



Beaver genetics in Scotland

Dr Helen Taylor
Conservation programme manager





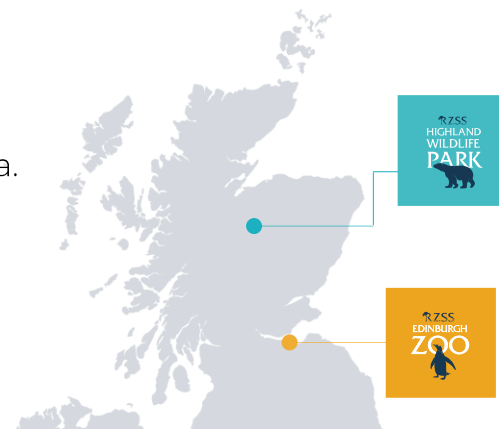
THE ROYAL ZOOLOGICAL SOCIETY OF SCOTLAND

A wildlife conservation charity with a bold vision: **a world where nature is protected, valued and loved**. Our strategic conservation goal is to **reverse the decline of 50 species by 2030**.

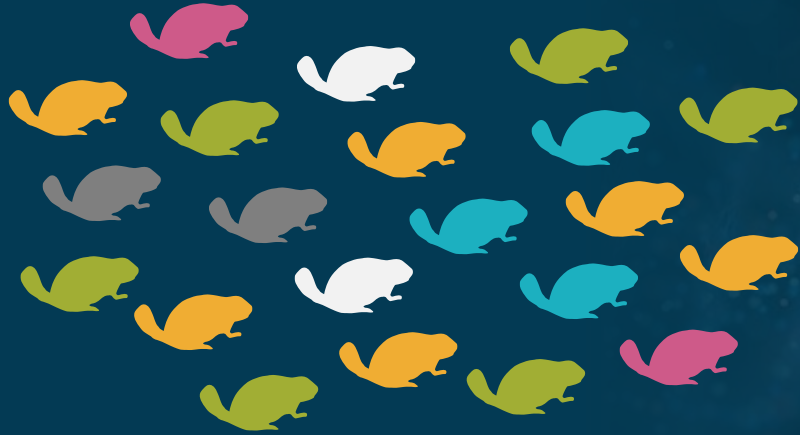
- Zoos in Scotland, but 30 conservation projects around the world.
- Own onsite conservation genetics lab, **WildGenes**.
- Reintroduced beavers to Scotland and partula snails to French Polynesia.
- Support large-scale initiatives in Brazil and Uganda.
- Working to save Scotland's wildcats.



