

Cryptic diversity in the smooth snake (*Coronella austriaca*)

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Abstract. The smooth snake, *Coronella austriaca*, is a common snake species widespread in the Western Palearctic region. It does not form conspicuous morphological variants and, although several evolutionary lineages have been distinguished based on the analyses of the mitochondrial DNA sequences, only two subspecies with very limited distribution have been traditionally recognized. Here we present an mtDNA phylogeography of the species using geographically extended sampling while incorporating biogeographically important areas that have not been analyzed before, such as Anatolia, Crimea, and Iran. We find that the smooth snake comprises 14 distinct phylogenetic clades with unclear mutual relationships, characterized by complex genetic structure and relatively deep divergences; some of them presumably of Miocene origin. In general, the biogeographic pattern is similar to other Western Palearctic reptiles and illustrates the importance of the main European peninsulas as well as the Anatolian mountains, Caucasus, and Alborz Mts. in Iran for the evolution of the present-day diversity. Considerable genetic structure present in the smooth snake populations within these large areas indicates the existence of several regional Plio-Pleistocene refugia that served as reservoirs for dispersal and population expansions after the glacial periods. The current taxonomy of *C. austriaca* does not reflect the rich genetic diversity, deep divergences, and overall evolutionary history revealed in our study and requires a thorough revision. This will only be possible with an even higher-resolution sampling and integrative approach, combining analyses of multiple genetic loci with morphology, and possibly other aspects of the smooth snake biology.

Keywords: Asia, Colubridae, Europe, glacial refugia, phylogeny, refugia-within-refugia, Serpentes, speciation.

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Supplementary material