Ribosomal DNA second internal transcribed spacer (ITS2) sequences of *Anophele culicifacies* (Diptera :Culicidae) species B and E in Sri Lanka and their phylogeneti relationship to other members of the complex

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Cytogenetically identified two forms designated as *Anopheles culicifacies* species B and found in Sri Lanka were analysed to see any sequence divergence in ITS2 of the rDN cistron. The sequence data of the ITS2 region of species B and E were complete identical and the length of the region is 367bp.

The genetic relatedness of Sri Lankan species to the same (B & E) and the differe counterpart siblings (A, C & D) of *Anopheles culicifacies* from different geographic regior (India, Cambodia, Iran and China) was investigated using the sequence derived from th internal transcribed spacer 2 (ITS2) of rDNA cistron. Previously deposited 17 ITS sequences of *An. culicifacies* siblings were retrieved from the GenBank. The phylogenet tree was constructed by Maximum Likelihood method with molecular clock version 3.573 after aligning the ITS2 sequences of *An. culicifacies* by the computer programm CLUSTER W. Phylogenic analysis revealed two main lineages categorizing siblings B, & C into one group and A & D into another, which were further divided into 8 levels c scrutiny. Amongst these with few exceptions, siblings B & E were found to have a identical sequence, similarly, A & D. Further, analysis pointed out that sibling B genetically diverse than that of its other sibling counterparts as they fell into thre genetically distinct levels in the phylogentic tree. This suggests that sibling B is mor polymorphic than the others. Finally, using the nucleotide difference between the two ma lineages, node time and length we estimate that the divergences between these lineage may have occurred much earlier and over a longer period of time, while the present siblir species have evolved in the recent past at a high evolutionary rate.

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