

TITLE: DIFFERENT PROFILES OF *Staphylococcus aureus* ISOLATED FROM CAPRINE MASTITIS AFTER TREATMENT WITH ENROFLOXACIN

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ABSTRACT:

The objective was to verify changes in the clonal, resistance and virulence profiles of *Staphylococcus aureus* isolated from the milk of goats with mastitis before and after treatment with enrofloxacin. Nine animals with clinical mastitis caused by *S. aureus* were treated with enrofloxacin, 5 mg / kg for 7 days. Of these nine animals, 18 *S. aureus* isolates were obtained. The techniques of Multilocus Sequencing Typing (MLST) and pulsed field gel electrophoresis (PFGE) techniques were used for the clonal profile. The resistance profile of the isolates was determined by the minimum inhibitory concentration (MIC, E-test®) and PCR (resistance genes and multidrug efflux system genes). From the MLST, all isolates of *S. aureus* belonged to the same ST 133, except for the two isolates, one, before treatment, belonged to ST 5 and another was classified as a new ST, after the treatment both presented the ST 133. The MICs ranged from 0.125 to 125 µg/mL in the isolates before to treatment, whereas in the isolates after treatment, antimicrobial MICs ranged from 0.19 to 96 µg/mL. The smallest MICs were observed for enrofloxacin and ciprofloxacin, while the largest MICs were for tetracycline and oxacillin. After treatment, three isolates increased the MIC for vancomycin, four isolates for gentamicin and penicillin, five isolates for enrofloxacin, ciprofloxacin and oxacillin and only one isolate increased MIC for tetracycline. There were differences in the presence of resistance genes and efflux systems after treatment with enrofloxacin. Resistance genes were detected before and after treatment (*ant(4')-Ia*, *ermB*, *bla_Z*, *ermA*, *mecA*, *tetM*, *tetK*) in three isolates there was an increase in the number of resistance genes, with addition of two to four genes after treatment. Nine isolates before treatment did not have the genes of the multidrug efflux system and after treatment three genes were detected. Sixteen virulence genes tested, only nine genes (*hla*, *fnbA*, *fnbB*, *eta*, *etb*, *sea*, *sec*, *seh* and *sej*) were detected before and after treatment. The genes *hla*, *eta* and *etb* genes were further detected after treatment, while the remaining six genes remained unchanged. The *hla*, *eta* and *etb* genes were the most detected in isolates after treatment. Despite the use of the recommended dose and duration of treatment, the presence of enrofloxacin may have led to increased selection pressure. The persistence of *S. aureus* in the mammary gland of goats can be result of changes in the bacteria after treatment, which may be associated with stimulation by mutation, horizontal transfer of resistance genes and efflux pump genes.

Keywords: Goat, Intramammary infection, selection pressure

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