

## Microbiology Congress 2018: Prevalence of enterotoxin genes and antibacterial susceptibility pattern of *Staphylococcus aureus* strains isolated from animal originated foods in west of Iran - Rasoul Y Mashouf - Hamadan University of Medical Sciences

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Raw milk may be contaminated by enterotoxigenic coagulase-positive staphylococci (CPS). Several of these microorganisms show antimicrobial resistance, which poses a potential risk for consumers. The aim of this study was to determine the occurrence of enterotoxin genes and antimicrobial resistance of CPS isolated from cow milk. A total of 115 samples were analyzed for the presence of CPS according to the International Organization for Standardization standard (ISO 6888-2). The genes were identified using 2 multiplex PCR assays. Resistance of the isolates to 10 antimicrobials was determined using the minimum inhibitory concentration method. Overall, 71 samples (62%) were contaminated with CPS and 69 isolates were further analyzed. Among them, 20 (29%) strains harbored the enterotoxin genes. The most commonly detected staphylococcal enterotoxin markers were *sed*, *sej*, and *ser*, whereas none of the analyzed isolates possessed the *seb* and *see* genes. Almost one-half of the tested strains (43%) were resistant to one or more antimicrobial agents. Resistance to penicillin was the most common, followed by sulfamethoxazole and chloramphenicol. On the other hand, all strains were susceptible to ciprofloxacin, erythromycin. None of the strains was positive for the *mecA* and *mecC* (methicillin-resistant *Staphylococcus aureus*) genes. These results indicate that enterotoxigenic and antimicrobial-resistant CPS strains are present in raw milk, which may be a potential risk for public health.

**Objectives:** The aims of our study were to evaluate the prevalence of *Staphylococcus aureus* strains in food samples of animal origin, examine their antibacterial susceptibility pattern and to detect staphylococcal enterotoxin (SEs) genes and the *mecA* gene in isolated *S. aureus* strains using the polymerase chain reaction (PCR).

**Methods:** A total of 1050 food samples including 671 raw milk and dairy products and 379 raw meats were collected between September 2013 and June 2014 in Hamadan, Iran. Food samples were analyzed for *S. aureus* identification. The antibiotic susceptibility pattern of all isolates was determined using the disk agar diffusion method followed by detecting *mecA* resistance gene using PCR. In addition, harboring of SE genes were determined using a multiplex PCR assay targeting nine genes.

**Results:** A total of 98 (9.3%) *S. aureus* strains were isolated from 1050 food samples. Of the 98 isolates examined, the most frequent resistance was observed to erythromycin

(30.6%), followed by tetracycline (29.6%), gentamicin (27.6%), clindamycin (26.5%), ciprofloxacin and rifampin (24.5%), trimethoprim-sulfamethoxazole (14.3%), and ceftiofur (5.1%). All ceftiofur resistant isolates were positive for *mecA*. The prevalence of SEs was 77.6% (n=76). Among the genes that code classic enterotoxins, *sea* was the most frequent and was carried by 25.5% of isolates, followed by *see* in 18.4%, *sed* in 11.2%, *sec* in 5.1%, and *seb* in 4.1% of isolates. Among the detected enterotoxins, *seg* was the predominantly identified enterotoxin gene in isolates with prevalence of 35.7%. The *seh* gene with prevalence of 1% and *sei* gene with 3.1% were other detected enterotoxins with low frequencies

**Conclusions:** The high prevalence of SE genes detected indicates a potential risk for causing animal-originated food poisoning. The increasing prevalence of community-acquired MRSA and its emerging antibiotic resistance in foods is a serious problem for public health.