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PROGRAMME & ABSTRACTS









University of Pannonia 22–27 August 2013



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Tibor Navracsics, Deputy Prime Minister, Minister of Public Administration and Justice

Organising Institutions:

Societas Europaea Herpetologica (www.seh-herpetology.org)
Hungarian Ornithological and Nature Conservation Society, MME/Birdlife Hungary (www.mme.hu)
University of Pannonia, Department of Limnology, Veszprém (ornithology.limnologia.hu)
Hungarian Natural History Museum, Budapest (www.nhmus.hulen)

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Welcome

Dear Colleagues,

Welcome to Veszprém, Hungary!

The 17th SEH European Congress of Herpetology is hosted by the University of Pannonia, and co-organised by the Hungarian Ornithological and Nature Conservation Society (MME) and the Hungarian Natural History Museum.

Participants from six continents (39 countries) registered for the event, giving the meeting a global perspective on the science of herpetology.

The scientific programme includes four invited talks on topics of broad interest (evolution of reptile venom, invasive species, biogeography and systematics) and 113 talks in 11 different parallel sessions. On the symposia day, four symposia will be presented on relevant topics such as invasive alien species, chytridiomycosis in Europe, monitoring of Natura 2000 species and herpetofauna and transport systems. There will also be 120 poster presentations divided between two poster sessions.

Wine will be served during the poster sessions and a morning raffle will be held with valuable prizes to be won. There will be a contest for the best student talk and poster, and for the first time in the history of SEH European Congress of Herpetology, a silent auction will take place.

The welcome party, the wine tasting in Balatonfüred-Csopak Wine Region and the gala dinner all provide further opportunities to meet the other delegates.

Although August is not the best time for field herping, locations have been chosen for congress excursions where sightings of amphibians and reptiles are guaranteed. These locations are the Kis-Balaton and the Hungarian Meadow Viper Conservation Center in Kiskunság.

On behalf of the Local Organising Committee I wish you an exciting and interesting meeting.

Kind regards, Judit Vörös CLIMATE CHANGE PHYLOGEOGRAPHY

What limits range overlap of common and Syrian spadefoot toads: climate or competition?

Ruben Iosif¹, Ciprian Samoila¹, Monica Papefl², Dan Cogălniceanu¹

Four species of the spadefoot toad genus Pelobates, mostly allopatric, are distributed over parts of Europe, North Africa, Caucasus, and the Middle East. Ranges of P. fuscus (Pf) and P. syriacus (Ps) overlap over a narrow strip in Dagestan and along Danube, in the Balkans. Our study focused on investigating (i) factors limiting the range overlap of the two species (climate or competition), and (ii) possible changes in their geographic ranges under future climate change scenarios. We computed climatic suitability models using MaxEnt and projected their distribution onto future (i.e., A1B, A2, B1 scenarios) and past conditions (i.e., Last Interglacial and Last Glacial Maximum). Additionally, we used fossil occurrences to test the predictive accuracy of past projections. Finally we assessed the degree of range overlap between the studied species using metrics implemented in ENMTools. The present climatic niche was slightly extended outside the known geographic range, in the Caucasus and the Balkans, south for Pf and north for Ps. The last interglacial distribution of Pf included British Isles, and broad areas in western, central and northern Europe, and extended farther north in the Balkans for Ps. Validation with fossil records revealed an excellent predictive performance (Omission error = 4.1% for Pf and 16.6% for Ps). Last Glacial Maximum maintained only isolated refugia in southern Europe, Pannonian Basin and Caucasus for Pf, and Israel, Southern Balkans, and Caucasus for Ps. Present potential distributions revealed a narrow range overlap (Range Overlap = 0.44), while under Last Glacial Maximum the two species had nearly disjunct allopatric distributions (Range Overlap = 0.17). The range overlap is projected to increase towards the end of this century. The species' absence from climatically suitable areas supports the hypothesis that dispersal barriers and competition limit their geographic range.

Mitochondrial phylogeography of three species of slow worms (Anguis) in the Balkans

Daniel Jablonski¹, Georg Džukić², David Jandžik^{1,3}, Dušan Jelić⁴, Katarina Ljubišavljević², Peter Mikulíček¹, Jiří Moravec⁵, Nikolay Tzankov⁶, Václav Gvoždík^{5,7}

The Balkan Peninsula has played a role of a speciation and radiation centre in evolutionary history of slow worms (Anguis spp.). Four from five known species are present in the region. However, knowledge of the detailed distribution ranges of the species and their contact zones in the Balkans remains insufficient. In the first step of this project we genotyped 193 individuals from 152 localities of this region based on mitochondrial DNA (ND2) to map distributions and contact zones of mitochondrial lineages/species and to screen their mtDNA diversity. According to our results, A. fragilis is relatively widespread in the north-western and central Balkans, south-westward from the Danube River. Relative genetic uniformity of this species suggests a recent dispersal within the Balkans. Anguis colchica has been identified in the north-eastern and eastern Balkans in Romania, Serbia and Bulgaria. This species forms several divergent evolutionary lineages within the Balkans, probably related to different Pleistocene refugia. Anguis graeca was, beside Greece, Albania and southernmost Montenegro, newly detected in Republic of Macedonia. In comparison to the other species, this Balkan endemic shows much higher and complex genetic variation. This finding corresponds to the hypothesis of multiple Pleistocene microrefugia in the southern Balkans, the pattern similar to other endemic species. Further investigations will evaluate variation in nuclear genes allowing detection of historical or recent hybridization events.

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