

TITLE: PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF ANTIMICROBIAL RESISTANCE OF *STAPHYLOCOCCUS AUREUS* IN THE SWINE PRODUCTION CHAIN

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ABSTRACT:

Brazil is a great producer of swine, and due to the large production of these animals, breeding systems have become almost exclusively intensive, which requires greater use of prophylactic and therapeutic drugs. *Staphylococcus aureus* constitutes the natural skin microbiota and respiratory organs and can be present both in humans and in swine. In this context, *S. aureus* stands out as a public health problem due to its ability to develop mechanisms of antimicrobial resistance. The objective of this study was to track the presence of *S. aureus* in the whole production line of swine from creation through processing and evaluating its antimicrobial resistance profile, phenotypically and genotypically. The study was conducted on 10 pig farms and finished in a slaughterhouse located in the west of Paraná. 540 samples were collected along the production chain, subject to isolation of *S. aureus*, through protocol ISO 6888-2/1999. All the isolates that exhibited compatible biochemical profile were subjected to a polymerase chain reaction for confirmation, by *femA* gene detection. All isolates identified as *S. aureus* were evaluated with regard to resistance to 10 different antibiotics through breakpoint susceptibility test in accordance with the limits of resistance established by Clinical and Laboratory Standards Institute (CLSI, 2016). The profile of genotypical resistance of the isolates was evaluated for the genes *femB*, *blaZ*, *mecA*, *mecC*, *vanA* and *tetK*. It was possible to detect *S. aureus* in 13 samples only, and these generated 18 isolates. As for phenotypic results, 100% of *S. aureus* isolates showed multidrug resistance. In addition, all of the isolates were resistant to sulfamethoxazole, penicillin, erythromycin and tetracycline. Approximately 95% showed resistance to ciprofloxacin and chloramphenicol, and almost 90% showed resistance to gentamicin. Only three isolates (16.6%) demonstrated resistance to oxacillin, vancomycin and rifampicin all samples were sensitive. Genotypic results genes *mecC*, *vanA* e *tetK* were not detected. *femB* gene was detected in five isolated, *blaZ* in 15 and the *mecA* in nine. Despite the low isolation of *S. aureus* along the production chain, the fact that all the isolates were multidrug-resistant demonstrates great concern for public health.

Keywords: multidrog, farm, slaughterhouse

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