Population genetic structure after 125 years of stocking in sea trout (Salmo trutta L.)

Stocking can be an effective management and conservation tool, but it also carries the danger of eroding natural population structure, introducing non-native strains and reducing genetic diversity. Sea trout, the anadromous form of the brown trout (Salmo trutta), is a highly targeted species that is often managed by stocking. Here, we assess the present-day population genetic structure of sea trout in a backdrop of 125 years of stocking in Northern Germany. The study area is characterized by short distances between the Baltic and North Sea river watersheds, historic use of fish from both watersheds for stocking, and the creation of a potential migration corridor between the Baltic and North Sea with the opening of the Kiel Canal 120 years ago. A survey of 24 river systems with 180 SNPs indicates that moderate but highly significant population genetic structure has persisted both within and between the Baltic and North Sea. This genetic structure is characterized by (i) heterogeneous patterns of admixture between the Baltic and North Sea that do not correlate with distance from the Kiel Canal and are therefore likely due to historic stocking practises, (ii) genetic isolation by distance in the Baltic Sea at a spatial scale of < 200 km that is consistent with the homing behaviour of sea trout, and (iii) at least one genetically distinct Baltic Sea river system. In light of these results, we recommend keeping fish of North Sea and Baltic Sea origin separate for stocking, and restricting Baltic Sea translocations to neighbouring river systems.

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