Panton-valentine leukocidin, mecA, and SCCmecV in methicillin-resistant Staphylococcus aureus isolates sampled from hospitalized patients in Northern Iran

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Abstract

Introduction: Panton-Valentine Leukocidin (pvl) is associated with strains of Staphylococcus aureus that produce a high level of virulence. The aim of this study was to investigate the prevalence of pvl gene and its relationship with mecA and SCCmecV in isolated samples taken from hospitalized patients in northern Iran.

Materials and Methods: During a 6-month treatment period, a total of 92 clinical isolates of S. aureus were obtained. Resistance to methicillin was determined, and the prevalence of pvl gene was estimated through running a polymerase chain reaction (PCR) on chromosomal DNA. The pvl positive isolates were further analyzed for mecA and SCCmecV genes by PCR.

Results: In total, 18 isolates (19.56%) were shown to be positive in terms of their carrying the pvl gene, and from among them, 15 isolates were methicillin-resistant S. aureus (MRSA), 3 were methicillin-susceptible S. aureus, and 8 were positive for mecA gene. None of the pvl positive samples had the SCCmecV gene cassette.

Conclusions: The study found that the majority of pvl positive isolates were MRSA, and almost half of them had the mecA gene. Based on the results, it could be postulated that there is a significant relationship between these two variables; however, they were not correlated in regard to SCCmecV.

Key words: mecA, methicillin, methicillin-resistant Staphylococcus aureus, Panton-Valentine Leukocidin, SCCmec

INTRODUCTION

Staphylococcus aureus a Gram-positive cocci is similar in appearance to a bunch of grapes under a microscope and produces relatively big yellow colonies on culture medium. It is often isolated from the nose, mouth, and digestive tract. It is also responsible for most hospital-acquired infections as well as intravascular infection.[1] It is often isolated from cases of pneumonia, arthritis, endocarditis, osteomyelitis, and septicemia infections. Pathogenicity of S. aureus relates to a product of compounds, including viscous matrix molecules (such as mass maker factor), extracellular proteins (such as coagulase and hemolysin), enterotoxins, exfoliative toxins toxic shock syndrome toxins, and Panton-Valentine Leukocidin (pvl).[2] Panton-Valentine is one of the most important factors of virulence isolated by Panton and Valentine from a patient with furunculosis in 1932. The toxin consists of two protein parts of S (38 KDa) and F (32 KDa) controlled by LukS/pv and Lukf/pv, respectively. Its main target is the extracellular membrane of polymorphonuclear, monocytes, and macrophages. Depending on the level of toxin concentration, it leads to the opening of calcium channels as well as of necrosis and apoptosis in leukocytes.[3,4] pvl is associated with methicillin-resistant S. aureus (MRSA) strains; however, LukS/LukF-PV genes can be carried by strains of methicillin-susceptible S. aureus (MSSA) as well.[4] Strains of the pvl
positive *S. aureus* produce a high level of virulence which is often associated with skin abscesses and acute necrotic infection. The genes for MRSA and *SCCmec* are SCC chromosomal cassettes of a relatively large DNA fragment, which are integrated into the orf x gene within *S. aureus* chromosome. SCCs can code resistance to antibiotics and/or agents of virulence determinants. Considering that SCCs can be divided into *SCCmec* and non *SCCmec* groups, all MRSA strains contain *SCCmec*, which codes for the *mecA* genes. Meticillin-resistant strains produce a new type of penicillin-binding protein (PBP) known as PBP2, which has a low affinity with meticillin or any other β-lactam antibiotics. Accordingly, peptidoglycan synthesis continues inside the cell wall of bacteria despite the presence of these drugs. The *mecA* gene and its regulatory elements comprise the *mec* complex altogether. Until today, 11 *SCCmec* types have been identified that can be differentiated from each other by their carrying the *ccr* gene complex. In terms of size, *SCCmecI*, *SCCmecII*, and *SCCmecIII* are larger, and *SCCmecIV* and *SCCmecV* are smaller. In recent years, numerous studies have shown an increase in the variety of meticillin resistance and of *pvl* positive *S. aureus*. Considering its importance, the current study, then, sought to investigate the prevalence of the *pvl* gene and its relationship with *mecA* and *SCCmecV* in strains isolated from hospitalized patients in Northern Iran.

### MATERIALS AND METHODS

#### Bacterial isolates

From February to July of 2015, a total of 92 clinical *S. aureus* strains were isolated from wounds, blood, urine, splinter, and body fluids of hospitalized patients in Rasht, Northern Iran. Clinical specimens were initially inoculated in Mannitol Salt Agar and incubated at 37°C for 18–24 h. Colonies were examined for catalase production, coagulase, hemolysin, DNase, as well as mannitol fermentation.

