

Genetic variation in brown trout *Salmo trutta* across the Danube, Rhine, and Elbe headwaters: a failure of the phylogeographic paradigm?

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Population genetic screening ($N = 97$) of brown trout *Salmo trutta* across the Danube/Rhine/Elbe catchments of Austria and Bavaria revealed a counter-intuitive phylogeographic structure with near fixation of the Atlantic lineage in the Bavarian Danube. Along the Austrian Danube, phylogeographic markers (mtDNA and LDH-C1) revealed increasing percentages of Danube-specific alleles with downstream distance. Pure Danube lineage populations in Austria were rare, occurring as isolate relicts either within or on the edge of previously glaciated regions north, south, and east of the Alps, whereby unglaciated regions revealed high percentages of Atlantic lineage genotypes. Both empirical data and simulated hybrid comparisons support that trout in non-glaciated regions of Austria have an admixed origin largely based on natural colonization from Atlantic basin watersheds. In contrast, most trout populations in glaciated regions of Austria south of the Alps revealed admixture based primarily on human-mediated release of hatchery strains. Despite the extensive use of Atlantic lineage hatchery strains in management, little evidence of first generation stocked fish or F_1 hybrids between stocked and wild fish was found.

The distribution pattern of the Atlantic and Danube lineages, as well as the clear signal of natural admixture is difficult to explain without invoking strong biological mechanisms in combination with a not-yet-visualized complex paleo-hydrological scenario. We conclude that the Atlantic lineage of brown trout is native to regions of the upper Danube and has been a very successful invader into unglaciated regions of the Austrian Danube north and east of the Alps, but there is no sign of its natural occurrence on the previously glaciated south slopes of the Alps.

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