



POPULATION DIVERSITY, STRUCTURE AND ADAPTATION IN THE SUGAR KELP - *SACCHARINA LATISSIMA*

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POPULATION BASELINE

APPLIED

- A baseline for future monitoring and impact assessments
- Map the selection of populations/strains available for cultivation
- Inform management decisions on translocation, conservation, hatchery development etc.

KNOWLEDGE

- Insight into geographic scale of diversity/phylogeography
- ID of putative genes under selection and potential mechanisms of ecological adaptation
- Mapping the genetic basis for functional traits of interest (GWAS, QTL etc)

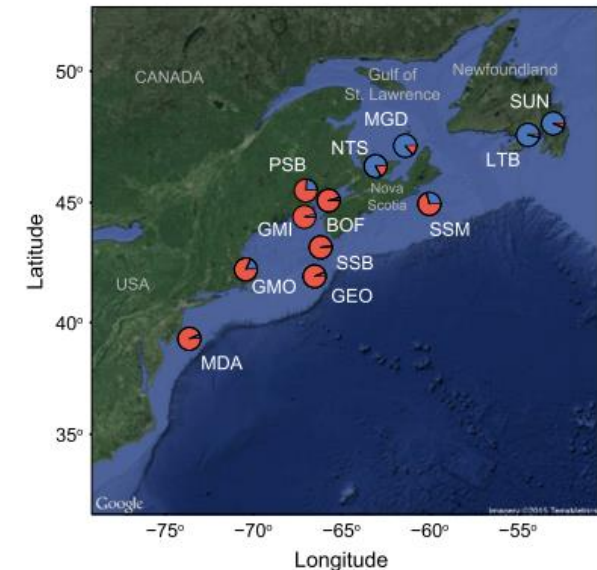
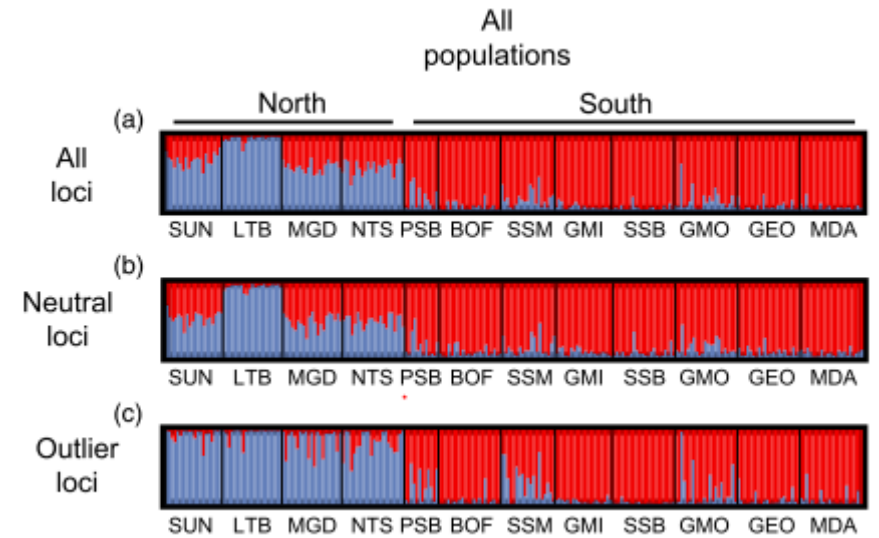


FIGURE 4 Plots of individual admixture for 12 populations of *P. magellanicus* at $K = 2$ determined using the program STRUCTURE and the ΔK method to select the optimal number of genetic clusters in the data. Results are presented for all populations at (a) all loci, (b) neutral loci and (c) outlier loci

GENETIC INTROGRESSION & DEPRESSION

- The artificial mixing of wild and introduced populations
- Concerns including:
 - Genetic pollution → reduced fitness
 - Genetic dilution/homogenization → loss of local diversity and resilience
 - Outcompeting
- Precedent in the salmon farming industry (Glover et al. 2017)
 - In Norway evidence of introgression in up to half of ~150 known populations
 - Long-term consequences expected to reduce lifespan, productivity and resilience of wild populations