#### Susceptibility testing and polymerase chain reaction (PCR)

An antibiotic susceptibility test was carried out by capitalizing on the disk diffusion method based on Clinical and Laboratory Standards Institute (CLSI) 2015 protocols. The antibiotic disks that were tested involved vancomycin (30 μg), oxacillin (1 μg), teicoplanin (30 μg), gentamicin (10 μg), tetracycline (30 μg), ciprofloxacin (5 μg), cefoxitin (30 μg), and linezolid (10 μg). In addition, a DNA extraction kit (Roche High Pure PCR Template Preparation Kit, Germany) was used to extract DNA from bacterial colonies. In this study, *S. aureus* (ATCC33591-*mecA* gene), *S. aureus* (ATCC49775-*pvl* gene), and *Staphylococcus epidermidis* (ATCC12228) considered as a methicillin resistance of positive, positive and negative controls, respectively. Using specific primers for the *pvl* gene, a PCR was used for detection of this gene in the genomic DNA of all *S. aureus* isolates. Those samples which were found to be positive for the *pvl* gene were subjected to additional PCR assays in an attempt to search for *mecA*, *LukS-PV-F*, *mecA*, and *SCCmecV* genes. The sequences of all primers used are summarized in Table 1. Primers were evaluated by the oligo analysis online software and NCBI base. The collected data were analyzed by the help of a Chi-square test and using SPSS-v16.

PCR was performed in a final 25 μl volume reaction containing PCR buffer (×10), magnesium chloride (2 mM), deoxynucleotide triphosphates (0.2 mM), forward and reverse primers (10 pmol/μl), template DNA (1 μl), Taq DNA polymerase (1.5 μl), and deionized water. The PCR method was performed in a thermal cycler (Bio-Rad, USA) according to the following program: Initial denaturation (95°C, 30 s), 32 cycles each composed of initial denaturation (95°C, 30 s), primer annealing (62°C, 30 s), and extension (72°C, 60 s). Positive control for *mecA*, *pvl*, *SCCmec V* genes, and negative control (distilled water) was also regarded in each series of the PCR reaction. The PCR product was subjected to electrophoresis in 1% agarose gel containing DNA safe stain and was documented using gel documentation (UVI TEC, Cambridge, UK).

### RESULTS

A total of 92 *S. aureus* were recovered from hospitalized patients in Rasht, Northern Iran. They were obtained from 20 urine specimens, 39 wounds, 17 blood samples, 9 chips, and 7 body fluid samples [Figure 1]. The antibiotic susceptibilities of these isolates are illustrated in Table 2.

As can be seen, the PCR assays suggest that 18 isolates (19.56%) were positive in terms of the existence of *pvl* gene, and from among these, 15 isolates (83.33%) were MRSA, 3 (16.66%) were MSSA, and 8 (8.69%) were in possession of *mecA*. Out of the 18 *pvl* positive isolates, 9 were obtained...

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5’–3’)</th>
<th>Size</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>mecA- F</td>
<td>GTGAAGATATACCAAGGTGATT</td>
<td>146bp</td>
<td>[13]</td>
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<tr>
<td>mecA- R</td>
<td>ATGCCGCTATAGTTGATGAAGGA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Luk pvL- F</td>
<td>TCATTAGGTTAAATGTCGACATGATCCA</td>
<td>433bp</td>
<td>[13]</td>
</tr>
<tr>
<td>Luk pvL- R</td>
<td>GGATCAAGTGTATTGAGGACAAAGC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SCCmec V- F</td>
<td>GAACTTGTACTAAATGAGGCG</td>
<td>325bp</td>
<td>[14]</td>
</tr>
<tr>
<td>SCCmec V- R</td>
<td>TGAAAGTTGTACCTTGACACC</td>
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<td></td>
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PCR: Polymerase chain reaction

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>Resistant</th>
<th>Intermediate</th>
<th>Sensitive</th>
</tr>
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<tbody>
<tr>
<td>Vancomycin</td>
<td>2 (2.17)</td>
<td>30 (32.6)</td>
<td>60 (65.21)</td>
</tr>
<tr>
<td>Oxacillin</td>
<td>43 (46.4)</td>
<td>25 (27.17)</td>
<td>25 (27.17)</td>
</tr>
<tr>
<td>Teicoplanin</td>
<td>12 (13.04)</td>
<td>36 (39.13)</td>
<td>44 (47.82)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>22 (23.91)</td>
<td>31 (33.69)</td>
<td>39 (42.39)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>21 (22.82)</td>
<td>45 (48.91)</td>
<td>26 (28.26)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>28 (30.43)</td>
<td>16 (17.39)</td>
<td>48 (52.17)</td>
</tr>
<tr>
<td>Cefoxitin</td>
<td>14 (15.21)</td>
<td>45 (48.91)</td>
<td>33 (35.86)</td>
</tr>
<tr>
<td>Linezolid</td>
<td>26 (28.26)</td>
<td>29 (31.52)</td>
<td>37 (40.21)</td>
</tr>
</tbody>
</table>

S. aureus: Staphylococcus aureus

from specimens, 3 from urine, 3 from body fluids, 2 from blood, and 1 from splinter. None of pvL- positive samples had the gene cassette. The PCR amplification of mecA and pvL genes has been shown in Figure 2. The results were analyzed by Fisher test with 95% confidence. The results revealed that there is no linear correlation among pvL, mecA, and SCCmecV genes (.8% Cramer test).

