INTISARI

Senyawa antimikroba memegang peran penting dalam kehidupan manusia sebagai agen pengendali patogen penyebab penyakit. Namun, penggunaan senyawa antimikroba secara masif dan berlebihan dalam berbagai sektor, termasuk pertanian dan peternakan telah mendorong munculnya fenomena *antimicrobial resistance* (AMR). Gen AMR dapat tersebar dengan cepat melalui 2 mekanisme utama, yaitu *vertical gene transfer* (VGT) dan *horizontal gene transfer* (HGT). Tanah dan pupuk kandang diketahui merupakan reservoir utama bagi gen AMR. Sebagai bakteri tanah, *Streptomyces* berpotensi berperan sebagai agen penyebaran gen AMR di lingkungan. Penelitian ini bertujuan untuk mendeteksi keberadaan gen AMR pada isolat *Streptomyces* yang berasal dari sampel limbah organik di PIAT UGM serta melakukan identifikasi molekuler pada isolat pembawa gen AMR. Deteksi gen AMR dilakukan menggunakan metode multiplex PCR dan PCR konvensional dengan primer spesifik untuk 7 gen resistensi, yaitu *cmIV, blaOXY, mcr-1, aac-Iva, vanTC_2, ermX_2,* dan *tetX5*. Identifikasi molekuler didasarkan pada hasil sekuensing gen trpB. Hasil penelitian menunjukkan bahwa seluruh isolat yang diuji mengandung gen AMR dengan komposisi gen yang bervariasi pada masing-masing isolat. Gen *mcr-1, tetX5,* dan *ermX_2* terdeteksi pada seluruh isolat uji. Gen *aac-Iva, blaOXY,* dan *cmIV* tidak terdeteksi pada sebagian kecil isolat (1-2 isolat), sedangkan gen *vanTC_2* terdeteksi pada 3 isolat. Seluruh isolat berpotensi mengalami *multidrug resistance* (MDR) karena mengandung > 1 gen resistensi. Isolat WTP-1 diketahui memiliki hubungan kekerabatan yang dekat dengan *Streptomyces* sp. WAC00288 dan *Streptomyces cinereoruber* strain ATCC 19740.

Kata kunci: *antimicrobial resistance* (AMR), *Streptomyces*, gen resistensi antibiotik, limbah organik, PCR

ABSTRACT

Antimicrobial compounds play an essential role in controlling disease-causing pathogens. However, the excessive and widespread use of antimicrobials in various sectors, including agriculture and livestock production, has accelerated the emergence of antimicrobial resistance (AMR). AMR genes can spread rapidly through vertical gene transfer (VGT) and horizontal gene transfer (HGT), with soil and manure acting as major environmental reservoirs. As soil-dwelling bacteria, *Streptomyces* spp. have the potential to contribute to the dissemination of AMR genes in the environment. This study aimed to detect AMR genes in *Streptomyces* isolates obtained from organic waste samples at PIAT UGM and to perform molecular identification of AMR gene–carrying isolates. AMR gene detection was conducted using multiplex PCR and conventional PCR targeting 7 resistance genes, namely *cmIV, blaOXY, mcr-1, aac-Iva, vanTC_2, ermX_2,* and *tetX5*. Molecular identification was based on sequencing of the trpB genes.The results showed that all tested isolates harbored AMR genes, with varying gene compositions among isolates. The *mcr-1, tetX5,* and *ermX_2* genes were detected in all isolates. The *aac-Iva*, *blaOXY*, and *cmIV* genes were not detected in a small number of isolates (1–2 isolates), whereas the *vanTC_2* gene was detected in three isolates. All isolates exhibited potential multidrug resistance (MDR) due to the presence of more than one resistance gene. Isolate WTP-1 showed a close phylogenetic relationship with *Streptomyces* sp. WAC00288 and *Streptomyces cinereoruber* strain ATCC 19740.

Keywords: antimicrobial resistance, *Streptomyces*, antibiotic resistance genes, organic waste, PCR