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PS-031. Molecular phylogeny of Ochlerotatus species inferred from COI sequences

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Accurate identification of mosquito species is essential in epidemiological studies of vector-borne pathogens. Among these vectors, Ochlerotatus is a large highly varied group of cryptic species with similar morphological characters shared by members of species complexes. Here we presented molecular identification of three Ochlerotatus species using a short fragment of the mitochondrial cytochrome c oxidase subunit I (COI) sequence serving as a DNA bio-barcode. The nucleotide sequence from each specimen was compared with barcode sequences on NCBI using nucleotide Basic Local Alignment Search Tool (BLASTn). The results of the BLASTn search in the Genbank data base retrieved highest homology to the species including Ochlerotatus caspius (99%), Ochlerotatus detritus (98%) and Ochlerotatus provocans (96%). To our knowledge, this study represents the first report of the emergence of O. provocans in Muğla Province. Neighbour-joining trees were drawn based on DNA barcodes and all the specimens were clustered in agreement with their taxonomic classification at species level. Nucleotide composition and haplotype diversity of DNA barcodes were also presented in our study. Furthermore genetic distances, including intraspecific and interspecific pairwise sequence divergence along with nearest-neighbour distance, were calculated using the Kimura-2- parameter. As a result data obtained from this study clearly demonstrate that DNA barcodes could be used as an efficient molecular tool in identification of especially cryptic species.

Keywords: Cytochrome c oxidase oxidase subunit I, DNA barcoding, Ochlerotatus sp., Phylogenetic analysis, new record