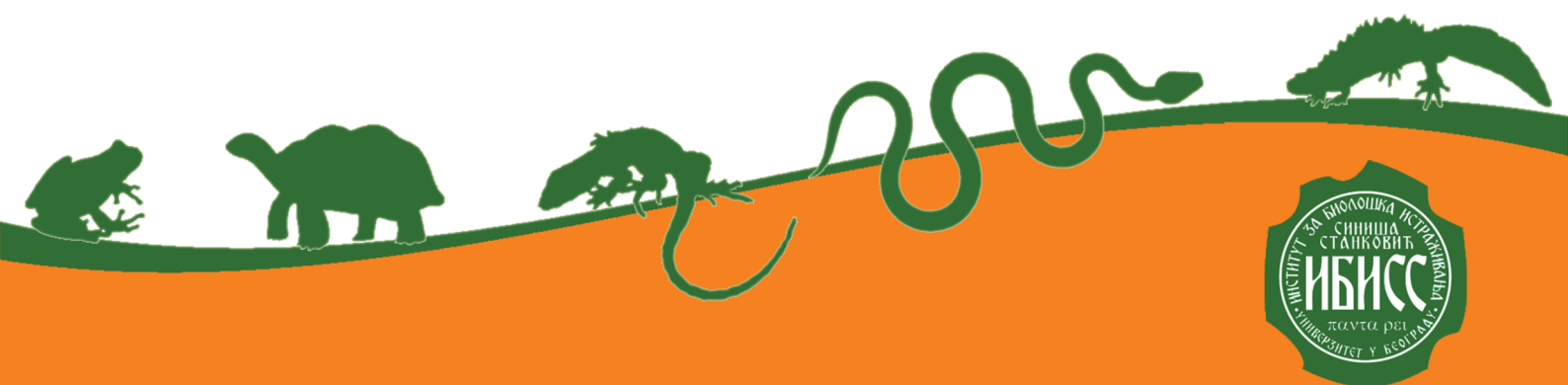




Program & Book of Abstracts

**Belgrade
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Institute for Biological Research “Siniša Stanković”
National Institute of Republic of Serbia
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EDITORS

Jelka Crnobrnja-Isailović
Tanja Vukov
Tijana Vučić
Ljiljana Tomović

CONGRESS LOGO DESIGN

Dejan Brajović

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Tanja Vukov, Marko Mirč

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Poster presentation

Spatial genomics of the *Vipera ammodytes* species-complex may help delineate Balkan subrefugia

Thanou E.^{1,*}, Jablonski D.², Kornilios P.^{1,3}

¹Molecular Ecology Backshop, G. Lekka 16, Loutraki, Greece

²Department of Zoology, Comenius University in Bratislava, Bratislava, Slovakia

³Section of Genetics, Cell Biology and Development, Department of Biology, University of Patras, Rio, Greece

*Corresponding author (e-mail): Evanthia Thanou (thanouevanthia@gmail.com)

Presenting author: Daniel Jablonski

Despite often treated as a single refugium, it is now well-documented that multiple subrefugia integrate the Balkan region. Although their number and location is mostly unknown, phylogeographic analyses, complemented with past and present niche projections, are useful tools for their delineation. In this concept, we applied comparative genomic and niche analyses to study the spatial and temporal evolution within the iconic nose-horned viper species-complex (*Vipera ammodytes*) and explore the putative topographic and climatic agents that may have shaped its speciation.

We used ddRAD sequencing to build a time-calibrated species-tree and detect genetic clusters and evidence of past and current gene flow. We revealed a geographically structured genetic diversity with multiple hybrid zones throughout the Balkan Peninsula. Deep divergence corresponds well to old and imminent biogeographical barriers while two well-differentiated clades, currently lacking any evidence of gene-flow, are respectively distributed on the Northwestern and the Southeastern Balkans. In most other cases, speciation is incomplete with uninterrupted gene-flow detected in all possible contact zones. Despite the fact that most divergent subclades can be geographically referred to a putative glacial subrefugium disconnected from adjacent regions by extended glaciations, there is no evidence of ecological divergence. This suggests that speciation probably occurred in niche-pockets of analogous environments.

Comparing the genomic to the mitochondrial phylogeny and coupling genetic with niche analyses, we discuss (1) an evolutionary scenario that resolves all mitochondrial conflicts (2) the complex processes that have shaped the history of *V. ammodytes*, (3) the need for a taxonomic update that would better reflect the phylogenetic relationships within this complex and (4) the usefulness of combined genomic and climatic evidence as a tool to pinpoint the biodiversity hotspots for amphibians and reptiles in the Balkan region.



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