

TITLE: VIRULENCE GENES IN *Staphylococcus aureus* ISOLATED FROM CLINICAL AND SUBCLINICAL CAPRINE MASTITIS

AUTHORS: LIMA, M.C.; PENA, J.L.; CASTRO, L.K.; GUIMARÃES, S.H.S.; BARROS, M.; MOREIRA, M.A.S.

INSTITUTION: LABORATORY OF BACTERIAL DISEASES (LDBAC), PREVENTIVE VETERINARY MEDICINE AND PUBLIC HEALTH SECTOR, VETERINARY DEPARTMENT; UNIVERSIDADE FEDERAL DE VIÇOSA, VIÇOSA, MG (AV. PH ROLFS, S/N, CAMPUS UNIVERSITÁRIO, CEP 36570-900, VIÇOSA – MG, BRAZIL)

ABSTRAT:

Staphylococcus aureus is the pathogen most prevalent in caprine mastitis, responsible for clinical and subclinical form of the disease. The virulence factors of microorganisms are important in the mechanisms of adhesion, invasion, colonization and immune system evasion. The goal of this work was detecting and comparing virulence genes from different *S. aureus* isolated from goats with clinical and subclinical mastitis. A total of 116 *S. aureus* obtained from dairy goats located in the mesoregion of the Zona da Mata of Minas Gerais, were used, 101 from subclinical mastitis and 15 from clinical mastitis. Detection of 17 virulence genes (*sea*, *seb*, *sec*, *sed*, *see*, *seg*, *seh*, *sei*, *selj*, *fbnA*, *fbnB*, *hla*, *LuckDE*, *eta*, *etb*, *tst*, *nuc*) was performed using conventional PCR and multiplex PCR. In the isolated obtained from subclinical mastitis were found 14 genes, eight genes encoding enterotoxins: *sea* (17.8%; 18/101), *seb* (13.8%; 14/101), *sec* (9.9%; 10/101), *sed* (1%; 1/101), *see* (8.9%; 9/101), *seg* (7.9%; 8/101), *seh* (6.9%; 7/101) and *selj* (22.8%; 23/101), and other six genes: *fbnA* (8.9%; 9/101) and *fbnB* (6.9%; 7/101) associated with adhesion; *hla* (38.8%; 39/101), Alpha-toxin; *etb* (10.9%; 11/101), exfoliative toxin; *nuc* (17%; 17/101), termonuclease and *tst* (17%; 17/101), Toxic Shock Syndrome. Eleven genes were detected in isolated from clinical mastitis, five genes encoding enterotoxins: *sea* (13.3%; 2/15), *sec* (40%; 6/15), *sed* (6.6%; 1/15), *selj* (26.6%; 4/15) and *seh* (6.6%; 1/15), and others six genes: *fbnA* (80%; 12/15), *fbnB* (20%; 3/15), *etb* (46.6%; 7/15), *nuc* (20%; 3/15), *hla* (46.6%; 7/15) and *tst* (20%; 3/15). The genes *LuckDE*, *sei* and *etb* were not detected in isolated either from clinical or subclinical mastitis. Based on the quantification and function of the virulence genes detected in *S. aureus*, isolated from subclinical mastitis have a higher enterotoxigenic capacity, except for the *sec* gene, detected fourfold in isolated from clinical mastitis. On the other hand, isolated from clinical mastitis have greater capacity of adhesion, invasion and immune system evasion. Although the development of a disease is a complex process, there was a predominance of a clonal type which carries a set of genes in isolated from clinical mastitis and another set in subclinical mastitis in goats. Thus, these data require more studies.

Keywords: Bacteria; Dairy goats; Intramammary infection; Pathogenicity

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