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Original Research Article

Prevalence and risk factors of panton valentine leukocidin-producing *Staphylococcus aureus* in Iran

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Abstract: *Staphylococcus aureus* (*S. aureus*) causes a wide spectrum of clinical disorders with pathogenic factors such as various toxins. The aims of this study were analysis of the prevalence of *pvl* gene among MSSA, MRSA, HA-MRSA, CA-MRSA and MSSA+MRSA groups in Iran. The prevalence of Panton-valentine leukocidin in Iran was searched from searching engines such as Google, Google Scholar, PubMed, Sciverse and so on. The terms PVL, MRSA, MSSA, Iran were investigated. Data was entered in Excel and Graph Pad Prism 6 for the analysis. Both children and adults were included in the study. Twenty-one previous publications on *pvl* gene prevalence were found. According to the results, the most prevalence of *pvl* gene was in MRSA, particularly in CA-MRSA group. However, the prevalence among HA-MRSA and MSSA groups was 17 and 25 percent respectively, showing a growing number of these strains encoding Panton valentine leukocidin toxin. The highest prevalence of *pvl* gene among previous publications was detected in CA-MRSA (74%), followed by 66.26% in HA-MRSA, 60% in HA+CA MRSA, 50% in MSSA+MRSA and 40.9% in MSSA+MRSA. On the other hand, the lowest prevalence was found in MSSA (3.3%) and 6% in MSSA+MRSA. Furthermore, previous hospitalization, carrier subjects, and age of them were possible risk factors in this case. The prevalence of *pvl* gene is significantly higher in MRSA than MSSA ($p<0.05$) and likewise higher in CA-MRSA than HA-MRSA strains. There is an increasing rate of presence of *pvl* gene in MSSA and HA-MRSA, showing transmission of related SAG prophage to methicillin susceptible and also healthcare associated strains. Previous hospitalization, carrier subjects, and age of them were possible risk factors in this case.

Keywords: Panton valentine leukocidin, Methicillin-susceptible *Staphylococcus aureus*, Iran.

INTRODUCTION

The pathogenicity of *S. aureus* is related to various staphylococcal surface components and extracellular proteins [1-3]. The frequent isolation of staphylococcal strains that produce leukocidal toxins from patients having deep skin and soft tissue infections, in particular cutaneous abscesses, furunculosis, severe necrotizing pneumonia, and also UTIs, supposes that the Panton-Valentine leukocidin (PVL) is a major virulence factor that has a key role in pathogenicity [4-6]. PVL-producing strains are associated with wound infections, accounting for 96 percent of the cases [7]. PVL has also been associated with harsh infections, such as pneumonia, purpura fulminans and osteomyelitis [8, 9]. PVL is carried by approximately 2% of *S. aureus* isolates. Two thirds of these are caused by meticillin sensitive strains of *S. aureus* (PVLMSSA) and the remaining one third are due to meticillin resistant strains (PVL-MRSA). PVL is mainly associated with community-associated MRSA (CA-MRSA) infections and distinguishable from nosocomial MRSA by a narrow drug resistance and carriage of the type IV staphylococcal chromosome cassette element (SCC*mec* type IV) [10-12]. The changing trend of MRSA epidemiology, exhibited the use of PVL gen detection as a marker of CA-MRSA isolates, in addition to non multi resistance pattern and SCC*mec* type IV or V [13, 14]. It has been recently revealed that both community and hospital associated strains contain the pvl gene, because of transmission of encoding SAG prophage to the healthcare settings[15]. At least eight PVL-encoding phages belonging to the *Siphoviridae* family Including 108PVL, PVL, SLT, Sa2958, Sa2MW, Sa2usa, Mut and 7247PVL, This *Siphoviridae*, comprises of Six functional modules lysogeny, DNA replication, packaging, head, tail, and lysis. PVL genes are located in the same situ, between the lysis module and the attachment site (*attP*) within the lysogeny genes. PVL horizontal transfer is performed through different bacteriophages.The major factor contributing to its high level occurrence in the wounds is the fact that the PVL toxin is a bi-component

cytotoxin that is preferentially linked to cutaneous abscesses, soft tissue infections, furuncles, cellulitis and severe necrotic skin infections [16-19]. The toxin subunits bind to cell membrane of leukocyte, causing proceeding of trans-membrane pore formation and subsequent cell lysis [20]. The *pvl* gene in carried by a prophage named as SGA group. Crowded population and poor hygiene are associated with increase of the risk of infection due to *S. aureus* strains (including MSSA, MRSA and pvl-producing strains) [21]. Data from Iran has not shown that if the prevalence of *pvl* gene is significantly different between MRSA and MSSA or between HA-MRSA and CA-MRSA strains or if there is a high prevalence among MSSA or healthcare associated strains. The aims of this study were meta-analysis of the prevalence of *pvl* gene among MSSA, MRSA, HA-MRSA, CA-MRSA and MSSA+MRSA groups in Iran.

MATERIALS AND METHODS

The prevalence of Panton-valentine leukocidin in Iran was searched from searching engines such as Google, Google Scholar, PubMed, Sciverse and so on. The terms PVL, MRSA, MSSA and Iran were investigated. Data was entered in Excel and Graph Pad Prism 6 for meta-analysis. Both children and adults (all the age ranges) were included in the study. Moreover, both hospital and community acquired MRSA strains and also VISA strains were included. Studies from veterinary sources were excluded.

