

Analysis of presence mecA gene of *S. aureus* isolates from bovine subclinical mastitis in a single herd in Brazil

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The use of antibiotics for the elimination of mastitis and possible sources of contamination in dairy herds are important control measures. However, one of the main responsible for bovine mastitis, *Staphylococcus aureus* has shown resistance to a lot of antimicrobials. *S. aureus* methicillin-resistant (MRSA) has been found in cattle, these strains carried the mecA gene that is localized in an island genomic called SCCmec which is a mobile region that allows the interchange between different species of staphylococcus, doing occurs more spread of this pathogen. Due to the great importance of epidemiological, the aim of this study was to evaluate the antimicrobial susceptibility profile and the presence of the mecA gene in *S. aureus* strains obtained from cows with subclinical mastitis in a single Brazilian herd. A total of 65 *S. aureus* strains identified by the presence of the nuc gene were subjected to disc-diffusion test according to CLSI (2012). The tested antibiotics were: vancomycin (1 µg), streptomycin (10 µg), gentamicin (10 µg), oxacillin (1 µg), ceftiofur (30 µg), tetracycline (30 µg), erythromycin (15 µg), clindamycin (2 µg), tobramycin, trimethoprim-sulfamethoxazole (1.25 / 23.75 µg), tetracycline (30 µg), cephalothin (30 µg). The strains with resistance to oxacillin and ceftiofur were subjected to PCR for detection of the mecA gene. We noticed 48 (73,8%) sensitive strains to all antibiotics and 17 (26,2%) intermediate susceptibility or resistance to at least one of the antibiotics tested. We found 6 resistance strains to oxacillin, among these, 5 also proved resistance to ceftiofur. The mecA gene was observed in 3 strains. The presence of MRSA strains in dairy herds complicates the control of mastitis and possible contamination of other animals, causing economic losses in dairy industries.

Palavras-chaves: mastitis, antimicrobial, methicillin, *Staphylococcus aureus*

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