

عنوان مقاله:

Genetic diversity of Mahisefid (*Rutilus frisii kutum* Kamensky ۱۹۰۱) in different rivers of the south Caspian Sea using PCR-RFLP

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خلاصه مقاله:

Mahisefid is the most popular fish in Iran with the highest economic value. The analysis of mitochondrial DNA has been extensively used as a marker for population genetic studies and is a powerful tool in studies of gene flow and evolutionary biology. Two hundred ninety four samples were collected from Sefid Rud River (۱۰۰), Lamir River (۹۸), Shir Rud River (۴۸) and Tajan River (۴۸) during spawning season. Out of ۲۴ enzymes tested, four enzymes, namely *TasI*, *HaeIII*, *HinfI* and *HincII* were selected for this study. In the present study, the haplotype and nucleotide diversity of Mahisefid in four important rivers where fingerlings are produced, were carried out by using PCR-RFLP at mtDNA ND۵/۶ region. A total of ۲۰ haplotypes were studied so that AAAA and BAAA haplotypes had the most frequency. The average haplotype frequency of AAAA and BAAA haplotypes were ۲۹.۹۳% and ۲۷.۵۵%, respectively. The maximum nucleotide diversity was ۰.۹۴%, the minimum was ۰.۸۰% and the average was ۰.۸۸%. Divergence between Lamir and Sefid Rud River and Shir Rud was ۰.۲% and between Lamir and Tajan, and Shir Rud River it was ۰.۱%. The average evolutionary distance was ۰.۰۱۵. The maximum evolutionary distance was ۰.۲۹۴ between ADAA and AAAB, ABAB and BDBA, BBAA and AABB. The average number of bases surveyed was ۱۲۱.۲ and the average number of fragments was ۳۰.۳۰. The study suggests that there was a low genetic variability in four populations of Mahisefid in the south of Caspian Sea. Mahisefid population can be divided into two main clusters, the first clade consists of Shir Rud River and Lamir River populations and the second clade consists of Tajan River and Sefid Rud River populations. The clustering of Mahisefid populations was not in accordance with their geographical areas or river systems.

کلمات کلیدی:

Rutilus frisii kutum, Genetic characteristics, mtDNA, Iran

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