

MRSA COLONIZATION IN PREGNANT WOMEN: RESISTANCE PROFILE, VIRULENCE, AND POTENTIAL FOR MATERNAL-NEONATAL TRANSMISSION

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a multidrug-resistant (MDR) pathogen associated with both healthcare-associated and community-acquired infections. Pregnant women and neonates constitute vulnerable populations and, when infected, may develop severe clinical outcomes. In addition, healthy individuals may be colonized by this bacterium, making pregnant women a potential source of transmission to neonates. Therefore, the aims of this study were to investigate the frequency of MRSA colonization in pregnant women and neonates, characterize the resistance and virulence profiles of the isolates, and evaluate the impact of potential maternal-neonatal transmission. Nasal swabs were collected from 597 pregnant women and 36 neonates at a maternity hospital during prenatal care or delivery between September 2021 and May 2023. Following bacterial identification by MALDI-TOF, the disk diffusion method was performed to determine phenotypic resistance profiles against twelve antimicrobials. PCR assays were used to investigate eleven resistance genes and five virulence genes (toxin genes). MRSA identification was performed using the ceftioxin disk test and detection of the *mecA* gene, followed by SCCmec typing. Among the 597 pregnant women evaluated, 39 (6.5%) were colonized by *S. aureus*, whereas none of the neonates showed colonization. MDR strains were identified in 22 pregnant women (3.7%), including nine MRSA (1.5%) carrying SCCmec types IVa or V. Among the MRSA strains, four exhibited additional resistance to antimicrobial classes other than beta-lactams. The highest resistance frequencies among *S. aureus* strains were observed for penicillin (87.2%), erythromycin (53.9%), clindamycin (38.5%), and gentamicin (20.5%). The detected resistance genes included *ermC*, *msrA*, *msrB*, *mecA*, *aac(6')-Ie-aph(2'')-Ia*, and *tet(L)*. Among the virulence genes, *lukS-PV/lukF-PV* (23.5%), *tst* (5.1%), and *eta* (2.6%) were identified, with the first two detected in MRSA strains. Colonization of pregnant women by MRSA and other MDR strains represents a relevant concern due to the limited therapeutic options available. The observed phenotypic and genotypic characteristics suggest the circulation of community-associated strains. Furthermore, MRSA strains carrying resistance and toxin genes may complicate the treatment of possible infections in pregnant women and represent a potential risk if transmission to neonates occurs. Maternal-neonatal transmission could not be confirmed, since *S. aureus* was not isolated from the evaluated neonates. Nevertheless, the detection of resistant and potentially virulent strains among pregnant women reinforces the need for surveillance of these

populations due to the risk of dissemination and infection.

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