



Rapid molecular identification of hospital-acquired methicillin resistant *Staphylococcus aureus* (HA-MRSA) lineages

Abstract

Background: MRSA infection accounts for high percentage of all *S. aureus* infections in most healthcare facilities. Epidemiological typing is usually done to identify outbreaks or track local spread of strains, and this helps in infection control programmes. A restriction-modification test (RM test) is a rapid, simple and inexpensive method to classify HA-MRSA strains into their appropriate clonal lineage.

Objective(s): Phenotypic and genotypic identification of MRSA isolates from clinical specimens at Fayoum University Hospital (FUH). Detection of *mecA* and *pvl* genes by PCR and using RM test to classify HA-MRSA strains into their appropriate clonal lineage were also performed.

Methodology: Seventy non duplicated *S. aureus* isolates collected from various clinical specimens at FUH were screened for methicillin-resistance and antibiotic resistance profile. Duplex PCR reaction was done for *mecA* and *pvl* genes detection and three RM tests for detection of MRSA isolates clonal lineage were also performed.

Results: MRSA prevalence among clinical *S. aureus* isolates was 87.1%. 17.5% were *pvl*+. Five different lineages were detected (CC1, CC2, CC3, CC4 and CC5).

Clonal lineage CC4 was the predominant one. CC3/ST3 was not detected at all.

Eight isolates (9.0%) were negative for this test. *pvl* gene was detected in three different clonal lineages; CC2, CC4 and CC1 in variable proportions.

Conclusion: RM tests are simple, easy and inexpensive tests that are suitable for detection of clonal lineages of MRSA isolates at healthcare settings with limited resources. Effective infection control programmes are needed to control the rapidly spreading MRSA at Egyptian hospitals.