

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

Sara Kurland¹, Nima Rafati², Nils Ryman³, and Linda Laikre³

¹Stockholms University Department of Zoology

²SciLifeLab

³Stockholm University

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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 ($F_{ST}=0.16$) 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 genome-wide 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.

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