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





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Genomic information

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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 change<sup>2</sup> this has not been investigated using genomic data.

## **DATA INPUT**

- 384 non-invasive mussel DNA samples at 30 locations collected between 2019 and 2021.
- 3-4x low coverage whole genome sequencing by Feb 2023.

# **RESEARCH AIMS** 1. Species Distribution

Define the niche and spatial distribution of the Scottish metapopulation and predict the change in distribution under climate change<sup>3</sup>.



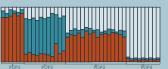
**Ecological models** (e.g species distribution models)

> **GOAL: Identify Scottish freshwater** pearl mussel populations at risk of loss under future climate scenarios.

#### 2. Population Genomics

Modelling

Define the genomic structure of multiple pearl mussel populations across Scotlandunderstanding connectivity, gene flow and the impact of genetic drift<sup>4</sup>.



### 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.















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1. Capblancq, T. et al. (2020) 'Genomic Prediction of (Mal)Adaptation Across Current and Future Climatic Landscapes', Annual Review of Ecology, Evolution, and Systematics, 51(1), pp. 245-269.

t. Wilson, C.D., Roberts, D. and Reid, N. (2011) 'Applying species distribution modelling to identify areas of high conservation value for endangered species: A

4. Gladstone, N.S. et al. (2022) 'Population genomics reveal low differentiation and complex demographic histories in a highly fragmented and endangered reshwater mussel', Aquatic Conservation: Marine and Freshwater Ecosystems, 32(8), pp. 1235-1248.