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Prevalence of enterotoxin genes and antibacterial susceptibility pattern of *Staphylococcus aureus* strains isolated from animal originated foods in west of Iran

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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 cefoxitin (5.1%). All cefoxitin 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.

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