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*Original Article*

# Prevalence of PVL and TSST-1 genes in nasal *Staphylococcus aureus* carriage among healthcare workers in a tertiary hospital

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## Abstract

Introduction: *Staphylococcus aureus* is an important pathogen associated with nosocomial and community-acquired infections. The main reservoirs of *S. aureus*/MRSA in hospitals are the colonized asymptomatic healthcare workers (HCWs) and patients. The aim of this study was to investigate the prevalence of MSSA and MRSA nasal carriage and their association with *pvl* and *tsst1* genes among HCWs.

Methodology: A cross-sectional study was performed. A total of 230 HCWs and 200 controls were screened for nasal carriage of *S. aureus.* All isolates were identified by conventional microbiological methods and confirmed by Vitek. Antimicrobial susceptibility was tested using disk-diffusion and MIC method. PCR was used to detect the *mecA*, *pvl* and *tsst1* genes.

Results: *S. aureus* nasal colonization was significantly higher ($p < 0.0001$) among HCWs, 23% (53/230) compared to the control 0.5% (1/200). Prevalence of MRSA was 9.6% (22/230) among HCWs. All isolates were susceptible to vancomycin and linezolid. Highest resistance was observed with ciprofloxacin and erythromycin among both - MSSAand MRSA. One MSSA isolated showed high-level mupirocin resistance (MIC > 1024 µg/mL). PVL and TSST-1genes were detected 7.4% and 0.8% of HCWs, respectively, with higher prevalence in MRSA isolates.

Conclusions: A high rate of *S. aureus*/MRSA carriage among HCWs was observed . The presence of PVL and TSST-1 raises concern due to poor infection control compliance. Periodic screening and improved infection prevention protocols are recommended.

**Key words:** *Staphylococcus aureus*; MRSA; *pvl*; *tsst1*; healthcare workers.

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## Introduction

*Staphylococcus aureus* is one of the most well-known pathogens associated with nosocomial as well as community acquired infections [1]. *S. aureus* causes various infections, such as skin and soft-tissue infections, endocarditis, toxic shock syndrome and food poisoning. *S. aureus* is a member of commensal microflora and anterior nares, rectum, perineum, axillae, vagina, hands are frequently colonized for varying time periods, however the main reservoir being the anterior nares [2-4]. The main sources of *S. aureus* in the hospital environment are the colonized asymptomatic health care workers and patients and they serve as reservoirs or vectors for *S. aureus*/MRSA [5]. Factors which contribute to dissemination in the healthcare facilities include overcrowding, contact with patients and breach in infection control protocols.

Since the introduction of β-lactam antibiotics, the spread of methicillin-resistant *S. aureus* (MRSA) has increased globally. Resistance to β-lactam antibiotics (as in MRSA) is due to the acquisition of the *mecA* gene. *mecA* gene encodes an altered penicillin-binding protein (PBP), PBP2A/PBP2B, which has reduced affinity for β-lactam antibiotics . Infections with MRSA are associated with limited therapeutic options like vancomycin and also associated with increase length of hospital stay, morbidity, mortality in patients and cost of treatment [6,7].

Several virulence factors such as toxins, enzymes and adhesion factors are involved in the unique pathogenicity of *S. aureus*. Toxins produced by *S. aureus* include Panton–Valentine leukocidin (PVL), hemolysin, toxic shock syndrome toxin-1 (TSST-1), exfoliation toxin, and staphylococcal enterotoxin [7]. PVL is a pore-forming leukotoxin, encoded by the *pvl* gene, that has the ability to target and kill host leukocytes by perforating the plasma membrane along with intracellular organelle membranes. However, another toxin known as TSST-1, encoded by the *tsst1* gene, is also produced by *S. aureus* strains, and its expression is associated with life-threatening acute toxic shock syndrome (TSS), with rash, fever, and

multi-organ dysfunction [8].