©Philip Price



POPULATION BOTTLENECKS AND GENETIC DIVERSITY

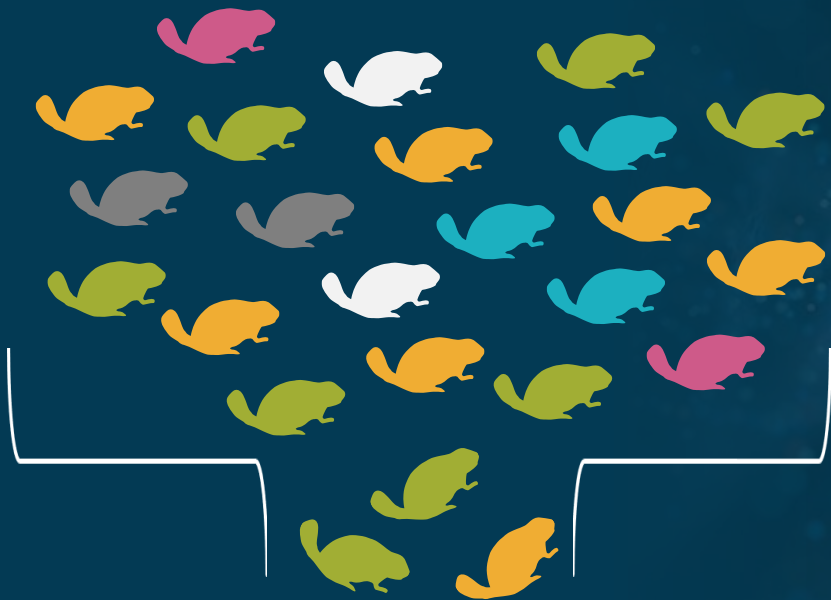


POPULATION BOTTLENECKS AND GENETIC DIVERSITY



TRANSLOCATION = POPULATION
BOTTLENECK

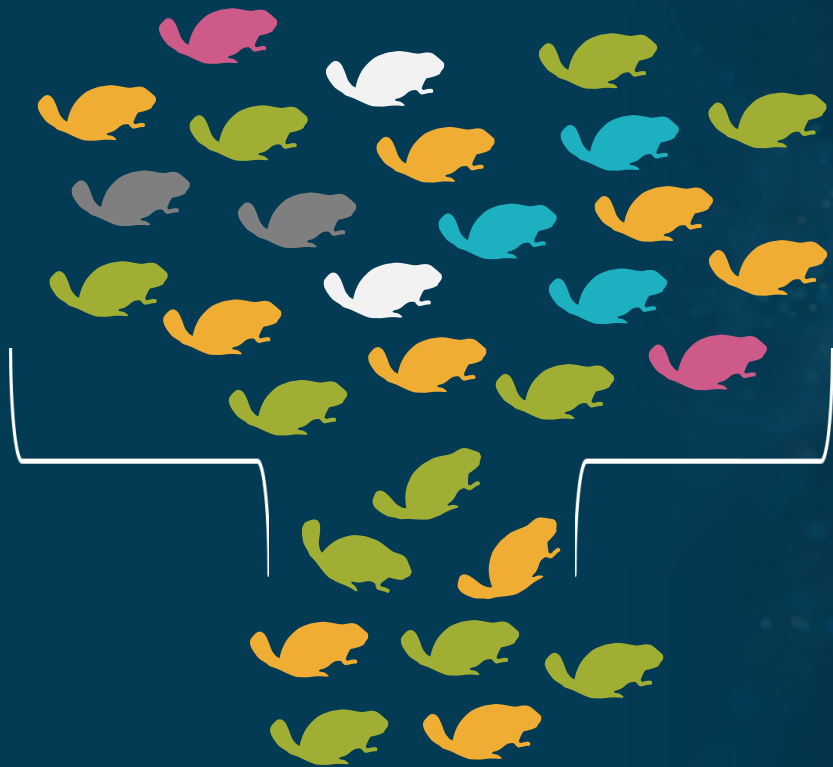
POPULATION BOTTLENECKS AND GENETIC DIVERSITY



TRANSLOCATION = POPULATION
BOTTLENECK

NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

POPULATION BOTTLENECKS AND GENETIC DIVERSITY

