

**Genomic signatures of local adaptation in natural populations of Atlantic cod: implications for interactions between aquaculture and wild cod populations**

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Marine fish display low levels of genetic structuring and associated high levels of gene flow, suggesting limited or a lack of local adaptations among populations. We investigated 98 gene-associated single nucleotide polymorphisms (SNPs) in local populations of Atlantic cod (*Gadus morhua*) across the species distribution. Genome scan tests for selection revealed eight loci with very high support for a statistical model of local selection compared with a model of neutral population divergence. On a south/north transect of central and eastern Atlantic populations, seven loci displayed strongly elevated levels of genetic differentiation consistent with adaptive evolution at the studied or closely linked loci. In general, outlier loci were not only associated with one or a few particularly divergent local populations. Temporal stability of allele frequencies within populations was confirmed by assessing SNP variation in DNA retrieved from historical otoliths. Our study of wild cod populations found that adaptive population divergence may be prevalent in cod on various geographical scales. This finding may have a number of strong implications for future sustainable aquaculture management and conservation of adaptive genetic diversity within the species.

Keywords: adaptive evolution, genome scan approach, marine fish, local adaptation, landscape genomics.

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