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## BACKGROUND & OBJECTIVE

- 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;
- During the COVID-19 pandemic, changes in personal behavior, hygiene care and usage of antibiotics may have contributed to changes in microbiota and MDR emergence;
- Objective: to determine MRS anovaginal colonization rates among pregnant women considering the periods before (January 2019 to March 2020; 521; **T<sub>1</sub>**), during (May 2020 to June 2021; 360; **T<sub>2</sub>**) the pandemic and after the implementation of COVID-19 immunization protocols and relaxation of non-pharmaceutical interventions in Rio de Janeiro, Brazil (July 2021 to August 2022; 443; **T<sub>3</sub>**).

## METHODS

- Anovaginal samples (1324) were collected from pregnant women between the 35th and 37th gestational weeks and streaked on chromogenic media.

## RESULTS

- Overall, 534 (40.4%) samples were positive for MRS, including 9 distinct species;
- In general, MRS anovaginal colonization rates among pregnant women significantly increased from 8.6% (45) to 59.1% (213) during the onset of COVID-19, and to 62.3% (276) during the third period;
- S. haemolyticus* was the most prevalent species (MRSH), followed by *S. epidermidis* (MRSE), *S. saprophyticus* (MRSS), *S. aureus* (MRSA), and *S. sciuri* (MRSSC) (Figure 4);
- Non-susceptibility to sulfamethoxazole/trimethoprim and levofloxacin decreased significantly over time, whereas non susceptible samples to tetracycline had a significant increase over time (Figure 5); 35.4% (189) of the MRS strains were resistant to at least 3 different antimicrobial classes (MDR).
- Most of MRS strains carried SCCmec type V (54.9%) or could not be typed due to new combinations of *ccr* and *mecA* complex genes (Figure 6).

## CONCLUSION

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.

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## TAKE HOME POINTS...

- MRS colonization rates increased significantly during the COVID-19 pandemic;**
- S. haemolyticus* carrying SCCmec type V was the most prevalent amongst MRS isolates;**
- 35.4% of the MRS strains presented a MDR phenotype;**
- During the COVID-19 pandemic, the percentage of strains with non-typeable SCCmec increased significantly, being the combination *ccr* type 2, *ccr* type 5 and *mecA* class C the most common.**

Figure 4: MRS species colonization rates during different time periods.

