

Emergence of Vancomycin Resistant and Methcillin Resistant Staphylococcus aureus in Patients with Different Clinical Manifestations in Khartoum State, Sudan

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Abstract : Staphylococcus aureus (Staph. aureus), a major cause of potentially life-threatening infections acquired in healthcare and community settings, has developed resistance to most classes of antimicrobial agents as determined by the dramatic increase. The present study aimed to determine the prevalence of MRSA, and VRSA in patients with different clinical manifestations in Khartoum state. The study population (n, 426) were males and females with different age categories, suffering either from wound infections (105), ear infections (121), or UTI (101), in addition to nasal carriers of medical staff (100). Cultures, Gram staining, and other biochemical tests were performed for conventional identification. Modified Kirby-Bauer disk diffusion method was applied and DNA was extracted from MRSA and VRSA isolates and PCR was then performed for amplification of arc, mecA, VanA, and VanB genes. The results confirmed the existence of Staph. aureus in 49/426 (11.5%) cases among which MRSA were isolated from 34/49 (69.4%) when modified Kirby-Bauer disk diffusion method was applied. Ten out of these 34 MRSA were confirmed as VRSA by cultures on BHI agar containing 6µg/ml vancomycin according to NCCLS criteria. PCR revealed that out of the 34 MRSA isolates, 26 were mecA positive (76.5%) while 8 (23.5%) were arcC positive. No vanA or VanB genes were detected. Molecular method confirmed the results for MRSA through the presence of either arcC or mecA genes while it failed to approve the occurrence of VRSA since neither VanA or VanB genes were detected. Thus, VRSA may be attributed to other factors.

Keywords : antibiotic resistance, Staphylococcus aureus, VRSA, MRSA, Khartoum, Sudan

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