
Spatial patterns of COI haplotype diversity in response to environmental factors – case study on *Merodon aerarius* (Diptera, Syrphidae)

Iva Gorše^{*†1}, Ljiljana Šašić Zorić², Marija Miličić², Mihajla Djan¹, Gunilla Ståhls³, and Ante Vujić¹

¹University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia – Serbia

²University of Novi Sad, BioSense Institute – Research Institute for Information Technologies in Biosystems, Novi Sad, Serbia – Serbia

³University of Helsinki, Finnish Museum of Natural History, Helsinki, Finland – Finland

Abstract

Understanding the processes responsible for shaping the spatial genetic patterns and distribution of species is critical for predicting evolutionary dynamics and defining significant management units. Here, we aim to obtain insight into environmental factors contributing to the dispersion and mitochondrial genetic structuring of *Merodon aerarius* - a widespread hoverfly species present on the mountain ranges of central Europe and the Balkan Peninsula, as well as on the islands of Sardinia and Corsica, as well as to establish its current potential distribution. In this regard, we assayed genetic variation at 5'COI gene sequences in 97 specimens of *M. aerarius* collected from 30 sites throughout its range. A Median-joining network of haplotypes was constructed employing the software PopART. Species distribution modelling using MAXENT algorithm was used in order to establish current potential distribution of *M. aerarius*, while the DISTLM routine implemented in PERMANOVA+ was performed to examine the association between distribution of haplotypes and environmental variables. A total of 19 haplotypes were obtained from our dataset, whereby the pattern of Median-joining network indicated grouping of haplotypes from the related sampling areas. The association between environmental and genetic variation revealed that 7 environmental/geospatial variables (LON, LAT, bio2, bio4, bio13, bio15, bio18) had statistically significant role in shaping the spatial patterns of haplotype distribution. This study highlights the utility of landscape studies to better understand the processes shaping geographic patterns of genetic diversity and distribution of hoverflies. This research was supported by the Science Fund of the Republic of Serbia, Ideje - SPAS #Grant No 7737504 and H2020 Project - ANTARES, GRANT No 739570, DOI: <https://doi.org/10.3030/739570>

Keywords: DNA barcode, haplotype distribution modelling, hoverflies, species distribution modelling

^{*}Speaker

[†]Corresponding author: iva.gorse@dbe.uns.ac.rs