

Abstract

Endemic Sicilian Brown Trout Endangered by Hatchery Introgression and Low Gene Diversity [†]

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Abstract: Brown trout (*Salmo trutta*) populations living in Mediterranean peninsulas and the surrounding islands belong to old evolutionary lineages that persisted during Quaternary glaciations. Many of these populations inhabit marginal areas along the south limit of the distribution of the species, where they face hard environmental conditions (drought, high temperatures and sudden shifts in water flow) that can get worse by anthropogenic activities and climate change. In islands, this vulnerable situation is exacerbated by geographical isolation. Sicilian trout remain only in the south-eastern part of the island and, based on their morphological characteristics, they have been recognized as a distinct species named *Salmo cetti*. Despite their genetic singularity among other Italian trout (a unique Italian native trout of Atlantic origin), the mitochondrial DNA haplotypes that were found in Sicily are clearly related with the brown trout Atlantic lineages from North Africa and the Iberian Peninsula. In the present study, brown trout in four rivers from north-eastern Sicily were genetically analysed. Based on the genotyping of mitochondrial (control region) and nuclear (LDHC, GP1, GP14, GP31, GP34, GP37, GP38, GP42, SS2 and SL) genes, this study aimed to: evaluate the impact of past stocking practices in natural populations; estimate mitochondrial and nuclear gene diversity; and reconstruct the phylogenetic relationships of Sicilian trout. The initial results showed that only trout from the Tellesimo River remain free from hatchery introgression. Gene diversity was low in most populations, and both mitochondrial and nuclear phylogenetic reconstruction related Sicilian trout with old Atlantic lineages.

Keywords: introgression; mitochondrial DNA; phylogenetics; *Salmo trutta*; *Salmo cetti*



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