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

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Background

- Genomic 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.

Genomic information

NatureScot

<u>Data</u>

- 5486 SNPs from 156 individuals non-invasively swabbed at 18 locations between 2019 and 2021.
 872 across-Scotland
- presence/absence points.

Research aims

1. Adaptive landscape

Define the genomic structure of multiple pearl mussel populations across Scotland and investigate genomeenvironment association.



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2. Predicting climate change response

Conduct genomic offset with identified putatively adaptive loci and compare with a more traditional species distribution model.

3. Drivers of decline

Use Scotland-wide recruitment data coupled with local pressures identified in the report to identify other factors beyond climate driving decline, such as pollution from sewage, dredging and hydrological management.

Major threats: pearl fishing, pollution, river engineering, host fish, climate change Cosgrove, *et al.* (2016) ENDANGERED > EN

References:

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. 2. Cosgrove, P. et al. (2012) 'Scotland's Freshwater Pearl Mussels: The Challenge of Climate Change', in River Conservation and Management. John Wiley & Sons, Ltd, pp. 121–132.

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



Ecological models

(e.g species distribution

models)