

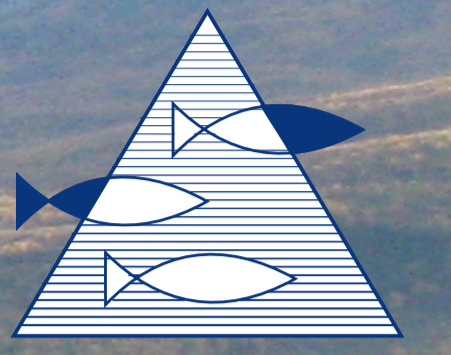
Farming of Atlantic cod *Gadus morhua* in the vicinity of major spawning sites for Norwegian coastal cod populations - is it hazardous?



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Introduction

Waters along and adjacent to the coast of northern Norway are unique in housing two major populations of Atlantic cod with very different life histories. The Northeast Arctic cod (NEAC) has its nursery and feeding grounds in the Barents Sea but migrates to the coast of northern Norway to spawn. Norwegian coastal cod (NCC) is more stationary, spawns mainly at local sites in individual fjords but to some degree also overlap with the spawning sites of NEAC (Fig.1). These distinctive patterns in life history are reflected in a clear-cut genetic divergence between the two populations. Various molecular genetic markers (scnDNA, microsatellites and SNPs) have displayed genetic differences between NEAC and NCC which are remarkable for marine fish with a comparable gene flow potential (cf. Sarvas and Fevolden 2005, Wennevik et al. 2008, and Westgaard and Fevolden 2008 for recent updates).



Ullsfjord



Figure 1. Approximate outer boundaries for Northeast Arctic cod (NEAC) and Norwegian coastal cod (NCC). Sampling sites indicated by filled circles.

Concern for cod farming

The unique biology and genetic make-up of the two cod populations needs to be taken into consideration when designing a management regime for cod farming in northern Norway. In contrast to captive Atlantic salmon, the iteroparous and batch spawning Atlantic cod may spawn over extended periods allowing escapement of the pelagic eggs and larvae in addition to adults (Jørstad et al. 2008). Thus, strict criteria should be set on the choice of brood stocks, using preferably native populations, and avoid producing hybrids between NEAC and NCC despite potential production advantages they might have. The list of reservations against an impetuous development in cod farming is extensive and should be founded entirely on the unique characteristics of the natural cod populations of concern.



Ullsfjord

Simulated genetic effects of farmed escaped cod

Given farmed escaped and wild cod interbreed, a simple simulation study on the genetic effects of escapees on a native fjord population is outlined by considering farming of typical North East Arctic cod (NEAC) in a fjord known to be a spawning site for Norwegian coastal cod (NCC). Thus, two genetically known samples from wild cod populations were used, NEAC sampled off Bear Island (Barents Sea) and NCC from the inner part of Ullsfjord (Troms County). Five molecular markers were included in the simulation study. They were four SNPs, all showing high adaptive divergence between NEAC and NCC, with F_{ST} values from 0.20 to 0.47 between the two populations. In addition, we analysed the *Pan I* locus (in reality also a SNP), which displays extreme allele frequency differences between NEAC and NCC ($F_{ST} = 0.71$).

Table 1. Allele frequencies for the five markers and two samples of wild cod populations, plus F_{ST} estimates between them.

| Allele: | NCC (Ullsfjord) | | NEAC (Barents Sea) | | F_{ST} |
|--------------|-----------------|-------|--------------------|-------|----------|
| | 1 | 2 | 1 | 2 | |
| Gm335_0159 | 0.643 | 0.357 | 0.982 | 0.018 | 0.31 |
| Gm240_0209 | 0.366 | 0.634 | 0.902 | 0.098 | 0.47 |
| Gm1086_0345 | 0.795 | 0.205 | 1.000 | 0.000 | 0.20 |
| Gm1077_0787 | 0.321 | 0.679 | 0.000 | 1.000 | 0.31 |
| <i>Pan I</i> | 0.802 | 0.198 | 0.065 | 0.935 | 0.71 |

By means of the software Hybridlab 1.0 (Nielsen et al. 2006) we simulated the effect of introgression between farmed NEAC and the native NCC population. The simulations were carried out with 1, 5, 10, and 25 % introgression of genetic material from NEAC. Given the high numbers of fish in a single cod farm and the notorious *Houdini*-talent of captive cod, the introgression levels employed here are deemed realistic for many northern Norwegian fjords designated for cod farming.

Figure 2 visualizes the effect on allele frequency distribution of the least common allele in native NCC by various levels of introgression from farmed NEAC. The *Pan I* exhibits the highest effect of introgression by escapees, in accordance with its displaying the largest divergence (F_{ST}) between the farmed and native population. The GM240_0209 locus displays the highest divergence and most profound effect among the SNP loci.