Few studies have investigated the nasal carriage rates of MSSA/MRSA and prevalence of *pvl* and *tsst1* among HCWs and control. Studies on *S. aureus* nasal carriage among HCWs in India have reported MRSA prevalence between 1.8% and 42% [9,10]. However, data regarding the prevalence of *pvl* and *tsst1* genes in nasal carriage *S. aureus* isolates in HCWs in India is unavailable. The aim of the current study was to determine the prevalence of MSSA and MRSA nasal carriage among HCWs and controls, along with evaluating their association with *pvl* and *tsst1* gene as well as establishing the antimicrobial resistance profile.

## Methodology

*Study setting*

The present study was conducted in Department of Microbiology, VMMC and Safdarjung Hospital, New Delhi.

*Participants and specimens*

A total of 230 healthcare workers (HCWs) (130 doctors and 100 nurses) from various clinical departments and 200 newly inducted medical students (not exposed to patients) represented the control group were screened for nasal carriage of *S. aureus* after informed written consent was received. HCW with working duration of less than 6 months in the current hospital, hospitalization within last 6 months or any antibiotic consumption within last 1 week were excluded from the study. The questionnaire included details regarding demographic data, risk factors and area of posting (clinical and laboratory) of HCWs were recorded. Two nasal swabs were collected using sterile cotton swab from both anterior nares. The specimens were processed within 2 hours of collection after transport at room temperature. HCWs and pre-clinical medical students who were hospitalized within the last 6 months, had received antibiotics in the previous week and were not directly involved in patient care (non-clinical departments) were excluded.

*Specimen collection*

Sterile cotton swabs pre-wetted with sterile trypticase soya broth (HiMedia Laboratories, Mumbai, Maharashtra, India) were rotated against both anterior nares of each participant. Swabs were inserted into a tube of Amie's transport media with charcoal (HiMedia Laboratories) and transported to the microbiology laboratory at Vardhman Mahavir Medical College (VMMC), Delhi.

*Isolation and identification*

Swabs were cultured on 5% sheep blood agar and 7.5% mannitol salt agar (MSA) and plates were incubated overnight at $37^0$C in aerobic condition. Presumptive identification of *S. aureus* was done by standard phenotypic methods consisting of β-hemolysis, gram staining, catalase test, coagulase test and deoxyribonuclease test. Final identification was done by Vitek 2 compact (Biomerieux India).

*Detection of methicillin resistance*

Phenotypic detection of MRSA was done by Cefoxitin (30 µg) and Oxacillin (1 µg) discs. Final confirmation of methicillin-resistant *S. aureus* (MRSA) was done by the amplification of *mecA* gene.

*Antimicrobial susceptibility testing*

Antimicrobial susceptibility testing was performed by Kirby–Bauer disk diffusion method for penicillin (10 µg), cefoxitin (30 µg), erythromycin (15 µg), clindamycin (2 µg), gentamicin (30 µg), ciprofloxacin (5 µg), linezolid (30 µg) and MIC of vancomycin and mupirocin were determined by E-test (Liofilchem diagnostics, Italy). All disks were procured from HiMedia Ltd (India). Breakpoints for sensitive and resistant were defined as per CLSI guidelines (Clinical Laboratory Standards Institute, USA, 2017). *S. aureus* ATCC 29213 was used as control strain.

*DNA extraction and PCR for detection of mecA, pvl and tsst1 genes*

DNA was extracted by boiling preparation [11]. PCR was performed for molecular confirmation of MRSA by amplifying *mecA* gene and for the detection of *pvl* and *tsst1* genes. Sequences of primers, target genes and amplicon size are given in Table 1. Primers were procured from Eurofins, India. PCR was performed in a 25 µl volume reaction by using template

**Table 1.** Details of primer sequences with their amplicon size used in the study.

| Primer | Target | Sequence (5′–3′) | PCR product (bp) | Reference |
|---|---|---|---|---|
| MecA P4 | *mecA* | TCCAGATTACAACTTCACCAGG | 162 | [8] |
| MecA P7 | *mecA* | CCACTTCATATCTTCTAACG | 162 | [8] |
| PVL-F | *lukS-PV* | GCTGCACAAAACTTCTTGGAATAT | 85 | [8] |
| PVL-R | *lukS-PV* | AGGACACCAATAAATTCTGGATTG | 85 | [8] |
| GTSST-1-1-1R-1 | *tsst1* | ACCCCTGTTCCCTTATCATC | 326 | [12] |
| GTSST-1-1-1R-2 | *tsst1* | TTTTCAGTATTTGTAACGCC | 326 | [12] |

