

ABSTRAK

Ruth Natalia Siagian, NIM 4213520006 (2021). Identifikasi Bakteri Endofit Penghasil Enzim L-Asparaginase Pada Tumbuhan Mangrove (*Excoecaria agallocha*) Menggunakan Pendekatan Metagenomik.

Tumbuhan mangrove *Excoecaria agallocha* merupakan habitat potensial bagi bakteri endofit yang mampu menghasilkan berbagai senyawa bioaktif, termasuk enzim L-Asparaginase yang memiliki aplikasi penting dalam terapi kanker dan industri pangan. Penelitian ini bertujuan untuk mengidentifikasi bakteri endofit penghasil enzim pada daun *Excoecaria agallocha* dengan menggunakan pendekatan metagenomik. Isolasi DNA dilakukan menggunakan ZymoBIOMICS DNA Miniprep Kit, kemudian dianalisis melalui *Next Generation Sequencing* (NGS) pada gen 16S rRNA (V1-V9) dan diolah dengan Oxford Nanopore Technologies (ONT). Hasil analisis menunjukkan bahwa komunitas bakteri endofit pada daun *Excoecaria agallocha* memiliki keanekaragaman yang tinggi, dengan dominasi filum *Pseudomonadota* (41,76%) dan *Bacillota* (23,53%). Genus yang paling banyak ditemukan antara lain *Bacillus*, *Pantoea*, *Enterobacter*, *Aeromonas*, *Klebsiella*, dan *Vibrio*. Beberapa spesies seperti *Bacillus altitudinis*, *Pantoea anthophilam* dan *Cytobacillus firmus* teridentifikasi berpotensi menghasilkan enzim L-Asparaginase berdasarkan hasil analisis bioinformatika. Temuan ini dapat memperkaya sumber alami enzim L-Asparaginase melalui tanaman mangrove untuk aplikasi bioteknologi.

Kata kunci : *Excoecaria agallocha*, bakteri endofit, L-Asparaginase, metagenomik.

ABSTRACT

Ruth Natalia Siagian, NIM 4213520006 (2021). Identification of Endophytic Bacteria Producing L-Asparaginase Enzyme in Mangrove Plant (*Excoecaria agallocha*) Using a Metagenomic Approach.

The mangrove plant *Excoecaria agallocha* serves as a potential habitat for endophytic bacteria capable of producing various bioactive compounds, including the enzyme L-Asparaginase, which plays an important role in cancer therapy and the food industry. This study aimed to identify endophytic bacteria producing L-Asparaginase from the leaves of *Excoecaria agallocha* using a metagenomic approach. DNA isolation was performed using the ZymoBIOMICS DNA Miniprep Kit, followed by *Next Generation Sequencing (NGS)* targeting the 16S rRNA (V1-V9) gene region and analyzed using Oxford Nanopore Technologies (ONT). The result revealed a high diversity of endophytic bacterial communities, dominated by the phyla *Pseudomonadota* (41.76%) and *Bacillota* (23.53%). The predominant genera included *Bacillus*, *Pantoea*, *Enterobacter*, *Aeromonas*, *Klebsiella*, and *Vibrio*. Bioinformatics analysis indicated that several species such as *Bacillus altitudinis*, *Pantoea anthophila*, and *Cytobacillus firmus* have the potential to produce L-Asparaginase. This study broadens the understanding of the potential of mangrove endophytic bacteria as a natural source of L-Asparaginase for biotechnological applications.

Keywords : *Excoecaria agallocha*, endophytic bacteria, L-Asparaginase, metagenomics.