

Comparative population genetic analysis of brown trout (*Salmo trutta*) from Kalkalpen National Park

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Keywords

Salmo trutta, population genetics, mtDNA, microsatellites

Summary

Central Europe is known to be a contact zone between the so-called Atlantic and Danubian lineage of brown trout (*Salmo trutta*) with the Atlantic lineage being native to river systems draining into the Atlantic Ocean and the Danubian lineage being the autochthonous lineage in the catchment area of the Danube (BERNATCHEZ 2001). Natural contact as well as the anthropogenic introduction of hatchery reared fish from the Atlantic lineage through extensive stocking activities throughout Europe have led to admixture of the Atlantic and Danubian lineage (SCHENEKAR 2015). The screening of about 200 brown trout populations throughout Austria revealed that most populations show admixture between these two lineages and only 10 (~ 5%) appear to be of a purely native Danubian origin. All other populations showed medium to high levels of genetic introgression with Atlantic basin fish – most presumably of hatchery origin (LERCETEAU-KÖHLER et al. 2013).

The aim of this study was to genetically characterize brown trout populations in the Kalkalpen National Park in Austria to gain a detailed overview of the current genetic make-up of populations within this national park as well as to identify potential source populations for future reintroduction and managing efforts. Emphasis was placed upon the genetic structure within and among these populations, particularly in relation to the presence of Danubian and Atlantic lineages. The analysis and interpretation was based on three different kinds of molecular markers – sequences of the control region of the mitochondrial DNA (mtDNA), a diagnostic site in the LDH-C1* gene, and allele size variance across a set of ten microsatellites.

The screening of eight small streams in the Kalkalpen National park led to the surprising result that six of these populations appear to be of purely Danubian origin, representing the most dense collection of such populations that has thus been discovered in Austria. In total, 19 different Danubian mtDNA haplotypes were resolved in the national park, illustrating the great diversity within the Danubian lineage. The analyses showed that populations belonging to the different sub-drainages were clearly distinguishable from each other. Autochthonous populations from the Krumme Steyring drainage (Krumme Steyring, Rumpelmayrbach & Schafgrabenbach) are genetically clearly differentiated from populations from the Großer Bach drainage (Saigerinbach & Stöffalmgraben) and Niklbach (Paltenbach drainage) with the latter stemming most likely from a different colonization event than the other populations.

These three sub-drainages drain an area at the northernmost edge of the last glaciation and a region that was covered by small mountain glaciers about 20.000 years ago. We speculate that these populations represent glacial relicts that were already isolated from downstream areas of the Enns catchment before the Würm glaciation. Fortunately, little to know stocking of foreign stocks of fish has been carried out in these streams, and it seems that the fish have survived the last 10,000 years without influence from foreign gene flow. Thus, these fish are a very valuable genetic resource for the Kalkalpen National Park. The data presented in this study can be of use for future management and potential reaturation plans elsewhere in the national park or neighbouring regions where native Danubian fish – clearly adapted to the unique characteristics of the region – are needed. Additional genome-wide scanning using state-of-the-art technology that is currently in progress may provide a deeper insight into the population structure of the brown trout populations in the Kalkalpen National Park and will help to further identify the relationship of these fish with other autochthonous populations in Austria and Bavaria.

Acknowledgements

I would like to thank my supervisor Assoc. Prof. Dr. Steven Weiss from the University of Graz; Dr. Reinhard Haunschmid and Florian Keil, MSc from the Bundesamt für Wasserwirtschaft for providing the brown trout samples; the Kalkalpen National Park for financial support (through a joint grant with the Federal Ministry of Agriculture, Forestry, Environment and Water Management and the European Union LE 14-20); and Dr. Erich Weigand in particular for his valuable support throughout the project.

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