

KARAKTERISASI MOLEKULER GEN 16S rRNA BAKTERI SIMBIOTIK PADA *Aedes aegypti* Linn

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INTISARI

Sekitar 15% spesies serangga termasuk *Aedes aegypti* memiliki bakteri simbion. Bakteri tersebut sebagai mikrobiota ditemukan pada berbagai lokasi di dalam rongga tubuh inang antara lain organ reproduktif, usus, *haemolymph* dan kelenjar ludah. Penelitian ini bertujuan untuk menganalisis keanekaragaman bakteri simbiotik di dalam tubuh populasi *Ae. aegypti* dan mengidentifikasi bakteri simbiotik tersebut secara molekuler berdasarkan analisis gen 16S rRNA. Pelaksanaan penelitian ini meliputi isolasi bakteri, deteksi dan identifikasi isolat bakteri simbiotik berdasarkan karakter morfologi, biokimia dan molekuler (analisis amplifikasi dan sekuensing gen 16S rRNA). Hasil penelitian menunjukkan adanya 2 tipe bakteri, yaitu tipe bakteri yang dapat dikulturkan (sembilan isolat) dan tipe bakteri yang tidak dapat dikulturkan. Berdasarkan hasil analisis keanekaragaman dan kemelimpahan menunjukkan bahwa perut *Ae. aegypti* merupakan bagian tubuh nyamuk yang memiliki indeks keanekaragaman bakteri paling tinggi, isolat dengan kemelimpahan tertinggi yaitu BAbL2.5 dan BAbL2.6. Analisis morfologi, biokimia dan molekuler diperoleh sembilan isolat bakteri simbiotik berbentuk batang, bersifat Gram positif mirip dengan golongan *Bacilli* yaitu *Bacillus cereus* (BThL1.8), *Lysinibacillus fusiformis* (BAbL2.4 dan BAbL2.9), bersifat Gram negatif mirip dengan golongan *Gammaproteobacteria* yaitu *Serratia oryzae* (BAbL2.5 dan BAbL2.7), *Aeromonas taiwanensis* (BLaL2.1 dan BLaL2.3) dan *Alphaproteobacteria* yaitu *Asaia bogorensis* (BAbL2.6 dan BAbL2.8). Sembilan isolat tersebut merupakan bakteri yang dapat dikulturkan (bakteri *culturable*) dengan ukuran basa gen 16S rRNA sekitar 1351-1655 bp.

Kata kunci : Bakteri simbiotik, mikrobiota, midgut, gen 16S rRNA, *Aedes aegypti*, karakterisasi molekuler

MOLECULAR CHARACTERIZATION 16S rRNA GENE OF SYMBIOTIC BACTERIA ON *Aedes aegypti* Linn

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ABSTRACT

Almost 15% of all insects including *Aedes aegypti* possess bacterial symbiont. This bacteria as microbiota were found in various site of insect's body including the reproductive organs, intestines, haemolymph and the salivary glands. The aims of this research were to analyzed the diversity of symbiotic bacteria in the body of *Ae. aegypti* population and to identify the symbiotic bacteria based on 16S rRNA gene analysis. The implementation of this research including bacterial isolation, detection and identification of symbiotic bacterial isolates based on morphological, biochemical and molecular characters (amplification and sequencing of 16S rRNA gene analysis). The results of this research showed there are 2 types of bacteria, i.e. culturable bacteria (nine isolates) and unculturable bacteria. Based on diversity and abundance analysis showed that abdomen of *Ae. aegypti* was part of mosquitoes body having highest bacterial diversity index, isolates having highest abundance were BAbL2.5 and BAbL2.6. Morphology, biochemical and molecular analysis obtained nine isolates of symbiotic bacteria were having rod-shaped, Gram positive similar to class of *Bacilli* i.e. *Bacillus cereus* (BThL1.8), *Lysinibacillus fusiformis* (BAbL2.4 and BAbL2.9); Gram negative bacteria similar to class of *Gammaproteobacteria* i.e. *Serratia oryzae* (BAbL2.5 and BAbL2.7), *Aeromonas taiwanensis* (BLaL2.1 and BLaL2.3), and class of *Alphaproteobacteria* i.e. *Asaia bogorensis* (BAbL2.6 and BAbL2.8). This isolates were could be cultured bacteria (culturable bacteria) with size of 16S rRNA gene bases about 1351-1655 bp.

Keywords : Symbiotic bacteria, microbiota, midgut, 16S rRNA gene, *Aedes aegypti*, molecular characterization