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ABSTRACT

Are Fisheries In Hot Water? Transcriptome-Wide Analyses Reveal Differential Gene Expression in Wild, Farmed and Hybrid Atlantic Salmon.

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Aquatrace is a EU funded project with 22 partners in the consortium provide multi-disciplinary expertise, ranging from molecular genomics to fish breeding. The collaboration aims to create forensically validated genetic techniques to reliably trace the origin of farmed fish, and to successfully gauge introgression between wild and farmed individuals.This project forms part of two work packages within the Aquatrace remit, using a transcriptomic approach with 44k chip analyses, we will attempt to highlight differential gene expression in wild, farmed and hybrid Atlantic salmon (*Salmo salar*).

Several strains of farmed salmon have been selected for aquaculture, specifically to improve several traits of commercial interest, such as faster growth rates and nutritional content. These hatchery broodstocks may also possess several other desirable traits, such as improved disease resistance and feeding efficiency. As the farmed salmon become selectively bred over multiple generations, genetic differences become apparent, resulting in altered gene expression and hormone or protein production, which can have both advantageous and detrimental effects on fitness in the wild. This study considers 8 different Norwegian strains, of wild and farmed origin, including reciprocal hybrids. These were sampled as sac-fry to prevent life-stage specific differences in gene expression being detected. Differentially expressed genes were illuminated with the use of 4x44k oligo-microarrays, providing a snapshot into the transcriptome of different strains of salmon at an identical life-stage.

Initial results show hundreds of genes differentially expressed between strains, indicating possible maternal and paternal effects through the use of reciprocal hybrids. In particular, we find genes related to metabolism, growth, immune response and transcription. These complex pathways and unexpected differences between wild strains from multiple origins are being investigated further. A clearer understanding of the similarities and differences between wild, farmed and hybrid salmon is necessary to identify candidate genes for domestication, selection and

introgression, and to aid the discovery of molecular genetic markers to reliably distinguish between wild and farmed salmon.

With a changing climate exerting effects, species must transition to new ranges or adapt *in situ* to survive within native environments. Species with a low tolerance for thermal stress could provide an informative source for investigating responses to climate change. Genomic and transcriptomic approaches can reveal evidence for environmental-mediated selection and highlight associated gene regions. With the arrival of capelin, cod, haddock and even salmon in the waters of Svalbard, the implications for native Arctic char (Salvelinus alpinus) are as yet uncertain. At the uppermost edge of its range where it is not subject to competition from other fishes, Arctic char demonstrate flexible habits. However, at lower latitudes, the diet of the Arctic char is thought to become limited under competition from higher temperature-tolerant species. Additionally, the Arctic chars ability to interbreed with closely related species introduces genetic changes that affect food chains producing other unexpected results. Since populations may vary in their susceptibility to climate change, applying genomic and transcriptomic technologies towards understanding responses to climate change could fill the current knowledge gap, providing insights into the management of a sustainable Arctic ecosystem.