

TITLE: VIRULENCE GENES OF *STAPHYLOCOCCUS AUREUS* ISOLATED FROM MILK OF COWS AND GOATS WITH CLINICAL AND SUBCLINICAL MASTITIS

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ABSTRACT

Intramammary infections (IMI) is the most significant cause of economic loss in the dairy industry worldwide. One of the most important causes of IMI is the *Staphylococcus aureus* (*S. aureus*), which is difficult to eradicate in dairy cattle and dairy small ruminant. The high pathogenicity of *S. aureus* strains is driven by multifactorial and complex virulence factors. Appropriate molecular typing methods and information about the genetic diversity of *S. aureus* strains in a particular region, may contribute to define effective strategies for epidemiological control. The aim of the present study was to determine the distribution of virulence factors genes among *S. aureus* strains isolated from cows and goats in three different geographical areas of Pernambuco state, Brazil. Therefore, the possibility that allelic variants at a given polymorphic locus of clumping factor (*clfA* and *clfB*) had an impact on the distribution of virulence factors genes was investigated. One hundred fifty strains (123 from bovines and 27 from goats) were included in the study. The virulence factors involved in adhesion to host cells (*fnbA*, *fnbB*, *clfA* and *clfB*), toxins (*sea*, *seb*, *sec*, *sed*, *seg*, *seh*, *sei*, *tsst*, *hla* and *hlb*), and capsular polysaccharide genes (*cap5* and *cap8*) were analyzed by PCR. The virulence factors relative to the intensity of mastitis (subclinical and clinical) no showed differences between groups. Three *clfA* and five *clfB* genotypes were identified. None of the strains harbored *see* gene. The *sec* and *tsst* genes were detected exclusively in strains from goat and the *seh* gene was detected exclusively in bovine's strains. The toxic potential, as indicated by the number of toxins genes per strain, show significant differences between the bovine's and goat's strains. Our data showed that *cap8* genotype had more virulence potential by the number of virulence genes per strain. The *cap5* genotype was the predominant, especially in bovine's strains in the semi-arid region. The results suggest that the distribution of virulence factors genes changes in relation to allelic variants of *clfA* and *clfB*. The inclusion of the potential virulence of the *Staphylococcus aureus* isolates from different geographical origins and hosts may contribute to mastitis control programs and could be used as an indicative of their potential risk to public health.

Keywords: molecular typing, *S. aureus*, genotyping, staphylococcal enterotoxin, capsular polysaccharide.

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