Genomic dynamics of brown trout (Salmo trutta) populations released to a novel environment

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Abstract

Understanding the consequences of human induced translocations on natural populations requires genetic monitoring. Salmonid fishes represent a group of species experiencing several such large-scale perturbations expected to affect microevolutionary processes. Here, two genetically separate brown trout populations with divergent life history traits are studied following their release into waters previously void of trout. We use a pooled sequencing approach to explore the genomic characteristics of the released stocks and of populations established in the wild in two lakes down-stream of the release site 30 years (4-5 generations) later. While most of the differences (FST=0.16) between the released stocks can be attributed to drift, we identify putatively adaptive differences between them in genes involved in immunity, hearing, skin and muscle texture. Higher levels of genomewide diversity in established populations compared to released stocks suggest extensive hybridization between stocks. However, released stocks are unequally represented in the established populations, with one stock mainly contributing to the lake closest to the release site, and the other dominating the lake further downstream. We also identify genomic regions putatively under directional selection in the new environment, where genes from one of the released populations, governing metabolism, appear advantageous. Our results demonstrate that hybridization, establishment, and adaptation can be rapid after release into novel environments. We show that such ongoing processes, important for conservation and management, are possible to monitor over contemporary time scales even for a species with relatively small local effective population sizes and a large, complex genome.

Hosted file

Stocks A (SA) and B (SB) released in 1979 and brown trout establishment confirmed. Void of fish not investigated for brown trout.

Haravatnet (HV) sampled 2011.

Lilla Bävervatnet (LB) sampled 2011.

Stora Bävervatnet (SB)

Waterfall prohibiting upstream migration.
Population

SA:SB

LB:HV

CHD23

Population

F_{ST}

\pi (x 10^{-3})

T_D

Position 10^6
A

Gene

F_{ST}

0.0
0.1
0.2

JAML
LHFPL6 FOXO1
LOC106602895
CAMLG FAXDC2 LARP1 RBM41 HINFP NCBP3

SA.SB
SA.LB
SA.HV
SB.LB
SB.HV
LB.HV

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