RESULTS

Twenty-one previous publications on *pvl* gene prevalence were found. According to the results, the most prevalence of *pvl* gene was in MRSA, particularly in CA-MRSA group. However, the prevalence among HA-MRSA and MSSA groups was 17 and 25 percent respectively, showing a growing number of these strains encoding Panton valentine leukocidin toxin. The highest prevalence of *pvl* gene among previous publications was detected in CA-MRSA (74%), followed by 66.26% in CA-MRSA, 60% in HA+CA MRSA, 50% in MSSA+MRSA and 40.9% in MSSA+MRSA. On the other hand, the lowest prevalence was found in MSSA (3.3%) and 6% in MSSA+MRSA [22-36]. Some few studies showed that lower ages, prolonged hospitalization and contact with carriers maybe possible risk factors of pvl-producing strains of *S. aureus* [35, 37].

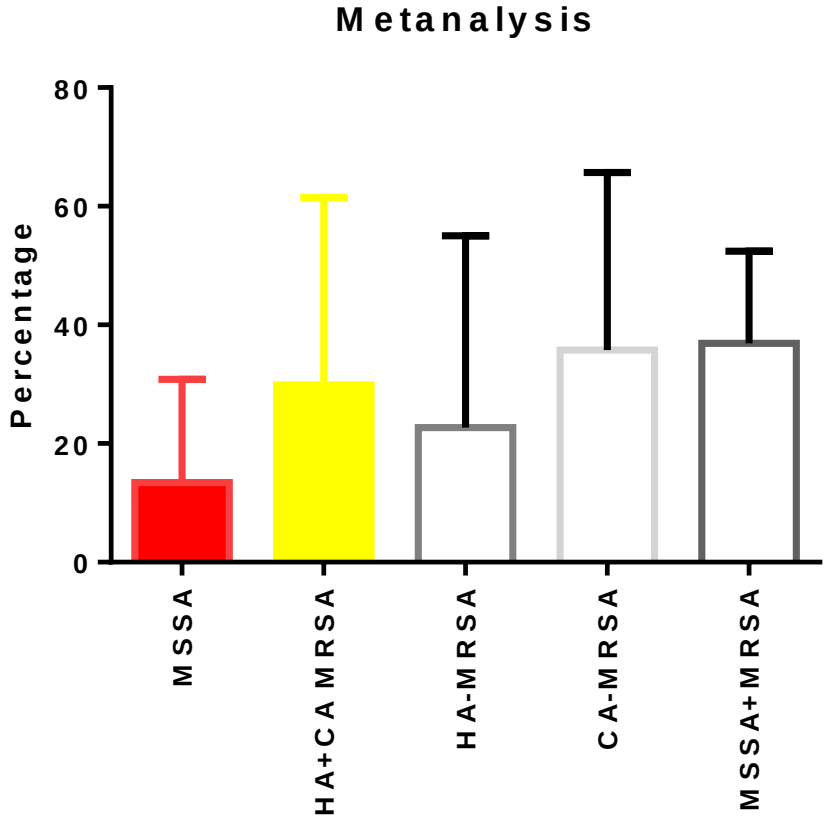

Fig-1: The prevalence of *pvl* gene among 5 various groups of MSSA, MRSA, HA-MRSA, CA-MRSA and MSSA+MRSA.

DISCUSSION

S. aureus causes a wide spectrum of infections in both healthcare and community. It causes severe infections in immune-compromised patients and children with various toxins; especially for PVL toxin. This toxin reportedly causes skin and soft tissue infections and pneumonia and several other clinical manifestations [38]. It is a concerning issue that PVL can be produced by MSSA and HA-MRSA strains. In the current study, twenty-one previous publications on *pvl* gene prevalence were found. According to the results, the most prevalence of *pvl* gene was in MRSA, particularly in CA-MRSA group. However, the prevalence among HA-MRSA and MSSA groups was 17 and 25 percent respectively, showing a growing number of these strains encoding Panton valentine leukocidin toxin. The highest prevalence of *pvl* gene among previous publications was detected in CA-MRSA (74%), followed by 66.26% in CA-MRSA, 60% in HA+CA MRSA, 50% in MSSA+MRSA and 40.9% in MSSA+MRSA. On the other hand, the lowest prevalence was found in MSSA (3.3%) and 6% in MSSA+MRSA [22-36]. Studies from other countries show that PVL toxin mainly is produced by CA-MRSA similar to that from Iran. However, similar to our country, recent investigations from several countries have shown that PVL is also produced by MSSA and HA-MRSA strains [15, 23, 39-41]. However, in Kilic's study, only 1.3% of S. aureus isolates were *pvl* positive [42]. It seems that crowded population and poor hygiene, carrier subjects, age and prolonged hospitalization are potential risk factors for infection acquisition with various strains of *S. aureus*.

CONCLUSION

The prevalence of *pvl* gene is significantly higher in MRSA than MSSA ($p<0.05$) and likewise higher in CA-MRSA than HA-MRSA strains in Iran. There is an increasing rate of presence of *pvl* gene in MSSA and HA-MRSA, showing transmission of related SAG prophage to methicillin susceptible and also healthcare associated strains. Following up the MSSA and HA-MRSA for *pvl* gene carriage is becoming a necessary procedure. Considering risk factors, surveillance, and control and management purposes although are in challenge, should be routinely considered and fulfilled for prevention of infection with these strains.

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