DNA, 1× PCR buffer, 0.2 µM of forward and reverse primers, 200 µM of each deoxy nucleoside triphosphate (dNTP), 1.5 mM $MgCl_2$ and 1U Taq DNA Polymerase. Amplification was done in Thermal Cycler (Eppendorf Mastercycler EPS thermo-module, Hamburg, Germany).

The detection of *mecA* gene was considered the gold standard for methicillin resistance.

*Statistical analysis*

All data was entered in WHONET software for analysis of susceptibility profile and MIC. Proportions of categorical variables were tested using Fischer's Exact test. All data was analysed using SPSS and values of significance were calculated by applying Pearson's $\chi^2$ test.

*Ethics statement*

The study was approved by the institutional ethics committee with the consent letter no. IEC/VMMC/SJH/thesis/October/2016. The ethical committee provided the consent on principles of respect for individuals, the right to make informed decisions in accordance with the declaration of Helsinki.

## Results

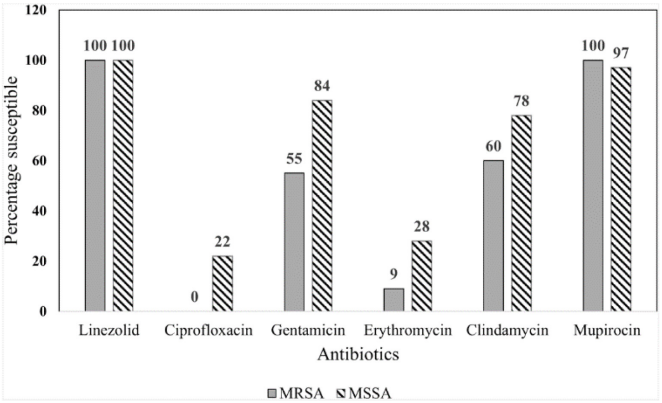
*Demographic data of study population*

A total of 230 HCW were screened for nasal carriage of *S. aureus* and the control group included 200 newly inducted medical students. Among 230 HCW, 130 (56.5%) were doctors and 100 (43.5%) were nurses. Age of HCWs ranged between 21–60 years with mean age of 34 years. The age of control group ranged between 18–24 years with mean age of 19.7 years. Male and female ratio among HCW and the control group was 1:1.32 and 1.4:1, respectively. The majority of HCWs screened were from the department of medicine (34%) followed by paediatrics (27%), critical care (26%) and surgery (13%).

*Screening for MRSA*

For the phenotypic screening of MRSA cefoxitin disk was used, and 22 *S. aureus* were identified as MRSA. All 22 MRSA isolates were genotypically screened by PCR for the *mecA* gene and the *mecA* gene was detected in all of them. There was 100% correlation between phenotypic and genotypic screening of MRSA isolates.

**Figure 1.** Antibiotic susceptibility profile of MRSA (n = 22) and MSSA (n = 32) isolates.




*Prevalence of MRSA and MSSA*

Prevalence of *S. aureus* among HCWs and the control group was 23% (53/230) and 0.5% (1/200), respectively. *S. aureus* colonisation was highest among HCWs from department of paediatrics (29.5%, 18/61), followed by medicine (26.5%, 21/79), critical care (20.3%, 12/59), surgery department (6.4%, 2/31). Among 53 *S. aureus* isolated from HCWs, 22 (41.5%) were MRSA and 31 (58.4%) MSSA. Only one *S. aureus* was isolated from the control group as MSSA. The results are given in Table 2.