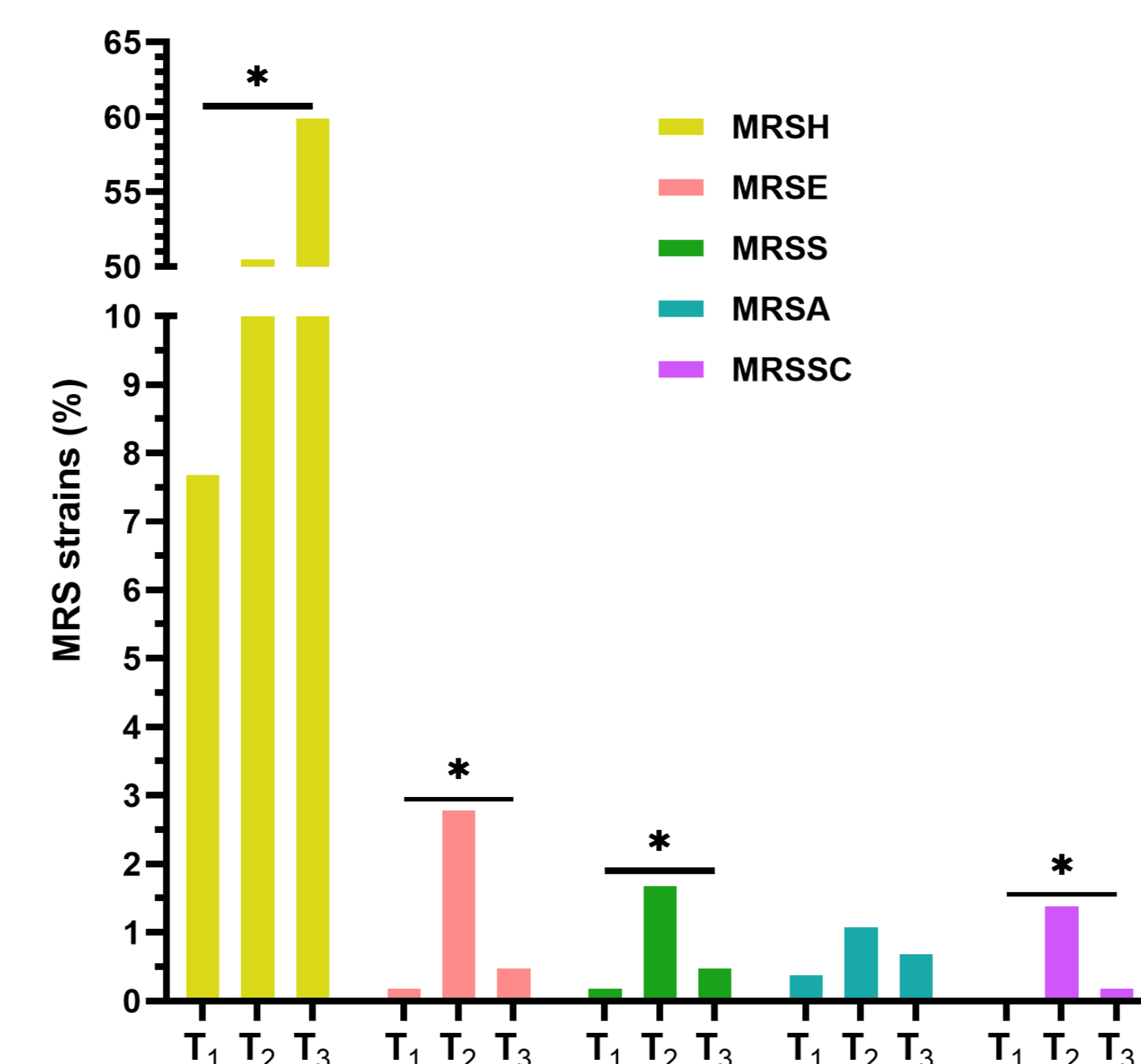


Figure 5: Non-susceptibility rates for MRS samples before and during COVID-19 pandemic.

