TITLE: METHICILIN-RESISTANT *STAPHYLOCOCCUS* SPP. COLONIZATION AMONG PREGNANT WOMEN CONSIDERING SCENARIOS BEFORE AND AFTER THE ONSET OF COVID-19 PANDEMIC IN BRAZIL

AUTHORS: RIO-TINTO, A.[1,4]; COSTA, N.S.[1]; ALVIM, D.C.S.S.[1]; ROCHA, A.A.[1]; GUTIERREZ, C.M.F.[1]; OLIVEIRA, L.M.A.[1]; SANTOS, K.R.N.[1]; OLIVEIRA, T.L.R.[1]; FRACALANZZA, S.E.L.[1]; TEIXEIRA, L.M.[1]; MARINHO, P.[2]; AMIM JR, J.[2]; TAYLOR, S.[3]; THOMAS, S.[3]; PINTO, T.C.A.[1]

INSTITUTION: [1]INSTITUTO DE MICROBIOLOGIA PAULO DE GÓES, UNIVERSIDADE FEDERAL DO RIO JANEIRO, RIO DE JANEIRO-RJ; [2]MATERNIDADE ESCOLA, UNIVERSIDADE FEDERAL DO RIO JANEIRO, RIO DE JANEIRO-RJ; [3]PUBLIC HEALTH ENGLAND, UNITED KINGDOM; [4] INSTITUTO BIOMÉDICO, UNIVERSIDADE FEDERAL DO ESTADO DO RIO DE JANEIRO, RIO DE JANEIRO-RJ.

ABSTRACT:

The emergence of multidrug-resistant (MDR) pathogens is a public-health threat. Methicillin-resistant *Staphylococcus* (MRS) is a leading cause of nosocomial infections and has been associated with neonatal infections, being the anovaginal colonization of pregnant women the main source of vertical transmission. The COVID-19 pandemic modified personal behavior and hygiene care and the usage policy of antibiotics, which may have been contributing to changes in microbiota composition. We determined MRS anovaginal colonization rates among pregnant women attended at a single maternity in Rio de Janeiro, Brazil before (January 2019 to January 2020; 481) and during (February 2020 to March 2021; 325) the pandemic. Anovaginal samples (806) were streaked onto chromogenic media after a pre-enrichment step and colonies were identified by MALDI-TOF MS. Antimicrobial susceptibility was evaluated according to CLSI. Detection of *mec*A and SCC*mec* typing was assessed by PCR. Overall, 215 (26.7%) samples were positive for MRS, including 9 distinct species. *S. haemolyticus* was the most prevalent (MRSH, 181; 84.2%), followed by *S. epidermidis* (MRSE, 11; 5.1%), *S. saprophyticus* (MRSS, 7; 3.2%) and *S. aureus* (MRSA, 5; 2.3%). MRS anovaginal colonization rates among pregnant women increased from 9.1% before to 52.6% after the onset of COVID-19. SCC*mec* type V was the most frequent among MRS (54.4%) and a high proportion of isolates (41.4%) could not be typed (NT) due to new combinations of *ccr* and *mec*A genes (being the combination *ccr*2, *ccr*5 and *mec*A class C genes the most common). The rate of SCC*mec* NT strains increased from 27.2% to 40.3% comparing before and during the pandemic. A total of 110 (51.2%) MRS strains were resistant to at least 3 different classes of antimicrobial agents, from which 65 (59%) harbored SCC*mec* type V. The increasing rates of MRS colonization among pregnant women included in the study indicate the need for continuing surveillance of this important group of multidrug-resistant pathogens within maternal and child population, and highlight possible effects of the pandemic in the dynamic of bacterial infectious diseases.