Norwegian salmon farming – Monitoring and research

Sten Karlsson

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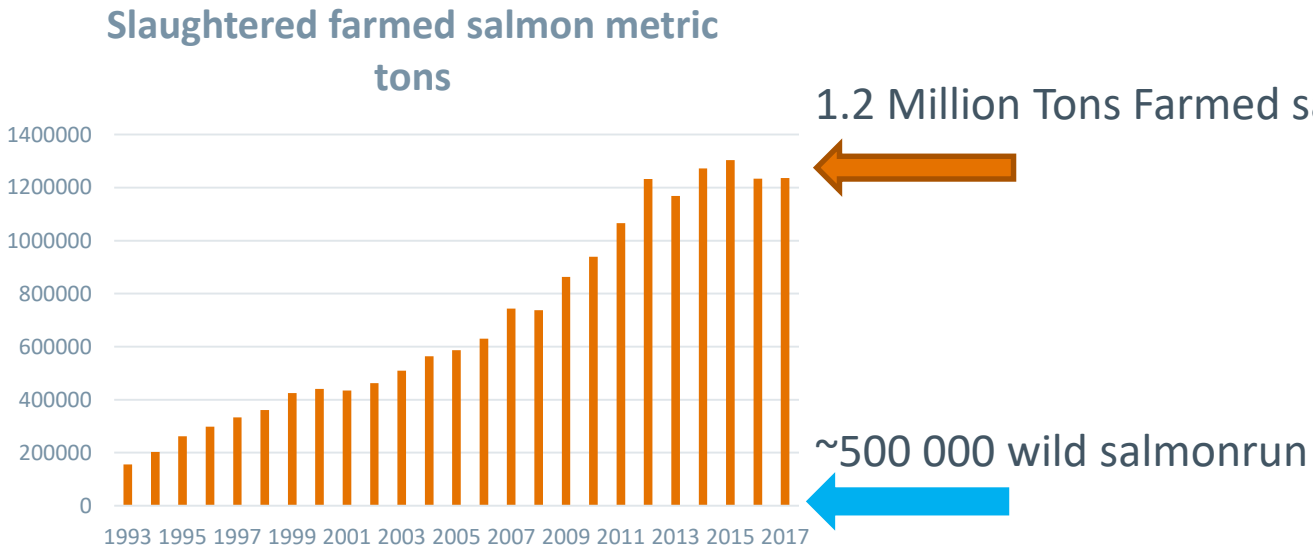
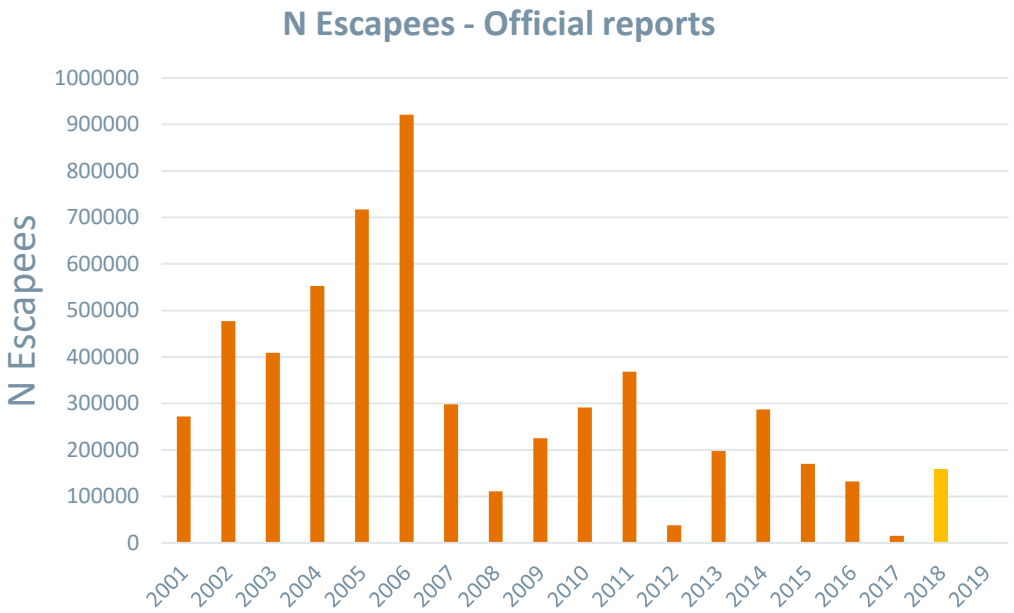
Norwegian Salmon farming



