Methicillin-Resistant *Staphylococcus aureus* colonization among Pregnant women in Eastern Sri Lanka: Prevalence, Antibiotic Resistance, *mecA* gene detection, associated factors and outcomes

Introduction

- Methicillin resistant *Staphylococcus aureus* (MRSA) is a resistant phenotype.
- Potential cause of neonatal sepsis.
- This study aimed to determine the prevalence of MRSA colonization, identify the antibiotic sensitivity patterns and presence of the *mecA* gene in the isolates, and identify maternal factors associated with colonization and its impact on neonatal outcomes.

Methodology

Ethical approval

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Informed consent, Questionnaire, Sample collection instruction sheet

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Samples: Nasal, rectal & vaginal swabs

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Routine biochemical tests

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Staphylococcus aureus identification

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ABST – CLSI disc diffusion test

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MRSA – Cefoxitin ≤ 21 mm

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Conventional PCR - *mecA* gene detection

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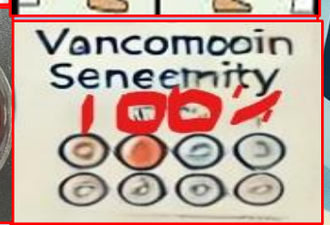
SPSS version 27.0

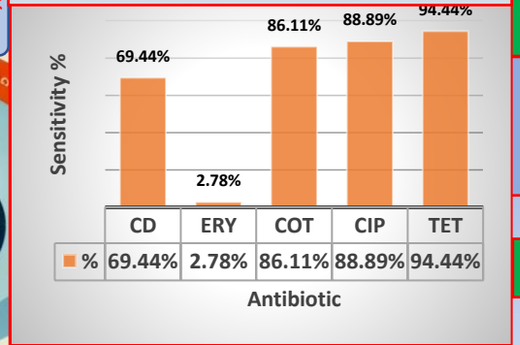


Results

Table 1: Prevalence of MRSA colonization

Bacteria	Number of pregnant women	Prevalence rate (%)
Nasal site only		
MRSA	9	3.83 %
Recto-vaginal site only		
MRSA	21	8.93%
Overall colonization		
MRSA	33	14.04 %

Table 2: Antibiotic sensitivity pattern of MRSA isolates



Vancomycin sensitivity – 100%

Table 3: Association between MRSA colonisation and maternal factors

Variable	Categories	Number of mothers	MRSA colonization	
			N	p-value
Admitted to hospital before delivery	No	176	27 (15.3%)	
	Yes	59	6 (10.2%)	0.391
Family history of skin disease	No	197	25 (12.7%)	
	Yes	38	8 (21.1%)	0.201
Anemic condition during pregnancy	No	221	28 (12.7%)	
	Yes	14	5 (35.7%)	0.032

Overall MRSA colonization and neonatal outcome

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No significant association

Conclusion

- MRSA colonization rate of 14.04%
- *mecA* gene present in 34 (94.44%) MRSA isolates

References

1. Nurjadi D et al., 2021
2. Chaurasia S et al., 2019