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**IDENTIFICATION OF *mecA* GENE ON CLINICAL ISOLATES
Staphylococcus aureus IN MOH. HOESIN GENERAL HOSPITAL (RSUP
MH) PALEMBANG**

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INTRODUCTION

Resistant to the antimicrobials and the spectrum of infection of *Methicillin resistant Staphylococcus aureus* (MRSA) remains serious problem worldwide. Resistance of MRSA was based on mutation of protein binding penicillin 2a encoded by *mecA* gene. Exact diagnosis of MRSA is to find the *mecA* gene¹.

METODE

The study was observational explorative to identify *mecA* gene of isolates from inpatients and outpatients in Moh. Hoesin General Hospital Palembang. We used PCR to identify the *mecA* according to Jonas et al (2002) with modification².

RESULT AND DISCUSSION

A total of 80 isolates we took and containing *Staphylococcus aureus*. A 23 isolates (28,8%) were pure of *Staphylococcus aureus* colonies, 5 isolates (6,3%) mixed with *Pseudomonas aeruginosa*, 5 isolates (6,3%) mixed with *Klebsiella pneumonia*, 3 (3,8%) isolates mixed with *Acinetobacter calcoaceticus*, 2 isolates (2,5%) mixed with *Escherichia coli*, 2 isolates (2,5%) mixed with *Proteus mirabilis*, 3 isolates (3,8%) mixed with *Candida sp* and the rest mixed with many species. We found 51 samples (63,8%) were positive of *mecA* gene. It was indicated that prevalence of MRSA high in our hospital³.



Picture 1. PCR result of *mecA* gene amplicon 147 bp. M is marker.

CONCLUSION

Prevalence of MRSA is high in our hospital.

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