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Molecular Characterization and Antimicrobial Profile of Methicillin Resistant *Staphylococcus aureus* in Palestinian Regions

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Background: Methicillin-Resistant *Staphylococcus aureus* (MRSA) is a major cause of hospital-acquired and community-acquired infections. This study aimed to investigate the epidemiological and genetic diversity of clinical MRSA isolates in healthcare settings in Palestine, from 2015 to 2017.

Methods: All MRSA isolates from nine major hospitals in Palestine were collected. Each strain was characterized by: antibiotic susceptibility pattern, staphylococcal chromosomal cassette mec (SCC*mec*), *Staphylococcus aureus* protein A (*spa*) accessory gene regulator (*agr*) groups and a panel of toxin genes (including: Panton-Valentine Leukocidin (PVL), *arc*A, Toxic Shock Syndrome Toxin-1 (TSST-1) and Exfoliative Toxin A (ETA)), and genes that encode microbial surface components recognizing adhesive matrix molecules (MSCRAMMs): *bbp*, *eno, cna*, *ebpS*, *fib*, *fnbA*, *fnbB*, *clfA* and *clfB*.

Results: All the 112 isolates of MRSA were susceptible to Vancomycin. Resistance was observed to erythromycin, ciprofloxacin, clindamycin, gentamicin and trimethoprim sulfamethoxazole (SXT), 63.4%, 39.3%, 34.8%, 23.2% and 18.7., respectively. Of all the isolates, 32 isolates (28.6%) were MDR (i.e., were resistant to at least three different non-β-lactam antibiotic groups). The majority of the isolates were identified as SCC*mec* type IV (86.6%). Molecular typing identified 29 *spa* types representing 12 MLST clonal complexes (CC). The most prevalent spa types were t386 (CC01) (12.5%), spa t044 (CC80) (10.7%) and t008 (CC8) (10.7%). All four *agr* groups were present; *agr* group 1 and 3 were predominant (40.2%, 43.7%, respectively). PVL genes were detected in (29.5%) of all isolates, while *ArcA* genes were present in 18.8 % of all isolates and 23.2% had the TSST-1 toxin gene. The two most common spa types among TSST-1-positive isolates were the *spa* type t223 (CC22) and t021 (CC30). All *spa* type t991 was ETA positive (5.4%). In this study, USA300 clone (positive for PVL and *ArcA* genes) was found in 9 isolates (8.0%). None of the isolates harbored *bap.* Moreover, 92.8% isolates were positive for *eno,* 85.7% for *clfA* and *clfB*, 83.9% for *fnbA*, 66.9% for *ebpS*, 71.4% for *fib*, 48% for *can* and 29.5% for *fnbB*.

Conclusions: Our results provide insights into the epidemiology of MRSA strains in Palestine. We report a diversity of MRSA strains in hospitals in Palestine, with frequent SCC*mec*IV carriage and the genetic variations of adhesion genes require further investigation.

Keywords: MRSA, spa, SCCmec, PVL, ETA, TSST1, arcA, Biofilm

Biography:

Kifaya Azmi has completed her PhD from Charite University School of Medicine, Berlin. She is one of the staff members of Al-Quds University, faculty of medicine, Teaching biochemistry and molecular biology. Recently working on MRSA project, published more than 35 papers in reputed journals.

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