The first large-scale genetic analysis of the vulnerable noble crayfish

Major global changes (e.g., human impact or climatic cycles) have a severe impact on the distribution and diversity of species such as the vulnerable European noble crayfish Astacus astacus. This is the first large-scale study regarding haplotype diversity of A. astacus in central and southeastern Europe. We analyzed a partial sequence of the mitochondrial gene cytochrome oxidase subunit I from 416 specimens of 92 crayfish stocks of three European river basins (Black Sea, North Sea and Baltic Sea). Twenty-two haplotypes were identified, and one common haplotype was found across the whole study area. We detected differences in the genetic diversity between major river catchments (ΦST: 0.03481 to 0.20387). The high haplotype diversity (HD = 0.794 ± 0.024) and high number of private haplotypes suggests a glacial refuge in the Balkan area. The very low haplotype diversity in central Europe (HD = 0.299 ± 0.038 and HD = 0.163 ± 0.058) could be a result of human translocation and/or founder effects due to postglacial re-colonization. Nevertheless, the high frequency of private haplotypes in all major catchment areas indicates a differentiation of noble crayfish populations throughout Europe despite the extensive human translocation of crayfish. The results of this study support the establishment of conservation management plans for this vulnerable species.

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