

Deteksi *Multi-Drug Resistant* (MDR) *Staphylococcus aureus* dari Kasus Medik Veteriner dan Manusia di Yogyakarta Berdasar Analisis Genomik Gen Resisten Berbagai Antibiotika

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INTISARI

Munculnya strain *Methicillin-Resistant Staphylococcus aureus* (MRSA) sebagai bakteri patogen berbahaya pada kasus medik veteriner dan manusia terus menjadi perhatian utama kesehatan masyarakat. Prevalensi MRSA sebagai penyakit zoonosis berbahaya terus meningkat secara global. *World Health Organization* memprediksi pada tahun 2050 MRSA akan menjadi penyebab kematian tertinggi di dunia. Penelitian ini bertujuan untuk mendeteksi prevalensi MRSA pada isolat *Staphylococcus aureus* (*S. aureus*) dari kasus medik veteriner dan manusia di Yogyakarta, Indonesia. Sebanyak 98 kasus infeksi *S. aureus* yang diuji pada penelitian ini terdiri dari 32 isolat asal sapi, 17 isolat asal kambing, dan 49 isolat asal manusia. Seluruh isolat dikonfirmasi sebagai *S. aureus* berdasarkan kultur bakteri dan deteksi gen 23S rRNA dan termonuklease *nuc* secara *Polymerase Chain Reaction* (PCR). Berdasarkan hasil pengujian 98 isolat, 55 isolat (56,1%) diidentifikasi sebagai MRSA melalui deteksi gen *mecA* penyandi resistensi metisilin melalui PCR. Strain MRSA paling banyak ditemukan pada isolat asal manusia (98%) diikuti sapi (15,6%) dan kambing (11,8%). Strain MRSA juga mengalami multiresisten (*multidrug-resistant*, MDR) terhadap penisilin, tetrasiklin, aminoglikosida, erlamisetin, makrolida dan linkosamid melalui deteksi gen penyandi resistensi *blaZ*, *tetK*, *tetM*, *aacA-D*, *ermC*, *msrB* dan *linA* secara berurutan dengan prevalensi sebanyak 56,1%. Resistensi terhadap tetrasiklin merupakan kejadian paling tinggi (100%) pada kedua kasus medik. Hasil sekuensing gen parsial 23S rRNA yang dianalisis menggunakan *Basic Local Alignment Search Tool* (BLAST) dan *software Molecular Evolutionary Genetics Analysis 11* (MEGA 11) menunjukkan bahwa isolat asal manusia dan hewan yang diuji identik 100% dan memiliki hubungan filogenetik yang sangat dekat (100%) terhadap *S. aureus* dari Jepang dan Mesir.

Kata kunci: Antibiotik, filogenetik, MRSA, *multidrug-resistant*, PCR

Detection of Multi-Drug Resistant (MDR) *Staphylococcus aureus* from Veterinary and Human Medical Cases in Yogyakarta Based on Genomic Analysis of Resistant to Various Antibiotics

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ABSTRACT

Emergence of Methicillin-Resistant *Staphylococcus aureus* (MRSA) a highly pathogenic bacteria strain in veterinary and human medical cases become public health concern. The prevalence of MRSA as dangerous zoonotic disease increased globally. World Health Organization estimates that by 2050 MRSA will be the leading cause of death. This study aimed to detect the prevalence of MRSA in *Staphylococcus aureus* (*S. aureus*) isolates from veterinary and human medical cases in Yogyakarta, Indonesia. A total of 98 cases of *S. aureus* infection were examined consisting of 32 cattle isolates, 17 goats isolates and 49 human isolates. All isolates were confirmed as *S. aureus* based on bacterial culture and 23S rRNA and *nuc* gene detection by Polymerase Chain Reaction (PCR). Among 98 isolates, 55 isolates (56.1%) were identified as MRSA by detected positive of *mecA* gene encoding methicillin resistance by PCR. The most common MRSA strains were found in human isolates (98%) followed by cattle isolates (15.6%) and goats isolates (11.8%). MRSA strain is also multidrug-resistant to penicillins, tetracyclines, aminoglycosides, erlamycetin, macrolides and lincosamides through the detection of resistance genes encoding *blaZ*, *tetK*, *tetM*, *aacA-D*, *ermC*, *msrB* and *linA* respectively, with prevalence was 56,1% on both setting. Resistance to tetracycline is the highest incidence (100%). Results of partial gene sequencing of 23S rRNA which were analyzed using the Basic Local Alignment Search Tool (BLAST) and MEGA 11 software showed that the isolates of human and animal origin tested were 100% identical and had a close phylogenetic relationship to *S. aureus* from Japan and Egypt.

Keywords: Antibiotics, phylogenetics, MRSA, multidrug-resistant, PCR