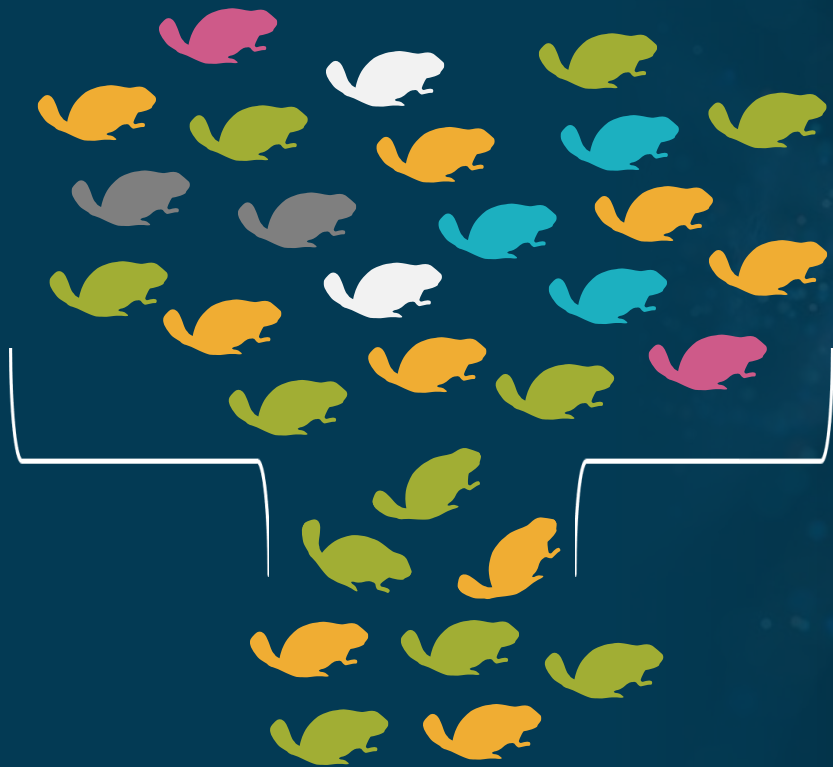


TRANSLOCATION = POPULATION
BOTTLENECK

NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

LESS GENETIC DIVERSITY IN NEW
POPULATION

POPULATION BOTTLENECKS AND GENETIC DIVERSITY



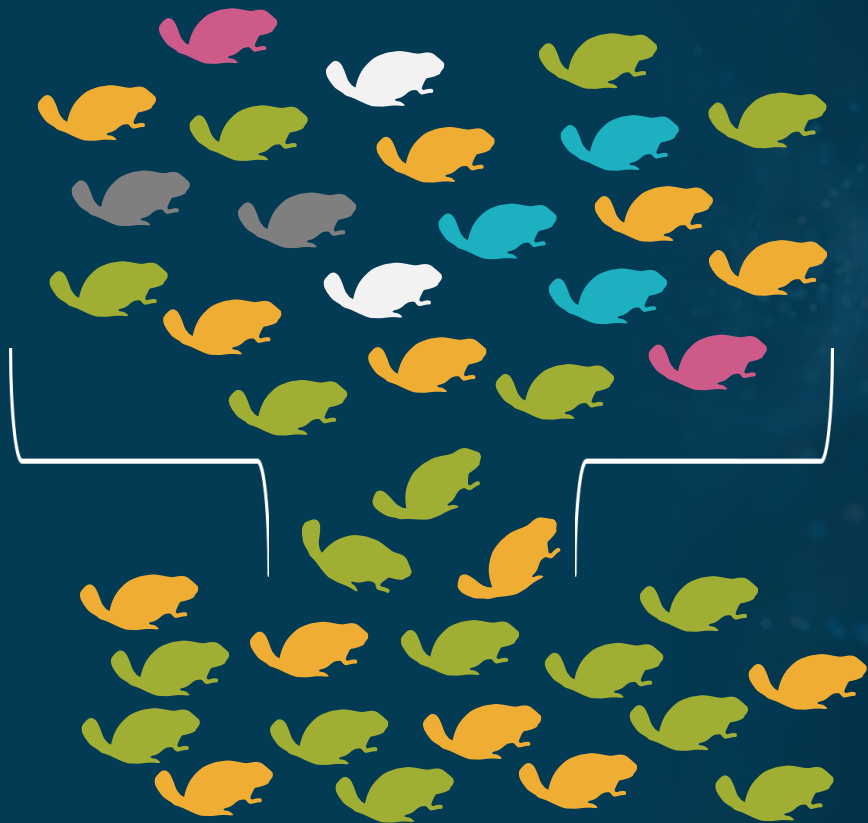
TRANSLOCATION = POPULATION
BOTTLENECK

NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

LESS GENETIC DIVERSITY IN NEW
POPULATION

INBREEDING MORE LIKELY