**DISCUSSION**

Antibiotic resistance has proved to be a growing problem in medical settings. The problem is especially menacing in regard to Staphylococci due to its inherent higher pharmaceutical resistance than other strains of bacteria. pvL is a virulence agent carried by a bacteriophage and can be transferred to other staphylococci. Strains of pvL positive S. aureus have a high level of virulence and are responsible for acute infections, including brain, bone and joint infections, and necrotizing pneumonia. Therefore, prompt diagnosis and eradication of pvL producing are of paramount importance. In a study conducted by Orrett and Land, of 243 strains of the S. aureus isolated from the hospital sources, 20.8% of them are MRSA. Cupane et al., 2015, reported that 75.0% of this S. aureus isolates possessed the pvL gene. Brown et al., 2012, checked 1055 isolates of S. aureus for LukSF/PV genes. In their experiment, 377 of these isolates (35.7%) were found to be positive for it. Miller et al., 2007, reported that 108 of their total 180 S. aureus isolates were MRSA. Molla-abasazdeh et al., 2013, reported that of their 100 S. aureus isolates, 18 (18.0%) were carriers of the pvL gene, and 94.4% of these were MRSA, and 5.6% MSSA. Darbi et al., 2012, who recovered S. aureus isolates from patients and hospital employers, reported rates of resistance to methicillin to be 90.0%. In line with the findings of the present study, most of pvL positive strains have been (up to 89.0%) MRSA, and only 11.0% of them have been MSSA. Its well-known that due to unnecessary consumption of antibiotics, genetics exchanges specifically resistance genes occurs through plasmids. Therefore, a partial resistance of S. aureus infectious treatment could be performed. In addition, ample evidence revealed that in 30–50% of S. aureus methicillin resistance process will take place by mecA gene. Of these isolates, 18 were harbored pvL genes all of which were collected from skin and soft tissue infections. In the present study, of 18 pvL positive isolates, 10 were isolated from wounds. In another study, of 119 isolates of S. aureus that were recovered from outpatients, 67.4% were MRSA. In 2014, of 131 MRSA isolates, which had been isolated from the nose and throat of healthy individuals in Mexico city, 21.4% were shown to be MRSA. Of them, 2.3% were harbored SCCmec V; however, this gene was not detected in this study. In a study conducted, in 2011, in Tehran, Iran, 7 MRSA isolates were identified in 154 nostril isolates of S. aureus. In this study, only one isolate had the pvL gene, and of 7 MRSA isolates, only one was positive for SCCmec V. Of 202 S. aureus isolates collected in Chinese hospitals, SCCmec and pvL gene were observed in 10 isolates, and three of these were harbored SCCmec V. In this study, of 93 isolates of S. aureus, 44 (47.82%) were found...
to be MRSA. 18 isolates (19.56%) were positive in terms of the pvl gene, and among these, 83.33% were MRSA, and three (16.66%) were MSSA. Eight cases (8.69%) were positive for mecA, and none of the pvl-positive samples had the SCCmecV gene cassette. In a study conducted in 2015, 30% of the total 200 S. aureus isolates had mecA gene in which 6% contained pvl gene, and interestingly, none of the mecA positive isolates were pvl positive.[20,46] Related to the existence of PBP2a protein, it is codified by the mecA gene and has a low compound tendency to β-lactams. It is placed in the chromosomal staphylococcal (SCCmec) cassette of the mecA gene.[21,47]

On the basis of these findings, sensitivity or resistance pattern in S. aureus to routine antibiotics treatment is different around the world, therefore, the control of antibiotics medication should have a critical role in resistance inhibition process. It should be noticed that production of toxins through S. aureus is an important issue in individual health, so, using an appropriate laboratory method should be considered to the recognition of infectious factor that could be beneficial strategy for rapid diagnosis in other species and toxins.

ACKNOWLEDGMENTS

We also thank Dr. Amir Monfaredan and personnel the Islamic Azad University of Rasht for their assistance and cooperation in the use of equipment.

REFERENCES


Source of Support: Nil. Conflict of Interest: None declared.