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Esox flaviae, population genomics revealed entangled origin and differentiation of the Italian populations

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In 2011, *Esox flaviae*, commonly known as the Southern pike, was identified as a distinct species from the Northern pike (*Esox lucius*) (Lucentini et al. 2011). It is classified as endangered on the IUCN Red List due to the threat of hybridization with the exotic species *E. lucius*, which was introduced for angling purposes. It is crucial to understand the population structure and dynamics of *E. flaviae* to protect it from local extinction, loss of genetic diversity, and loss of local adaptation. There have been few efforts to investigate the structure and substructure of this new species (Gandolfi et al. 2017). In this study, the genomes of 62 pikes, including 50 *E. flaviae* from six locations and 12 *E. lucius* from two locations outside Italy, were examined to detect genome-wide hybridization between and admixture among populations. The goal is to analyze the population's structure and dynamics at a higher resolution and to evaluate the consistency of phylogenetic relationships across chromosomes. The phylogenetic-based approach employed indicates variable relationships among populations through the chromosomes, suggesting admixture among the Po population and other populations studied. ABBA-BABA indicates admixture events that were not evident in the initial structure analysis, with the Po population being the most affected by these events. Such mixing, likely caused by human-mediated translocation for angling, complicates conservation efforts. This study lays the foundation for determining conservation units (CUs) and developing informed management plans for these populations. Preserving the adaptive potential of a species or population is crucial for its ability to adapt to changing environments

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