Figure 3 shows the effect on F_{IS} for each locus in the native population by introgression from farmed NEAC. For *Pan I* and GM240_0209, F_{IS} becomes increasingly negative by higher introgression rates, that is, the population deviates more and more from Hardy-Weinberg expectations due to excess of heterozygotes, a typical hybridization effect.

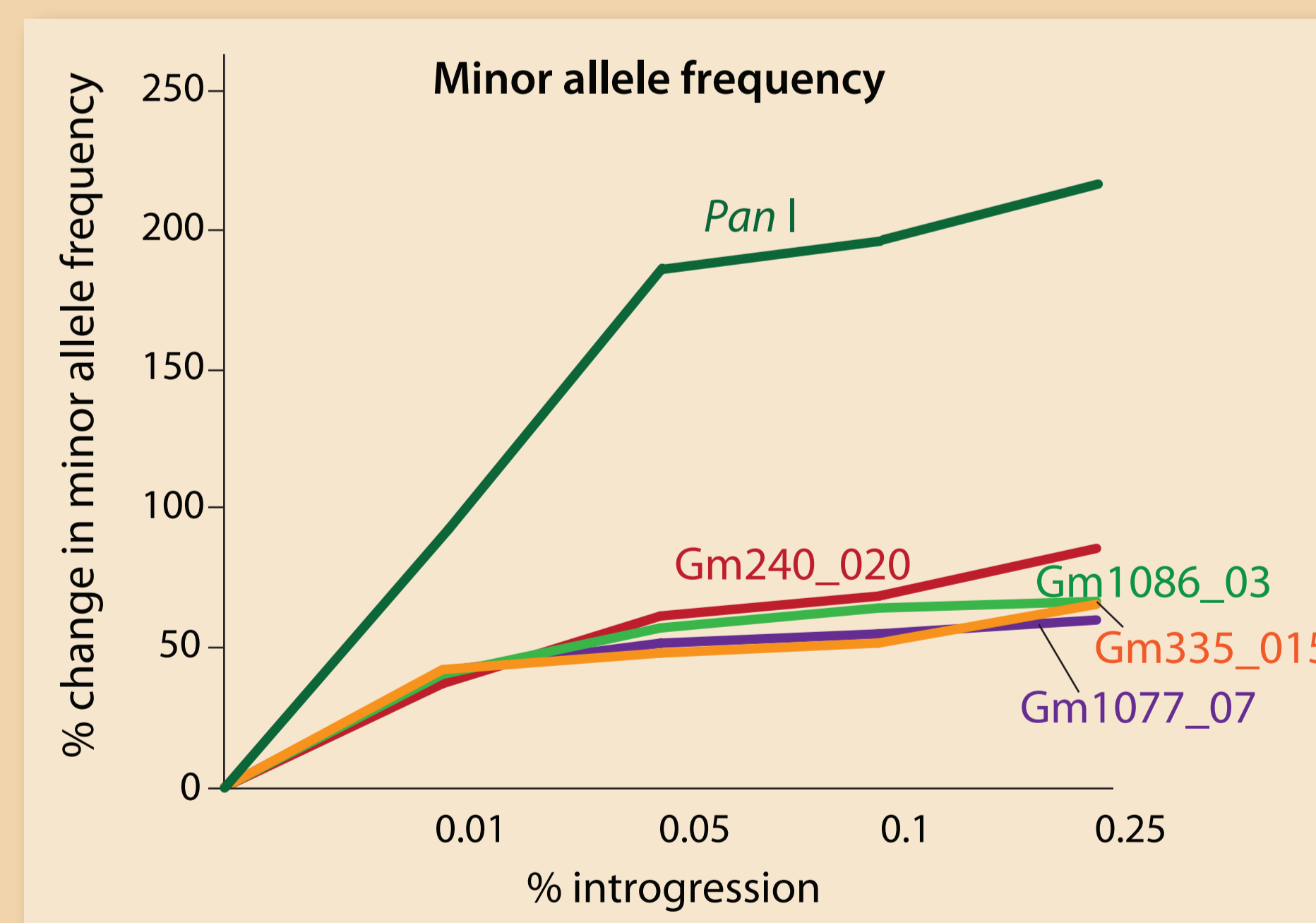


Figure 2. Changes in frequencies of the less frequent allele at five markers in the F1 generation of the native population of coastal cod (NCC) at different levels of introgression by escaped farmed Northeast Arctic cod (NEAC). Values are means of ten simulation runs.

