Abstract

In this research, Inter Simple Sequence Repeat (ISSR) analysis was performed in order to Investigation of genetic diversity of *Capoeta trutta* population in Kurdistan province. Six dinucleotide primers (AG)9C, (GA)9C, (AC)9T, (CA)9T, (GT)9C and (TG)9C were properties. In Six using of primers recluse of three (AG)9C, (GA)9C and (AC)9T) primers generated clear, repetitive and handicap bands in Polymerase Chain Reaction (PCR) condition. A total of 115 individuals belonging to Six populations were screened using 3 different ISSR primers. A total of 56 loci were produced in the 6 studied populations %64.29, %69.64, %67.86, %85.71, %69.64 and %58.93 of these loci were polymorphic over all the genotypes tested in Sirvan, Gaverood, Gheshlagh, choman, Garmab and Shovey populations, respectively. The total number of loci and polymorphic loci detected by single primer ranged from 16 to 21 and 14 to 18. The average heterozygosities of Sirvan, Gaverood, Gheshlagh, Choman, Garmab and Shovey populations were %11, %14, %13, %21, %13 and %10, respectively. Compared with the Six populations, showed significant genetic differences including a smaller number of total loci ($P \leq 0.05$), a smaller number of total polymorphic loci ($P \leq 0.05$), a smaller number of genotypes ($P \leq 0.05$) and a smaller Shannon index ($P \leq 0.05$). The ISSR fingerprinting technique used was confirmed to be a reproducible and sensitive tool for the study of population genetics of *Capoeta trutta*. Genetic diversity, heterozygosity, Shanon index, observed alleles and drastic alleles in the populations in this study showed essence medium diversity in this populations.

Keywords : genetic diversity, *Capoeta trutta*, ISSR marker, polymorphism

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The Thesis Submitted for the Degree of M.Sc

(In the Field of Fisheries)

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October 2011

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The Thesis Submitted to the Postgraduate Studies Office in Partial Fulfillment of the Requirements for the Degree of M.sc in Fisheries

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The above thesis was evaluated and approved by the following members of the thesis committee with mark

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