1.2 Million Tons Farmed salmon

~500 000 wild salmonrun



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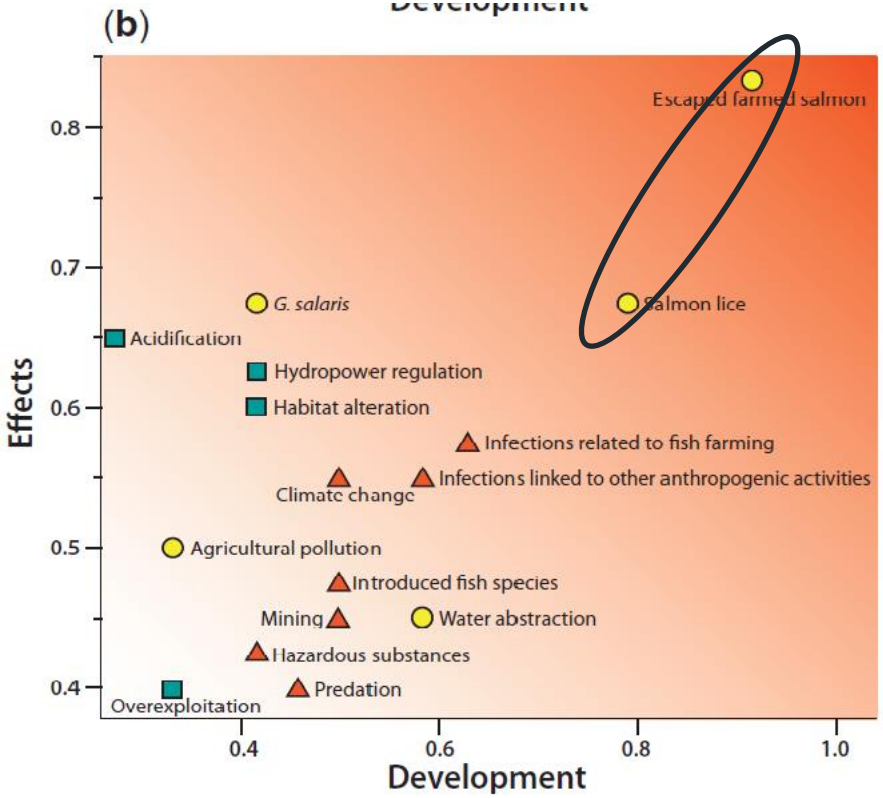
Nowegian wild salmon

