

The Present Genetic Structure of Vendace (Coregonus albula (L.)): Populations in Latvian Lakes as a Result of Its Management and Conservation †

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- † Presented at the IX Iberian Congress of Ichthyology, Porto, Portugal, 20–23 June 2022.
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Abstract: The European vendace (Coregonus albula (L.)) is often treated as one of the glacial relicts of the animal world, and it is a widespread species in the waters of the Holarctic. Together with whitefish and salmonid, vendace belongs to a list of economically valuable fish species. In Latvian lakes, its share in the fishery is not big, and it is insignificant and unstable. The objectives of this study evaluate the influence of vendace translocations on the flourishment of a population and following a decline. The present research used nine microsatellite markers to study vendace populations from nine Latvian Lakes. The indices of genetic variation include the following: number and frequency of alleles at a locus, occurrence of private alleles, observed and expected heterozygosity levels, and the richness of alleles and private alleles were determined. Additionally, the genetic structure and differentiation of the populations were accessed. Investigated vendace populations have a high level of expected heterozygosity, with a high mean allelic richness and private allelic richness in Lake Riču suggesting that this vendace population is indigenous. Three clustering methods reveal similar groupings in three genetic groups. At the present time, the vendace populations of the investigated Latvian lakes seem to be a "mixture" of several populations and, therefore, may not differences may be caused by the consequences of the translocations and genetic drift, which influence allele frequencies in different ways and could be driven by some environmental factors. The results of the study allow the acceptance of each of the studied populations as a different management unit and

Keywords: population genetics; fish transfer; indigenous population; divergence; translocation

were to reveal the genetic structure and variability of the vendace gene pool in Latvian Lakes and to check for updates Citation: Oreha, J.; Škute, N. The be fully indigenous. The level of genetic variability differs among the studied populations. Such prompts the development of an optimal strategy for their effective conservation and management.

Present Genetic Structure of Vendace (Coregonus albula (L.)): Populations in Latvian Lakes as a Result of Its Management and Conservation. Biol. Life Sci. Forum 2022, 13, 110. https:// doi.org/10.3390/blsf2022013110

Academic Editor: Alberto Teodorico Correia

Published: 16 June 2022

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Author Contributions: Methodology, Validation, Formal analysis, Investigation, Data Curation, Writing—Original Draft, Visualization, J.O.; Conceptualization, Resources, Review & Editing, Supervision, Project administration, funding acquisition, N.S. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The datasets generated during and/or analyzed during the current study are available from the corresponding author on a reasonable request.

Conflicts of Interest: The authors declare no conflict of interest.