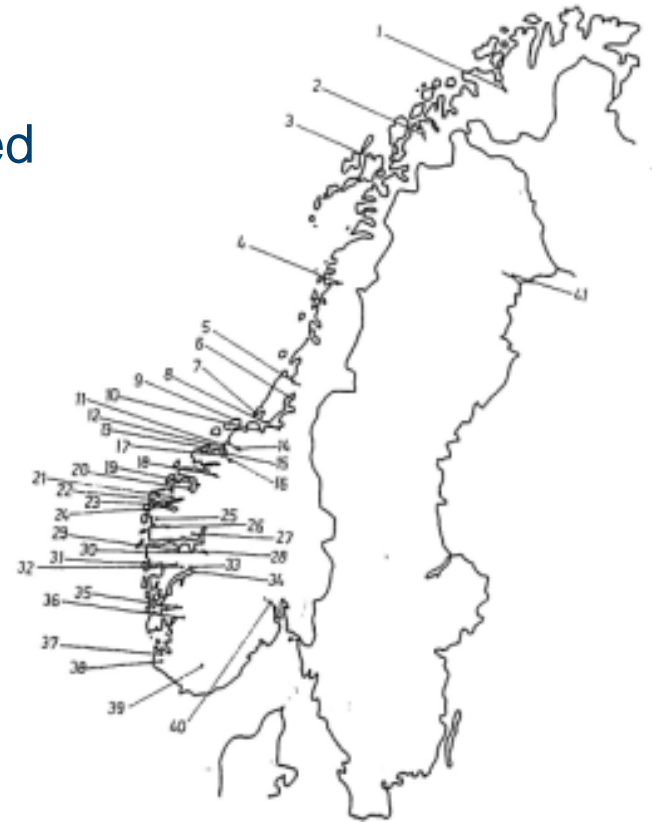


Genomic tools to trace and monitor the genetic impact of aquaculture escapes

Céleste Jacq

Norwegian Farmed Atlantic Salmon

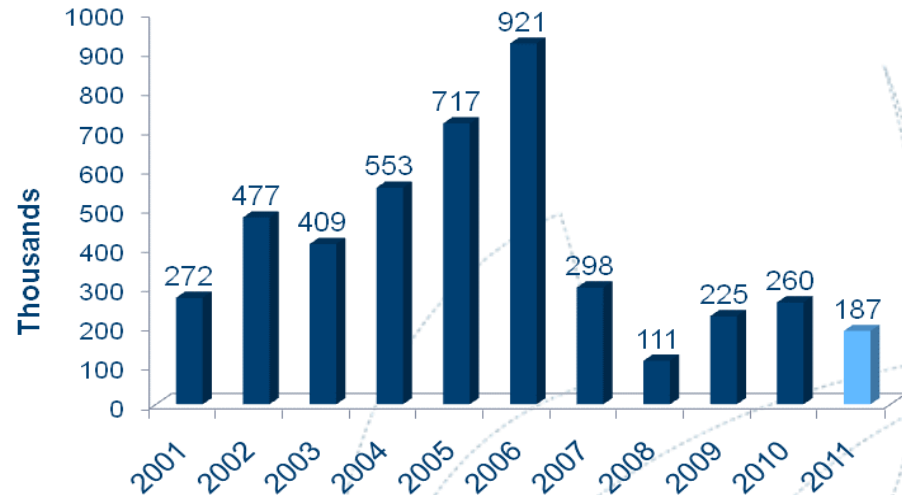
- In 1970s wild salmon collected from 40 rivers in Norway
- These salmon form the basis for the farmed Atlantic salmon material both in Norway and in many other parts of the world
- Individuals and family-based selection on this material for up to 10 generations for:
 - Growth
 - Delayed sexual maturity
 - Disease resistance
 - Flesh quality traits (colour, fat, etc)
- 900 000 tonnes farmed salmon produced by Norway in 2010 (ca. 200 million individuals)



Escapes of Atlantic salmon in Norway

Pose special threats:

- Norwegian farmed salmon originate from Norwegian wild salmon
 - Genetically similar
 - Max. 10 generations separate farmed from wild
 - Small changes at many loci rather than large changes at few
- Important phenotypic differences:
 - Size (growth)
 - Later sexual maturation



Source: Norwegian Directorate of Fisheries – Aug., 2011

We know that:

- In some rivers % escaped salmon immigrants greater than % natural wild immigrants (strayers)
- Escapees can breed with wild fish, but have lower lifetime survival (success)
 - Offspring of escapees also have lower success

Effect of farmed escapees on wild populations is dependant on:

1. Adaptation to local environment
2. Size of population
3. Degree of migration (straying) between neighbouring populations
4. Number of escapees & frequency of influx

Wild populations respond in different ways

- Complex life history
 - Anadromous / freshwater-restricted populations
 - Varies between & sometimes within rivers
 - Results in different selection pressures at different stages
 - Time spent at sea (1 SW – 5 SW)
- Genetic, ecological, biological differences between populations:
 - Phylogeographic differences (historical evolutionary divides)
 - Homing facilitates local adaptation
 - Straying facilitates genetic diversity
 - Meta-population structuring (sub-populations exchange migrants within larger population)

Genetic influences of farmed salmon:

- Some wild populations that receive farmed escapees show changes in genetic variation over time:
 - Temporal shift in (neutral) allele frequencies
 - Temporal change in LD
 - With or without accompanying loss in genetic diversity
- Other wild populations show no temporal change despite presence of farmed salmon
- Few studies have looked at changes in adaptive diversity

What we *DON'T* know is:

- Are temporal genetic changes observed in wild populations due to:
 - Hybridisation & introgression of "farmed" gene variants?
 - Natural selection acting on wild population to out-compete farmed immigrants?
 - Other anthropogenic issues (damming, river acidification, etc)?
- To what degree will natural selection act on farmed immigrants to "naturalise" them?
- What is the relative lifetime survival of farmed fish in different rivers?
- What is the actual genetic contribution from farmed fish in the wild?