- About 400 salmon rivers

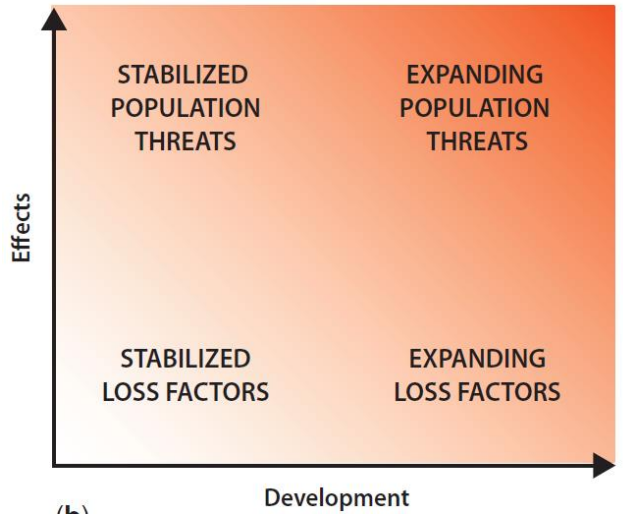


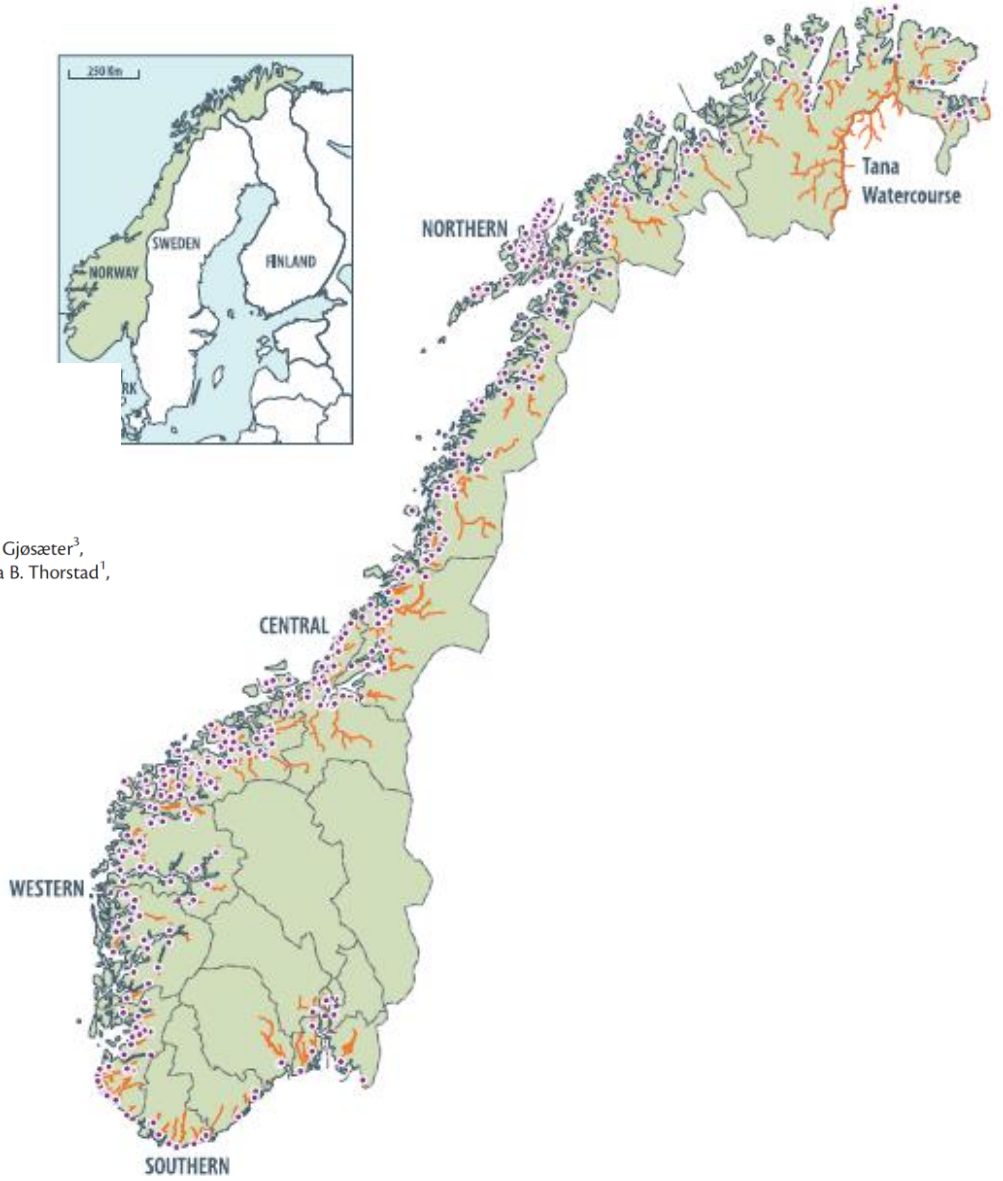
ICES Journal of Marine Science (2017), doi:10.1093/icesjms/fsx020

Review article

The major threats to Atlantic salmon in Norway

Torbjørn Forseth[1,*], Bjørn T. Barlaup[2], Bengt Finstad[1], Peder Fiske[1], Harald Gjøsæter[3], Morten Falkegård[1], Atle Hindar[4], Tor Atle Mo[1,5], Audun H. Rikardsen[6], Eva B. Thorstad[1], Leif Asbjørn Vøllestad[7], and Vidar Wennevik[3]





