MOLECULAR TECHNIQUE FOR ANGUILLA ANGUILLA AND A. JAPONICA SPECIMENS DISCRIMINATION BASED ON COMPARISON OF HOMOLOGOUS mtDNA D-LOOP REGION SEQUENCES

Adomas Ragauskas¹, Dalius Butkauskas¹, Aniolas Sruoga² ¹Nature Research Center, Akademijos str. 2, LT-08412 Vilnius, Lithuania Tel. +370 5 272 9287; e-mail: adomas.ragauskas@gmail.com ²Vytautas Magnus University, K. Donelaičio str. 58, LT-44248 Kaunas, Lithuania; e-mail: a.sruoga@gmf.vdu.lt

Summary. In order to clarify whether declared eels belong to *A. japonica* species or not, molecular technique which is based on PCR with Ang1 primer pair and alignment of newly obtained sequences with homologous *A. anguilla*, *A. rostrata* and *A. japonica* sequences from the GenBank, was used. It was shown that identification of *A. anguilla*, *A. rostrata* and *A. japonica* species based on analysis of 450-455 bp homologous mtDNA D-loop region sequences is reliable. After the study of 31 eels of uncertain origin it became clear that all investigated mtDNA D-loop region sequences belong to *A. japonica* species. Since this molecular technique is a powerful tool for *A. anguilla* and *A. japonica* discrimination, thus it could be used as an alternative to other methods.

Keywords: Anguilla sp., molecular technique, D-loop, species identification.