

SUMMARY

Investigation of Virulence Genes of *Enterococcus faecalis* Strains Isolated from Mastitic Bovine Milk

In this study, it was aimed to investigate the potential virulence genes (gelatinase [*gelE*]), adhesion-associated protein [*EfaAfs*], enterococcal surface protein [*esp*], cytolytins [*cylA*, *cylM*, *cylB*], sex pheromones [*cpd*, *cob*, *ccf*], aggregation substance [*aggA*], enhanced expression of pheromone [*eep*]) of *Enterococcus faecalis* strains isolated from mastitic bovine milk samples with polymerase chain reaction (PCR). A total of 56 *E. faecalis* isolates, which were previously isolated from 600 mastitic bovine milk samples were used as material. After the isolation of enterococcus in selective media, identifications based on genus and species were also performed with PCR. 1.8 % and % 3.6 of the strains harbored eight and seven virulence determinant, while there was no enterococci enterococcal isolate having virulence gene. The *efaAfs* gene was the predominant (% 94,6) virulence gene among the enterococci investigated followed by *cpd* (% 91,0), *gelE* (% 87,5), *esp* (% 51,7), *ccf* (% 42,8), *cob* (% 10,7), *eep* (% 8,9), *aggA* (% 7,1), *cylA* and *cylM* (% 1,78). None of the strains harbored *cylB* gene. Finally, it can be said that *E. faecalis* strains isolated from mastitic bovine milk have high pathogenicity and have zoonotic contamination risk and have high infection capability in humans. It is thought that further studies should be conducted on the definition of virulence factors related to severity of the infection and expending traits of enterococcus and their relationships with some kind of antibiotics should also be revealed.