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Molecular Characterization of *S. aureus* Isolated from Renal Hemodialysis (HD) Patients from Saudi Arabia

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ABSTRACT

Staphylococcus aureus, including methicillin resistant *S. aureus* (MRSA) is the most common isolated pathogen in hospitals worldwide. The aim of present study was molecular characterization of *Staphylococcus aureus* isolated from renal hemodialysis (HD) patients from Ha'il region of Saudi Arabia. A total of 392 samples were screened from 204 HD patients for colonization of *S. aureus*. The isolated bacteria were identified by MALDI-TOF-MS. Antibiotic susceptibility testing was performed using Microscan. Among these isolates, 72 *S. aureus* (43% MRSA and 57% MSSA) were identified. The isolates were considerably resistant with varied profile to the antibiotics tested except being 100% susceptible to vancomycin, linezolid and teicoplanin. Of the isolates, 22.2% were positive for biofilm assay. Four representative MRSA isolates were selected and whole genome sequence analysis was performed using MiSeq. Two out of the 4 MRSA were found to be ST-1 and 2 were found to be ST-32. Among MRSA isolates, 25.8% were negative for *mecA* and all of them were negative for *mecC* gene. A high prevalence of MRSA in HD patients as well as high percentage of biofilm production in MRSA isolates from highlights the vital role for standardized surveillance along with validated molecular typing methods to evaluate the incidence of MRSA and accordingly to control its spread.

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