

## RINGKASAN

Bakteri *Streptomyces* spp. asal rhizosfer tanaman mangrove *Bruguiera* sp., *Sonneratia* sp., *Rhizophora* sp., *Aegiceras corniculatum* dan *Avicennia marina* telah berhasil diisolasi. Bakteri *Streptomyces* spp. tersebut terbukti menghasilkan aktivitas antibakteri yang mampu menghambat pertumbuhan *Stapylococcus aureus* dan *Eschericia coli*. Seleksi isolat potensial dilakukan berdasarkan pada tingginya kemampuan isolat dalam memproduksi aktivitas antibakteri. Sebanyak lima isolat potensial dianalisis lebih lanjut pada tahap molekuler dan kekerabatan spesies.

Penelitian ini bertujuan untuk mendeteksi adanya gen Nonribosomal Peptide Synthetase (NRPS) pada bakteri *Streptomyces* spp. yang mampu menghambat pertumbuhan *S. aureus* dan *E. coli*, mengetahui karakteristik gen tersebut dan mengetahui hubungan kekerabatan isolat *Streptomyces* spp. berdasarkan gen penyandi NRPS. Deteksi gen NRPS dilakukan melalui tahapan isolasi DNA bakteri *Streptomyces* potensial, amplifikasi gen NRPS melalui teknik PCR, elektroforesis gel, sekuensing DNA, analisis sekuen DNA menggunakan *software* BioEdit, analisis prediksi produk metabolit sekunder menggunakan program AntiSmash dan analisis filogenetik menggunakan program MEGA.

Hasil analisis menunjukkan 5 isolat yang diteliti terdeteksi memiliki gen NRPS, dengan ukuran nukleotida sekitar 700 bp. Sebanyak 3 isolat berhasil terkualifikasi untuk dianalisis sekuensing. Berdasarkan jarak genetik pada sekuen setiap isolat, isolat *Streptomyces* sp. E401, *Streptomyces* sp. E403, dan *Streptomyces* sp. E461 memiliki nilai kekerabatan yang cukup dekat karena memiliki nilai jarak genetik 0,4-0,6. Hasil analisis sekuen homolog dapat digunakan untuk prediksi metabolit sekunder *Streptomyces* spp. Secara umum, prediksi sekuen NRPS *Streptomyces* spp. memiliki homologi dengan beberapa klaster gen, meliputi *Streptomycin biosynthetic gene cluster* dan *Syringomycin biosynthetic gene cluster*. Prediksi metabolit sekunder yang dihasilkan menunjukkan Streptomisin dan Siringomisin.

**Kata Kunci** : *Streptomyces*, kekerabatan, gen NRPS, antibakteri, metabolit sekunder

## SUMMARY

*Streptomyces* spp. bacteria obtained from *Bruguiera* sp., *Sonneratia* sp., *Rhizophora* sp., *Aegiceras corniculatum* and *Avicennia marina* mangrove plants rhizosphere were isolated. Those *Streptomyces* spp. bacteria positively produced antibacterial activity that capable to inhibit the growth of *Staphylococcus aureus* and *Escherichia coli*. Selection of potential isolates was performed based on the high ability of isolates to produce antibacterial activity. Five potential isolates were further analyzed at the molecular and genetic relationship levels.

This study aims to detect Non Ribosomal Peptide Synthetase (NRPS) encoding gene in *Streptomyces* spp. bacteria capable to inhibit the growth of *S. aureus* and *E. coli*, to know their gene characters and genetic relationship based on NRPS encoding gene. The research was performed by following steps: DNA isolation of potential *Streptomyces* spp. bacteria, Amplification of NRPS gene using PCR technique, Gel electrophoresis, DNA sequencing, Analysis of DNA sequence using BioEdit software, prediction analysis of secondary metabolite products using AntiSmash program and Phylogenetic analysis using MEGA program.

The analysis showed that 5 isolates studied had NRPS encoding genes, with nucleotide size around 700 bps. Three isolates were successfully qualified for sequencing analysis. Based on genetic distance in each isolate sequence, *Streptomyces* sp. E401, *Streptomyces* sp. E403, and *Streptomyces* sp. E461 isolates showed high similarity because they had 0.4-0.6 genetic distance value. The homologous sequence analysis results can be used to predict secondary metabolites generated from *Streptomyces* spp. In general, predicted sequences have homology in several clusters of genes, including Streptomycin biosynthetic gene cluster and Syringomycin biosynthetic gene cluster. The secondary metabolites synthesized were predicted as Streptomycin and Siringomycin.

**Keywords:** *Streptomyces*, genetic relationship, NRPS gene, antibacterial, secondary metabolites

