

Methicillin–Resistant *Staphylococcus* spp. Colonization Among Pregnant Women Considering Scenarios Before and After the Onset of COVID–19 Pandemic in Rio de Janeiro, Brazil



BactiVac

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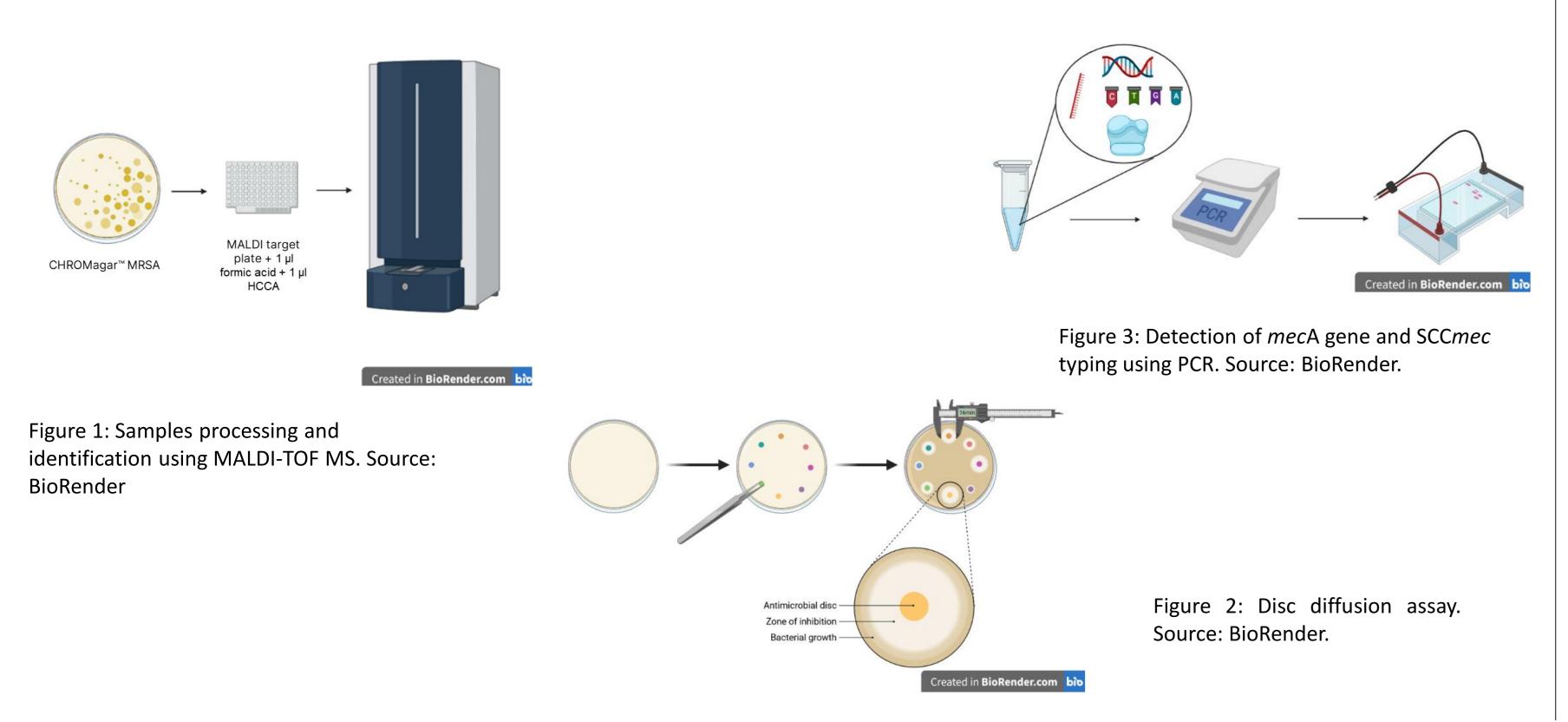
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INTRODUCTION & OBJECTIVE

Methicillin-resistant *Staphylococcus* (MRS) comprises multidrug-resistant (MDR) species of the *Staphylococcus* genus which are a public-health threat. MRS are associated with neonatal infections, with colonization of the anovaginal tract being one of the ways of transmission to the newborn. The COVID-19 pandemic changed the patterns of personal behavior and use of some antimicrobials in the population, which may have impacts on the constitution of the microbiota and on the antimicrobial susceptibility profile of these microorganisms. Our aim was to determine MRS colonization rates among pregnant women attending a single maternity in Rio de Janeiro, Brazil, before (January 2019 to March 2020; 521) and during (May 2020 to March 2021; 285) COVID-19 pandemic.