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Farmed escapees

ICES Journal of Marine Science (2019), doi:10.1093/icesjms/fsy202

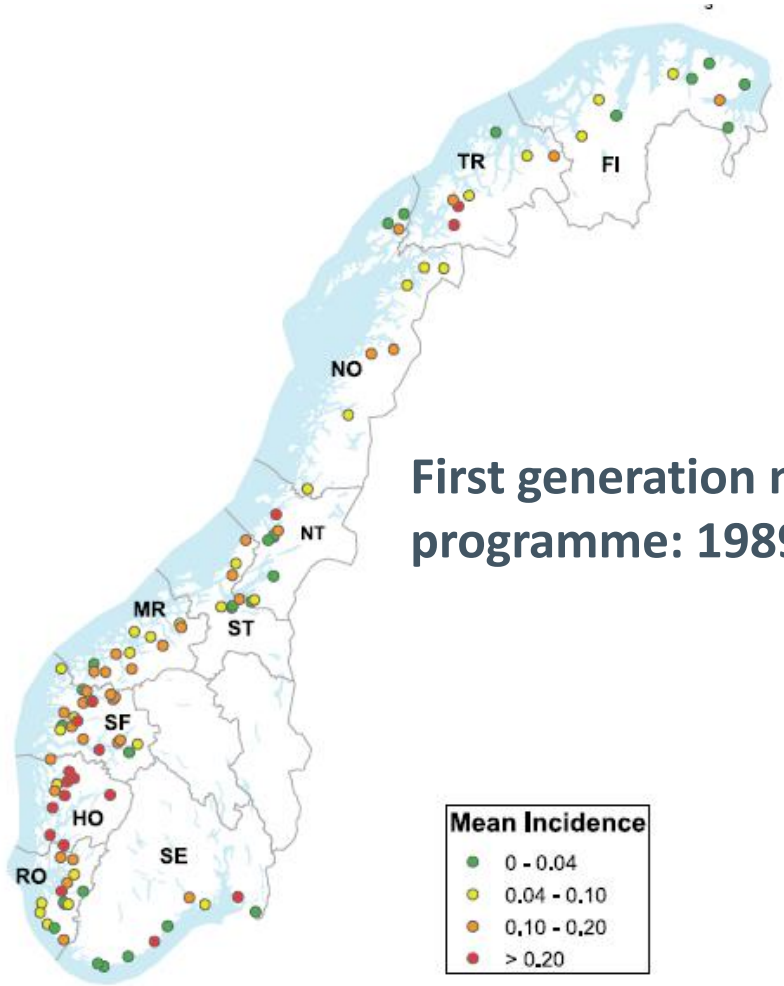
Escaped farmed Atlantic salmon in Norwegian rivers during 1989–2013

