

A FIRST STEP FOR SUSTAINABLE BREEDING PROGRAMMES IN PIKEPERCH (*Sander lucioperca*) THROUGH THE EVALUATION OF THE GENETIC VARIATION IN DOMESTICATED BROODSTOCKS AND NATURAL POPULATIONS

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Abstract

The pikeperch is a temperate Eurasian freshwater/brackish water fish species with growing interest for the European aquaculture. Wild populations of pikeperch show signs of decline in many areas of its natural range of distribution (from Finland to the Aegean Sea, and East to the Aral and Caspian basins) due to human activities, such as the destruction of natural habitats and/or overfishing. The species has been introduced in northern Russia, Italy, Spain, Turkey, the North African countries (from Morocco to Tunisia) and many other regions. There are only a few commercial hatcheries that produce pikeperch in Europe. In principle, each farm uses its own stock, captured either from the wild or supplied by another farmer. Therefore, pikeperch populations differ from one farm to another depending upon the geographical origin of the captured wild populations, which were at the base of the captive stocks. The main objective of the present study was to develop and use highly informative and efficient for the species, multiplex panels of microsatellite loci, in order to assess the genetic variability of thirteen domesticated populations from commercial farms and of eight wild populations. In total, DNA from 971 fish samples (fin clips) was extracted using standard protocols. Two multiplexes (4-plex & 7-plex) were developed, optimized and finally used for genotyping of samples while all 21 populations were analyzed for basic population genetics parameters (allelic richness, heterozygosity indices, inbreeding coefficients). The genetic differentiation among locations was quantified by F_{ST} values. Genotyping of wild and domesticated populations and the comparative evaluation of their genetic status are extremely useful for the future establishment of genetic breeding programmes for sustainable optimal performance through domestication of pikeperch. Results indicate that most of the populations show medium to low levels of genetic diversity and some of them may be inbred. Differentiation between broodstocks was high in most cases, while lowest values were estimated for pairs of known common origin or geographic proximity.

Keywords: microsatellites, differentiation, freshwater aquaculture

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