

Prevalence of *mecA* Gene of Methicillin Resistant *Staphylococcus spp.* Isolated from Nosocomial Infections and Environmental Specimens in Sanandaj Hospitals, Kurdistan, Iran

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Received: 17 Apr 2015

Revised : 20 May 2015

Accepted: 2 Jun 2015

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DOI: 10.7508/rmm.2015.03.008

Abstract

Background: Methicillin resistant *Staphylococcus aureus* (MRSA) is one of the major agents for increasing number of serious hospital and community acquired infections. The aim of this study was to investigate the occurrence of the MRSA and *mecA* gene among nosocomial and environmental specimens in Kurdistan hospitals and determining the antibiotic resistance of the isolates.

Materials and Methods: A total of 264 clinical and environmental *Staphylococcus* was isolated from Kurdistan medical University Hospitals, in February 2011 to June 2012 Iran, and their susceptibility patterns to different antibiotics were determined. Furthermore, agar screen method was used to determine oxacillin resistant isolates. Finally, using PCR, the oxacillin resistant isolates were tested for the presence of *mecA* gene.

Results: In this study, from 88 (93.18%) *Staphylococcus aureus* isolates, 82 were found resistant to oxacillin using agar screen method and *mecA* gene was detected in 66 strains (75%). Our results showed that the agar screen method is more reliable in determination of MRSA strains compared to PCR.

Conclusion: In this research the studied MRSA were found with high prevalence and *mecA* was widespread in *S. aureus* isolates in Sanandaj.

Keywords: Nosocomial infections; Methicillin resistance; MRSA; *mecA*

Please cite this article as: Ramazanzadeh R, Salimizand H, Shahbazi B, Khonshah M, Narenji H. Prevalence of *mecA* Gene of Methicillin Resistant *Staphylococcus spp.* Isolated from Nosocomial Infections and Environmental Specimens in Sanandaj Hospitals, Kurdistan, Iran. Res Mol Med. 2015; 3 (3): 38-42

Introduction

Staphylococcus aureus (*S. aureus*) is one of the most frequently isolated bacteria from both hospital and the environment (1, 2). Clinical infections with this bacterium are most common in care units, nursing homes, and other chronic care facilities. Also, methicillin-resistant *S. aureus* (MRSA) as an emerging and important community-acquired pathogen due to resistance to all of the available β -lactam antibiotics (3, 4). Infections with MRSA are rapidly expanding throughout the world (5) soon after the first isolation of MRSA in the United Kingdom in 1961 (2). MRSA transmission in healthcare usually occurs via contaminated hands, garments, or equipment of healthcare laborer (7, 8). This kind of transmission has been a major factor

accounting for the raise in the incidence and prevalence of MRSA in acute care facilities (8). Barrier precautions are often included in recommended control measures for MRSA. For example, contact isolation in a single room has been recommended by the Centers for Disease Control (CDC) and prevention since 1983 for patients colonized or infected with MRSA (9). *mecA*, a particular penicillin-binding protein (PBP) gene called PBP2A with low affinity for methicillin and most other β -lactam drugs, is reported as the main cause of non-susceptibility to methicillin (10). However, *mecA* is also present in methicillin-resistant coagulase negative staphylococcus (MRCoNS) isolates, which could be detected both,

simultaneously, to rapidly distinguish MRSA from MRCoNS (11). Recent studies have revealed an increase in the worldwide prevalence of MRSA. European countries have maintained low rates of MRSA (12). Although, there are many reports from different cities of Iran, however, the average rate of MRSA in Iran hospitals is still unknown (6).

In this study we investigated the occurrence of MRSA and *mecA* gene among isolates from nosocomial infections and environmental specimens in Kurdistan hospitals and determined the antibiotic resistance of the isolates.

Materials and methods

Bacterial collection

A total of 264 isolates was collected from patients and healthy individuals. Of which, 156 staphylococci strains were isolated from clinical samples, 49 from the environment and 59 from the staff in wards of hospitals in Sanandaj. Characterization of isolates was confirmed by biochemical tests (catalase, coagulase, mannitol fermentation and DNase activity).