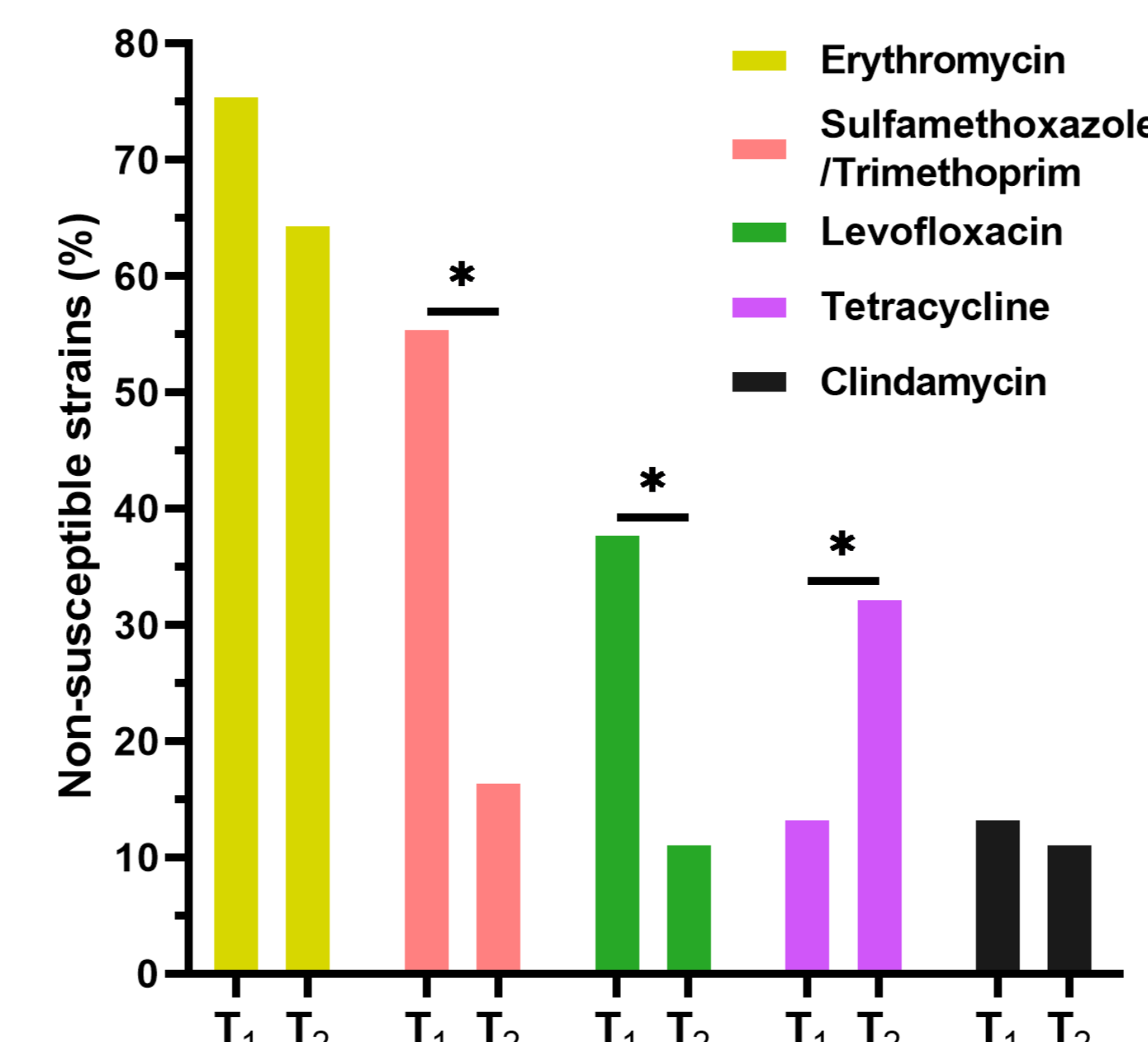
