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Prevalence of virulence and high level aminoglycoside resistant genes in *Enterococcus faecalis* strains

Alireza Dolatyar Dehkharghani¹, Mohsen Imani¹ and Mohsen ghelman²

¹Ministry of Health and Medical Education

²Iran University of Medical Sciences, Iran

Background: *Enterococci* have increasingly emerged as a cause of serious nosocomial and community-acquired infections, including bacteraemia and endocarditis. *Enterococcus* is capable of acquiring resistance genes, including high-level resistance (HLRA) to aminoglycoside antibiotics. It is believed that nosocomial *enterococci* might have virulence elements that increase their ability to colonize hospitalized patients.

Objectives: The genetic and molecular basis of high-level aminoglycoside resistant (HLAR) and the prevalence of genes encoding virulence factors in high-level aminoglycoside resistant *Enterococcus faecalis* were investigated.

Material and Methods: Bacterial identification was performed by biochemical tests and phenotypification was done. Antibiotic susceptibility was evaluated by disc diffusion and microdilution methods. Aminoglycoside resistance genes and virulence genes *aceI*, *agg*, *gelE* and *efaA* were analysed by PCR-based methods.

Results: In this study, 24% of *E. faecalis* were high-level-resistant to gentamicin. The *aac(6')-Ie-aph(2'')*-I gene was responsible for high-level resistance to gentamicin in *E. faecalis*. The *aph(3')-IIIa* and *ant(4')-Ia* genes responsible for resistance to amikacin were also isolated in *E. faecalis*. The *efaA* gene was detected in 80% of the isolates. *aceI* gene was present in 55%, *agg* gene in 23.1%, and *gelE* gene in 46% of the clinical isolates.

Conclusion: The spread of the *aac(6')-Ie-aph(2'')*-Ia gene was responsible for high-level resistance aminoglycoside among *Enterococci* isolated from patients. Virulence genes of *E. faecalis* also were isolated from clinical strains. We evaluated prevalence of virulence genes among isolated high-level resistant to aminoglycoside strains and understood *efaA* gene has the most frequency. More studies will be necessary to establish an association between two parameters.

ardityr@gmail.com