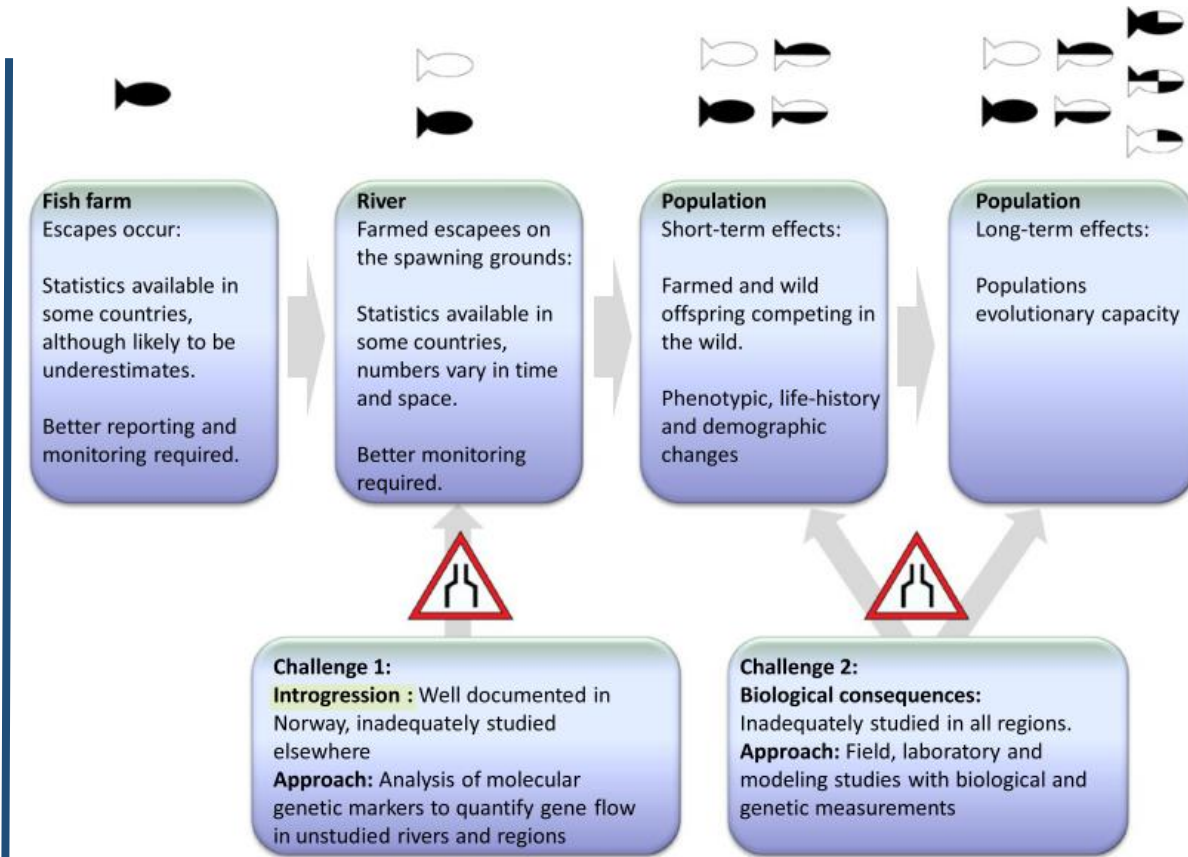


FIGURE 3 The two major challenges limiting current documentation of genetic impact of farmed escaped Atlantic salmon on wild populations. It is important to note that challenge 1 has recently been addressed in ~150 Norwegian rivers (Glover et al., 2013; Karlsson et al., 2016), but challenge 2 remains more or less completely unaddressed (Glover et al. 2017)



CURRENT KNOWLEDGE

- No previous studies on UK populations
- Microsatellite analysis of European populations (Paulino et al 2016; Guzinski et al 2016)
 - Further analysis on localised ecological adaptation in Danish populations (Moller Nielsen, 2016)
 - Strong inter-population diversity recorded but disagreement on levels of intra-population diversity.
- No genome-wide SNP-based analysis of *S. latissima* populations published.

