

Determination of ecovars, antibiotic susceptibility and *tst* gene frequency in *Staphylococcus aureus* isolated from dairy food products

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Abstract

S. aureus is a major cause of food borne diseases throughout the world. The aim of the present study was the identification of source contamination and *tst* gene in *Staphylococcus aureus* isolated from food of animal origin in Hamedan city. In this study, the contamination sources of 65 *S. aureus* isolates which had previously been isolated from cream pastry (45 isolates) and traditional Iranian white cheese (20 isolates) were evaluated using biotyping method. Meanwhile, the identification of *tst* gene by PCR method and susceptibility of the isolates against several antibiotics was examined using standard disk diffusion test. Of the 65 biotyped isolates, 52.3% (34 isolates) and 44.6% (29 isolates) belonged to the host specific (HS) and non-host specific (NHS) biotypes, respectively, and 3.1% of the isolates (2 isolates) were not placed in certain types. Besides, human ecovars in cream pastry and bovine ecovars in cheese samples were predominant. The prevalence rate of *tst* gene in the isolates was 4.6% (3 isolates), and according to the results of antimicrobial susceptibility test, HS biotypes showed higher resistance rather than NHS biotypes. Due to the abundance of human and bovine Staphylococcal ecovars in cream pastry and cheese samples, respectively, it can be concluded that the contamination of cream pastry and cheese samples may be originated from humans and cattle. Also, because of high antibiotic resistance and presence of *tst* gene among HS biotypes and the possibility of their circulation in the community can have a potentially alarming effect on general health of community.

Key words: *Staphylococcus aureus*, Biotyping, *tst* gene, Antibiotic susceptibility test

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