Antibiotic susceptibility testing

Sensitivity to antibiotics was determined by Kirby-Bauer methods with gentamicin (10µg), vancomycin (30µg), ciprofloxacin (5µg), and erythromycin (15µg) according to the guidelines of Clinical and Laboratory Standards Institute (CLSI) (13). Then, agar screening containing 6 µg/mL oxacillin was used

to find MRSA isolates (14).

Molecular assay of *mecA* gene

DNA from isolates was extracted by commercial kit (Cinnapure-DNA, CinnaGen, Iran). Uniplex PCR assays for *mecA* gene were performed in a reaction volume of 25 µl. Primers were 3'-AAA CTA CGG TAA CAT TGA TCG CAA C-5' as forward and 3'-CTT GTA CCC AAT TTT GAT CCA TTT-5' as reverse. To make the 25 µl reaction mixture we mixed 2X-PCR Master mix (CinnaGen, Iran) 12.5µl, DW 8.5µl, 1 µL of each primer and 2 µl of the DNA. The cycling profile for *mecA* was as follows: initial denaturation at 95 °C for 5 min, and 35 cycles of denaturation at 95 °C for 45s, annealing at 57.5 °C for 45s, extension at 72 °C for 1 min and final extension at 72 °C for 10 min. The expected amplicon were 321 bp.

Ethics Statement

Since bacteria were under experiments, there was no need to consider research ethics.

Results

A total of 264 strains from patients and healthy individuals (101 men, 104 women; 49.27% and 50.73%, respectively) were isolated. Sources and types of Staphylococcus isolates are mentioned in Table 1.

Table 1. Prevalence of Staphylococcus strains isolated from the samples.

Organism	Staff	Environmental	Clinical	Total (%)
<i>S. aureus</i> -n (%)	18 (36.73)	20 (33.9)	50 (32.05)	88 (33.3)
<i>S. epidermidis</i> - n (%)	31 (63.27)	38 (64.41)	101 (64.74)	170 (64.39)
<i>S. saprophyticus</i> -n (%)	0	1 (1.69)	5 (3.21)	6 (2.27)
Total - n (%)	49 (18.56)	59 (22.35)	156 (59.09)	264 (100)

Among the 264 isolates tested by disk diffusion method, vancomycin was the most effective antibiotic against *staphylococcus* species (69.7%). The frequency of resistance to ciprofloxacin was 43.94%, gentamicin 28.3% and erythromycin 9.09%. The data analysis showed that most of the strains were resistant to at least more than one antibiotic.

Screen agar for detection of MRSA strains

After culturing Staphylococcus strains on Muller Hinton agar (Merck, Germany) containing 4% NaCl and 6 mg / L oxacillin (Sigma, Germany), the isolates were incubated for 24 hours and the results were evaluated. In total, 6 (6.82%) isolates were

methicillin susceptible and 82 (93.18%) of the isolates were resistant to methicillin (Table2).

mecA amplification

PCR for *mecA* gene was performed (Figure1). Results revealed that 66 (75%) out of 88 *S. aureus* isolates harbored *mecA* gene.

Discussion

S. aureus, as the most frequently isolated bacteria in both hospital and environment, has reported as a causative agent of clinical infections especially in care units, nursing homes, and other chronic care facilities (1, 2). MRSA, as an emerging pathogen, due

to resistance to all of the available β -lactam antibiotics has become a barrier in treatment of staphylococcal infection (3, 4). Data of prevalence and the rate of infections occurred by *S. aureus* isolates can help in reducing the rate of mortality and morbidity related to this pathogen.

Table 2. Frequency of methicillin resistance in *S. aureus* and coagulase negative staphylococcus groups based on agar screen method.

Organisms	Frequency (%)
MRSA	82 (93.18)
MSSA	6 (6.82)
MRCONS	151 (85.79)
MSCONS	25 (14.21)

MRSA, Methicillin-resistant *S. aureus*; MSSA, Methicillin Sensitive *S. aureus*; MRCONS, Methicillin-resistant Coagulase-negative staphylococcus; MSCONS, Methicillin Sensitive Coagulase-negative staphylococcus.