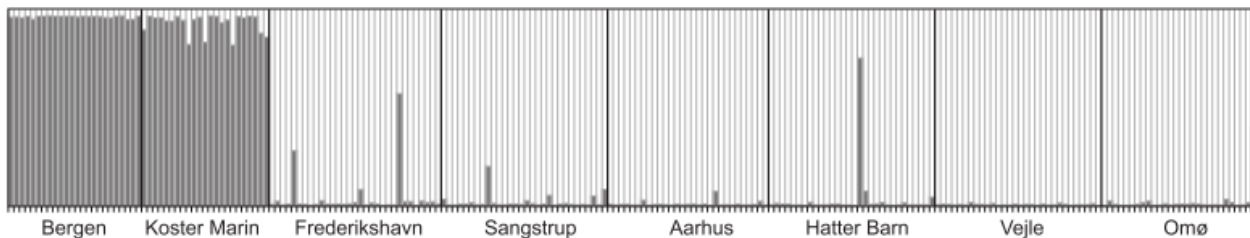
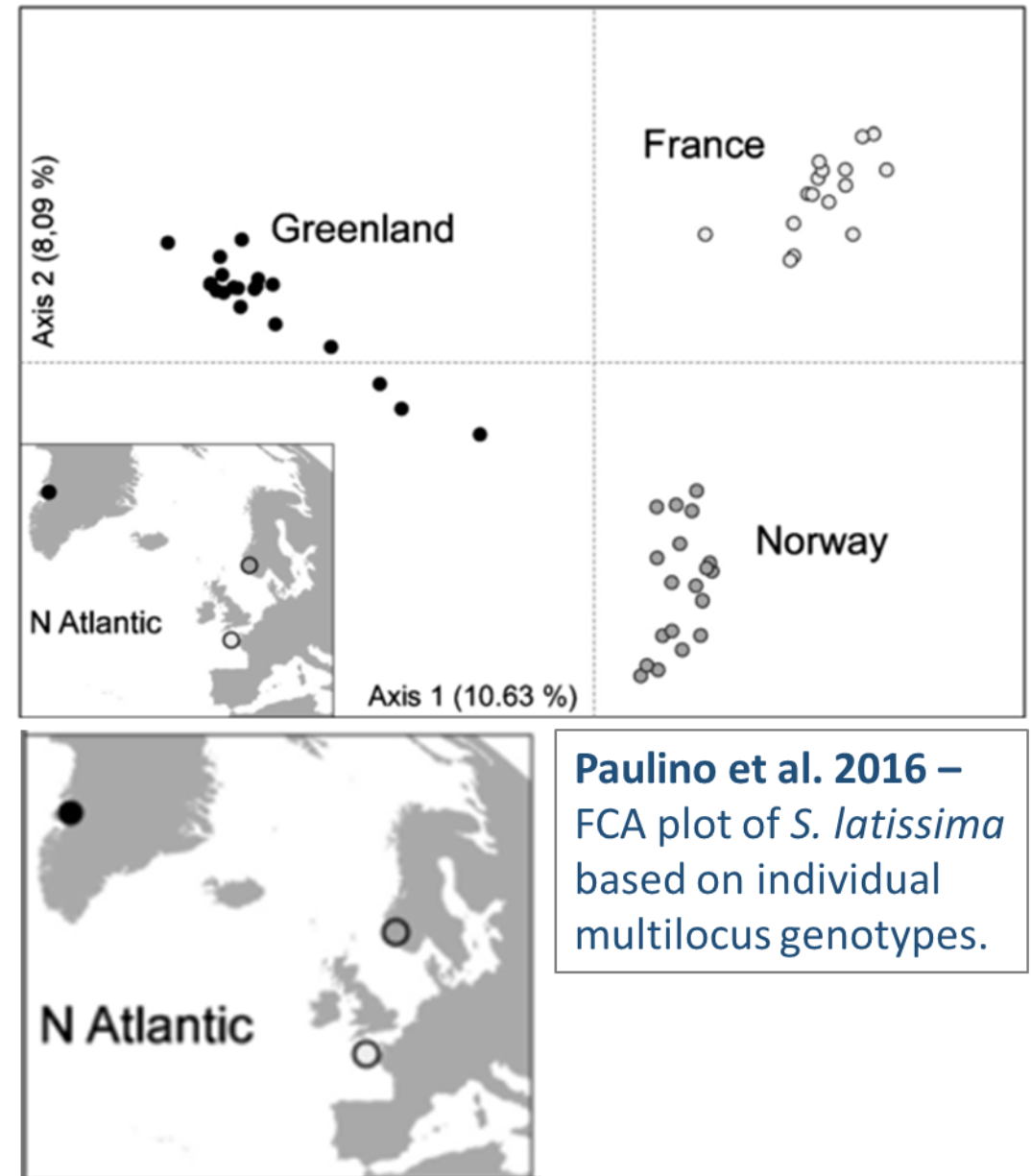


