XV Congresso Nazionale
A.I.I.A.D.

“La fauna ittica nello scenario dei cambiamenti globali”

CONSERVATION GENETICS OF SOUTHERN PIKE: HOW MANY DIFFERENT MANAGEMENT UNITS?

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Northern pike (*Esox Lucius* L. 1758) is one of the most prized game fish targeted by anglers worldwide and a commercial food fish locally reared and transplanted by professional fisherman. As a consequence, pike populations are heavily managed throughout its entire native distribution area, through translocation and restocking activity.

Statistically significant differences were described, in recent scientific literature, regarding phenotypic features (skin colour pattern), meristic characters (number of scales in the lateral line) and mtDNA (cyt-b and COI sequences) and ncDNA (AFLP, SNPs) genetic traits, pointing to a clear differentiation between a first lineage of northern pike, widely distributed in the palearctic region, and a second lineage of southern pike, naturally occurring in Italy. Based on differentiation and diagnosability of these two recently separating evolutionary entities, pike populations from Italy were proposed to belong to a newly described endemic species, southern pike (*E. flaviae* Lucentini et al., 2011). At present, however, no clear genetic evidence has been gained on a possible hybridization or introgression between the two species, due to the repeated stocking of European pike in Italy. Moreover, the level and structure of genetic differentiation between different natural populations in Italy is not known.

The present work preliminary investigated the ability and the power of molecular markers to fill both these gaps in available data, aiming at the definition of correct conservation and management plans for the residual populations of the native Italian pike populations.

Based on data from a mtDNA sequence marker (cyt-b) and 17 ncDNA microsatellite markers analysed on populations collected from different Italian sites, we here show that i) the introgression of *E. lucius* in *E. flaviae* is proved by genetic data; ii) a significant population substructuring can be observed in the *E. flaviae* sample from different hydrological districts, pointing to the definition of different Management Units in order to correctly preserve the remnant genetic heritage of this Italian endemic fish. According to the data here presented, particular attention needs to be adopted in translocation and restocking measures aimed at supporting angling activities and professional fishing. The extension of partial sampling coverage preliminarily accomplished in the present study will thus provide a more adequate and complete support to the definition of scientifically based local management plans for *E. flaviae*.