



## **Population genetics of *Capoeta aculeata* as determined from mitochondrial DNA variation of the control region**

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### **Abstract**

Mitochondrial DNA (mtDNA) control region sequences were analyzed to evaluate the population genetic structure of *Capoeta aculeata*. A total of 120 specimens were collected from the three rivers of the Kohgiluyeh and Boyer-Ahmad Province in Iran. MtDNA control region was amplified using PCR. Direct sequencing was performed according standard method. The results showed that 21 haplotypes were observed between 120 samples in the method. The highest numbers of haplotypes were observed in Maroun River in which five haplotypes (D1, D, F, G and I) among them were specific for the river and were not observed in the other rivers. The average haplotype diversity ( $h$ ) and nucleotide diversity ( $\pi$ ) were  $0.822\pm 0.073$  and  $0.0135\pm 0.005$ , respectively. The results of  $F_{ST}$  based on kimura- 2 parameters method and analysis of molecular variance (AMOVA) demonstrated that most variations occurred between samples from Maroun River and that the samples include two distinct population segment including Maroun River and Beshar River ( $P < 0.001$ ). As mtDNA control region is hypervariable segment, this can be provide potential marker for identifying probable populations and for determining their management and conservation units, leading to the useful application of molecular genetics in investigating conservation biology of *Capoeta aculeata*.

**Keywords:** *Capoeta aculeata*; mitochondrial DNA; genetic variation