

INVESTIGATION INTO GENETIC VARIABILITY OF PARASITIC AND NON-PARASITIC LAMPREYS INHABITING WESTERN RIVERS IN LITHUANIA

Robertas Staponkus¹, Dalius Butkauskas¹, Vytautas Kesminas¹, Aniolas Sruoga²

¹Nature Research Centre

Akademijos 2, LT-08412 Vilnius, Lithuania; e-mail: robertas.staponkus@gmail.com

²Vytautas Magnus University

K. Donelaičio 58, LT-44248 Kaunas, Lithuania

Abstract. The river lamprey (*Lampetra fluviatilis*) is fish ectoparasites that parasitize the herring (*Clupea harengus*), the sprat (*Spattus sprattus*) and other commercial fish species in the Baltic Sea. On the other hand, the river lamprey is a valuable commercial catch itself in the Lithuanian, Latvian, Estonian, as well as northern Swedish and Finnish rivers. According to the latest molecular studies of the parasitic river lamprey and the non-parasitic non-migratory brook lamprey (*Lampetra planeri*) in the populations of Western Europe, there is insufficient evidence to separate the two by molecular markers. This initial study was carried out in order to determine if the hypervariable region of the D-loop could be used as an informative marker for recognising parasitic and non-parasitic lampreys. We established a data set from control region I sequences and identified 21 unique haplotypes unequally distributed among 5 populations. The phylogenetic analysis revealed one highly differentiated lineage among the obtained data set of sequences. This lineage consisted of two haplotypes shared by few individuals from the geographically close populations distributed in two drainages corresponding to the same region. Sequences of these two haplotypes differed by $5.7\% \pm 1.9\%$ (\pm SE) ($p < 0.01$) from all the rest D-loop sequences belonging to *L. fluviatilis* and *L. planeri* individuals and expressed a greater similarity to the Ukrainian lamprey (*Eudontomyzon mariae*) compared to the *Lampetra* genus. It could be guessed that a part of the non-parasitic lamprey population inhabiting some rivers in northern Lithuania harbour forms of mtDNA considered as belonging to an undescribed species which is the most closely related to *E. mariae*. A lack of highly differentiated clades in *L. planeri* and *L. fluviatilis* representing different drainages suggests possible intensive hybridisation or recent divergence of the two species.

Keywords: *Lampetra*, *Eudontomyzon*, identification, D-loop, Lithuania