*Antimicrobial susceptibility profile of S. aureus isolates*

All 54 S. aureus isolates from HCWs (n = 53) and control group (n = 1) were tested for antibiotic susceptibility against penicillin, linezolid, ciprofloxacin, gentamicin, erythromycin and clindamycin. All MSSA and MRSA isolates were resistant to penicillin and susceptible to vancomycin and linezolid. Resistance to ciprofloxacin was high in both MRSA (100%) and MSSA (78%). Resistance to erythromycin and clindamycin was higher among

**Table 2.** Prevalence of MSSA and MRSA among HCWs (doctors and nurses) and controls (medical students).

| Study population | No. screened | *S. aureus* n (%) | MSSA n (%) | MRSA n (%) |
|---|---|---|---|---|
| **Doctors** | | | | |
| Resident | 116 | 28 (24) | 18 (15.5) | 10 (8.62) |
| Faculty | 8 | 4 (50) | 3 (37.5) | 1 (12.5) |
| Interns | 6 | 3 (50) | 1 (16.6) | 2 (33.3) |
| **Nurses** | | | | |
| Nursing Officer | 100 | 18 (18) | 9 (9) | 9 (9) |
| **Total HCWs** | **230** | **53 (23)** | **31 (13.5)** | **22 (9.6)** |
| **Control group: MBBS 1st Professional** | **200** | **1 (0.5)** | **1 (0.5)** | **0** |

MRSA isolates (91% and 40%, respectively) in comparison to MSSA (72% and 22%, respectively). It was observed that resistance to ciprofloxacin (p = 0.0001), erythromycin (p = 0.0003) and clindamycin (p = 0.0012) was significantly high in MRSA. All isolates were susceptible to vancomycin with MIC range 0.19–1.5 µg/mL. The majority of MRSA and MSSA were sensitive to mupirocin with MIC of 0.064 µg/mL. Only one isolate of MSSA showed high-level resistance to mupirocin with MIC of > 1024 µg/mL. Data are given in Figure 1.

*Prevalence of pvl and tsst1 genes*

Overall, the pvl gene was more frequently detected among MRSA (36.4%, 8/22) in comparison to MSSA (22.5%, 7/31) isolates. Highest prevalence of the pvl gene was observed from HCWs in the department of paediatrics (11.4%, 7/61), followed by critical care (8.5%, 5/59), surgery (3.2%, 1/31) and lowest in medicine (2.5%, 2/79). The tsst1 gene was detected in 2 (9%) isolates, both of which were MRSA. An equal number of tsst1 gene was observed from paediatrics (n = 1) and medicine department (n = 1). The difference in prevalence of pvl and tsst1 among MRSA and MSSA was not statistically significant (p = 0.354 and 0.161, respectively). Details are given in Table 3.

## Discussion

HCWs asymptomatically colonized with *S. aureus*/MRSA are the major source of cross-transmission of *S. aureus*/MRSA in healthcare settings. HCWs can acquire *S. aureus*/MRSA from colonized patients and as well as from the community [5]. MRSA isolates with virulence factors such as *pvl* and *tsst1* have the ability to produce toxins encoded by these genes responsible for severe infections such as TSS and necrotic pneumonia with morbidity and mortality up to 75% [13]. HCWs colonized with MRSA and toxin-producing isolates can be a source of transmission within healthcare facilities [8-9], especially in immunocompromised patients. So, the screening of HCWs for MRSA and toxin-producing isolates is important for the implementation of infection-control policy, which will be useful to prevent transmission of MSSA and MRSA. A periodic decolonization strategy should be implemented for HCWs working in critical areas of the healthcare system. Data on the prevalence of *S. aureus*/MRSA and their association with virulence factors (*pvl* and *tsst1*) among HCWs is also sparse from India. Screening of *S. aureus*/MRSA and eradication should be part of infection-control policy, which helps to control transmission within the healthcare setting.

