

Population genetic analysis on different pikeperch (*Sander lucioperca*) populations based on microsatellite markers

Population genetic analysis was done by eight species-specific microsatellite markers on four different pikeperch populations with 20 individuals per population. In the four sampled fish populations there were three originated from Hungary (two pond reared /Akasztó-AK and Attala-AT/ and one wild population from Danube-D) and one from Romania-RO (cultured in an intensive system). The following population genetic parameters were investigated:

- The average allele number in each locus;
- detected number of alleles in each locus per population;
- expected and observed heterozygosity;
- deviations from Hardy-Weinberg population equilibrium;
- calculation of polymorphic information content (PIC) for each locus;
- calculation of allelic richness of each locus;
- genetic distance of the populations from each other by F-statistics (F_{ST} , D_A);
- fixation index of the alleles in each population (estimation of inbreeding);
- analysis of molecular variance (AMOVA);
- population assignment based on molecular marker information.

In this section, some of the main results are shown in tables and graph.

1. Table: PIC (Polymorphic Information Content) scores of the applied microsatellite markers by pikeperch populations and by locus, furthermore the average scores by locus.

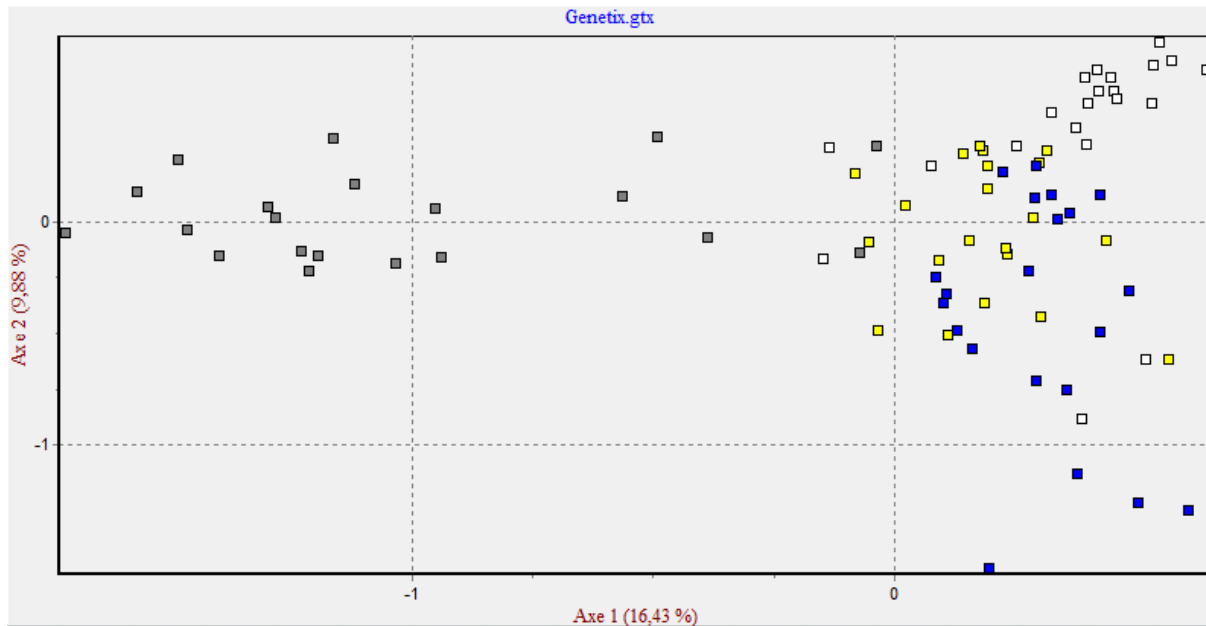
Microsatellite locus								
Pop. code	MS192	MS195	MS198	MS260	MS268	MS397	MS84	MS203
AK	0,2392	0,7204	0,1878	0,7091	0,375	0,375	0,3856	0,3975
AT	0,4728	0,5262	0,3126	0,4371	0,3744	0,3744	0,0526	0,6719
D	0,4889	0,5386	0	0,6758	0,2149	0,1239	0,2484	0,6448
RO	0,3725	0,3715	0	0,4422	0,3589	0,3589	0,3711	0,4741
Average	0,3933	0,5392	0,1251	0,5661	0,3308	0,308	0,2644	0,5471

2. Table

	AK	AT	D	RO
AK	0,000	0,044	0,073	0,108
AT	0,048	0,000	0,102	0,148
D	0,083	0,112	0,000	0,182
RO	0,091	0,135	0,181	0,000

Pairwise F_{ST} matrix (Weir and Cockerham, 1984; 1000 iterations) values (below diagonal) and Nei minimum distance D_A (above diagonal) in four pikeperch populations based on eight microsatellite marker.

The indicated numbers with bold is the minimum and maximum values of F_{ST} and D_A .



1. Graph. Multiple correspondence map based on the genotypes of the pikeperch individuals by eight molecular markers.

To summarize the results of this study, we can conclude that the least genetic distance can be found in the two pond reared pikeperch populations ($F_{ST;AK-AT}=0,048$) it assumes that the two pond reared populations are originating from the same population. However, based on the allele fixation indices stronger genetic constriction can be seen at the AT population ($F_{IS}=0,109$). The D population is genetically more separated from the other populations however, the genetic distance to AK and AT populations is closer ($F_{ST;D-AK}=0,083$ and $F_{ST;D-AT}=0,112$), thus it is presumable that the AK and AT pond reared pikeperch populations are originating from the Danube. The RO population has the largest genetic distance from the other populations ($F_{ST;RO-AK}=0,091$, $F_{ST;RO-AT}=0,135$ and $F_{ST;RO-D}=0,181$), which primarily arise from the segregation effect of geographical distance among populations.