

## A POPULATION GENETIC STUDY OF THE PIKE-PERCH (*Sander lucioperca L.*) WITH NEW MICROSATELLITE MARKERS

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For the pike-perch, many research teams are developing intensive farming technologies -among others- all across Europe. However, little is known about the genetic background of this species, its populations, stocks or varieties, these technologies could further be improved with molecular biological tools.

Our aim is to isolate new, specific genetic markers – microsatellites – from pike-perch that besides allowing the genetic analysis of the species itself, could also be used for other closely related species.

In order to generate microsatellite enriched libraries we used the slightly modified method of Travis C. Glenn and N. A. Schable (Glenn, T.C. and Schable, N.A. 2005. Methods in Enzymology 395:202-222.).

4 libraries were established, from which more than 100 clones were sequenced. 98,3% of the sequences contained microsatellite type repeats. The redundancy was less than 6%. 44 flanking sequences of repeat containing clones were determined and primers were designed for specific amplification. Until now 24 new microsatellite markers were isolated for the pike-perch.

10 polymorphic markers were chosen to analyze the natural population of the Lake Balaton (Hungary) (60 individuals) and an artificially propagated (captive bred) population from Dalmand (Hungary) (46 individuals).

Both populations showed moderate allelic diversity (Mean number of alleles/locus = 4,8 and 4,5; number of alleles = 2-11) and moderate gene diversity ( $H_s = 0,426$  and  $0,388$ ;  $H_d = 0,443$  and  $0,449$ ). PIC value of the 10 screened microsatellite loci varied widely between 0,064 and 0,784. The  $F_{st}$  values showed significant genetic difference among populations. The information on the genetic structure obtained in this study is useful for setting up suitable guidelines for future genetic management and stock improvement through selective breeding.

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Number of genomic DNA libraries highly enriched for microsatellites	4
Number of positive colonies	117
Number of sequenced inserts	115
Number of microsatellite sequences	101
<b>Number of new, applicable microsatellite markers</b>	<b>24</b>