MOLECULAR CHARACTERIZATION 16S RRNA GENE OF ENDOSYMBIOTIC BACTERIALISOLATESFROM AEDES AEGYPTI MOSQUITOE

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Abstract - Almost 15% of all insects including Aedes aegypti possess bacterial endosymbiont. This bacteria as microbiota could be found in various site of insect's body including the reproductive organs, intestines, haemolymph and the salivary glands. The aim of this research was to analize the diversity of symbiotic bacteria in the bodyof Ae. aegypti population and to identify the symbiotic bacteria based onbiochemical and 16S rRNA gene analysis. The implementation of this research including bacterial isolation, detection and identification of endosymbiotic bacterial isolates based on biochemical and molecular characters (amplification and sequencing of 16S rRNA gene analysis). The results of this research showed there are nine bacterial isolates was discovered in Ae. aegypti. Based on phylogenetic molecular analysis, amplification and sequencing of 16S rRNA gene analysis indicated thatalmost all of isolates belongs to the Gammaproteobacteria, Alphaproteobacteria, and Firmicutes.Symbiotic bacterial isolates were rod-shaped cells, Gram positivebacteria (three isolates), Gram negativebacteria (six isolates), and located in the cytoplasmic cells of mosquitoe's midgut. Identification results of Gram positive bacterial isolates were having properties similar to Bacillus cereus (strain B.TH.L1.8), Lysinibacillus fusiformis (strain B.AB.L2.4 and B.AB.L2.9); the Gram negative bacterial isolates were resembled to Rahnella sp. (strain B.AB.L2.5 and B.AB.L2.7), Asaia bogorensis (strain B.AB.L2.6 and B.AB.L2.8), Aeromonas hydrophila (strain B.LA.L2.1) and Aeromonas dhakensis (strain B.LA.L2.3). Conclussion of the research showed that most of the bacterial endosymbionts were gram negative bacteria, having rod-shaped with bases size of 1351-1655 bp.

Keywords - Endosymbiotic bacterial, Aedes aegypti, 16S rRNA gene, molecular characterization