Azimian et al. in 235 *S. aureus* isolated from clinical samples in Iran showed that 127 strains (54%) were methicillin susceptible and 108 strains (46%) showed resistance, also PCR for *mecA* gene showed that 110 strains (47%) had *mecA* gene (15). In another study, Japoni et al. that isolated 109 *S. aureus* from nosocomial infections and environmental specimens in Iran found vancomycin as the most effective antibiotic against all of the MRSA strains (16). A survey carried out in 300 U.S.A laboratories, between 1998 and 2005, about three million microbial isolates were recovered. In which, *S. aureus* was the most prevalent in inpatients (18.7%) and the second in outpatients (14.7%). Also, the frequency of MRSA was 59% in ICU patients, 55% in non-ICU patients and 48% in outpatients (17). These studies in concert with others showed that MRSA has become an important problem in hospitals worldwide and MRSA strains as the major nosocomial pathogens.

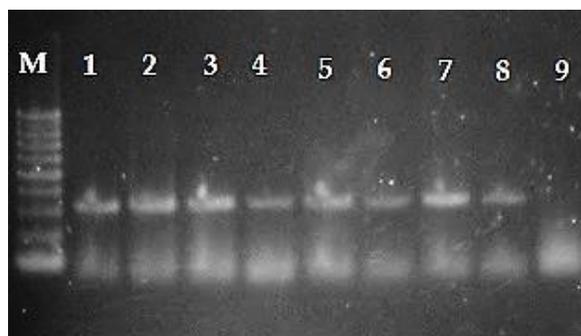


Figure 1. Product of PCR : Lane 1, 100 bp DNA marker; Lane 2 to 8 *mecA* gene 321 bp; Lane 9, Negative control.

Serious infections can be created by MRSA such as

bacteremia, osteomyelitis, and sepsis (14, 18). *S. aureus* is the major pathogen in both community and hospital acquired infections (19). Moreover, It has been a causative of outbreaks in hospitals especially those which are resistant to beta-lactamases and erythromycin (10, 15). In the present study, 93.18 % of *S. aureus* isolates were found methicillin resistant in screen agar method and 75% *mecA* carrier by PCR. It can be concluded that screen agar is more reliable than PCR to detect methicillin resistant isolates; however, for epidemiology studies *mecA* PCR followed by sequencing of this gene is required.

Various studies reported the prevalence of MRSA in different countries. For instance, Eftekhari et al. from Iran reported MRSA in 90.9% of isolates in screen agar method, although, 75% of isolates were MRSA in PCR method (20). Also, Najari Piraye et al. in 174 *S. aureus* that isolated from clinical samples in Iran showed that 47.7% of isolates were MRSA in screen agar method. moreover, PCR for *mecA* gene showed that 48.2% had *mecA* gene (21) which is in contrast with our findings. Perez et al. from USA reported 99.4% and 41.4% of isolates were MRSA in screen agar and PCR method, respectively (22). Our results are compatible with Eftekhari and Perez studies that indicate a wide distribution of *mecA* gene in the world, which has the potential of the risk of MRSA infection occurrence. In another study by Kumer et al. from India 45% of strains were resistant to methicillin (23). Nafisi et al. from Iran found 44% of the strains resistant to methicillin (24). Askaryan et al. showed that in 186 *S. aureus* isolated from clinical samples in Iran 17.2 % were MRSA in screen agar method, and PCR showed that 17.2% had *mecA* gene (25). The rise of methicillin resistance may be due to antibiotic-resistant genes spread in the community, hospitals and healthy staff (26). But the common thread among all of these studies, illustrate the variety of *mecA* gene in the risk of occurrence of resistant staph infections, Thus, health plans and control infection measures should be taken to prevent this problem.

Acknowledgments

This paper is a part of M.Sc. dissertation (submitted by H. Narenji). The authors wish to extend their gratitude to the Research Deputy of Kurdistan University of Medical Sciences for financial support.

Authors' contributions

RR and NH designed the project. ShB, KhM and NH did the experiments. NH wrote paper manuscript and SH revised the paper.

Support/Funding

This work was supported by Research deputy of

Kurdistan University of Medical Sciences.

Conflict of interest

The authors declare that there are no conflicts of interest.

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