POPULATION BOTTLENECKS AND GENETIC DIVERSITY



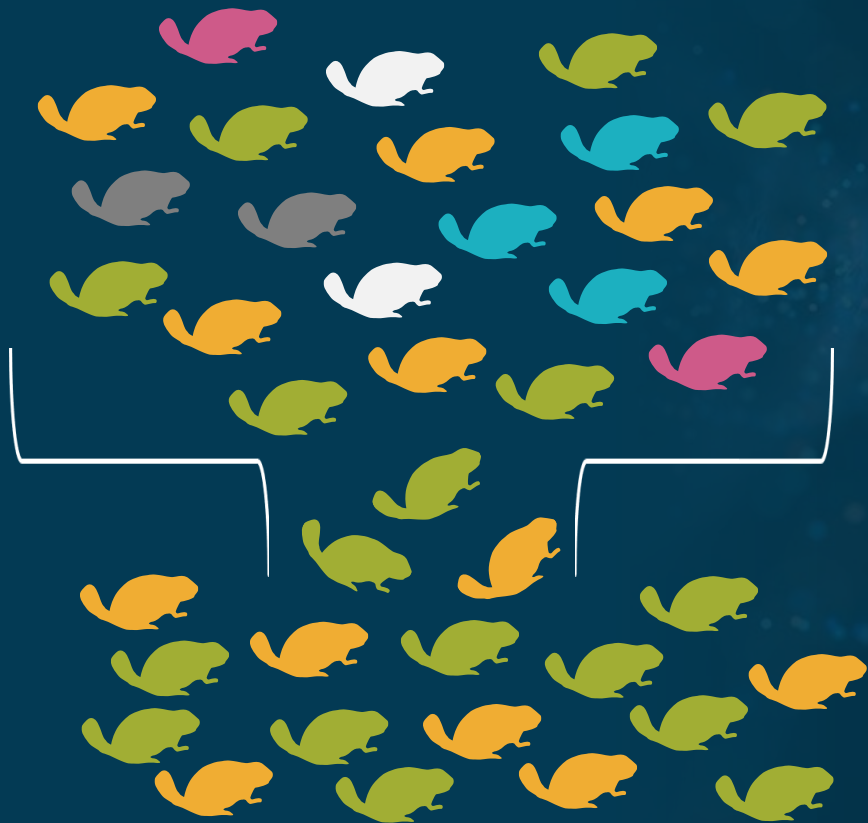
TRANSLOCATION = POPULATION
BOTTLENECK

NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

LESS GENETIC DIVERSITY IN NEW
POPULATION

INBREEDING MORE LIKELY

POPULATION BOTTLENECKS AND GENETIC DIVERSITY



TRANSLOCATION = POPULATION
BOTTLENECK

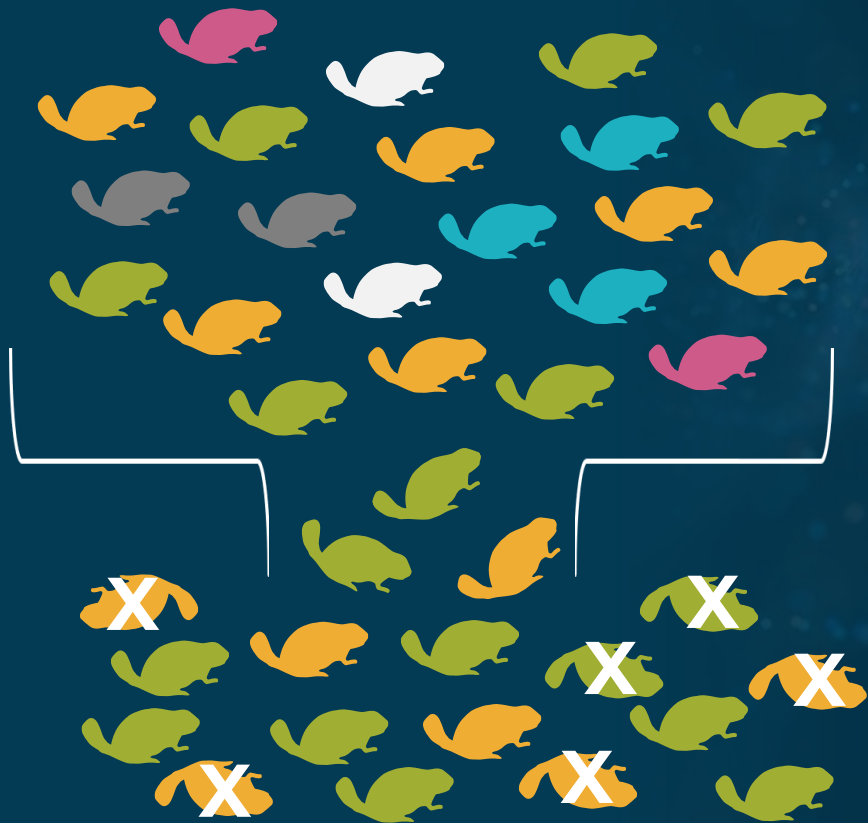
NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

