



Conference Abstract

Conservation genetics of the vulnerable stone crayfish using DNA barcoding and microsatellites

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Abstract

The stone crayfish *Austropotamobius torrentium* is a native European freshwater species with significant population declines caused by anthropogenic pressure onto its habitats, climate change and spreading of non-native invasive crayfish and their pathogens. Large-scale DNA barcoding based on sequencing a short fragment of the mitochondrial cytochrome c oxidase subunit I (*COI*) gene revealed this species represents a highly divergent taxon whose evolutionary heritage is preserved in genetically divergent mtDNA phylogroups, with majority of them having restricted distribution ranges. Guarding in mind vanishing populations trends and potential loss of genetic diversity, effective conservation planning and monitoring are needed for ensuring the persistence and long-term survival of this endangered species. Since genetic data are often critical for defining populations for conservation and management purposes, along with DNA barcoding, we employed microsatellites to examine samples of more than 400 individuals from 17 populations across its entire distribution range in Croatia, known as the stone crayfish diversity hot spot. Microsatellite analyses revealed high level of genetic diversity and differentiation among studied populations that grouped according to their geographical position and mtDNA phylogroup. Almost all sampled populations represent a distinct genetic cluster, showing high level of differentiation and reflecting long periods of isolation. Results of genetic characterisation enabled selection of suitable donor populations for future restocking and reintroduction programs. Combination of DNA barcoding and microsatellites

provided good insight into genetic diversity and population structure as well as enabled sound conservation programs for this threatened species in Croatia.

Keywords

Austropotamobius torrentium, freshwater, mtDNA, COI, diversity

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