

DNA Barcoding for Identification of Dengue Vectors from Assam and Arunachal Pradesh: North-Eastern States in India

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Abstract : *Aedes aegypti* and *Aedes albopictus* are considered as two major vectors to transmit dengue virus. In North-east India, two states viz. Assam and Arunachal Pradesh are known to be high endemic zone for dengue and Chikungunya viral infection. The taxonomical classification of medically important vectors are important for mapping of actual evolutionary trends and epidemiological studies. However, misidentification of mosquito species in field-collected mosquito specimens could have a negative impact which may affect vector-borne disease control policy. DNA barcoding is a prominent method to record available species, differentiate from new addition and change of population structure. In this study, a combined approach of a morphological and molecular technique of DNA barcoding was adopted to explore sequence variation in mitochondrial cytochrome c oxidase subunit I (COI) gene within dengue vectors. The study has revealed the map distribution of the dengue vector from two states i.e. Assam and Arunachal Pradesh, India. Approximate five hundred mosquito specimens were collected from different parts of two states, and their morphological features were compared with the taxonomic keys. The analysis of detailed taxonomic study revealed identification of two species *Aedes aegypti* and *Aedes albopictus*. The species *aegypti* comprised of 66.6% of the specimen and represented as dominant dengue vector species. The sequences obtained through standard DNA barcoding protocol were compared with public databases, viz. GenBank and BOLD. The sequences of all *Aedes albopictus* have shown 100% similarity whereas sequence of *Aedes aegypti* has shown 99.77 - 100% similarity of COI gene with that of different geographically located same species based on BOLD database search. From dengue prevalent different geographical regions fifty-nine sequences were retrieved from NCBI and BOLD databases of the same and related taxa to determine the evolutionary distance model based on the phylogenetic analysis. Neighbor-Joining (NJ) and Maximum Likelihood (ML) phylogenetic tree was constructed in MEGA6.06 software with 1000 bootstrap replicates using Kimura-2-Parameter model. Data were analyzed for sequence divergence and found that intraspecific divergence ranged from 0.0 to 2.0% and interspecific divergence ranged from 11.0 to 12.0%. The transitional and transversional substitutions were tested individually. The sequences were deposited in NCBI: GenBank database. This observation claimed the first DNA barcoding analysis of *Aedes* mosquitoes from North-eastern states in India and also confirmed the range expansion of two important mosquito species. Overall, this study insight into the molecular ecology of the dengue vectors from North-eastern India which will enhance the understanding to improve the existing entomological surveillance and vector incrimination program.

Keywords : COI, dengue vectors, DNA barcoding, molecular identification, North-east India, phylogenetics

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