LESS GENETIC DIVERSITY IN NEW
POPULATION

INBREEDING MORE LIKELY

POSSIBILITY OF INBREEDING DEPRESSION

POPULATION BOTTLENECKS AND GENETIC DIVERSITY



TRANSLOCATION = POPULATION
BOTTLENECK

NOT ALL GENETIC DIVERSITY MAKES IT
THROUGH

LESS GENETIC DIVERSITY IN NEW
POPULATION

INBREEDING MORE LIKELY

POSSIBILITY OF INBREEDING DEPRESSION

INCREASED EXTINCTION RISK

Original translocations for the trial



2009-14

Scottish beaver trial

2009

11 beavers released

2010

5 beavers released

NORWAY

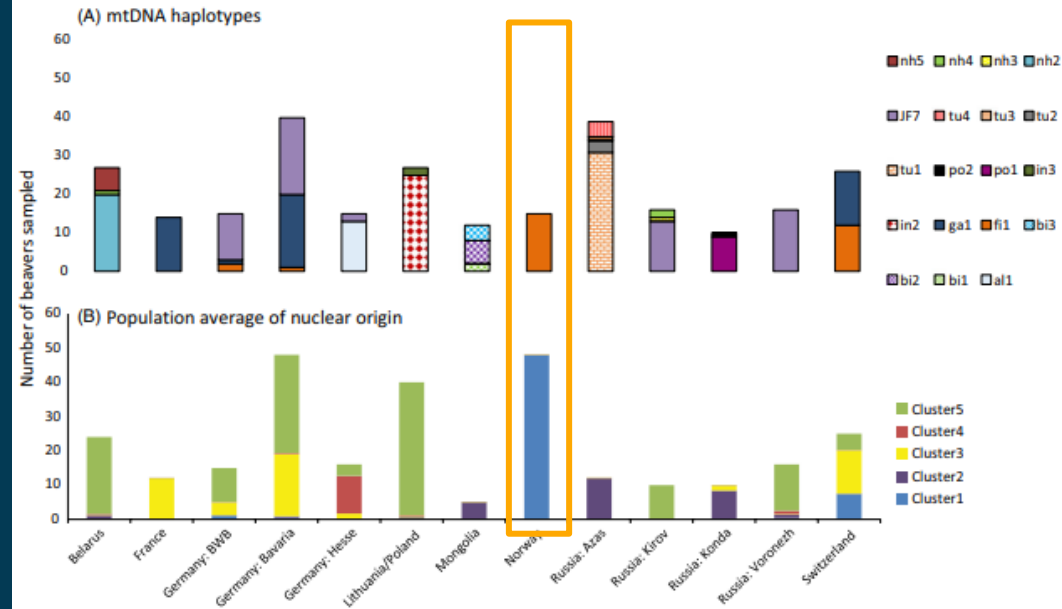
Source of all trial beavers



ORIGINAL ARTICLE

Nuclear and mitochondrial genetic structure in the Eurasian beaver (*Castor fiber*) – implications for future reintroductions

Helen Senn,¹ Rob Ogden,¹ Christiane Frosch,² Alena Syřůčková,³ Roisin Campbell-Palmer,¹ Pavel Munclinger,³ Walter Durka,⁴ Robert H. S. Kraus,² Alexander P. Saveljev,⁵ Carsten Nowak,² Annegret Stubbe,⁶ Michael Stubbe,⁷ Johan Michaux,⁸ Vladimir Lavrov,⁹ Ravchig Samiya,¹⁰ Alius Ulevicius¹¹ and Frank Rosell¹²



