

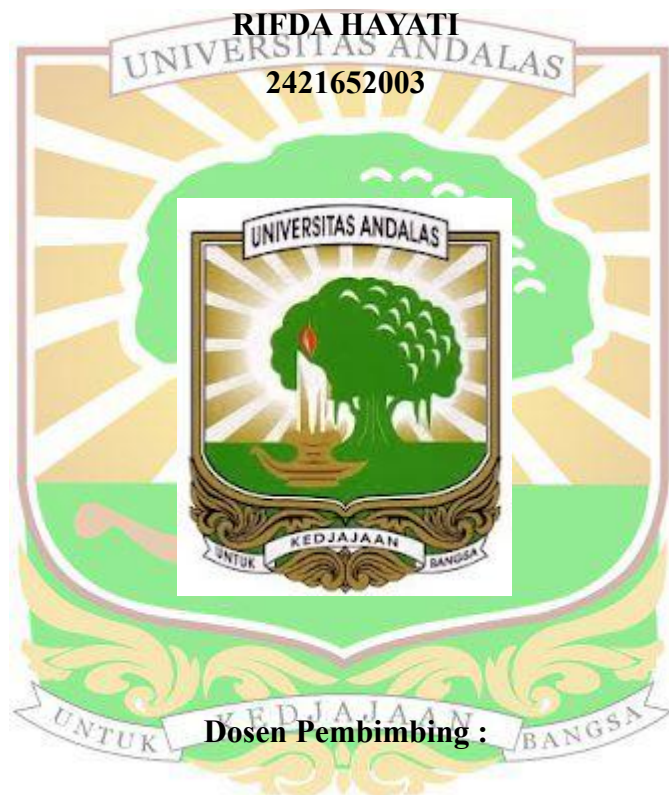
**KAJIAN METAGENOMIK KOMUNITAS BAKTERI DAN  
METABOLOMIK DARI GENUS *Streptomyces* ISOLAT  
TANAH MANGROVE KAWASAN MANDEH**

**TESIS**

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**PROGRAM PASCASARJANA**

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# KAJIAN METAGENOMIK KOMUNITAS BAKTERI DAN METABOLOMIK DARI GENUS *Streptomyces* ISOLAT TANAH MANGROVE KAWASAN MANDEH

Oleh : RIFDA HAYATI (2421652003)

(Dibawah bimbingan: Prof. apt. Marlina, MS., Ph.D dan Prof. Dr. Anthoni Agustien, M.Si.)

## Abstrak

Ekosistem hutan mangrove merupakan habitat unik dengan keanekaragaman mikroorganisme yang tinggi dan berpotensi sebagai sumber senyawa bioaktif. Penelitian ini bertujuan untuk mengkaji keanekaragaman komunitas bakteri tanah mangrove menggunakan pendekatan metagenomik serta mengidentifikasi potensi metabolit menggunakan pendekatan metabolomik dari genus *Streptomyces* di Kawasan Mandeh, Kabupaten Pesisir Selatan, Sumatera Barat. Analisis metagenomik dilakukan menggunakan teknologi *Next-Generation Sequencing* (NGS) berbasis *Oxford Nanopore Technology* (ONT) dengan target gen 16S rRNA region V1–V9. Isolasi dan identifikasi *Streptomyces* dilakukan secara morfologi dan molekuler, sedangkan analisis metabolomik dilakukan menggunakan metode *Liquid Chromatography–High Resolution Mass Spectrometry* (LC-HRMS). Hasil analisis metagenomik menunjukkan bahwa sampel tanah mangrove mengandung 4.309 spesies bakteri. Spesies yang mendominasi komunitas bakteri adalah *Ilumatobacter fluminis*. Isolat *Streptomyces* yang berhasil diperoleh dari tanah mangrove Kawasan Mandeh memiliki kekerabatan dengan *Streptomyces roseoviridis*. Analisis metabolomik menggunakan LC-HRMS berhasil mengidentifikasi sekitar 244 senyawa metabolit. Dari 30 senyawa yang dianalisis lebih lanjut, teridentifikasi dua senyawa yang berkaitan dengan aktivitas antibakteri, yaitu *betaine* ( $C_5H_{11}NO_2$ ) dan *neohydroxyaspergillic acid* ( $C_{12}H_{20}N_2O_3$ ). Hasil penelitian ini menunjukkan bahwa isolat *Streptomyces* yang diperoleh dari tanah mangrove Kawasan Mandeh memiliki potensi dalam menghasilkan metabolit antibakteri, serta mendukung penerapan pendekatan multi-omik dalam eksplorasi mikroorganisme lingkungan.

Kata kunci: mangrove, *Streptomyces*, metagenomik, metabolomik, antibakteri

# METAGENOMIC STUDY OF BACTERIAL COMMUNITIES AND METABOLOMICS OF THE GENUS *Streptomyces* ISOLATES FROM MANGROVE SOIL IN THE MANDEH REGION

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## Abstract

*Mangrove forest ecosystems are unique habitats with high microorganism diversity and potential as sources of bioactive compounds. This study aims to examine the diversity of mangrove soil bacterial communities using a metagenomic approach and to identify potential metabolites using a metabolomic approach from the Streptomyces genus in the Mandeh area, Pesisir Selatan Regency, West Sumatra. Metagenomic analysis was performed using Next-Generation Sequencing (NGS) technology based on Oxford Nanopore Technology (ONT) with the target gene 16S rRNA region V1–V9. Streptomyces isolation and identification were performed morphologically and molecularly, while metabolomic analysis was performed using the Liquid Chromatography–High Resolution Mass Spectrometry (LC-HRMS) method. The results of metagenomic analysis showed that mangrove soil samples contained 4,309 bacterial species. The species that dominated the bacterial community was *Ilumatobacter fluminis*. Streptomyces isolates successfully obtained from the mangrove soil of the Mandeh area were related to *Streptomyces roseoviridis*. Metabolomic analysis using LC-HRMS successfully identified approximately 244 metabolite compounds. Of the 30 compounds that were further analyzed, two compounds related to antibacterial activity were identified, namely betaine ( $C_5H_{11}NO_2$ ) and neohydroxyaspergillic acid ( $C_{12}H_{20}N_2O_3$ ). The results of this study indicate that Streptomyces isolates obtained from the mangrove soil of the Mandeh area have the potential to produce antibacterial metabolites and support the application of a multi-omic approach in the exploration of environmental microorganisms.*

*Keywords: mangrove, Streptomyces, metagenomics, metabolomics, antibacterial*