

MRSA Clinical Isolates Harboring mecC Gene Imply Zoonotic Transmission to Humans and Colonization by Biofilm Formation

ABSTRACT

This study was conducted for the molecular detection of the *mecA*, *mecC*, and *nuc* gene among MRSA and to investigate biofilm formation among the methicillin-resistant *Staphylococcus aureus* (MRSA) clinical isolates. A total of 208 different samples were collected and processed for phenotypic and genotypic identification of MRSA. All MRSA isolates were subjected to antibiotics sensitivity, cefoxitin disk diffusion test, and vancomycin minimum inhibitory concentration (MIC) E-test. The MRSA isolates were detected for the presence of *mecA*, *mecC*, and *nuc* genes. Congo red agar (CRA) method was used to assess the ability of isolates to form biofilms. The results of the study showed that the prevalence of MRSA was 48%. The MRSA isolates were highly resistant (100%) to penicillin, β lactamase inhibitors, cephalosporins, and macrolides. All the MRSA isolates were susceptible to vancomycin antibiotic drugs. Cefoxitin (30 μ g) disk diffusion test showed 100% sensitivity and specificity for the identification of MRSA phenotypically. A total of 100 MRSA clinical isolates were positive for the *mecA* and *nuc* gene. Only 3 MRSA isolates were positive for the *mecC* gene. Congo red agar method showed that 20 (20%) isolates formed moderate biofilm while 80 (80%) isolates were non-biofilm forming. Multi drugs resistant and *mecC* gene-positive MRSA isolates are rapidly emerging in Pakistan. Therefore, the *mecC* gene should be detected along with the *mecA* gene for the identification of MRSA clinical isolates. It also requires early identification of biofilm formation and necessary interventions for its effective treatment and control