

Conference Abstract

First results on the genetic variation of the Bulgarian populations of *Morimus asper funereus* (Mulsant, 1862) (Coleoptera, Cerambycidae)

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Abstract

There is an ambiguity about the taxonomic status of Morimus asper funereus (Mulsant, 1862), a saproxylic longhorn beetle, widespread in Bulgaria and other Balkan countries. It is a protected species under the Habitats Directive (Annex II) and under the Bulgarian Biodiversity Act. A recent molecular study, based on the cytochrome C oxidase subunit I (COI) and the second internal transcribed spacer (ITS2) gene seguences, found that all European and Turkish populations of Morimus should be referred to M. asper (Sulzer, 1776) (Solano et al. 2013). The territory of Bulgaria and some other Balkan countries remain as an unstudied gap in that research. Here we present preliminary results on the genetic divergence and diversity of Morimus populations on the Balkans based on COI gene sequences using material from Bulgaria and Albania and the haplotypes' sequences of Solano et al. (2013) obtained from GenBank. The material collected from Bulgaria and two localities in Albania was identified based on morphology characteristics as M. asper funereus (44 samples), M. verecundus bulgaricus Danilevski et all., 2016 (1 sample from the type locality), Morimus orientalis Reitter, 1894 (1 sample from Strandzha Mts.) and Lamia textor (Linnaeus, 1758) (1 sample) used as an outgroup. All obtained sequences were analyzed and haplotype diversity was estimated. The results show that Bulgarian populations of Morimus demonstrate relatively high haplotype diversity in correspondence

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to the diversity of the other European populations. Also, a phylogeographical hypothesis of the linkage between Bulgarian and other Balkan populations was developed. Four main lineages of divergence were identified. In addition, our results support the assumption that *M. verucundus* is a tentative subspecies of the morphologically and genetically variable *M. asper.*

Keywords

Longhorn beetles, Lamiinae, COI, genetic diversity

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References

Solano E, Mancini E, Ciucci P, Mason F, Audisio P, Antonini G (2013) The EU protected taxon *Morimus funereus* Mulsant, 1862 (Coleoptera: Cerambycidae) and its western Palaearctic allies: systematics and conservation outcomes. *Conserv Genet* 14: 683-694. https://doi.org/10.1007/s10592-013-0461-3