

Genetic comparison of Caucasian goby fish, *Knipowitischia caucasica* (berg, 1916), in the southeast coastlines of the Caspian Sea using microsatellite loci

Afieh Anvarinia¹

Eisa Jorjani²

Seyedeh Ainaz Shirangi^{3*}

Rahman Patimar⁴

Hadi Raeisi⁵

1. Ms.C graduated student of Fisheries, Faculty of Agriculture and Natural Resources, Gonbadkavous University, Gonbad Kavus, Iran.

2, 3. Assistant professor, Department of Biology, Faculty of Basic Sciences & Engineering, Gonbadkavous University, Gonbad Kavus, Iran.

4. Associate professor, Department of Fisheries and Forestry, Faculty of Agriculture and Natural Resources, Gonbad Kavous University, Gonbadkavous, Iran.

5. Assistant professor, Department of Fisheries and Forestry, Faculty of Agriculture and Natural Resources, Gonbad Kavous University, Gonbadkavous, Iran.

*Corresponding author:

ainazshirangi@gmail.com

Received date: 2020/01/22

Reception date: 2020/07/27

Abstract

In order to study the genetic structure of Caucasian goby fish (*Knipowitischia caucasica*) populations using microsatellite markers, 40 individuals were collected from the southeast of the Caspian Sea coastlines. Genomic DNA of the samples was extracted from the fish fins by phenol-chloroform method. The quality and quantity of extracted DNA were then investigated. PCR reaction was performed by 4 pairs of microsatellite loci. PCR product was used for electrophoresis by polyacrylamide 6% and colored by AgNO₃. Amount of allelic frequency, the numbers of observed and effective alleles, observed and expected heterozygosity, genetic distance, Hardy-Weinberg equilibrium, F_{ST} and gene flow were evaluated based on AMOVA test by using PopGene 32. From all of five pairs of microsatellite loci used for Caucasian goby fish, all of them except Pmic-02 showed the sharp band in appropriate range. All of 4 loci except locus Pmar-05 were polymorphic. The average of observed and effective alleles was 2.375 and 1.68, respectively. The mean H_O and H_e were evaluated 0.445 and 0.364, respectively. Deviation of HWE were not observed in none of loci except for Pmar-05 locus only in Gorgan bay and Pmar-08 in both of Gorgan bay and Gomishan wetland, (P>0.001). Furthermore, amount of F_{ST} and gene flow (N_m) between individuals of southeast of Caspian Sea were 0.481 and 0.269, respectively. Consequently, Caucasian goby fish from Gorgan bay and Gomishan wetland are belonged to two different populations.

Keywords: *Knipowitischia caucasica*, genetic variation, Genetic population, microsatellite, Caspian Sea.