

Title: VIRULENCE AND ANTIMICROBIAL RESISTANCE GENETIC CHARACTERIZATION OF *Staphylococcus aureus* ASSOCIATED WITH BOVINE MASTITIS

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Abstract:

Mastitis one of the most common infections of the bovine mammary gland causes significant economic losses to the dairy industry. *Staphylococcus* is one of the main causes of infection and *S. aureus* is most often isolated in subclinical mastitis. *S. aureus* related mastitis is correlated with extracellular factors and toxin production, in conjunction with adhesion and biofilm formation. Understanding the molecular profiles of *S. aureus* enhances epidemiological studies of pathogen dispersal on farms, contributing to the elucidation of pathogenesis mechanisms. Thus, strategies and prophylaxis protocols for *S. aureus* control can be managed appropriately. This study focused on the genetic characterization of bovine-associated *S. aureus* causing mastitis in order to derive data on the epidemiology of this microorganism. For the present study, 17 strains of *S. aureus* were selected from four farms from four cities in the state of Rio de Janeiro that presented subclinical mastitis confirmed through the CMT test. PCR was used to confirm the species identity and the prevalence of 31 virulence associated genes. Pulsed Field Gel Electrophoresis (PFGE) was performed to assess genetic diversity. Multi-locus sequence analysis (MLST) was performed on seven selected isolates to further subtype these strains. All isolates used in the study were tested for antimicrobial susceptibility using the National Antimicrobial Resistance Monitoring System (NARMS) broth microdilution assay. All strains tested were confirmed by PCR as *S. aureus*. Through the detection of virulence genes 17 different virulence profiles were identified. This leads us to conclude that *S. aureus* associated mastitis strains are quite different from each other. This fact is corroborated by the PFGE results that found a high diversity among the strains examined and the absence of clones. However, with the characterization of strains by MLST it was possible to observe that ST 126 (71.4%) was prevalent among selected strains. For antimicrobial susceptibility analysis most isolates were susceptible to the antimicrobials tested with the exception of Erythromycin and Penicillin where a low prevalence of resistance was observed (17.6% for both). The results obtained in this study demonstrate a high genetic diversity among *S. aureus* causing bovine mastitis, this fact confirms the importance of understanding the etiological complexity of mastitis caused by *S. aureus* so that we can elucidate the mechanism of pathogenesis.

Key words: Antimicrobial susceptibility, bovine mastitis, genetic profile, *Staphylococcus aureus*.

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