The present study was conducted to generate valuable data regarding the prevalence of *S. aureus*/MRSA nasal colonization and its association with *pvl* and *tsst1* among the HCWs. In the present study a total of 230 HCWs comprising of 130 doctors and 100 nurses, and 200 control were screened for *S. aureus* nasal colonization. The *S. aureus* nasal colonization rate among HCWs (23%, 53/230) was significantly high ($p < 0.0001$) in comparison to the control group. In the present study, among the HCWs, doctors had a higher prevalence of *S. aureus* nasal colonization (26.9%) compared to nurses (18%). A similar study from Nepal reported *S. aureus* nasal colonization was high among doctors (11.5%) [14], Similarly, in our study it was observed that the nasal colonization of *S. aureus*/MRSA was higher in doctors compared to nurses. In contrast, a study from Ethiopia found nasal colonization of *S. aureus*/MRSA was slightly higher in nurses (7.8%) than in doctors (7.7%) [15].

The prevalence of *S. aureus* nasal colonization is variable in India. Studies have reported colonization rates among HCWs ranging from 9 to 52%. In the present study *S. aureus* nasal colonization rate among HCWs was 23%, which is similar to study reported by Rutvi et al. (22%) [17]. However, a study conducted by Shibabaw et al. found a *S. aureus* colonization rate of 44.1% compared to 23% in the present study [18].

In the present study the MRSA colonization rate among HCWs was 9.6%. It was observed that the MRSA carriage rate was higher in comparison to developing and developed countries including India (6%), Germany (5.5%), Northern Ireland (7.5%), USA (6.6%), France (6.2%), Netherlands (0.4%), Portugal (4.8%), United Kingdom (2%) and the Republic of Ireland (4.8%) [19-20]. The carriage rate was lower compared to studies reported by Yemen (55.7%), Iran (32.8%), Nepal (21.9%) and the Gaza strip (25.5%) [21-24]. Studies in India have reported prevalence of MRSA nasal carriage between 1.33% and 30% [17,25-30]. Taken together these studies show that MRSA carriage rates among HCWs are highly variable. Part of

**Table 3.** Distribution of pvl and tsst1 genes among *S. aureus* isolates.

| Gene | *S. aureus* | MSSA | MRSA | *p* value |
|---|---|---|---|---|
| | n (53) (%) | n (31) (%) | n (22) (%) | |
| *pvl* | 15 (28.3) | 7 (22.5) | 8 (36.4) | 0.354 |
| *tsst1* | 2 (3.8) | 0 (0) | 2 (9) | 0.161 |

these variations may be attributed to methodological differences (in sample collection, sample size and laboratory techniques) along with other factors such as sanitation and infection-control practices.

To the best of our knowledge this is the first study in India investigating the prevalence of *pvl* and *tsst1* positive *S. aureus* nasal colonization among HCW. The prevalence of the *pvl* gene among *S. aureus* isolates was high at 28.3%. It was higher in MRSA isolates (36.4%) compared to MSSA isolates (22.5%). In addition, 3.9% (2/54) of *S. aureus* isolated from HCW were positive for *tsst1* and all were MRSA. These finding have important implications as a previous study by Tang et al. reported an outbreak of skin and soft-tissue infections caused by PVL-producing MRSA strains among children during vaccination and was proven to be transmitted from colonized HCWs [31]. Poor compliance with hand hygiene is an important factor that may facilitate spread of *S. aureus*/MRSA within hospitals. Presence of both *pvl* and *tsst1* among *S. aureus* and MRSA from colonized HCWs calls for strict infection-control practices in our hospital.

## Conclusions

Based on the observations in this study it can be concluded that there is a high rate of *S. aureus* and MRSA carriage among HCWs in Safdarjung hospital. Association of *pvl* and *tsst1* with nasal carriers represents a potential reservoir of highly virulent strains of *S. aureus* and MRSA. Guidelines should be formulated for periodic *S. aureus* and MRSA screening among HCWs, which will be useful for effective infection control and reducing, mortality and morbidity in the hospital. Hand hygiene compliance, periodic decolonization, judicious antimicrobial prescription use should be encouraged to control the colonization rate.

## Authors' contributions

RG: Conceived and designed the experiment, VR: manuscript writing and experimental work, AK: experimental work and provided data, AK: experimental work, MN: provided data. All authors have read and approved the manuscript.

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## Conflict of interest

No conflict of interest is declared.

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