O. H. Diserud[1]*, P. F
P. Orell[6], J. Erkinaro[6]

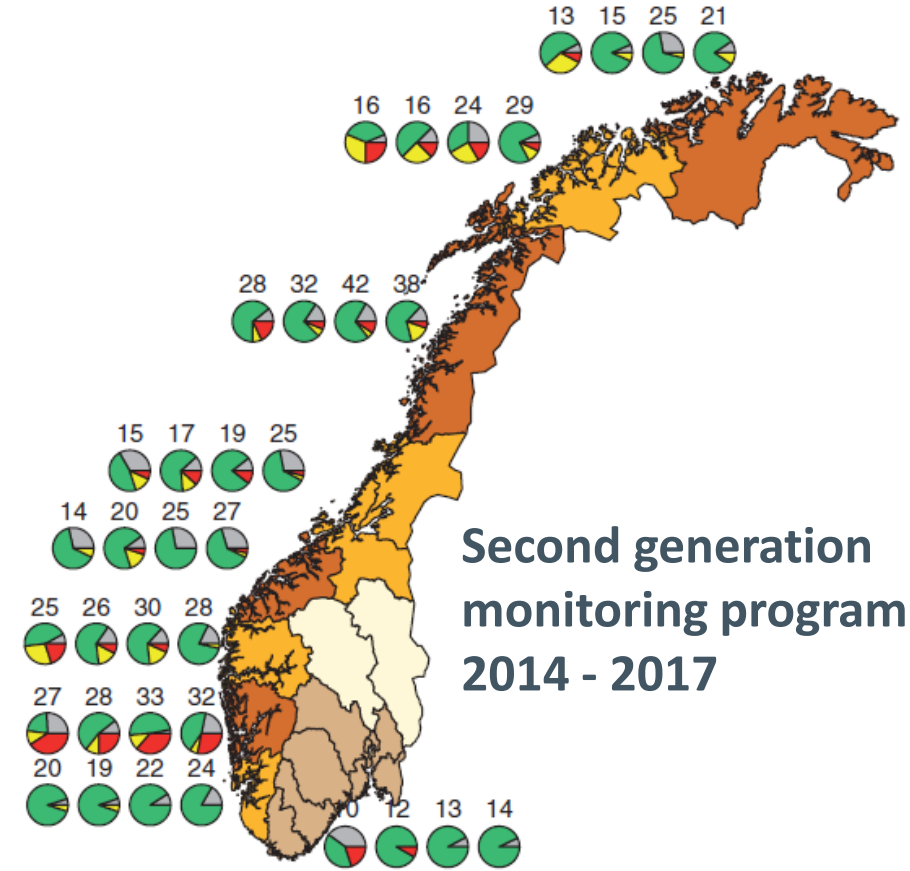
ICES Journal of Marine Science (2019), doi:10.1093/icesjms/fsy207

Domesticated escapees on the run: the second-generation monitoring programme reports the numbers and proportions of farmed Atlantic salmon in >200 Norwegian rivers annually

K. A. Glover[1,2]*, K. Urdal[3], T. Næsje[4], H. Skoglund[5], B. Florø-Larsen[6], H. Otterå[1], P. Fiske[4], M. Heino[1,2,7], T. Aronsen[4], H. Sægrov[3], O. Diserud[4], B. T. Barlaup[3], K. Hindar[4], G. Bakke[1], I. Solberg[3], H. Lo[6], M. F. Solberg[1], S. Karlsson[4], Ø. Skaala[1], A. Lamberg[8], Ø. Kanstad-Hanssen[9], R. Muladal[10], O. T. Skilbrei[11] and V. Wennevik[1]



First generation monitoring programme: 1989 - 2013



Second generation monitoring programme: 2014 - 2017

Figure 3. Pie-charts showing frequency of rivers displaying <10% (green), ±10% (yellow), and >10% (red) proportion of escapees from 2014 (left) to 2017 (right) for the different areas of Norway.

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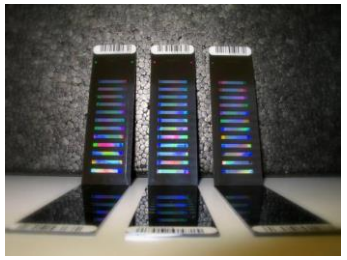
Farmed to wild genetic introgression

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**
*Nofima Marine, Arboretveien 6, N-1432 Ås, Norway, †Aqua Gen AS, PO Box 1240, N-7462 Trondheim, Norway, ‡Department of Animal and Aquacultural Sciences and Centre for Integrative Genetics, Norwegian University of Life Sciences, Arboretveien 6, N-1432 Ås, Norway, ¶Institute of Marine Research, PO Box 1870 Nordnes, N-5817 Bergen, Norway, **Norwegian Institute for Nature Research (NINA), PO Box 5685 Sluppen, N-7485 Trondheim, Norway

