

Prevalence of bacteriocin activities and bacteriocin encoding genes in enterococcal clinical isolates of Iran

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Background and Aims: The occurrence of multi-antibiotic resistance bacteria is a prevalent clinical problem worldwide and continues to get serious due to the lack of efficient therapeutic options by the time. In this regards, prokaryotic antimicrobial peptides with bactericidal or bacteriostatic activity which are directed against bacterial strains closely related to producer strains looks one of the promising alternative to conventional antibiotics. The aim of the project was to isolate and characterize the bacteriocin producer enterococci as well as determine the prevalence of enterocin structural genes in 187 enterococcal clinical isolates from North-West of Iran.

Methods: The isolates were screened for antibacterial activity against 18 different indicator strains. The proteinaceous nature of antimicrobial substances was confirmed by sensitivity to proteinase K and trypsin, their stability to heat treatment was tested at 60 °C and 100 °C for 30 and 10 min, respectively. The PCR method was applied to detect previous identified enterocin genes.

Results: Our results showed that 38 (20.3%) of enterococcal isolates were considered as potential bacteriocinogenic strains. Furthermore, genes encoding diverse bacteriocin are highly distributed among clinical enterococci and the strains with multi-bacteriocin genes displayed high antimicrobial activity. Enterocin A, enterolysin A and enterocin LA50A/B were the most abundant structural genes detected in bacteriocinogenic strains.

Conclusions: This work is the first survey on the prevalence of bacteriocin structural genes among clinical enterococci in Iran that has isolated strains with high antimicrobial activity which could potentially served as alternatives to antibiotics in pharmaceutics as well as feed supplements.

Keywords: Prevalence; Genes; Bacteriocin; Enterococci