

Virulence Factors and Drug Resistance of Enterococci Species Isolated from the Intensive Care Units of Assiut University Hospitals, Egypt

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Abstract : Background: The enterococci may be considered as opportunistic agents particularly in immunocompromised patients. It is one of the top three pathogens causing many healthcare associated infections (HAIs). Resistance to several commonly used antimicrobial agents is a remarkable characteristic of most species which may carry various genes contributing to virulence. Objectives: to determine the prevalence of enterococci species in different intensive care units (ICUs) causing health care-associated infections (HAIs), intestinal carriage and environmental contamination. Also, to study the antimicrobial susceptibility pattern of the isolates with special reference to vancomycin resistance. In addition to phenotypic and genotypic detection of gelatinase, cytolysin and biofilm formation among isolates. Patients and Methods: This study was carried out in the infection control laboratory at Assiut University Hospitals over a period of one year. Clinical samples were collected from 285 patients with various (HAIs) acquired after admission to different ICUs. Rectal swabs were taken from 14 cases for detection of enterococci carriage. In addition, 1377 environmental samples were collected from the surroundings of the patients. Identification was done by conventional bacteriological methods and confirmed by analytical profile index (API). Antimicrobial sensitivity testing was performed by Kirby Bauer disc diffusion method and detection of vancomycin resistance was done by agar screen method. For the isolates, phenotypic detection of cytolysin, gelatinase production and detection of biofilm by tube method, Congo red method and microtiter plate. We performed polymerase chain reaction (PCR) for detection of some virulence genes (*gelE*, *cylA*, *vanA*, *vanB* and *esp*). Results: Enterococci caused 10.5% of the HAIs. Respiratory tract infection was the predominant type (86.7%). The commonest species were *E.gallinarum* (36.7%), *E.casseliflavus* (30%), *E.faecalis* (30%), and *E.durans* (3.4 %). Vancomycin resistance was detected in a total of 40% (12/30) of those isolates. The risk factors associated with acquiring vancomycin resistant enterococci (VRE) were immune suppression ($P= 0.031$) and artificial feeding ($P= 0.008$). For the rectal swabs, enterococci species were detected in 71.4% of samples with the predominance of *E. casseliflavus* (50%). Most of the isolates were vancomycin resistant (70%). Out of a total 1377 environmental samples, 577 (42%) samples were contaminated with different microorganisms. Enterococci were detected in 1.7% (10/577) of total contaminated samples, 50% of which were vancomycin resistant. All isolates were resistant to penicillin, ampicillin, oxacillin, ciprofloxacin, amikacin, erythromycin, clindamycin and trimethoprim-sulfamethaxazole. For the remaining antibiotics, variable percentages of resistance were reported. Cytolysin and gelatinase were detected phenotypically in 16% and 48 % of the isolates respectively. The microtiter plate method showed the highest percentages of detection of biofilm among all isolated species (100%). The studied virulence genes *gelE*, *esp*, *vanA* and *vanB* were detected in 62%, 12%, 2% and 12% respectively, while *cylA* gene was not detected in any isolates. Conclusions: A significant percentage of enterococci was isolated from patients and environments in the ICUs. Many virulence factors were detected phenotypically and genotypically among isolates. The high percentage of resistance, coupled with the risk of cross transmission to other patients make enterococci infections a significant infection control issue in hospitals.

Keywords : antimicrobial resistance, enterococci, ICUs, virulence factors

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