

## Genetic diversity of the killifish *Aphanius fasciatus* paralleling the environmental changes of Tarquinia salterns habitat

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**Abstract** The habitat in the Natural Reserve of the Tarquinia salterns, located on the Tyrrhenian coast of central Italy, has undergone dramatic alterations over the last 10 years. After salt production was terminated in 1997 the site was abandoned until 2002, with consequent degradation of habitat quality and stiffening of the environmental conditions. From 2003 to 2006 ecological rehabilitation of the site was carried out, restoring water circulation to its previous equilibrium. The genetic variation in the killifish *Aphanius fasciatus* inhabiting the salterns was monitored using allozymes from 1998. The results showed that the genetic variability of the killifish strongly reduced through time: a high number of rare alleles were lost and both heterozygosity and allele richness were significantly decreased. The most recent samples, taken after the ecological restoration, showed that to date the genetic erosion of *A. fasciatus* gene pool has slowed down, since no significant differences have been detected for any genetic variability parameter. Concerning the mechanisms leading to the impoverishment of the genetic variability, the strong loss of rare alleles suggests a role of genetic drift, which accords with the fluctuation of the effective population size recorded over the period of study and with the low gene flow typical of this species. The low levels of gene flow reported for this species imply that once lost, the genetic variability can rarely be restored through immigration from highly variable populations.

**Keywords** *Aphanius fasciatus* · Allozymes · Tarquinia salterns · Genetic variability · Environmental changes

### Introduction

The link between the degree of environmental heterogeneity and genetic diversity has been the subject of extensive investigation, generating a bulk of studies showing that heterogeneous environments usually host genetically more variable populations (Nevo 2001; Nevo et al. 1986; Stanton et al. 2000). The main evolutionary forces maintaining high polymorphisms in variable environments have been identified as mutation, gene flow, and both stabilizing and cyclical selection (Nevo 2001). On the other hand, the occurrence of environmental impacts is expected to decrease population size and this might lower the overall levels of genetic variability (van Straalen and Timmermans 2002). In this case the evolutionary forces displaying their action are mainly genetic drift, inbreeding and directional selection (Nei et al. 1975), especially when coupled with lack of gene flow and sharp population size decline (Hoffmann and Willi 2008). This has been the rationale to hypothesize that neutral markers variation would allow detecting the effects of human impact such as pollution, habitat fragmentation or overexploitation on natural populations (Belfiore and Anderson 2001; Bickham et al. 2000; DiBattista 2008; Schwartz et al. 2007). Many data would suggest that the observed patterns in natural and experimental populations follow expectations, i.e., genetic variation decreases in the presence of pollutants (Maes et al. 2005; Nowak et al. 2009; Ungherese et al. 2010). Other data have shown that fishing pressure has reduced the genetic diversity of some marine fish species, by impacting their populations at both demographic and genetic levels

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