



Population genetic characterization of endangered Persian sturgeon (*Acipenser persicus*) in Caspian Sea based on mitochondrial DNA data

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Abstract:

The genetic variation and population structure of the Persian sturgeon, *Acipenser persicus* (Borodin, 1897) was investigated by means of PCR-RFLP analysis of the nucleotide dehydrogenase subunit 5 (*ND5*) of mitochondrial DNA (mtDNA). We compared these data with our previous study based on mtDNA control region sequences. A total of 225 individuals were collected from 23 sample sites in the south and 4 locations Turkmenistan, Azerbaijan, Russian Federation and Kazakhstan covering the three main geographic regions including South, Middle and North part of the Caspian Sea. The PCR products were digested with 25 restriction enzymes and five enzymes revealed polymorphism patterns (*Rsa* I, *Hinf* I, *Hae*III, *Mbo* I and *Cfr*13I). Thirty two composite haplotypes were revealed with the number of haplotypes in each population sample ranging from 6 to 13. Two regional (Sefidroud River and Russia) groups were clearly identified by cluster and molecular variance model (AMOVA) analyses. Each of these groups showed dominant haplotypes that were little in populations from the other geographic areas. The mean haplotype diversity (*h*) and nucleotide diversity (π) were 0.7610 ± 0.046 and 0.008332 ± 0.00421 , respectively. Based on heterogeneity test and Monte-Carlo with 1000



replicates, significant differences were showed for haplotype frequencies of the Persian sturgeon populations ($P < 0.0001$). These results and F_{ST} based on kimura- 2 parameters method showed that haplotype distribution in different location were significant ($P < 0.0001$). Results of this study determined independent populations of Persian sturgeon and will have noticeable implications for sturgeon conservation genetics in general.

Keywords: *Acipenser persicus*, Mitochondrial DNA, PCR-RFLP, Caspian Sea