Microsatellite markers indicate a different structure among three populations of the Caspian Roach, *Rutilus rutilus caspicus* (Jakowlew, 1870), in the Caspian Sea

(Osteichthyes: Cyprinideae)

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Abstract. The population structure of *Rutilus rutilus caspicus* (Jakowlew, 1870) from two locations on the Iranian coastline and one location in Russia was investigated using microsatellite DNA markers. Genomic DNA from 90 specimens and seven loci with reasonable polymorphism were amplified using a PCR approach The results showed that the lowest mean number of alleles per locus (6.42) was observed in the Russian population and the highest (7) in the Gorgan Bay population. The observed heterozygosity in the Anzali Wetland (0.59) population was higher than the other populations in Iran (Gorgan Bay: 0.5) and Russia (0.52). Significant to highly significant deviations from Hardy-Weinberg expectations were found at more loci in Iranian populations than in the Russian. Population differentiation was modest among all populations. The highest and significant (0.044; $p \leq 0.01$) population differentiation (F_{st}) value was between Iranian populations and Russian populations and the lowest and non-significant population differentiation (F_{st}) value was between Iranian populations (0.012; $p \leq 0.07$). The estimated gene flow (N_m) value between Iranian populations (Gorgan Bay and Anzali Wetland) across all the studied loci was the highest, while the N_m value between Iranian and Russian population was the lowest.

Key words. Microsatellite, *Rutilus rutilus caspicus,* genetic variation, Caspian Sea, Iran, Russia.

Introduction

The Caspian Roach, *Rutilus rutilus caspicus* (Jakowlew, 1870), is widespread throughout the north and southern parts of the Caspian Sea. This commercial fish has been included in the list of threatened species (KIABI et al. 1999) due to overfishing and the deterioration of its spawning ground. An effective strategy for the conservation of a particular species should include information on its genetic structure (FRANKLIN 1980). Microsatellites are highly polymorphic as a result of their hypermutability and thereby cause an accumulation of various forms in the population of a given species. Microsatellite polymorphism is based on size differences due to varying numbers of repeat units contained by alleles at a given locus. Microsatellite mutation rates have been reported as high as 10^{-2} per generation (WEBER & WONG 1993, REZVANI GILKOLAEI 1997, ELLEGREN 2000) which is several orders of magnitude greater than that of non-repetitive DNA (109) (LI 1997). The advantages of microsatellites as molecular markers include their abundance in genomes, even distribution, small locus size facilitating polymerase chain reaction (PCR)-based genotyping, codominant nature of Mendelian inheritance, and high levels of polymorphism. In previous studies, the genetic

Zoology in the Middle East 50, 2010: 67–73.
ISSN 0939-7140 © Kasparek Verlag, Heidelberg