

**THE ESTIMATION OF SPATIAL GENETIC DIVERSITY OF
VENDACE (COREGONUS ALBULA L.) POPULATIONS
IN LATVIAN-BELARUSIAN LAKELAND**

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Vendace (*Coregonus albula* L.) is a very plastic species of freshwater white fish and widespread in Europe. It has reached North-western Europe after glaciations. In Latvian-Belarusian Lakeland the populations of local Coregonidae fish are residues of Arctic freshwater faunal complex, and can be considered as glacio relicts and an indicator species of Lake ecosystem status. In Latvia and Belarus the areal of vendace populations is decreased, the catch is insignificant and unstable and this species is included into the list of specially protected fish species.

The extent of genetic diversity within and among populations is the outcome of interactions among genetic drift, selection, migration, mutation, and also anthropogenic activities. The estimation of the genetic structure of populations and determining the causes of genetic differentiation and the factors that promote variation between and within populations is fundamental for understanding adaptation and is, therefore a primary goal of population and conservation genetics.

Five microsatellite loci (BWF1, Cisco90, Cisco126, Cisco157, and Cisco106) were used to investigate the genetic structure within and between populations.

Genetic diversity was studied in seven vendace populations from Latvian-Belarusian Lakeland, namely Stirnu, Drīdzis, Sventes, Drisvjati, Rudakova, Strusto, Snudi.

Allelic variation was different in all investigated vendace populations, the observed and expected heterozygosity level was quite high. The estimates of genetic differentiation of population varied in all investigated loci. The F-statistic shows more accurate differentiation of studied population than the R-statistic. A bottleneck-induced distortion of allele frequency distributions were not revealed in any studied populations.

Structuring of the seven vendace populations were estimated by principal component analysis (PCA), Bayesian clustering (STRUCTURE) and by building UPGMA tree using Nei et al. (1983) genetic distance (Da). Bayesian-based STRUCTURE analysis suggested that there are two main genetic groups within our study area, separating Rudakova and Strusto into one and others studied populations into the other cluster.

These populations would be differentiated due to drift, reduced gene flow and possibly selection that promoting divergence.