Frequency of Panton–Valentine Leukocidin Gene among Clinical Isolates of Methicillin-Resistant *Staphylococcus aureus* in Eastern Province of Saudi Arabia

Sir,

Staphylococcus aureus is a common bacterial pathogen of human beings. Methicillin-resistant *S. aureus* (MRSA) could be community acquired or health care acquired (CA-MRSA or HA-MRSA). CA-MRSA and HA-MRSA show different genetic, phenotypic, epidemiological, and clinical characteristics.[1] The resistance is due to mutation in *mecA* gene, which is located in a region called the *Staphylococcal cassette chromosome mec* (*SCCmec*). While CA-MRSA carries either *SCCmec* IV or V, the HA-MRSA have *SCCmec* I, II, or III. Panton–valentine leukocidin (PVL) is a cytotoxin produced by *S. aureus*. The significance of PVL in virulence of CA-MRSA is well established, especially in skin and soft tissue infections.[2] Of late, there has been a worldwide increase in the PVL harboring *S. aureus* clinical isolates. Further, there are increasing reports of CA-MRSA being isolated from health-care settings and HA-MRSA circulating in the community. Saudi Arabia has seen a hike in the number of MRSA infections in recent years.[3] We undertook this study to estimate the prevalence of PVL among MRSA clinical isolates in Al-Ahsa city of Saudi Arabia and to determine PVL distribution among HA-MRSA and CA-MRSA.

Seventy-two consecutive, non-repetitive MRSA isolates from King Fahad Hospital, Al-Ahsa, and King Faisal University Health Centre were analyzed. Isolates were labeled as CA-MRSA or HA-MRSA based on the Centers for Disease Control and Prevention criteria. Standard bacterial identification methods and phenotypic determination of methicillin resistance by cefoxitin susceptibility testing were performed. A duplex polymerase chain reaction (PCR) was done with two primer sets (*mecA* and *PVL*).[4]

Cefoxitin disc diffusion test and PCR confirmed 71 isolates as MRSA [Figure 1]. Forty (56.3%) were identified as CA-MRSA and the remaining as HA-MRSA (30/71, 43.7%). PVL gene was detected among 27/40 (67.5%) and 9/31 (29%) of CA-MRSA and HA-MRSA strains, respectively.

Studies from other Arabian Gulf countries have demonstrated CA-MRSA infections in health-care institutions. There seems to be a shift in the epidemiology of MRSA as some CA-MRSA clonal types are increasingly reported causing health-care-acquired infections.[5] We assume that a good proportion of PVL-positive HA-MRSA in our study could be either SCCmec type I–III or SCCmec types IV or V attributed as CA-MRSA hitherto, but increasingly reported from health-care institutions.

In conclusion, our study demonstrated that a considerable number of MRSA identified as hospital acquired also possessed PVL gene, highlighting the significance of changing epidemiology of MRSA. Further studies need to be done for complete molecular characterization of MRSA including *SCCmec* genotype, clonal complexes, and multi-locus strain typing.

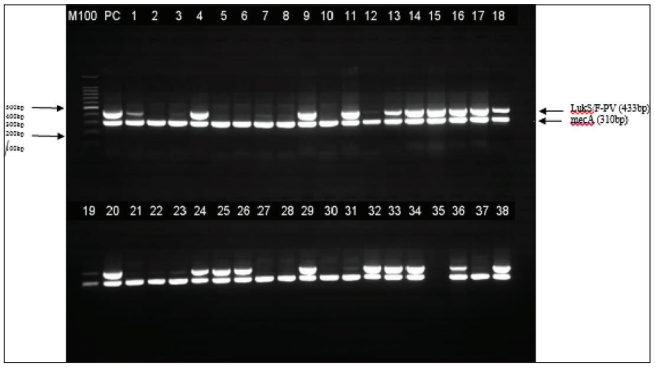

Figure 1: Gel electrophoresis photograph of duplex polymerase chain reaction

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Conflicts of interest

There are no conflicts of interest.

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