Several genetic clusters of beavers in Eurasia

Norwegian beavers show relatively low genetic diversity

Loch Coille-Bharr, North

Adults Millie, Bjornar and
an unknown number of offspring

Coille-Bharr outflow to Faery Isles

Two unidentified adult beavers

Lochan Beag

Very small amount of activity
from an unidentified animal

Loch Losgunn

Unidentified adult beaver

Lochan Buic and Lily Loch

Adults Eoghann and Trude

● Dam

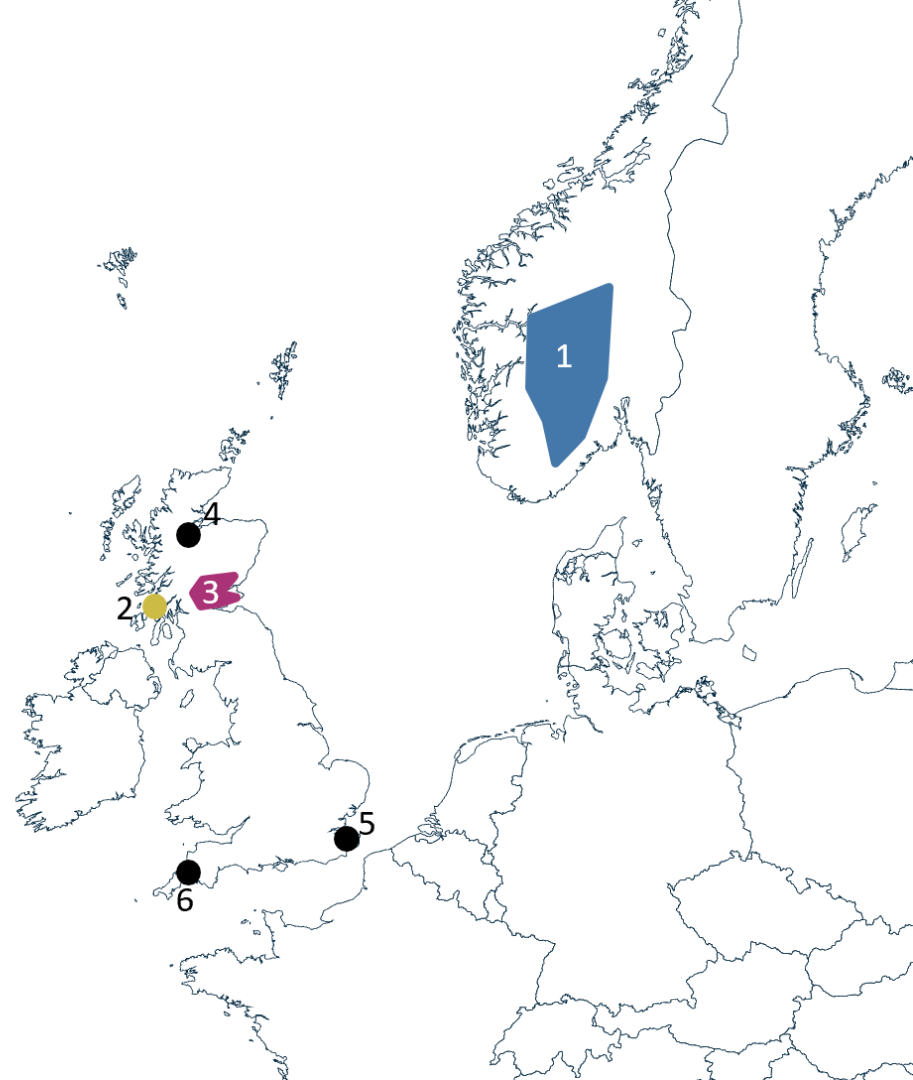
● Lodge

● other field signs

Follow-up survey 2017
8 known adults remaining

Beaver reinforcement options for Knapdale

- 1 ● Norway population
- 2 ● Knapdale population
- 3 ● Tayside population
- 4 ● Beaulieu population
- 5 ● Wildwood Trust
- 6 ● Derek Gow Consultancy



What is the genetic background of these other beavers?

COMMISSIONED REPORT

Commissioned Report No. 682

Genetic assessment of free-living beavers in and around the River Tay catchment, east Scotland

For further information on this report please contact:

James Scott
Scottish Natural Heritage
Great Glen House
INVERNESS
IV3 8NW
Telephone: 01463 725363
E-mail: james.scott@snh.gov.uk

This report should be quoted as:

McEwing, R. Senn, H. & Campbell-Palmer, R. 2015. Genetic assessment of free-living beavers in and around the River Tay catchment, east Scotland. *Scottish Natural Heritage Commissioned Report No. 682*.

This report, or any part of it, should not be reproduced without the permission of Scottish Natural Heritage. This permission will not be withheld unreasonably. The views expressed by the author(s) of this report should not be taken as the views and policies of Scottish Natural Heritage.