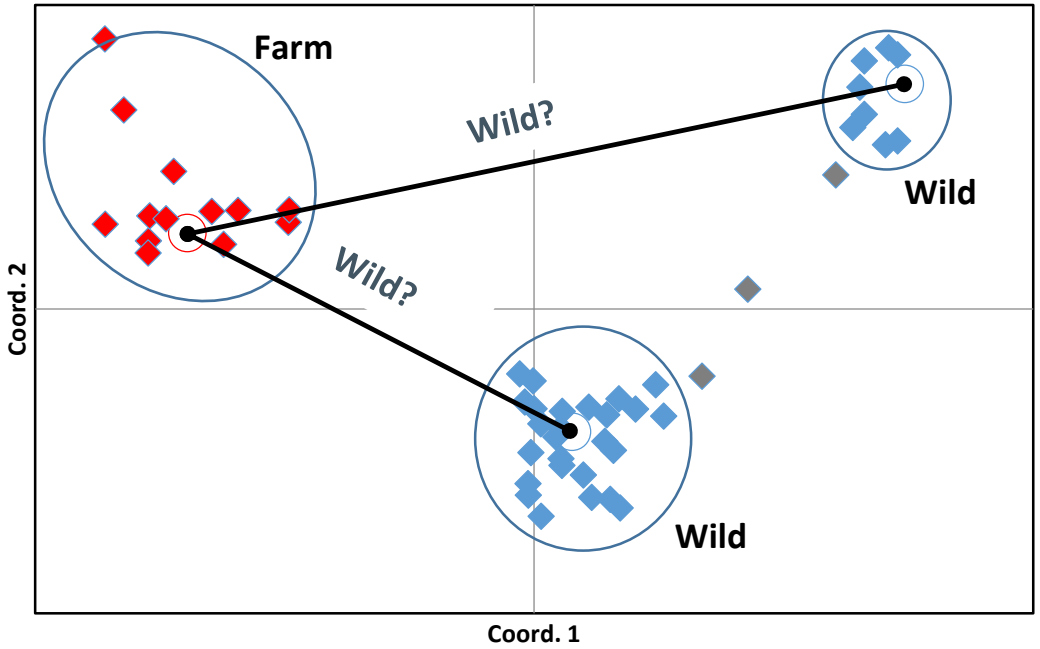


Finding genetic markers (SNPs) that generically differentiate between Norwegian wild and farmed salmon

Ecology and Evolution
Open Access

A standardized method for quantifying unidirectional genetic introgression

Sten Karlsson[1], Ola H. Diserud[1], Thomas Moen[2,3] & Kjetil Hindar[1]
[1]Norwegian Institute for Nature Research (NINA), P.O. Box 5685 Sluppen, N-7485 Trondheim, Norway
[2]AquaGen AS, P.O. Box 1240, N-7462 Trondheim, Norway
[3]Centre for Integrative Genetics, Norwegian University of Life Sciences, Arboretveien 6, N-1432 Ås, Norway



..P(wild)

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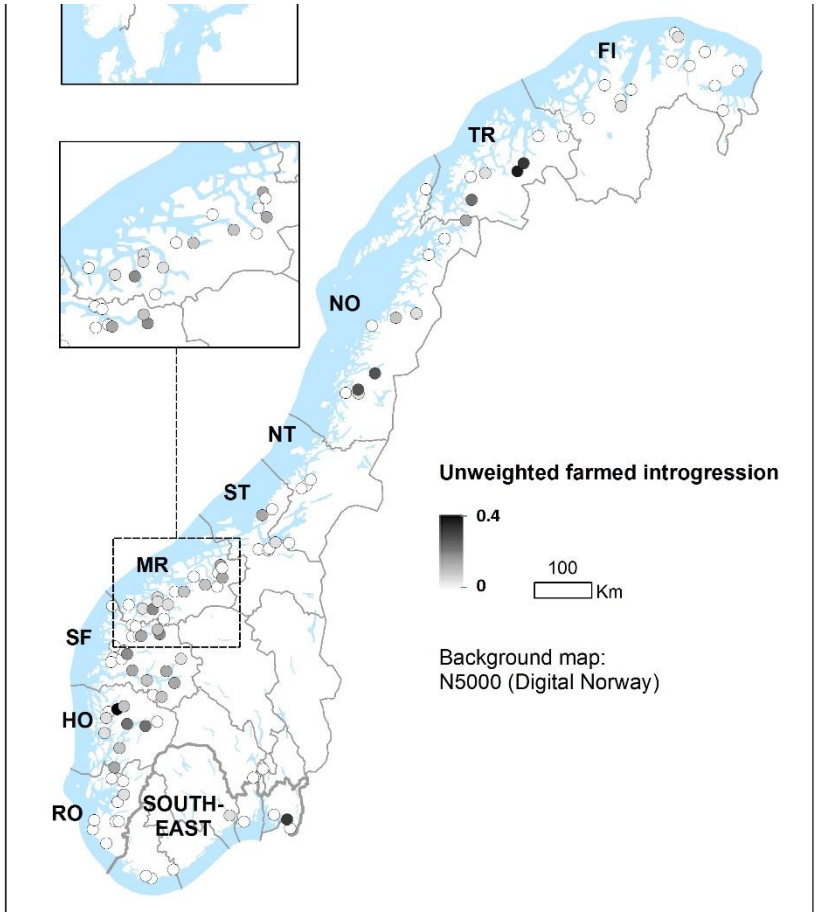
Farmed to wild genetic introgression

