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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

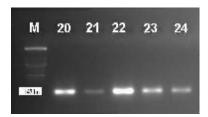
inpatients and outpatients in Moh. Hoesin General Hospital Palembang. We used

PCR to identify the *mec*A according to Jonas et al (2002) with modification².

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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 *mec*A gene. It was indicated that prevalence of MRSA high in our hospital³.



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

CONCLUSION

Prevalence of MRSA is high in our hospital.

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