

Different Histories, Different Destinies—Impact of Evolutionary History and Population Genetic Structure on Extinction Risk of the Adriatic Spined Loaches (Genus *Cobitis*; Cypriniformes, Actinopterygii)

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The region of Balkans is often considered as an ichthyologic “hot spot”, with a great number of species and high portion of endemics living in fresh waters in a relatively small area. The Adriatic watershed in Croatia and Herzegovina is inhabited by six spined loach species (genus *Cobitis*) whose extinction risk estimations were based solely on their extent of occurrence (and/or area of occupancy) and its fragmentation, and conservation proposals do not consider diversity below species level. In this investigation we employed molecular genetic methods to describe present genetic structure of the Adriatic spined loaches and reveal their demographic history. The divergence of the Adriatic lineages inside the genus *Cobitis* started in Miocene and lasted until Pleistocene epoch. Geological events responsible for shaping recent diversity of spined loaches in the Adriatic basin are: the Dinarid Mountains upwelling, the evolution of Dinaric Lake system, local tectonic activity, river connections during glaciations and differences in sea level. Even though all the investigated species inhabit karstic rivers located in the same geographic area and that were subject of similar geological events, the results obtained reveal great differences in their genetic diversity and structure and point out the necessity of different conservation measures to ensure their future viability. High level of genetic polymorphism is characteristic for species located more to the south. Two species comprised of more than one population have completely different intraspecific structure; populations of *C. illyrica* are genetically distinct and represent separate evolutionary significant units, whereas intraspecific structure of *C. narentana* corresponds to metapopulational pattern. Without population genetic data, evolutionary significant units could be easily misidentified. Furthermore, the obtained results affirm that population genetic measurements are able to detect differences among closely located and related species and estimate extinction risk even more accurately than currently applied IUCN criteria.