

Integrating genomics and modelling to predict climate change response in the endangered freshwater pearl mussel (*Margaritifera margaritifera*)



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BACKGROUND

- Whole genome sequencing offers a solution to predicting climate change adaptation in endangered species¹.
- Freshwater pearl mussels are critically endangered, keystone species. While their decline has been linked to climate change² this has not been investigated using genomic data.

DATA COLLECTION

This project will use low coverage whole genome sequencing data from non-invasive swabs of mussels from 30 rivers across Scotland.

RESEARCH AIMS

1. Species Distribution Modelling

Define the niche and spatial distribution of the Scottish metapopulation and predict the change in distribution under climate change³.

2. Population Genomics

Define the genomic structure of multiple pearl mussel populations across Scotland- understanding connectivity, gene flow and the impact of genetic drift⁴.

3. (Mal)adaptation of Populations

Identify adaptive components using genome scans, apply a predictive model and determine offset between adaptation to current and future climates¹.

