NEW GENETIC VARIATION OF AEDES ALBOPICTUS DENSOVIRUS ISOLATED FROM MOSQUITO C6/36 CELL LINE

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Abstract. Densovirus (DNV) is a small single-stranded DNA, non-enveloped virus belonging to the subfamily Densovirinae of the Parvoviridae family. This group of invertebrate viruses infects exclusively insects. Two of the major densoviruses, Aedes aegypti (AaeDNV) and Ae. albopictus (AalDNV), infect mosquitoes that carry viruses responsible for two important public health diseases, namely, dengue hemorrhagic fever and yellow fever. The present study describes cloning, sequencing and phylogenetic analysis of a new densovirus, AalDNV-4, from infected Ae. albopictus C6/36 cell line. The total nucleotide sequence (3.9 kb) of AalDNV-4 was obtained from sequencing of DNA fragments, and is 98% homologous to the initial AalDNV previously isolated, and distinguishable from other AalDNVs reported earlier. This full-length viral genome contains a 40-bp deletion at the left terminal region, 12 substitutions and 3 indels. Phylogenetic analysis of AalDNV-4 genome indicates that this virus is more closely related to the original AalDNV found in C6/36 cell line than to AaeDNV isolated from other mosquitoes. It was concluded that AalDNV-4 may have been derived from the original DNV found in the C6/36 cell line and has transferred worldwide from the exchange of this cell line among laboratories.

Keywords: Aedes albopictus, Densovirus, C6/36, genetic variation

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