Thesis Title Cloning and Sequencing of PDK 13 Vaccine Candidate of Dengue Virus Type 1

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ABSTRACT

An envelope (E) gene coding region of the dengue-1 16007 PDK13 candidate vaccine virus was sequenced, aligned, and compared with E gene of the dengue-1 16007 parental virus (sequence data obtained from Center for Disease Control, U.S.A). A comparison results show 9 of 1485 or 0.6 % nucleotide differences between the parental strain (dengue-1 16007) and its progeny (dengue-1 16007 PDK13), of which about 4 of 9 nucleotides are silent. The remaining 5 nucleotide changes led to 5 of 495 or 1.0 % amino acid alterations in E protein of the virus. Three amino acid changes are clustered around amino acid position 87, 88 and 108 within domain A of TBE E protein model (TBE E protein model was proposed by Heinz and coworkers). The remaining changes are amino acid position 384 and 401 which located

within domain B and C of TBE E protein model respectively. However, the molecular basis of attenuation of dengue-1 16007 PDK 13 virus, attributable to the E protein, remains unclear.