Detecting selection & hybridisation

- Can distinguish farmed from wild salmon in natural populations using 60 diagnostic SNP markers
 - Useful to measure gene flow from escapees up to F1 hybrids
 - Based on signatures of selection over genome
 - Breeding goals similar in different breeding companies
 - Therefore loci under selection evolve in same direction (away from wild populations)

MOLECULAR ECOLOGY RESOURCES

Molecular Ecology Resources (2011) 11 (Suppl. 1), 247–253

doi: 10.1111/j.1755-0998.2010.02959.x

SNP GENOTYPING AND APPLICATIONS

Generic genetic differences between farmed and wild Atlantic salmon identified from a 7K SNP-chip

STEN KARLSSON,* THOMAS MOEN,†‡ SIGBJØRN LIEN,‡ KEVIN A. GLOVER¶ and KJETIL HINDAR**

Detecting selection & hybridisation...

- 1st study to look at temporal changes in loci under selection in the wild following interactions with farmed escapees
- Found temporal change in number of loci putatively under selection when compared to farmed reference samples
 - Suggests wild population progressing toward "farmed-like" fish following introgression



Heredity (2011) 106, 500–510
© 2011 Macmillan Publishers Limited All rights reserved 0018-067X/11
www.nature.com/hdy

ORIGINAL ARTICLE

Temporal change in genetic integrity suggests loss of local adaptation in a wild Atlantic salmon (*Salmo salar*) population following introgression by farmed escapees

V Bourret¹, PT O'Reilly², JW Carr³, PR Berg⁴ and L Bernatchez¹

Relative fitness of farmed and wild salmon

- Only two studies of relative survival of farmed & wild salmon
 - Competitive exclusion of wild fish at young age, BUT...
 - Lifetime success better in wild fish than farmed and hybrid fish
 - Evidence of natural selection **against** farmed fish
- Contrast with Bourret et al. may be due to different population reactions:
 - Weak populations can't out-compete farmed immigrants
 - Strong populations have better overall fitness
- May also indicate that specific traits have a selective advantage in the wild, while others are at a disadvantage

Proc. R. Soc. Lond. B (2000) **267**, 1517–1523

Lifetime success and interactions of farm salmon invading a native population

Ian A. Fleming^{1*}, Kjetil Hindar¹, Ingrid B. Mjølnerød^{1†}, Bror Jonsson², Torveig Balstad¹ and Anders Lamberg¹

Fitness reduction and potential extinction of wild populations of Atlantic salmon, *Salmo salar*, as a result of interactions with escaped farm salmon

Philip McGinnity, Paulo Prodöhl, Andy Ferguson, Rosaleen Hynes, Niall ó Maoiléidigh, Natalie Baker, Deirdre Cotter, Brendan O'Hea, Declan Cooke, Ger Rogan, John Taggart and Tom Cross

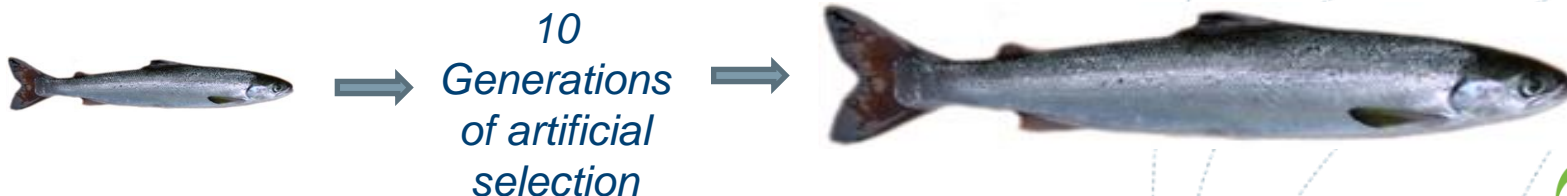
Proc. R. Soc. Lond. B 2003 **270**, 2443-2450

Genomics and the future...

- Annotated Atlantic salmon genome sequence available 2012 (?)
- Genomic re-sequencing becoming more affordable
- Higher density SNP chip being developed (~200K)

These technologies will lead to:

- Improved mapping of QTL's
- Temporal sampling over generations in breeding program can provide information on heavily selected genes:
 - What are the functions of the genes underlying commercially important traits?
 - How different is the farmed genome from the wild genome?



Genomics and the future...

- Temporal surveys of farmed + wild populations can tell us:
 - Which traits selected for in the breeding programs also have selective advantages in the wild?
 - Through polymorphisms underlying these traits we can assess the rate of selection for (and against) these traits in the wild
 - What are the consequences of introgression of these traits on long-term population fitness?
- This information will enhance predictions of which populations are most at risk - More effective management strategies...