## **Exploring genetic diversity and hybridisation patterns of mussels in**

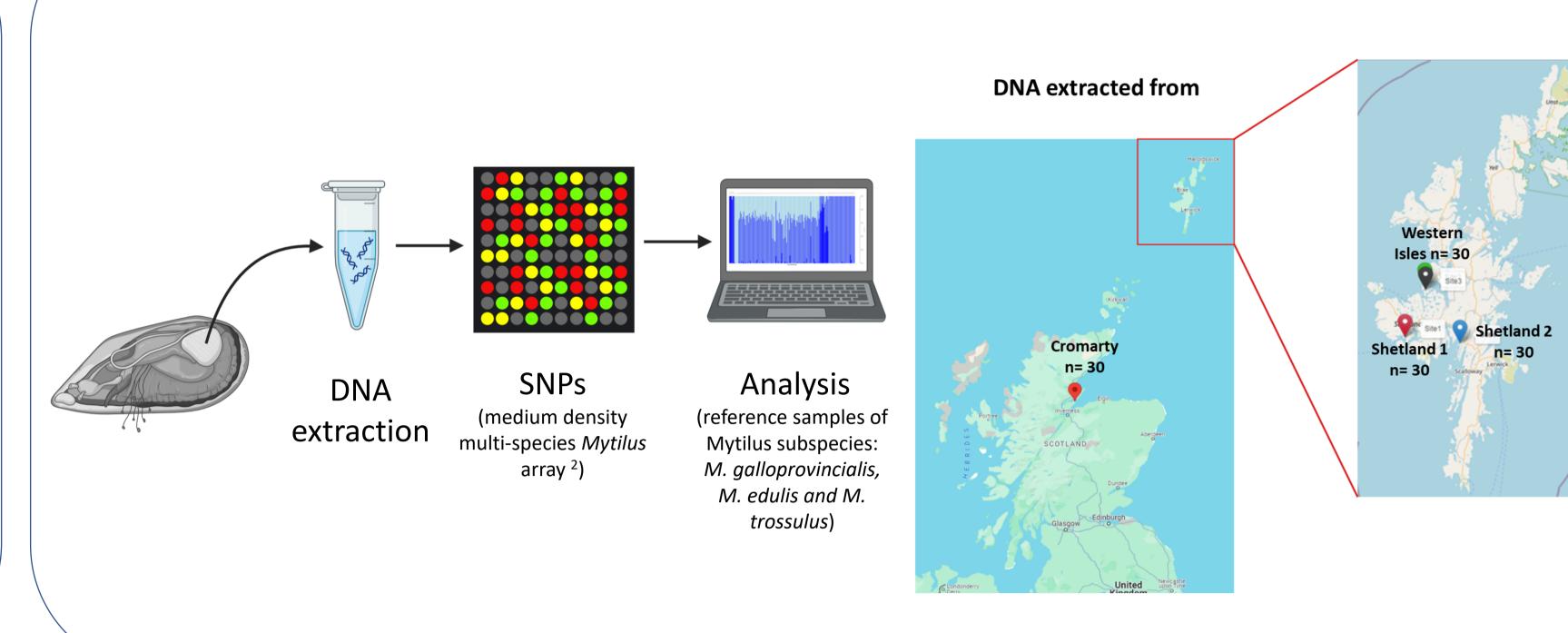
### Northern Scotland.

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#### Background

- Understanding mussel genetic diversity and gene flow informs aquaculture sustainability.
- Mussel farming depends on wild spat collection after natural spawning, sometimes moving stock to different environments with mixed success.
- Little is known about mussel population genetics, hybridisation, host-associated microbiomes, and the impact of moving individuals between populations

