

Phylogeographie, Artbildung und postpleistozäne Einwanderung mitteleuropäischer Reptilien

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Phylogeography, speciation and post Pleistocene invasion of central European reptiles

A phylogeographic analysis of 7 species complexes of European reptiles was executed using different molecular methods. While mitochondrial genes (here mainly cytochrome b sequences) enabled us to draw conclusions about phylogeographic history and differentiation, the additional application of bisexually inherited markers was helpful to determine which stage had been reached in speciation. As species with similar distribution patterns in southern and central Europe had been selected, matching phylogeographic branching patterns could be used to draw some general conclusions:

- Highest genetic diversity among the analyzed species complexes was observed in their representatives in southern Europe, the Near East and the Caucasus. Obviously the differentiation took place in the Pleistocene refugia.
- The species complexes were found in different stages of speciation. In some cases, cryptic species could be detected.
- Evidence for multiple range retractions and expansions, which were postulated for the times of Pleistocene climatic oscillations, could be found in the Balkans, but in Central Europe their traces have been wiped out. Only the Holocene invasion has left imprints in the genomes from this area.
- The Balkans and the Pontic region were the origins of active invaders into Central and Northern Europe.
- Groups from the Iberic and Apennine peninsulas rarely conquered other regions. This limitation can be attributed to the barrier function of the Pyrenees and the Alps.

Key words: *Emys*, *Lacerta*, *Elaphe*, *Hierophis*, *Natrix*, phylogeography, phylogeny, taxonomy, Pleistocene refugia, colonization.

Zusammenfassung

Sieben Artenkomplexe europäischer Reptilien wurden einer phylogeographischen Analyse unterzogen, wobei verschiedene molekulargenetische Methoden eingesetzt