Population genetic analysis of wild and domesticated pikeperch (Sander lucioperca, Linnaeus, 1758) populations in Europe

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Abstract

The pikeperch (or zander Sander lucioperca, Linnaeus, 1758) is a Eurasian freshwater fish species with wild populations showing signs of decline in many areas of its natural range of distribution due to human activities whilst it presents growing interest for the European aquaculture. Pikeperch is considered still a wild species for the aquaculture industry and in principle each pikeperch farm uses its own stock, captured either from the wild or supplied by another farmer. The species has been recently introduced in southern European and northern African countries and many other regions. We developed and used two highly informative and efficient microsatellite multiplex panels (in total 10 loci) in order to assess the genetic variability in approximately 1,000 fish from twenty-one populations of the species: thirteen domesticated (from commercial farms) and eight wild populations. Partial Cytochrome b gene sequences were also used to infer phylogeographic relationships between populations. Results indicate that the majority of the populations show medium to low levels of genetic diversity and some of them may suffer from inbreeding. Differentiation between domesticated broodstocks was high in most cases, while lowest values were estimated for pairs of populations with already known common origin or geographic proximity. Finally, we provide evidence that pikeperch populations in Europe belong to at least two genetically differentiated groups: the first is found in northern Europe from Netherlands/Denmark to the West and Poland to the East to the North of Finland and the second one comprises all remaining populations in Central and Southern Europe.

Keywords: microsatellites, Cytochrome b, differentiation, freshwater fish

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