

GENETIC DIVERSITY OF *Aedes aegypti* (DIPTERA: CULICIDAE) ISOLATED FROM FIVE CITIES IN NORTH COAST AREA OF CENTRAL JAVA, INDONESIA

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Abstract. The tropical mosquito *Aedes aegypti* is the major vector in the transmission of human arboviruses, including chikungunya, dengue and yellow fever viruses. All provinces in the Indonesian archipelago have reported incidences of dengue. In order to study the genetic diversity and the dispersal of *Ae. aegypti* in Central Java, genetic analyses based on mitochondria cytochrome oxidase 1 gene (mtCOI) were performed on *Ae. aegypti* isolated in five cities along the national North Coast road of Central Java. Seventeen representative mtCOI fragments from either larvae or adult mosquitoes were PCR-amplified, sequenced and analyzed for sequence polymorphism, haplotype and genetic differentiation. A phylogenetic tree was constructed using maximum likelihood method and general time reversible model. There were seven haplotypes and the presence of different haplotypes in the cities was indicative of the heterogeneity of *Ae. aegypti* in Central Java. Gene flow and genetic differentiation analyses revealed no differentiation among populations from the cities. The possible gene flow between populations may reflect an active dispersal of *Ae. aegypti* among the cities as a result of movement of traffic along the national North Coast road of Central Java.

Keywords: *Aedes aegypti*, haplotype, mitochondria COI, Central Java, Indonesia

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