ABSTRACT

DETERMINATION OF THE DISTRIBUTION PATTERN AND GENETIC STRUCTURE OF *OCHLEROTATUS ZAMMITII* (DIPTERA: CULICIDAE) IN MEDITERRANEAN AND AEGEAN COAST OF TURKEY

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The Mariae group, which consists of three species, namely *Ochlerotatus mariae*, *Ochlerotatus phoeniciae* and *Ochlerotatus zammitii*, has a limited distribution worldwide. All of the three species are found in the rocky habitats on the coastal areas of Mediterranean countries. *Ochlerotatus phoeniciae* and *Oc. zammitii* species of the Mariae group are found in Turkey. The aim of this study is to determine the distribution pattern and genetic structure of the *Oc. zammitii* species in the Mediterranean and Aegean regions. For this purpose, the larval and adult samples of *Oc. zammitii* were collected in 20 different rocky locations in the coastal regions of Antalya, Muğla, Aydın, İzmir, Balıkesir and Çanakkale provinces. DNA isolation was performed primarily from the obtained samples. After DNA isolation, the mtDNA *ND4* gene region of the samples, which were collected from each localities, was amplified by using suitable primers with *Polymerase* Chain Reaction. As a result of the analyses that were made with the sequences of *ND4* gene regions, which were obtained from *Oc. zammitii* samples, 22 haploptypes of the *ND4* gene were detected in the distribution region of the species. AMOVA was applied to sampling localities, separated into seven different groups depending on the geographical distance and $Gamma_{st}$ values. The variation between the groups was 67.25%, the variation between the locations was 2.93%, while the variation within the locations was 29.82%. Furthermore, the gene flow between the populations was calculated and it was concluded that the gene flow between the nearby locations was found to be high. Meanwhile, the gene flow between the groups was very low in the classifications based on the genetic distance tree.

Key words: *Ochlerotatus zammitii*, Mitocondrial DNA, *ND4*, Mediterranean, Aegean.