FIG. 2. Genetic subdivision of *Saccharina latissima* individuals based on STRUCTURE. Each individual multilocus genotype is represented by a vertical bar, showing its proportional assignment to the inferred genetic clusters. Black lines separate individuals from different populations, according to the names shown below the plot.

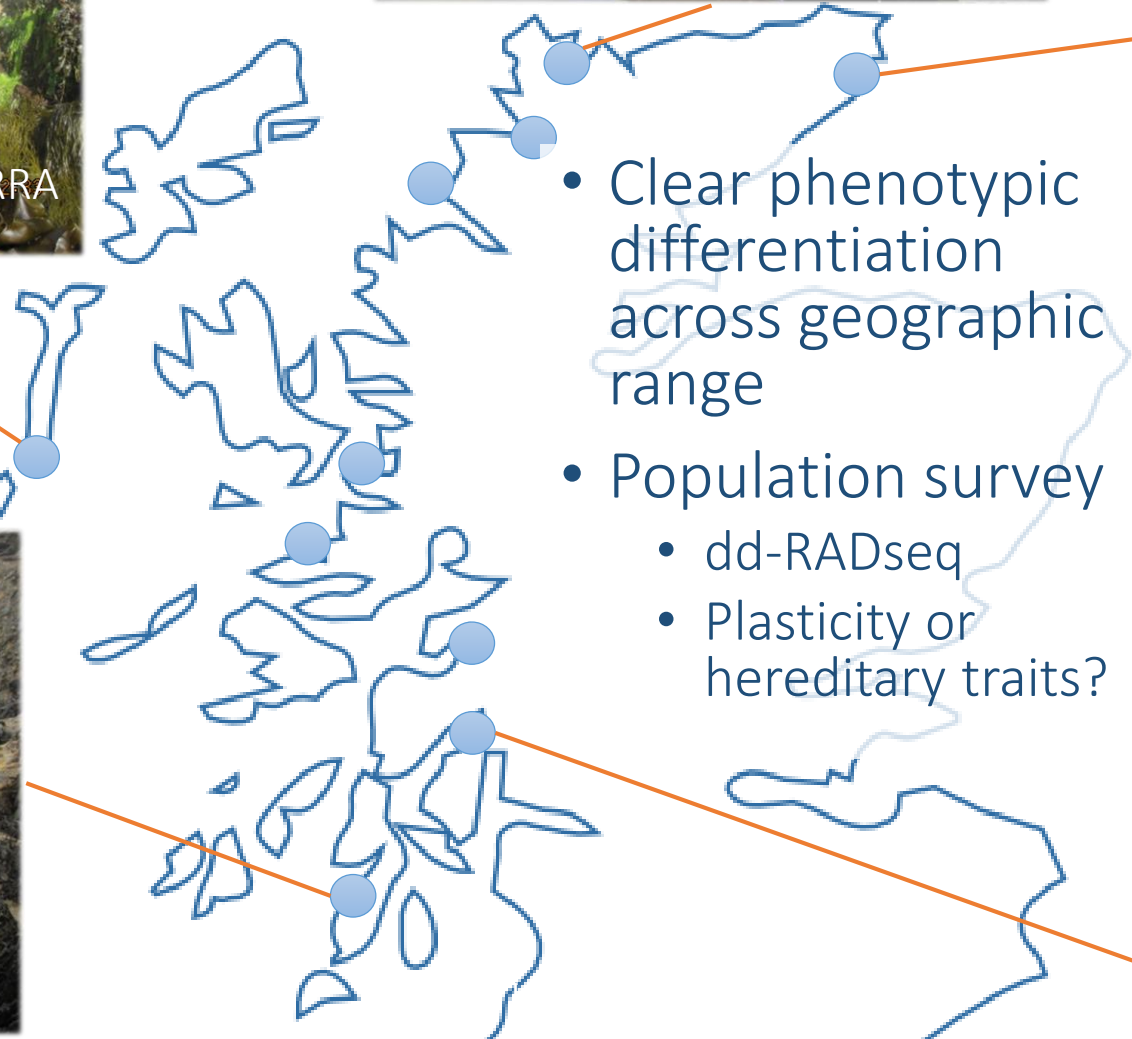
from Moller-Nielsen et al. 2016



METHODS AND PROTOCOLS

- Sampling design & implementation
- Extraction
- RADseq & double digest RADseq
- Library construction
- Downstream analysis
 - STRUCTURE
 - GWSS and Outlier tests





- Clear phenotypic differentiation across geographic range
- Population survey
 - dd-RADseq
 - Plasticity or hereditary traits?





POPULATION GENOMICS AND GWSS

- STRUCTURE – population analysis
 - Neutral and outlier loci
- GWSS
 - Fst tests and outlier scans
 - Inferring selection from outlier scans
 - Follow up: annotation and RT-PCR
- SNP Chips and genotyping arrays
 - Streamlining macro-algal genotyping
 - Development of genetic toolbox

