarjani and Skalicky et al [(15)]., examined the capacity of *S. aureus* strains isolated from hospital wastewater to form biofilms and their profiles of resistance to antimicrobial agents, demonstrating significant rates of biofilm formation and resistance to several antibiotics. Similarly, Silva-de-Jesus et al [(16)]., emphasised the significance of *S. aureus* biofilms in spreading antibiotic resistance across the meat production chain. They stressed the importance of implementing appropriate control measures to reduce this risk. Tummanapalli and Willcox et al [(17)]., also addressed the rise of antibiotic-resistant ocular bacteria, highlighting the immediate requirement for innovative therapeutic strategies, such as antimicrobial peptides, to effectively treat ocular infections. Present study offers important findings regarding the distribution of Staphylococcus strains based on gender and their antibiotic resistance profiles. This emphasises the necessity for customised infection control measures and efforts to promote responsible use of antimicrobials in order to combat the increasing problem of antimicrobial resistance in Staphylococcus infections.

Conclusion:

The study explores the prevalence of Staphylococcus colonisation and antibiotic resistance among dentistry students and staff in a Chennai, India, dental institution. It reveals gender disparities in colonisation rates, with males carrying more Staphylococcus strains. The study also reveals complex patterns of resistance, particularly in beta-lactamase, cefoxitin, gentamicin, and ciprofloxacin. Despite a high prevalence of erythromycin resistance in *S. aureus* strains, no resistance was observed to clindamycin, suggesting the need for alternative treatment options. The findings underscore the need for tailored infection control measures and antimicrobial stewardship programmes to combat antibiotic resistance in Staphylococcus infections.

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No competing interests

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Journal of Chemical Health Risks

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