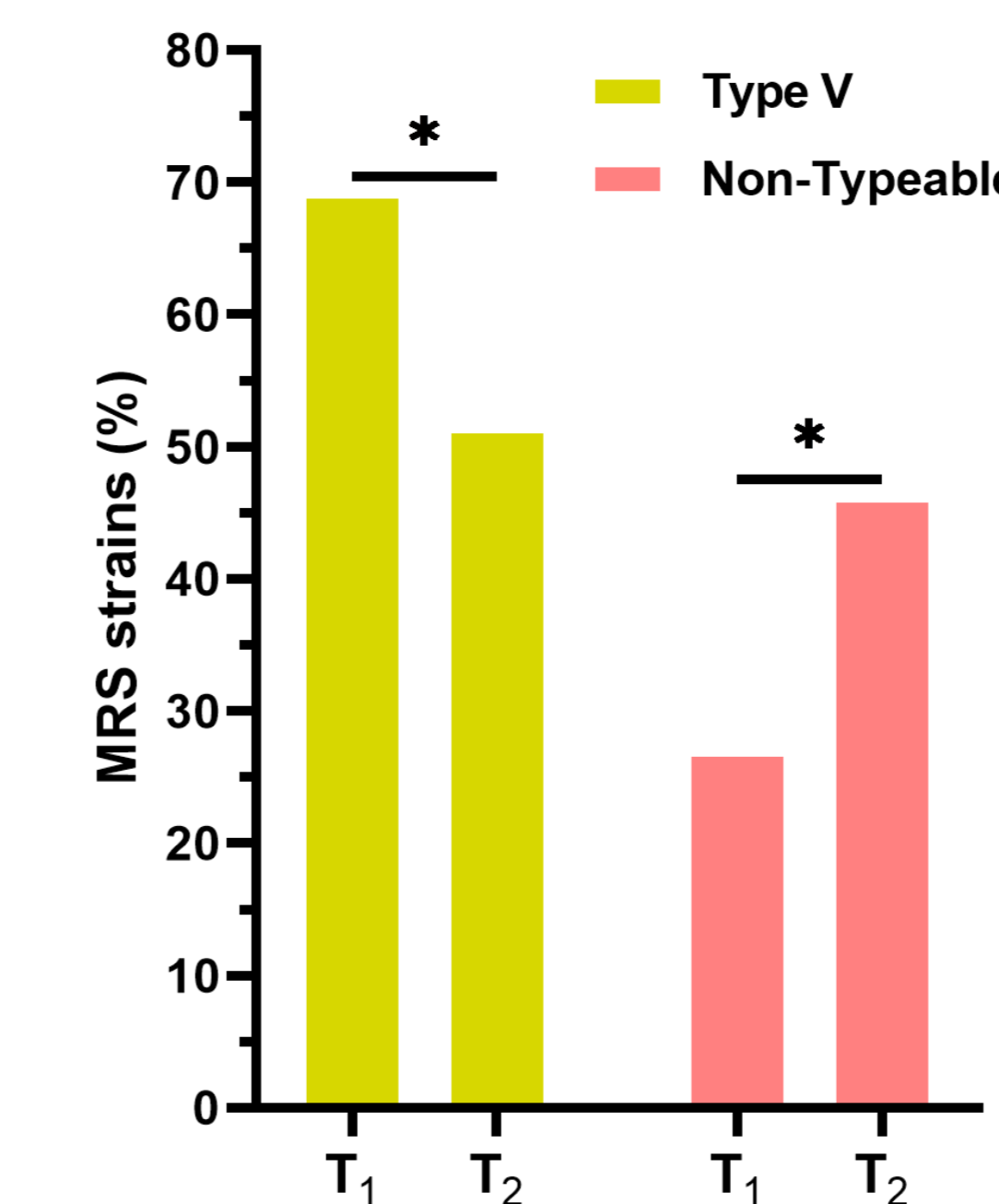


