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Prevalence of selected virulence factors of *Staphylococcus aureus* isolated in bovine mastitis in Chaharmahal and Bakhtiari province- Iran

Behnam Rozbahan[1], Naser Shams Esfandabadi[2*], Ali Kadivar[3], Azam Mokhtari[4] and Najmeh Davoodian[5]

[1] DVSc Student of Theriogenology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[2] Professor, Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[3] Associate Professor, Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[4] Associate Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord , Iran
[5] Associate Professor, Research Institute of Animal Embryo Technology, Shahrekord University, Shahrekord, Iran

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Abstract

It has been determined that there is a direct relationship between the severity of mastitis and the virulence factors produced by bacterial agents. Identifying bacterial virulence factors is neccecary for designing suitable vaccines against mastitis. The aim of the present study was molecular diagnosis of selected virulence factors of endemic isolates of *S. aureus* involved in bovine mastitis. A total of 180 milk samples were collected from cows with clinical (37 samples, 20.6%) and subclinical (143 samples, 79.4%) mastitis from 8 semi-industrial dairy farms of Chaharmahal and Bakhtiari province, Iran. After culture and purification, coagulase, catalase and oxidase tests were performed. DNA was extracted from *S. aureus* suspected colonies. Final confirmation was performed using PCR test on the specific 23S rRNA gene of the bacteria. Thirty one (17.22%) out of the 180 collected samples were found to be positive for *S. aureus* by PCR, of which 2 cases were related to clinical mastitis and 29 cases were related to subclinical mastitis. The highest frequency of virulence genes was related to the Coa gene (90.32%), followed by ClfB (87.09%), LukD, and fnbB (80.64%), LukE (77.41%), fnbA (74.19%), Hla (48.38%). The lowest frequency was related to the Hlb gene (45.16%). Based on the obtained results, the diagnosis of the virulence factors of *S. aureus* has the potential of being used in the development of vaccines for the prevention of mastitis.

Key word: Mastitis, *Staphylococcus aureus*, Virulence factors

[*] **Corresponding Author**: Naser Shams Esfandabadi, Professor, Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
E-mail: drn_shams@yahoo.com

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