
عنوان مقاله:

Prevalence of resistance and toxin genes in community-acquired and hospital-acquired methicillin-resistant Staphylococcus aureus clinical isolates

محل انتشار:

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خلاصه مقاله:

Objective(s): Methicillin-resistant Staphylococcus aureus (MRSA) is one of the major health hazards and became of greater public health concern since the emergence of community-acquired MRSA. This work aimed to study the prevalence of mecA, femA, femB, lukS-PV, lukF-PV (PVL), intI, and intII genes among community-acquired (CA) hospital-acquired (HA) MRSA to increase vigilance in the diagnosis and management of suspected infections. Materials and Methods: S. aureus isolates recovered from clinical samples were classified into community or hospital-acquired and tested for their antibiotic susceptibility against 19 antibiotics. All isolates were screened for mecA, femA, femB, lukS-PV, lukF-PV, intI, and intII genes. Statistical correlations were carried out.Results: Out of 338 S. aureus isolates, only 105 were MRSA and classified as 77 CA-MRSA and 28 HA-MRSA. mecA and femA genes were present in all HA-MRSA and CA-MRSA isolates. femB was found in all HA-MRSA and 93.5% of CA-MRSA isolates. PVL genes were detected in 28.6% HA-MRSA isolates and 92.2% CA-MRSA. intI gene was recovered from 60.7% HA-MRSA isolates and 37.7% CA-MRSA isolates while the intII gene recovered from only 10.7% HA-MRSA isolates and 6.5% CA-MRSA.Conclusion: The high prevalence of MRSA colonizing the groin, axilla, and nose may play a significant role in endogenous infection, re-infection, and also acts as a route for MRSA transmission. mecA and femA genes could be used as a sole and fast step for identification of MRSA, while PVL genes cannot be used as a sole .stable marker for CA-MRSA identification

کلمات کلیدی:

Community, fem, Hospital, Integron, mecA, MRSA

لینک ثابت مقاله در پایگاه سیویلیکا: