**Original Article**

**Antibiotic Resistance Pattern and Frequency of meca Gene in Staphylococcus aureus Isolated from Shohada Hospital, Tabriz**

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**INTRODUCTION**

*Staphylococcus aureus* strains had become pandemic in 1950s after becoming resistant to penicillin [1]. Methicillin-resistance in *S. aureus* was first reported in 1961, 2 years after introduction of methicillin for the treatment of penicillin-resistant *Staphylococcal* infections [2, 3], but the specific gene responsible for methicillin-resistance (meca) has not been identified over the next 20 years. This gene encodes a low-affinity penicillin binding protein (PBP2a) [4]. The meca gene that is located in a mobile cassette element improves our understanding of methicillin-resistance biology and provides an additional tool for clarifying the evolutionary relationships among methicillin-resistant *Staphylococcus aureus* (MRSA) strains [5].

At present, antibiotic resistance is a global problem and distributed widely in pathogenic bacteria. Emergence of community-acquired MRSA (CA-MRSA) and hospital-acquired MRSA (HA-MRSA) isolates has become increasingly blurred [6]. One of the causes of the success of *S. aureus* strains is their high variability, occurring at different periods and places with different clonal types and antibiotic resistance pattern. Infections with these resistant bacteria lead to serious problems in the general population, especially young children, the elderly, and immunocompromised patients [7]. Furthermore, the MRSA strains carrying meca LGA251 (a novel meca homologue) are present in different host species other than human and cattle; therefore MRSA surveillance and control measures seem to be necessary [8]. Two recommendations are emerging for the control of MRSA. The first is to screen and treat carriers, and the second is universally treat everyone and run the theoretical risk of exacerbating bacterial resistance and changing the microbiome of both patient and facility [9]. This study was conducted first to evaluate the presence of meca gene and MRSA isolates collected from inpatients with *S. aureus* infection in the orthopedic ward of Shohada Hospital in Tabriz by phenotypic and genotypic methods, and second to compare the frequency of MRSA in a period of three years.

**MATERIAL AND METHODS**

This study was carried out in the department of Medical Microbiology, Tabriz branch, Islamic Azad University and Shohada Teaching Hospital, Tabriz, Iran. One hundred and eighty two *S. aureus* isolates obtained from different clinical (blood and wound) specimens, were studied to determine antimicrobial sensitivity patterns and presence of meca gene. Identification of the organism was made by growth in blood and wound) specimens, were studied to determine antimicrobial sensitivity patterns and presence of meca gene. Identification of the organism was made by growth in blood agar, colony morphology, Gram stain, and positive results for catalase, coagulase and DNase. Coagulase and DNase positive *staphylococci* were considered as *S. aureus*.

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Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method, according to Clinical and Laboratory Standards Institute (CLSI) recommendation for screening of MRSA, the test was performed with the same discs for all the samples, because most of the isolates were from wound. The used antibiotics included: cefazolin (30 μg), methicillin (5 μg), tetracycline (30 μg), cefoxitin (30 μg) (Himedia, India), and oxacillin (1 μg) (Padtan Teb, Iran) [10]. The \textit{S. aureus} ATCC 25923 was used as control strain for susceptibility testing.

To extract bacterial genomic DNA, an overnight culture in LB broth was harvested by centrifugation and processed according to the procedure of Kalia \textit{et al.} [11]. The extracted DNA was stored at -20°C in 50 μl TE buffer for further use.

Genotypic identification of the isolates was done by tracking the presence of \textit{nuc} gene. Forward primer sequence (5'-GCG ATT GAT GGT GAT ACG GTT 3') and reverse primer sequence (5'-AGC CAA GCC TTG ACG AAC TAA 3') were used for amplification of 279 bp region [12]. The condition of PCR for this gene was first described by Brakstad \textit{et al.} [12] and modified as follows: an initial denaturation at 95°C for 3 min, followed by 30 cycles of initial denaturation at 94°C for 60 s, annealing at 55°C for 30 s, extension at 72°C for 1.5 min, and a final extension at 72°C for 3.5 min.

For amplification of \textit{mecA} gene (553 bp), the following primers were used: forward primer (5'-AAA ATC GAT GGT AAA GGT GGC-3') and reverse primer (5'-AGT TCT GCA GGT ACC GGA TTT GC-3') [13]. Each reaction mixture contained 5 μl of master mix buffer (Cinnagen Inc.), 0.5 μl of forward primer (30 mM), 0.5 μl of reverse primer (20 mM), 1μl of template DNA, and 3 μl of ddH2O.

