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**SS-016.**  **Molecular identification of mosquito species using DNA barcode analysis**

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Mosquitoes are a key threat to public health since they are involved in transmission of devastating pathogens and parasites. The current classification of these vectors is based on morphological characters which have many drawbacks such as being time consuming and error-prone due to variation of individual taxonomic expertise of the analysts as well as phenotypical variations. One of the most serious drawbacks of only using this approach for species identification is the fact that some traits or characters are apparent only during certain life cycle stages or in one gender. Therefore, DNA-based approaches can overcome many of the aforesaid problems. In this study we analyzed immature mosquito specimens collected from different habitats of Muğla Province, Turkey. A 658 base pair (bp) region of the cytochrome c oxidase (COI) gene used as a universal marker in order to identify mosquito species. Analyzed nucleotide sequences were found without pseudo genes and indels that match with high similarity to the mosquito sequences in NCBI database. The most common and abundant mosquito species were found to be Culex and Culiseta species. Individuals of the same species grouped closely together in a Neighborhood-Joining (NJ) tree with Kimura 2-parameter (K2P) distances based on COI sequence similarity. In conclusion COI gene based DNA barcoding is a reliable and standardized identification system for most mosquito species and for studies at the population level.

**Keywords:** Cytochrome c oxidase, DNA barcoding, Mosquitoes, Phylogenetic analysis

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