Methods

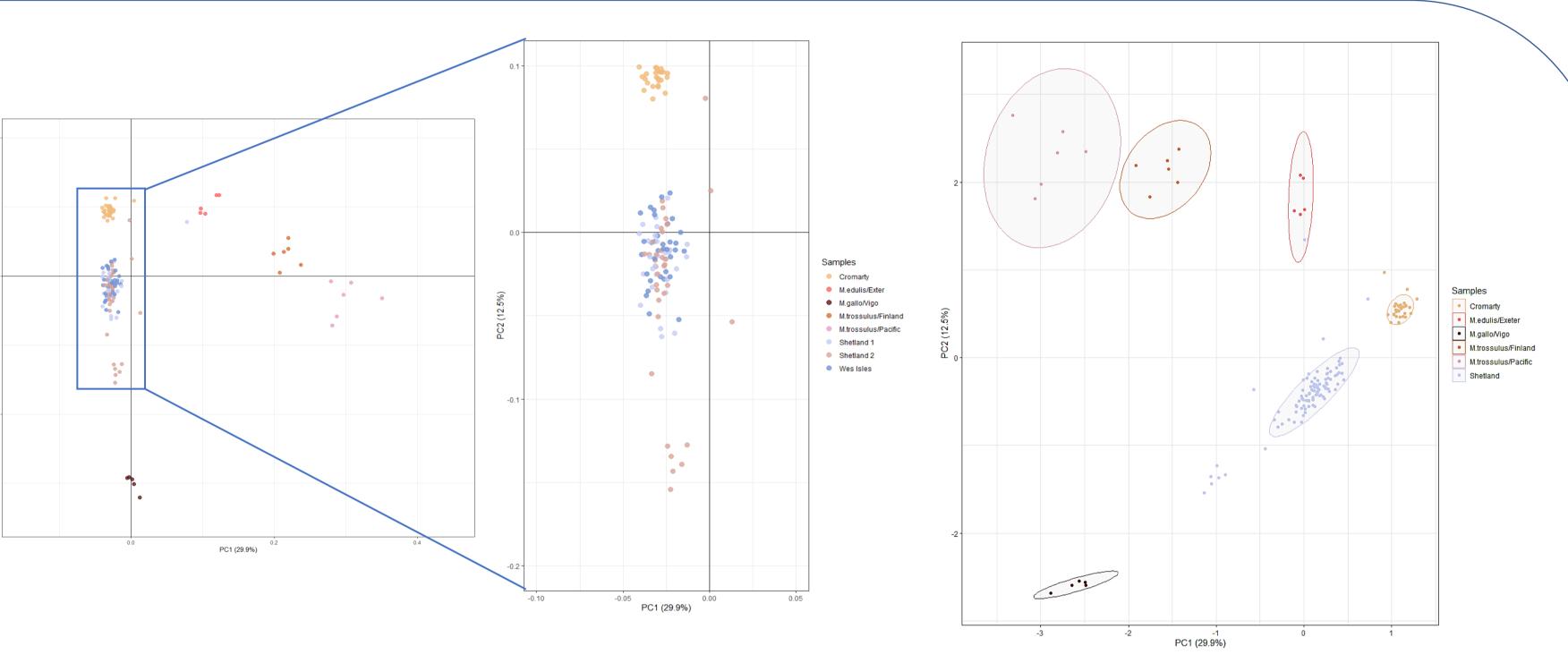


 Our study aims to compare genetic diversity and population structure between mussels from Cromarty Firth (north mainland) and from Shetland, the latter of which produces >60% UK mussels<sup>1</sup>.

#### Results

The initial analysis reveals:

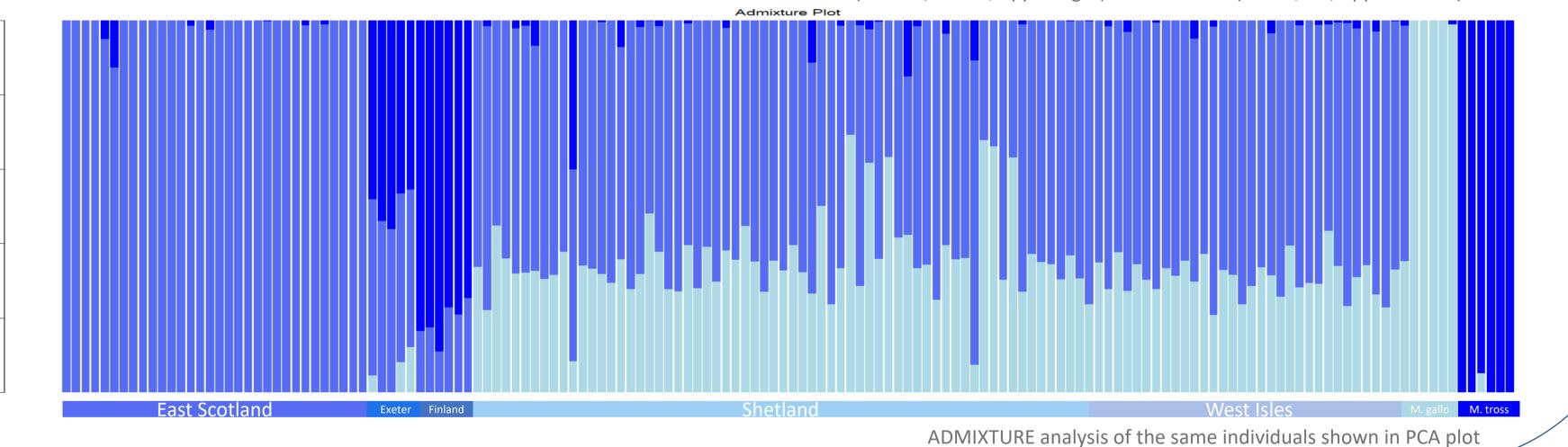
- Population in Cromarty appears to be predominantly composed of *M. edulis* background.
- On the other hand, mussels from Shetland and the Western Isles display levels of introgression with *M. galloprovincialis*.
- Higher levels of genetic conservation were seen in the Western Isles compared with the relatively diverse genetics observed in both Shetland populations.



PCA plotting using 60k SNP array data from each of the 4 populations against sub-species references for M. galloprovincialis (Spain, lower-left), M. trossulus (Finland/Pacific, upper-right) and M. edulis (Exeter, UK, upper-centre).

#### Conclusion

- The striking similarity between the Western Isles and Shetland populations suggests the potential for interconnectedness.
- The SNP array offers a robust platform for consistent genotyping, enabling further investigation into optimal growing environments to enhance mussel health and productivity.

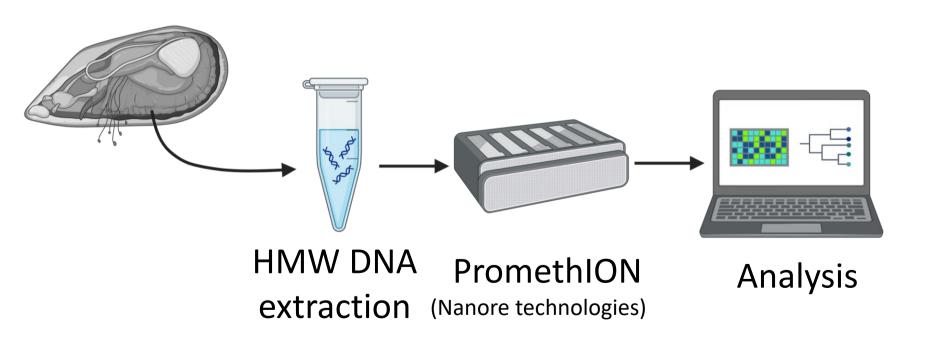


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#### Future work

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- Perform high molecular weight (HMW) DNA extraction from selected mussel samples representing populations from Cromarty, the Western Isles, and Shetland. Generate libraries and conduct long-read sequencing using Nanopore technologies.
- Analyse structural variations, metagenomic differences, and microbiome composition between the different mussel populations to understand the impact of their respective environments.



- Explore gene presence/absence variations and large-scale structural variations associated with environmental adaptation.
- Investigate the influence of ocean currents and spawning patterns on larval dispersal to better understand the extent of

connectivity between these mussel populations

1. Regan T, Bean TP, Ellis T, Davie A, Carboni S, Migaud H, Houston RD: Genetic improvement technologies to support the sustainable growth of UK aquaculture. *Reviews in Aquaculture* 2021, 13(4):1958-1985

2. Nascimento-Schulze, J. C., Bean, T. P., Peñaloza, C., Paris, J. R., Whiting, J. R., Simon, A., Fraser, B. A., Houston, R. D., Bierne, N., & Ellis, R. P. (2023). SNP discovery and genetic structure in blue mussel species using low coverage sequencing and a medium density 60K SNP-array. Evolutionary Applications, 16(5), 1044-1060.

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