METHODS

Anovaginal samples (806) were streaked onto chromogenic media, and after a 24h incubation period, suspicious colonies were identified by MALDI-TOF MS (Figure 1). Antimicrobial susceptibility was evaluated according to CLSI (Figure 2). Detection of *mec*A and SCC*mec* typing were assessed by PCR (Figure 3). Clinical samples were collected from pregnant women during routine antenatal care, between the 35th and 37th gestational weeks. All participants signed a consent form, as well as a questionnaire to obtain information about the pregnant woman's health history and sociodemographic data.

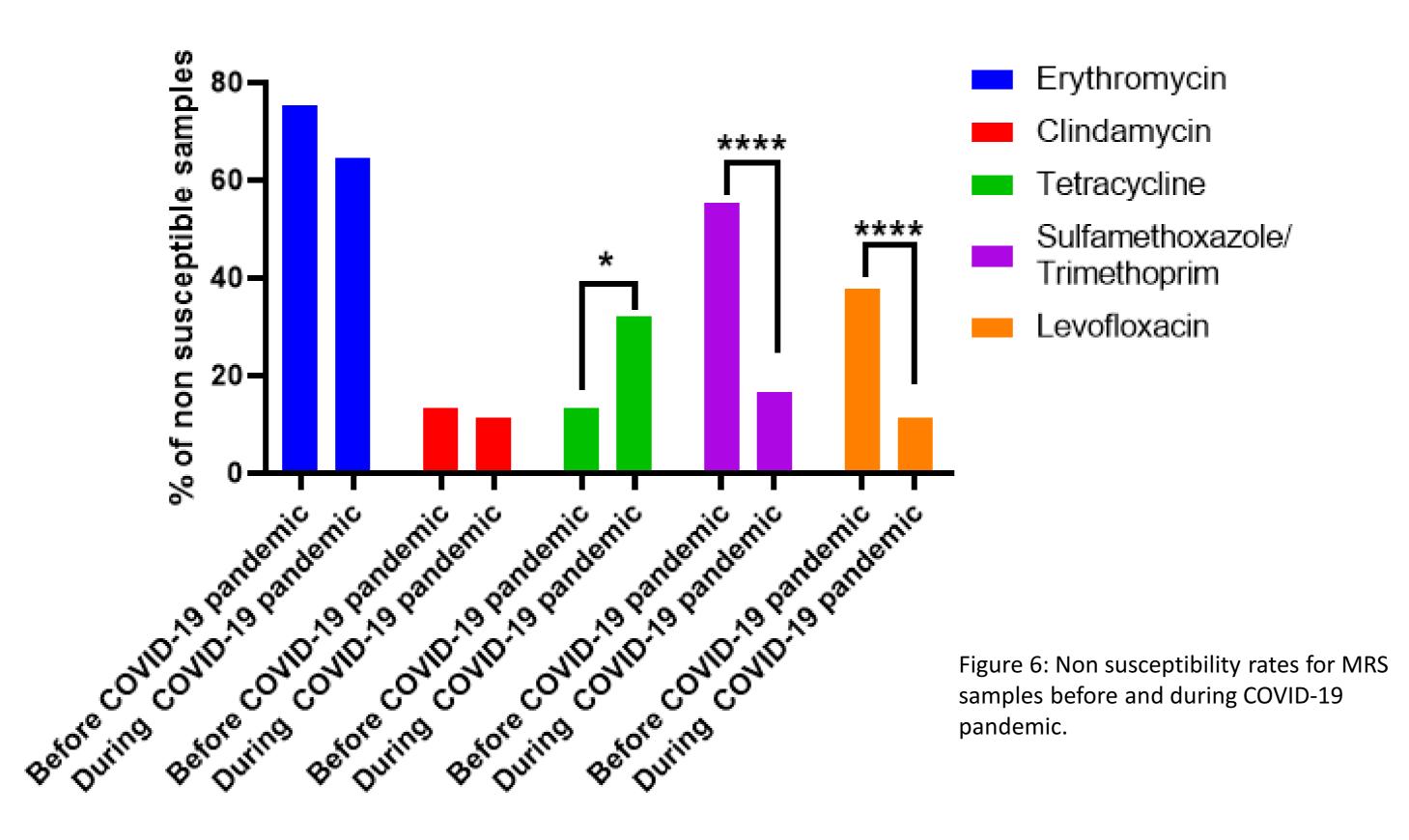


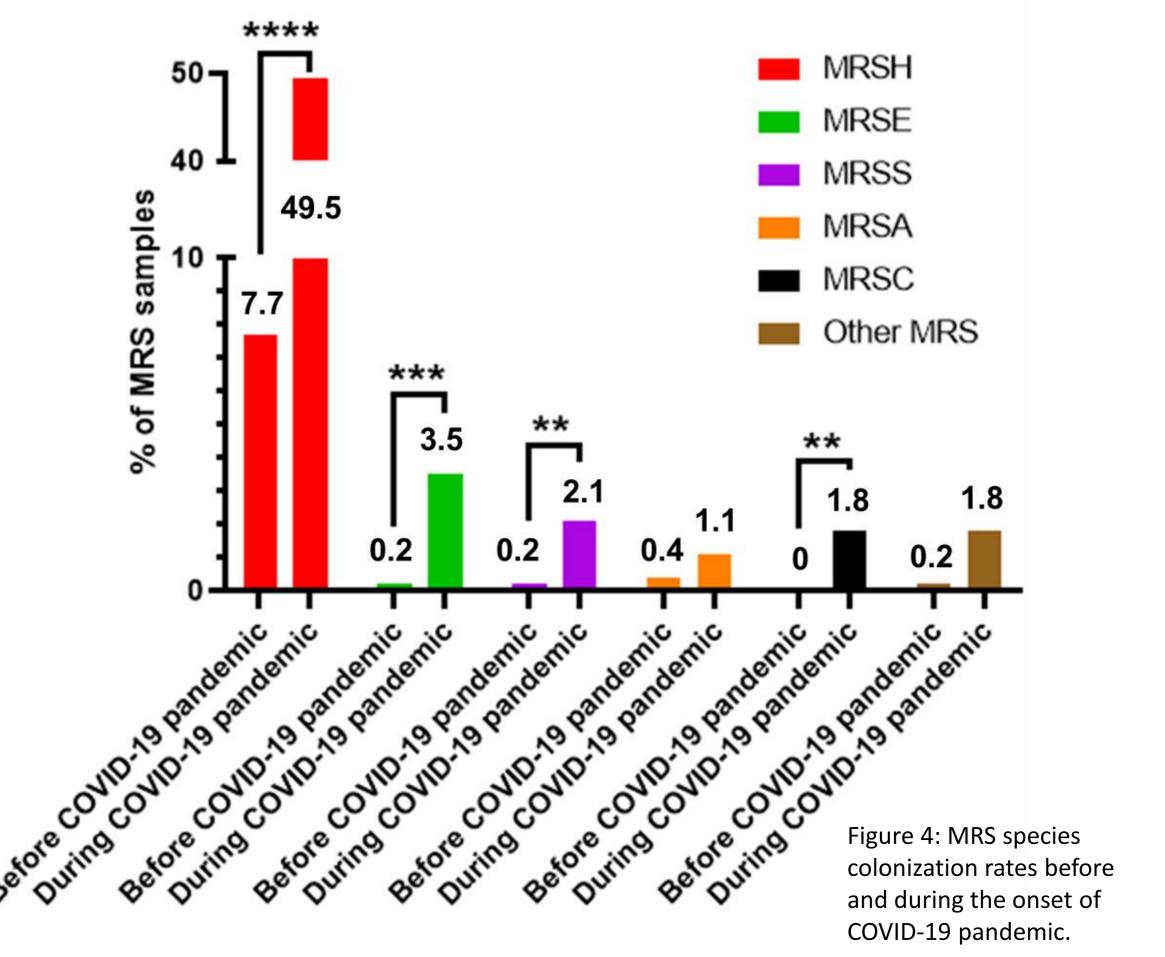
RESULTS

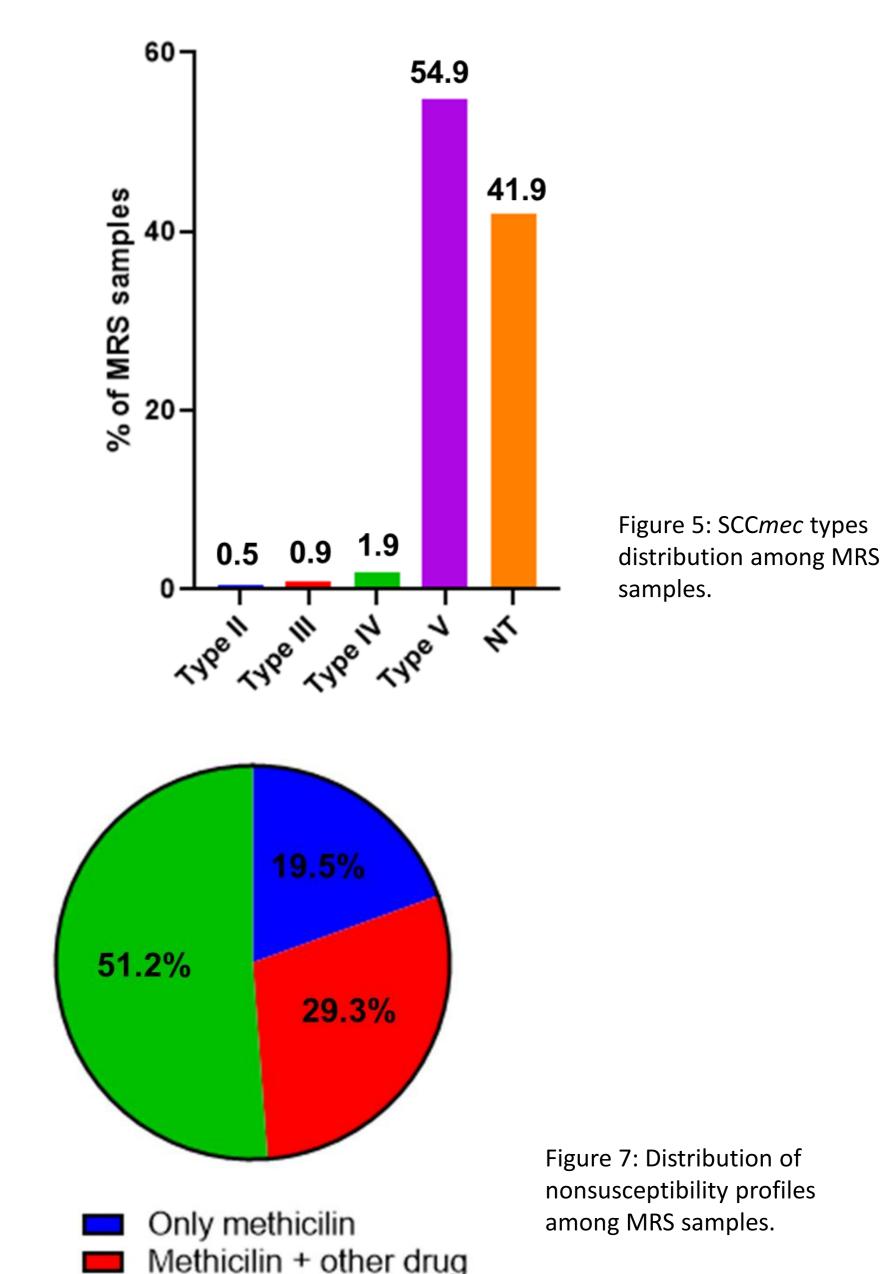
Overall, 215 (26.6%) samples were positive for MRS, including 9 distinct species. MRS anovaginal colonization rates among pregnant women increased from 8.6% before to 59.6% during the onset of COVID-19. *S. haemolyticus* was the most prevalent (MRSH, 181; 84.2%), followed by *S. epidermidis* (MRSE, 11; 5.1%), *S. saprophyticus* (MRSS, 7; 3.3%), *S. aureus* (MRSA, 5; 2.3%) and *S. sciuri* (MRSC, 5; 2.3%). All MRS colonization rates increased during the COVID-19 pandemic (Figure 4).

