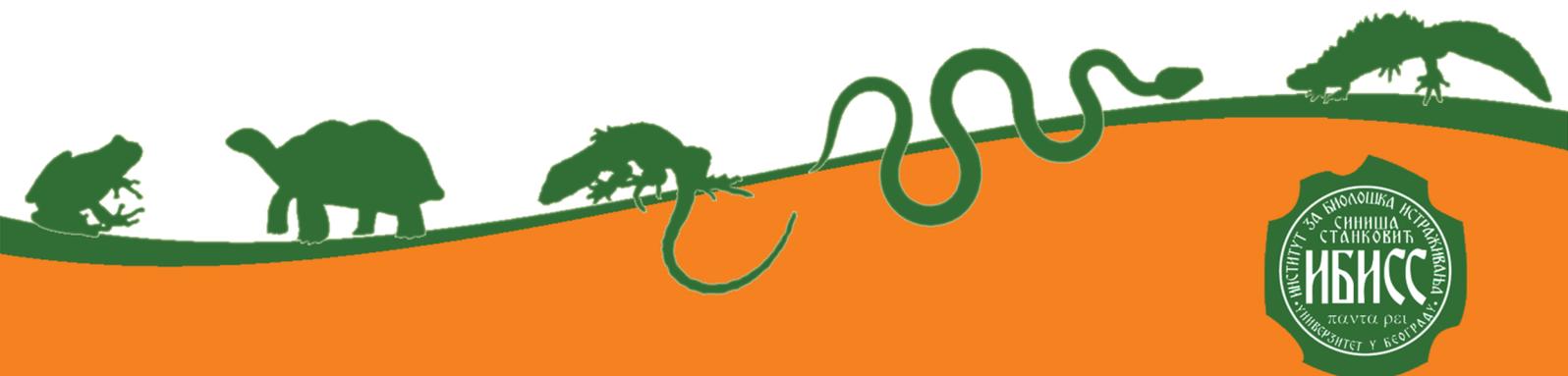




# Program & Book of Abstracts

Belgrade  
2022



Institute for Biological Research “Siniša Stanković”  
National Institute of Republic of Serbia  
University of Belgrade, Serbia

# **PROGRAM & BOOK OF ABSTRACTS**

21<sup>st</sup> European Congress of Herpetology



September 5<sup>th</sup>-9<sup>th</sup>, 2022  
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## *Oral presentation*

### **The effects of topography and climate fluctuations on the species and lineage richness of amphibians and reptiles living in the Balkan Peninsula**

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The Balkan Peninsula is one of the most biodiversity rich areas in Europe, including many endemic species and evolutionary lineages of amphibians and reptiles. Due to the high topographic and climatic complexity, the Balkans served both as a speciation center and as well as an important refugium in the last millions of years. Consequently, the Balkans is an excellent area for the study of macro and microevolutionary processes. In this study, we compiled a dataset of occurrence records of every amphibian and reptile species in the area to calculate species richness in 50×50-km cells. To estimate richness of evolutionary lineages, we reconstructed species concatenated phylogenetic trees and using phylogenetic interpolations we split occurrence records into allopatric lineages which we then summed in the same defined area. We then compared species and lineage richness as a function of terrain ruggedness and two measures of past climate changes. These were defined as the absolute value of the difference between the current climate (annual mean temperature and precipitation) and the Last Glacial Maximum of the Pleistocene and the middle of the Pliocene, using linear regressions. We found that terrain ruggedness positively influenced species and lineage diversity in both studied groups. Climate difference from the Pliocene usually had a significantly negative effect on richness values, while the climate difference from the Pleistocene was not significant or also negative, indirectly supporting the importance of climate stability in richness. Our study suggests that a better understanding of phylogenetic processes can greatly help in interpreting currently observed patterns of biodiversity.



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