**TITLE:** GENETIC DIVERSITY AND ANTIMICROBIAL RESISTANCE OF *STAPHYLOCOCCUS HYICUS* ISOLATED FROM SOWS WITH PURULENT VUVLAR DISCHARGE

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## ABSTRACT

Staphylococcus hyicus is an important pathogen in porcine production, mainly because it is the etiological agent of a skin infection in young pigs that occurs worldwide, known as exudative epidermitis. Besides, S. hyicus is also an important agent for reproductive infections in sows, known to be capable of causing uterine infections. Due to the lack of current information on the genetic behavior and antimicrobial resistance patterns of this agent in Brazilian farms, here we describe the genetic profiles of S. hyicus strains isolated from sows with purulent vulvar discharge and their minimal inhibitory concentrations for antibiotics used in swine farming. Samples were collected from four farms in four Brazilian states: SP, MG, PR and MT. Swabs from sows with purulent vulvar discharge were collected from the deep region of the vaginal canal using a sterile speculum. Thirty-eight S. hyicus strains were identified by MALDI-TOF mass spectrometry and analyzed by Single-enzyme Amplified Fragment Length Polymorphism (SE-AFLP). The antimicrobial resistance profiles were assessed by broth microdilution method. S. hyicus strains presented high genetic variability, with 15 profiles in the SE-AFLP analysis. This variation does not seem to be associated with the origin of the strains, nor with other epidemiological variables analyzed as year, animal or female parity. The strains presented high resistance rates to the tested antimicrobials. All strains (100%) were resistant to spectinomycin, clindamycin and tiamulin, followed by marbofloxacin (92.3%), enrofloxacin and florfenicol (89.7%), and sulfadimethoxine (79.5%). Elevated resistance rates were also observed for doxycycline and oxytetracycline (71.8 and 74.4%) and considerable indices for beta-lactams ampicillin and penicillin (51.3 and 66.7%). All strains presented resistance for at least three antimicrobial classes, and 53.8% of them presented resistance to five or six classes. Thus, strains of S. hyicus isolated from sows with purulent vulvar discharge presented high genetic variation, which could be associated to other genetic elements that still need to be evaluated, such as virulence factors genes. However, strains also presented a high and alarming antimicrobial resistance pattern, showing that S. hyicus cannot be neglected in reproductive infections of sows.

Keywords: uterine infection, bacterial resistance, MALDI-TOF, sows.

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