ICES Journal of Marine Science

ICES Journal of Marine Science (2016), doi:10.1093/icesjms/fsw121

Widespread genetic introgression of escaped farmed Atlantic salmon in wild salmon populations

Sten Karlsson*,†, Ola H. Diserud†, Peder Fiske, and Kjetil Hindar

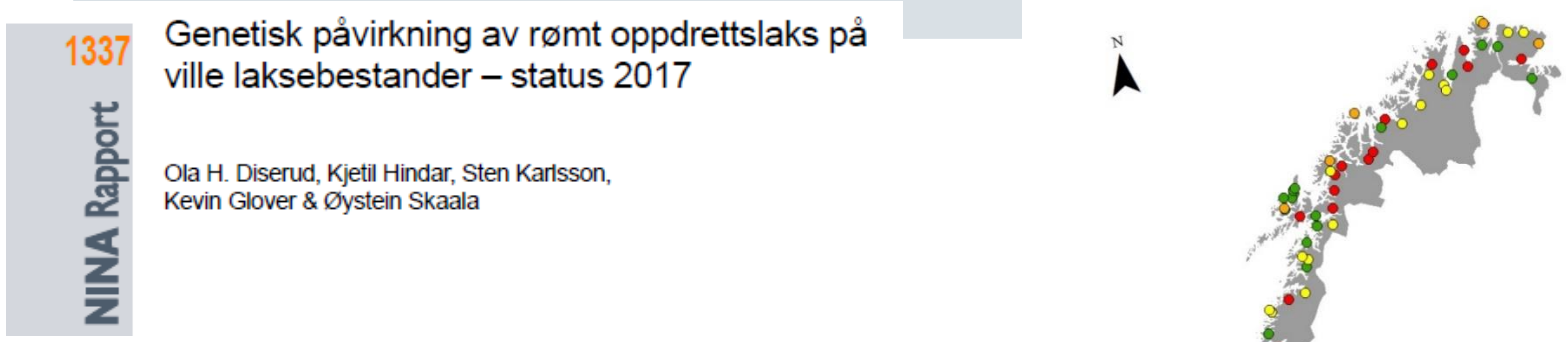


- 16 407 samples adult salmon
- 5155 samples of juveniles
- 109 populations
- Significant introgression in 51 (47%)
- Average introgression 6.4%,

