

Molecular characterization of the noble crayfish (



The genetic variability between individuals from five crayfish (*Astacus astacus* L.) populations was determined. The analysis was based on sequences variations of mitochondrial DNA (cytochrome oxidase subunit I (COI) and 16S ribosomal DNA. Mitochondrial DNA sequences are widely used to detect genetic variation within and between populations. Data analysis revealed the existence of two COI haplotypes – most common haplotype Hap01 and one new haplotype, differed only in one substitution. Analysis of the 16S rDNA sequences obtained showed no differences in nucleotide composition. The results of the analysis are important part of project “Active protection of noble crayfish in lakes of Pomeranian Complex Landscape Parks” financed by Financial Mechanism of the European Economic Area 2014–2016.

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