

Abstract

Genetic variability of the European grayling (*Thymallus thymallus*) in North Rhine-Westphalia, Germany: Implications for management and conservation strategies.

Christoph Köbsch, Sascha Krenek, Thomas Schiller and Thomas U. Berendonk

Information on the genetic diversity for the European grayling (*Thymallus thymallus*) is essential for the future genetic management and stocking strategy of the grayling and for the protection of its genetic diversity. Accordingly, this project endeavoured to close this gap of knowledge and has analysed several populations from different river catchments in North Rhine-Westphalia (NRW), Germany.

Throughout the years 2016-2018, a total of 12 origins from three river catchments were analysed: Meuse (n = 2), Rhine (n = 7) and Weser (n = 3). Additionally, individuals from 5 hatchery stocks were included in the analysis to assess their suitability as sources for stocking measures to support the wild populations. Furthermore, it was possible to develop a non-invasive approach to analyse forensically sampled DNA of grayling individuals. The genetic diversity of this species in NRW river catchments was assessed using mitochondrial and nuclear microsatellite markers. In total 535 Individuals were sampled and 506 individuals from 17 origins were successfully genotyped by the use of 12 microsatellite loci. In addition, the mitochondrial control region (CR), NADH Dehydrogenase subunits 1 (ND1) and 5/6 (ND5/6) were analysed for 189 individuals from 17 origins using sequence and RFLP-analysis for phylogeographic and population genetic inference.

The analysis of the mtDNA has shown that the main part of the observed genetic variance (approx. 63 – 76 %, respectively) was explained by the genetic variation between river basin districts. For the analysed wild populations, the results of the microsatellite analysis revealed heterozygosity rates between 0.24 and 0.43. Heterozygosity rates in hatchery stocks ranged from 0.15 to 0.55. These comparatively low values could be indicative for low effective population sizes and could reflect the phylogeography as well as life history traits of European grayling such as its strong homing and weak dispersal behaviour, the formation of family cohorts and its spawning behaviour.

The genetic differentiation based on F_{ST} -values between the investigated populations shows significant differentiations between the populations according to all hierarchical levels tested by AMOVA and pairwise comparisons. Most of the observed genetic variation was explained by differences between individuals within populations (61.41 %). Only one hatchery stock proved to be suitable for stocking measures in some of the analysed wild populations.

In summary, the analysed grayling populations show a comparatively low level of genetic variability with high levels of differentiation. If necessary, stocking management should therefore endeavour to use several individuals from the local population as parental generation for supportive breeding.