Range 0 – 42%

- Highest introgression in the most farming intensive regions

Farmed to wild genetic introgression



quality norm for wild Atlantic

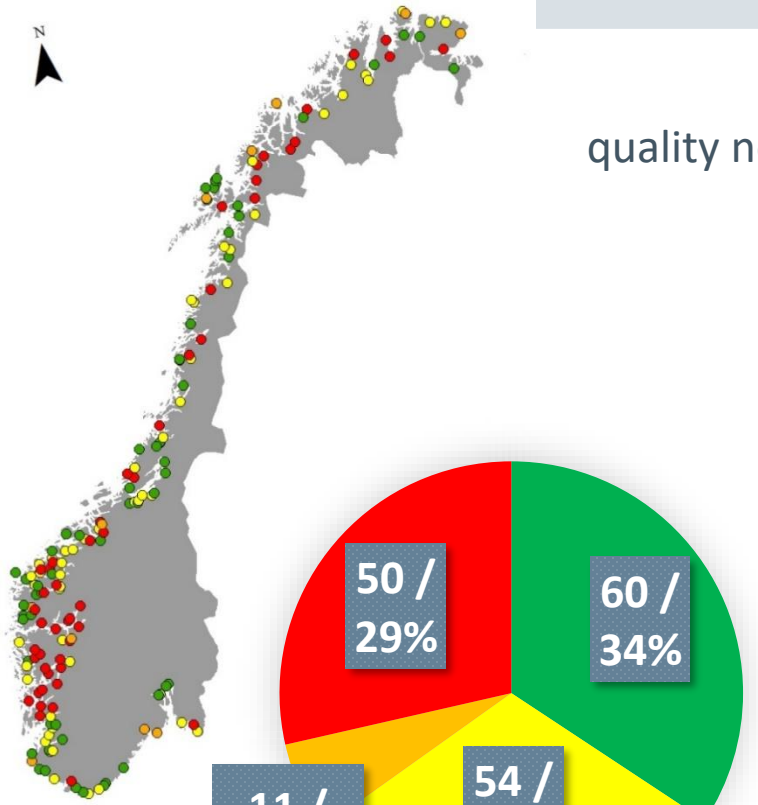
175 populations evaluated

60 No genetic changes observed

54 Weak genetic changes indicated

11 Moderate significant genetic changes

50 Large significant genetic changes



Now about 40 000 individuals from about 240 populations

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nature ecology & evolution ARTICLES
PUBLISHED: 10 APRIL 2017 | VOLUME: 1 | ARTICLE NUMBER: 0124

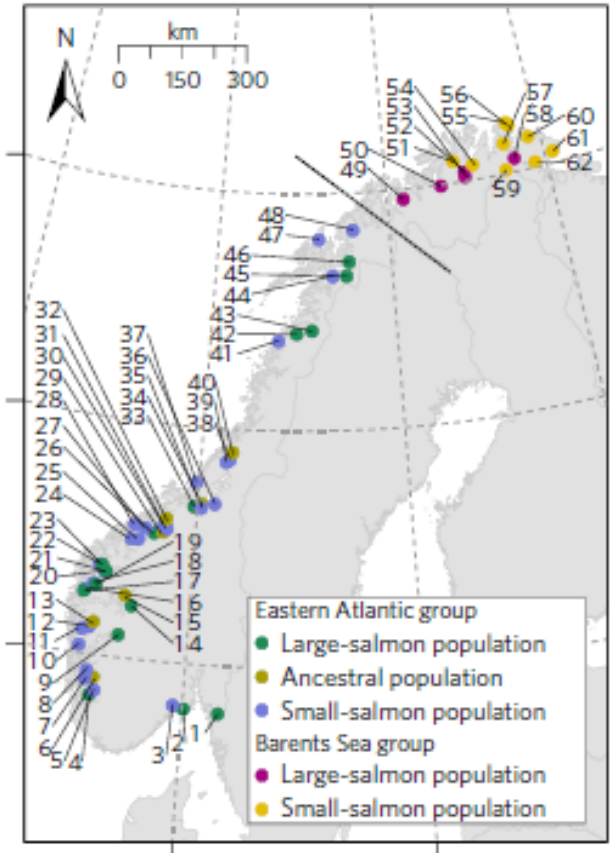
Consequences

Gene flow from domesticated escapes alters the life history of wild Atlantic salmon

Geir H. Bolstad[1*], Kjetil Hindar[1], Grethe Robertsen[1], Bror Jonsson[2], Harald Sægrov[3], Ola H. Diserud[1], Peder Fiske[1], Arne J. Jensen[1], Kurt Urdal[3], Tor F. Næsje[1], Bjørn T. Barlaup[4], Bjørn Florø-Larsen[5], Håvard Lo[5], Eero Niemelä[6] and Sten Karlsson[1]

Large effect on Sea-age and growth

- Different effect in males and females
- Different effect in large and small salmon rivers
- Phylogenetic origin matters - Different effect in the Atlantic and the Barents/White Sea Phylogenetic groups



- Atlantic Phylogenetic grouo
  - 3350 individuals
  - 22 Large-salmon rivers
  - 26 Small-salmon rivers
- Barents/White Sea – Phylogenetic group
  - 751 individuals
  - 6 Large-salmon rivers
  - 8 Small-salmon rivers

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Samarbeid og kunnskap for framtidas miljøløsninger

Foto. A. Staverløkk

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