Figure 6: SCCmec type V and non-typeable distribution among MRS strains.



## ACKNOWLEDGMENTS

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Figure 1: Samples processing and identification using MALDI-TOF MS. Source: BioRender

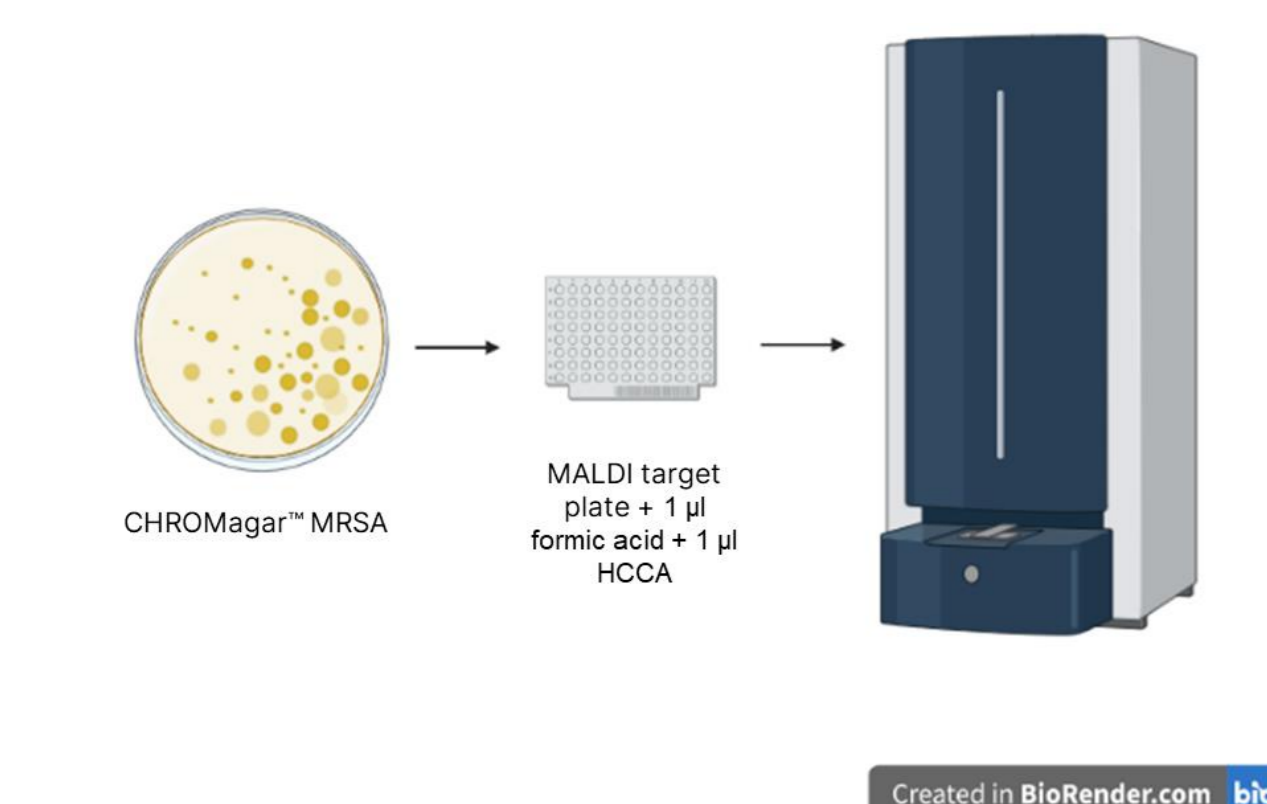


Figure 2: Disc diffusion assay. Source: BioRender.

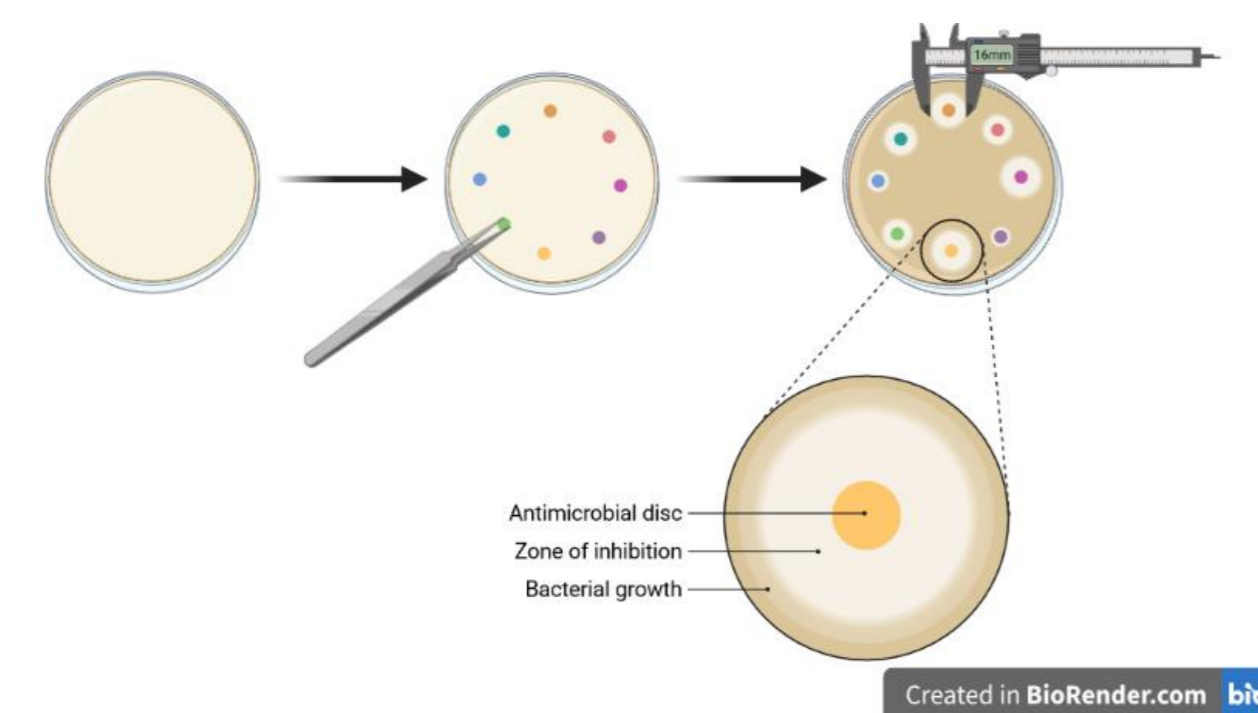


Figure 3: Detection of *mecA* gene and SCCmec typing using PCR. Source: BioRender.

