TITLE: CHARACTERIZATION OF MRSA ISOLATED FROM VAGINAL MICROBIOTA

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ABSTRACT:

Vaginal dysbiosis, caused by the alteration of *Lactobacillus*, contributes to the increase of pathogens that colonize the vaginal mucosa, which can cause vaginitis. Bacteria of the genus Staphylococcus can spread in this environment. The presence of methicillin-resistant Staphylococcus aureus (MRSA) is one of the significant obstacles in the treatment of staphylococcal diseases since these microorganisms are resistant to β-lactam antimicrobials. Thus, this study aimed to characterize MRSA isolated from vaginal contents of women in the fertile period. Two samples of vaginal contents from 102 patients who attended routine consultations at a gynecological and obstetric office of a private network from August 1, 2021, to March 1, 2022. The bacterial isolates were submitted to the PCR technique for identifying S. aureus through the sau gene and MRSA by detecting the mecA gene. The Staphylococcal Chromosome Cassette mec (SCCmec) was characterized by multiplex PCR. Staphylococcal enterotoxin A, B, C, D, and Toxic Shock Syndrome Toxin 1 (TSST-1) genes were screened by PCR. Eighty-three staphylococci were isolated from the studied samples, and of these, 10 (12%) were S. aureus. Among S. aureus, 9 (90%) MRSA were detected, 6 (66.6%) with SCCmec type I and 3 (33.3%) with SCCmec IV. Among the superantigens, the enterotoxin A gene (sea gene) was detected in 5 (50%) of S. aureus, in 4 MRSA with SCCmec I, and 1 MRSA with SCCmec IV. The data indicate a high frequency of MRSA among S. aureus isolates from vaginal contents, and its ability to produce enterotoxin A is worrisome. Enterotoxin A is a potent superantigen that contributes to spreading these bacteria in case of staphylococcal infections. Thus, the importance of therapeutic care among these women is emphasized, especially in antimicrobials.

Keywords: Staphylococcal diseases, MRSA, SCC*mec*, Enterotoxins

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