

ASSESSMENT OF DNA VARIATIONS OF THE NOBLE CRAYFISH (ASTACUS ASTACUS L.) IN GERMANY AND POLAND USING INTER-SIMPLE SEQUENCE REPEATS (ISSRS)



Conservation of the endangered noble crayfish (*Astacus astacus*) requires preservation of existing populations and reintroduction into suitable habitats, as currently underway in several regional projects in Germany and Poland. Therefore, knowledge about the genetic variation between populations is vital but, unfortunately, still restricted. By means of ISSR-PCR (Inter-Simple Sequence Repeats - Polymerase Chain Reaction) eight stocks in Germany and Poland were analysed. These semi-arbitrary multiloci markers had not previously been used in population studies of the noble crayfish. A total of 22 unambiguous and polymorphic markers were detected to use in the subsequent statistical analysis. The number of polymorphic loci in one population ranged from 4 to 19. Therefore the ISSR markers proved suitable for assessing within- and between-population DNA variations and establishing significant separation of most of the stocks. Shannon's Index, a relative estimate of genetic diversity within populations, ranged from 0.06 to 0.51. UPGMA cluster analysis based on pairwise ROGERS' (1972) genetic distance revealed two main clusters corresponding to populations sampled in the western and eastern part of the study area. Results are relevant on the local, regional and supra-regional (landscape) level. The implications for conservational management and restocking programs are presented.

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