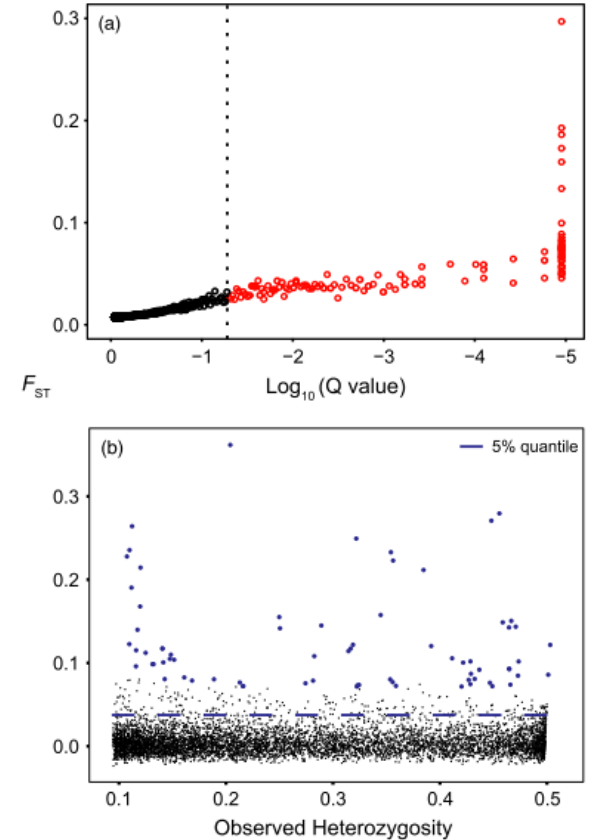


FIGURE 2 Results from (a) the Bayesian test for selection completed using the program BayeScan and (b) the hierarchical island model test for selection completed using the program Arlequin for 7163 loci sequenced in 12 populations of *P. magellanicus*. BayeScan outliers are defined as all loci with a q -value higher than .05 (highlighted in red). Arlequin outliers are defined as the loci that fall above the simulated 5% quantile of F_{ST} versus Heterozygosity ($q \leq .05$, highlighted in blue)

Van Wyngaarden et al. 2017

SUMMARY AND CONCLUSION

- Strong incentives to develop a genetic baseline in *S. latissima*
 - Monitoring & Impact assessment
 - Mapping diversity
 - Management
- Clear phenotypic diversity seen in field
- SNP identification through RADseq
- GWSS and Genomic Tools
 - Allows assessment of diversity and structure
 - Offers insights in to putative genes under selection and potential traits of interest



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