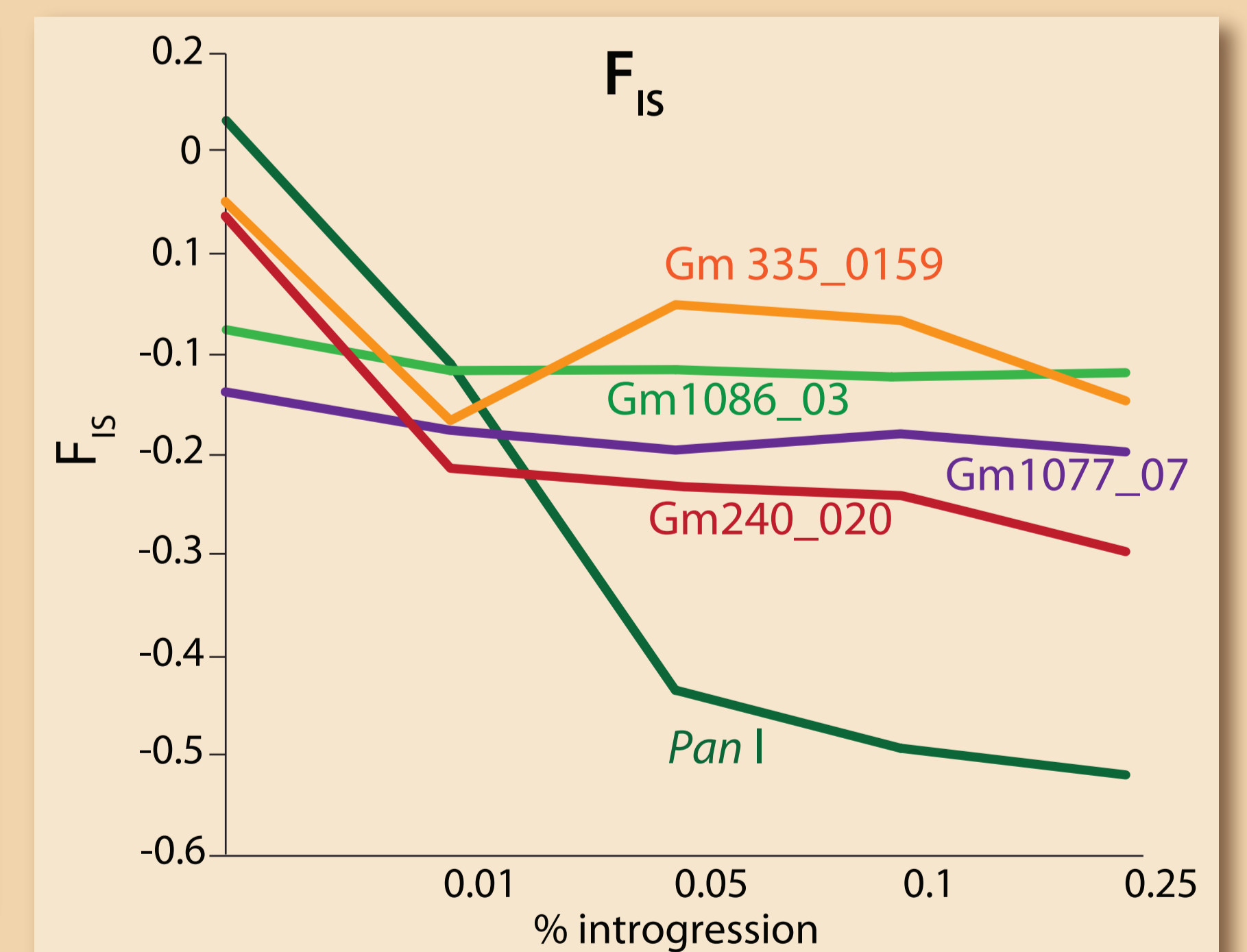


Figure 3. Changes in single loci F_{IS} values in the F1 generation of the native population of coastal cod (NCC) at different levels of introgression by escaped farmed Northeast Arctic cod (NEAC). Values are means of ten simulation runs.

References

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The simulations demonstrate that in cases where the farmed cod population (e.g. NEAC) is genetically very distinct from the native population (e.g. NCC) allele frequency alterations, even at low rates of introgression, have profound effects on the genetic profile of the native population. This clearly represents a genuine cause of concern.

Outstanding questions

The introduction of alien escaped cod inevitably raises several questions concerning the genetic impact on native cod in addition to the obvious ecological consequences.

- Long-term change in genetic profiles over generations?
- Change in migration and spawning patterns?
- Change in overall fitness and survival?