Most isolates presented SCC*mec* type V or could not be typed (NT) (Figure 5). The rate of SCC*mec* NT strains increased from 26.7% to 45.9% comparing before and during the pandemic.

During the COVID-19 pandemic, non susceptibility to sulfamethoxazole/trimethoprim and levofloxacin decreased significantly from 55.5% to 16.5% and 37.8% to 11.2%, respectively, whereas non susceptible samples to tetracycline had a significant increase from 13.3% to 32.3% (Figure 6). More than half of MRS strains were MDR (Figure 7), which 58.2% harbored SCC*mec* type V.







MDR

RESULTS

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 neonatal population and highlight possible effects of the pandemic in the dynamic of bacterial infectious diseases.

REFERENCES

Andrews WW, Schelonka R, Waites K, Stamm A, Cliver SP, Moser S. Genital tract methicillin-resistant Staphylococcus aureus: risk of vertical transmission in pregnant women. Obstet Gynecol. 2008 Jan;111(1):113-8. doi: 10.1097/01.AOG.0000298344.04916.11. PMID: 18165399. Argemi X, Hansmann Y, Prola K, Prévost G. Coagulase-Negative

Staphylococci Pathogenomics. Int J Mol Sci. 2019 Mar 11;20(5):1215. doi: 10.3390/ijms20051215. PMID: 30862021; PMCID: PMC6429511.

Becker K Both A Weißelberg S Heilmann C Robde H Emergence of

Becker K, Both A, Weißelberg S, Heilmann C, Rohde H. Emergence of coagulase-negative staphylococci. Expert Rev Anti Infect Ther. 2020 Apr;18(4):349-366. doi: 10.1080/14787210.2020.1730813. Epub 2020 Mar 2. PMID: 32056452.

Oliveira CF, Cavanagh JP, Fredheim EG, Reiter KC, Rieger A, Klingenberg C, d'Azevedo PA, Sollid JE. Coagulase-negative staphylococci in Southern Brazil: looking toward its high diversity. Rev Soc Bras Med Trop. 2016 May-Jun;49(3):292-9. doi: 10.1590/0037-8682-0015-2016. PMID: 27384825.

Del Vecchio VG, Petroziello JM, Gress MJ, McCleskey FK, Melcher GP, Crouch HK, Lupski JR. Molecular genotyping of methicillin-resistant Staphylococcus aureus via fluorophore-enhanced repetitive-sequence PCR. J Clin Microbiol. 1995 Aug;33(8):2141-4. doi: 10.1128/jcm.33.8.2141-2144.1995. PMID351.

Golińska E, Strus M, Tomusiak-Plebanek A, Więcek G, Kozień Ł, Lauterbach R, Pawlik D, Rzepecka-Węglarz B, Kędzierska J, Dorycka M, Heczko PB. Coagulase-Negative Staphylococci Contained in Gut Microbiota as a Primary Source of Sepsis in Low- and Very Low Birth Weight Neonates. J Clin Med. 2020 Aug 4;9(8):2517. doi: 10.3390/jcm9082517. PMID: 32759861; PMCID: PMC7464628.

Hirose M, Aung MS, Fukuda A, Murata Y, Saitoh M, Kobayashi N. Prevalence and Genetic Characteristics of Methicillin-Resistant Staphylococcus aureus and Coagulase-Negative Staphylococci Isolated from Oral Cavity of Healthy Children in Japan. Microb Drug Resist. 2019 Apr;25(3):400-407. doi: 10.1089/mdr.2018.0333. Epub 2019 Jan 29. PMID: 30694723

Ruppé E, Barbier F, Mesli Y, Maiga A, Cojocaru R, Benkhalfat M, Benchouk S, Hassaine H, Maiga I, Diallo A, Koumaré AK, Ouattara K, Soumaré S, Dufourcq JB, Nareth C, Sarthou JL, Andremont A, Ruimy R. Diversity of staphylococcal cassette chromosome mec structures in methicillin-resistant Staphylococcus epidermidis and Staphylococcus haemolyticus strains among outpatients from four countries. Antimicrob Agents Chemother. 2009 Feb;53(2):442-9. doi: 10.1128/AAC.00724-08. Epub 2008 Nov 10. PMID: 19001111; PMCID: PMC2630651.

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