APPLICATION OF *SPA-GENE* AS A MARKER OF MOLECULAR EPIDEMIOLOGY IN THE CASEOF *METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS* (MRSA) WHICH ITS FROM DAIRY COWS IN SURABAYA REGION

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ABSTRACT

The aim of this study was to isolate and identify the strain of *methicillin-resistant Staphylococcus aureus* (MRSA) from cow's milk in Surabaya and the determination of fragment *spa-Gene* in MRSA strains. Cow milk samples of 50 samples obtained from four dairy farm. The identification of 50 samples were obtained 19 samples (38%) positive bacterium *Staphylococcus aureus*. Antibiotic sensitivity testing using the antibiotic *oxacillin* and *erythromycin* showed 6 samples were resistant to the antibiotic *oxacillin* and 6 samples were resistant to the antibiotic *erythromycin*. MRSA confirmation test conducted on 6 samples obtained 5 positive of MRSA strain. The results of electrophoresis of *Polymerase Chain Reaction* (PCR) of 5 MRSA strain contained four positive samples showed the presence of fragment *spa-Gene*. Results showed that three models of picture fragments *spa-Gene*; The first has a length of 90 bp and 140 bp, second has a length 140 bp, and third with a length of 90 bp. This study reveals the nature of *spa-Gene* polymorphism of MRSA strains isolated from milk samples. It was concluded that the spa-gene can be used as a marker molecular epidemiology of MRSA strains.

Key words: *Staphylococcus aureus, methicillin-resistant Staphylococcus aureus* (MRSA), *spa-Gene,* polymorphism, epidemiology molecular