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corroborated as being of Neotropical origin, radiating to North America, Madagascar and Australia. The ancestral range of the Palaearctic species remains equivocal. Ancient DNA techniques were implemented for three mitochondrial gene sequences and applied to museum specimens (including holo- and paratypes) of three high elevation *Hyles* species to elucidate their much debated phylogenetic relationships. The Afghan endemic, *Hyles salangensis*, is only known from 15 males caught in the 1960s. The species status of the Nepal endemic *Hyles renneri* is corroborated and its known distribution extended by over a thousand kilometres eastwards. Sequences of *H. nepalensis* indicate no genetic differentiation between specimens from Nepal and low elevation Palaearctic *H. gallii*. Surprisingly samples from the NW-Himalaya are recovered in a monophyletic group that also includes samples from North America. This complex biogeographical history requires further study.

Keywords: cladistic biogeographic ancestral state analyses, phylogeny, moths, aDNA, Central Asia, taxonomy.

7.12 ✂ Implications of phylogeography and population genetics for the taxonomy of grass snakes (*Natrix natrix*)

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Grass snakes (*Natrix natrix*) represent one of the most widely distributed snake species of the Palaearctic region. Within *N. natrix*, up to 14 distinct subspecies are regarded as valid. In addition, some authors recognize big-headed grass snakes from western Transcaucasia as a distinct species, *N. megalcephala*. Based on phylogenetic analyses of a 1984-bp-long alignment of mtDNA sequences (cyt b, ND4+tRNAs) of 410 grass snakes, a nearly range-wide phylogeography is presented for both species. Within *N. natrix*, 16 terminal mitochondrial clades were identified, most of which conflict with morphologically defined subspecies. Hypotheses regarding glacial refugia and postglacial range expansions are presented. In Central Europe, there are two contact zones of three distinct mitochondrial clades, one of these contact zones was theretofore completely unknown. In agreement with previous studies using morphological characters and allozymes, there is no evidence for the distinctiveness of *N. megalcephala*. Therefore, *N. megalcephala* is synonymized with *N. natrix*. In addition, first preliminary results of 14 tested microsatellite loci are presented as an outlook on future work.

Keywords: Reptilia, grass snake, taxonomy, species delimitation, phylogeography

7.13 Performance of steppe plants in Central Europe – a comparative analysis of four steppe species based on fruit set and germination data

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A transect towards the (north-)westernmost distribution limit of rare and endangered Central European steppe species was not only used for studying genetic structure and diversity patterns at the absolute periphery of the species' distributions (see respective contribution by Kristina Plenk), but also for analyses of plant performance in the field and germination success. We hypothesised decreased performance values and lower germination rates, i.e. reduced overall fitness, towards the absolute distribution limit within our core project taxa *Carex supina* (Cyperaceae), *Inula germanica* (Asteraceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae) based on four representative populations within each of the three study regions (i.e. Central Hungary, Eastern Austria, Western Germany). To a small extent, the results show expected patterns in fruit set, weight of fruits, and germination (rates). But in general, most findings are more species-specific, and notably, strongly influenced by species' ability for vegetative propagation as well as by varying population sizes.

Keywords: steppe species, range edge, phylogeography, plant performance, germination, relict populations