ABSTRACT

The aim of this study was to utilize molecular techniques for the development of rapid molecular methods to detect methicillin resistant *Staphylococcus aureus* (MRSA) and subsequently to study important antibiotic determinants and molecular characterize MRSA isolates from three different Arab countries. Sixty seven clinical MRSA isolates were collected. Seventeen from West Bank of Palestine, 25 from Jordan, and 25 from Iraq. Conventional oxacillin disc diffusion test and PCR-based hybridization assay (Geno Type MRSA Direct) were used for simultaneous identification and detection of methicillin resistance gene to enable rapid identification of MRSA. All sixty seven strains (100%), identified as methicillin resistant phenotypically by conventional oxacillin disc were also positive by Geno Type MRSA assay specific for the *mec*A gene.

The prevalence of oxacillin, penicillinG, erythromycin, clindamycin, ciprofloxacin, gentamicin, cefotaxime, fusidic acid, ceftazidime and sulfamethoxazole-trimethoprim resistance among MRSA isolates was above 82%. Resistance rates of MRSA to other antibiotics were as follows: 64.2% resistant to each of amikacin and imipenem, 13.4% to teicoplanin. Vancomycin-resistant isolates were not observed in this study. Resistance to oxacillin/ penicillinG/ erythromycin/ clindamycin/ ciprofloxacin/ gentamicin/ cefotaxime/ fusidic acid/ amikacin/ imipenem/ ceftazidime/ sulfamethoxazole-trimethoprim was the most common pattern of multiple resistance in the three participant countries.

Nucleotide comparison and maximum likelihood phylogenetic analysis revealed the existence of two main clusters of MRSA in these three countries: Cluster (I) comprised 18.2% (n=2) of the isolates, and contained one representative isolates from each of Jordan and Iraq. Cluster (II) comprised most of the strains 81.8% (n=9), and contained 5 isolates from Palestine, two isolates from Jordan and two from Iraq. Since the strain distribution in these two clusters is characteristic, it denotes the existence of two main clones.

Phylogenetic analysis showed that isolates of cluster II is identical to international strains that have the accession number X61307, AM407300,

U54636 and EF094528 belonging to France, Switzerland, Brazil and Australia, respectively.

These results suggest that cluster II strains are globally disseminated and often multi drug resistant, which poses a global imminent threat. Thus, further studies are needed for the surveillance of MRSA strains using a combination of molecular typing techniques, to relate our strains to international epidemic clones and to provide a much larger view of molecular epidemiology of MRSA isolates in the Arab world.