The PCR condition was described by Al- Ruaily \textit{et al.} [13], and modified as follows: an initial denaturation at 94°C for 3 min, followed by 40 cycles of denaturation at 94°C for 30 s, annealing at 58°C for 30 s, extension at 72°C for 1 min, and a final extension at 72°C for 5 min. The \textit{S. aureus} ATCC 29213 and \textit{S. aureus} ATCC 33591 strains were used as negative and positive controls for \textit{mecA} gene, respectively. The PCR products of \textit{nuc} and \textit{mecA} genes were then electrophoresed on 1.2% agarose gel, and amplified bands were analyzed in UV transilluminator system (Intas, German).

\section*{RESULTS}

CLSI (2013) [10] has recommended cefoxitin disc screening test to be used instead of methicillin disc diffusion test for detection of MRSA, because cefoxitin is a good inducer of \textit{mecA} gene. In our study, in disc diffusion method 176 (96.7%) isolates, 27 (14.8%) isolates, and 81 (44.5%) isolates were identified as MRSA by methicillin, oxacillin, and cefoxitin discs, respectively. During the period of study (2010-2012), 43.3%, 39.3%, and 50.8% of the isolates were identified as MRSA by cefoxitin disc diffusion method. Sixty-six (36.3%) isolates were resistant to tetracycline and 23 (12.6%) isolates were resistant to cefoxitin. In our isolates, the presence of \textit{mecA} gene was confirmed in 97 (53.3%) cases (Figure 1). Table 1 shows antibiotic resistance and presence of \textit{mecA} gene in our isolates. No significant differences were found among the isolates over the three-year period of the study. Twenty-five (25.8%) isolates of MRSA were resistant to either tetracycline or cefoxitin. Out of 85 methicillin sensitive \textit{S. aureus} (MSSA) isolates, 85 (100%) isolates was susceptible to cefoxitin, but 25 (29.41%) isolates showed resistance to tetracycline.

\section*{DISCUSSION}

\textit{S. aureus} as an opportunistic pathogen plays an important role in community- and hospital-acquired infections [14]. Increasing frequency of MRSA poses a serious and growing global problem [15]. According to CLSI recommendation, cefoxitin disc screening test is better than methicillin or oxacillin disc screening test for detection of methicillin-resistance [10].

\begin{figure}[h]
\centering
\includegraphics[width=0.8\textwidth]{fig1.png}
\caption{Results of PCR for \textit{mecA} gene in \textit{S. aureus} isolates. Lane 1, Size marker 1 Kb; lane 2, \textit{S. aureus} ATCC 25923 (negative control); lane3, \textit{S. aureus} ATCC 33591 (positive control); lanes 4-21, Clinical isolates positive for \textit{mecA} gene.}
\end{figure}
The main mechanism of methicillin-resistance in S. aureus is production of low affinity penicillin-binding proteins (PBPs), which is identified by the presence of mecA gene [4-5].

In this study, most of the isolates were collected from male orthopedic inpatients (126 of 182 isolates). There was no significant difference in isolation of pathogenic bacteria over the three-year period of study, which indicates that programs have been unsuccessful in controlling or reducing MRSA frequency. The most effective drug was cefazolin, since 100% of MSSA isolates and 67% of MRSA isolates were sensitive to this antibiotic. The frequency of MRSA in Shohada Hospital of Tabriz was determined to be 96.7%, 14.8%, 44.8%, and 53.3% by methicillin disc diffusion method, oxacillin disc diffusion method, cefoxitin disc screening test, and PCR for mecA gene, respectively. There was no significant difference between cefoxitin disc screening test and PCR for mecA gene. There was a significance difference between methicillin-resistance (96.7%) and PCR (53.3%) for mecA gene confirming the validity of this disc in routine sensitivity tests.

Our findings were similar to those of Moghadami et al. [16] in Shiraz hospitals, which reported 52.7% MRSA, meta-analysis and systematic review by Askari et al. [17] with 52.7%±4.7% MRSA, Azimian et al. [18] in Tehran hospitals with 47% MRSA, and Jarvis et al. [19] in the USA with 50% MRSA in health care facilities. Johnson’s study [20] showed that more than one-third of European countries share >25% proportion of hospital-acquired infections caused by MRSA.

It is strongly believed that the dissemination of MRSA clones must be controlled via screening patients by culture from different sites of body [21], isolation and barrier nursing by contact precautions, hand hygiene, and frequent cleaning and disinfection of environmental surfaces in this teaching hospital.

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CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest associated with this manuscript.

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Phenotypic and Genotypic Detection of MRSA


