

[Phylogenetic relationships of Sakhalin taimen *Parahucho perryi* inferred from PCR-RFLP analysis of mitochondrial DNA].

[Article in Russian]

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Abstract

RFLP analysis of three amplified mtDNA fragments (Cytb/D-loop, ND1/ND2, and ND3/ND4L/ND4) was performed in the following taxa: *Parahucho perryi*, *Hucho taimen*, *Brachymystax lenok*, *B. tumensis*, *Salmo salar*, *Salvelinus leucomaenis*, and *S. levanidovi*. For mtDNA of *P. perryi*, a substantial decrease in the haplotype and nucleotide diversity was observed as a result of random genetic drift, caused by a reduction in the effective population size. Nucleotide divergence estimates between the mtDNA haplotypes were determined. Sakhalin taimen *P. perryi* was found to be approximately equally diverged from *S. salar* and from the charrs of the genus *Salvelinus*, by 11.0 and 10.0%, respectively. The divergence between *P. perryi* and *H. taimen* constituted 14.6%, between *P. perryi* and lenoks of the genus *Brachymystax*, 14.2%, and between *H. taimen* and *Brachymystax*, 7.7%. The analysis of possible phylogenetic relationships of the mtDNA from *P. perryi* among the group of taxa examined confirmed validity of the genus *Parahucho*. Phylogenetic reconstructions performed showed that robustness of the trees constructed for the complex of phylogenetically informative characters over three mtDNA fragments was considerably higher than that of the trees constructed for individual genes.