© Scottish Natural Heritage 2015.

Global Ecology and Conservation 24 (2020) e01275



ELSEVIER

Contents lists available at ScienceDirect

Global Ecology and Conservation

journal homepage: <http://www.elsevier.com/locate/gecco>



Original Research Article

Beaver genetic surveillance in Britain

R. Campbell-Palmer ^a, H. Senn ^b, S. Girling ^c, R. Pizzi ^c, M. Elliott ^d,
M. Gaywood ^e, F. Rosell ^{f,*}

^a Independent Beaver Consultant, Edinburgh, Scotland, UK

^b Conservation Department, Royal Zoological Society of Scotland, Scotland, UK

^c Veterinary Department, Royal Zoological Society of Scotland, Scotland, UK

^d Devon Wildlife Trust, Exeter, Devon, UK

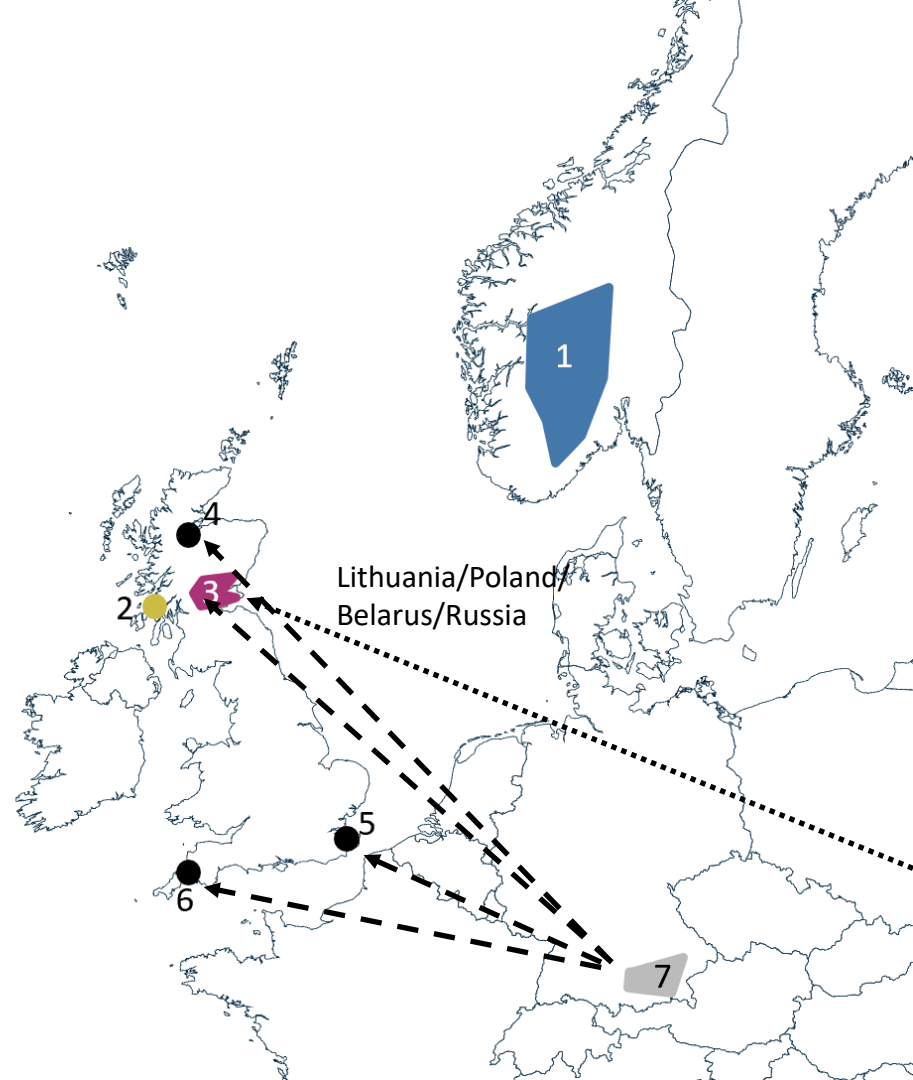
^e NatureScot, Great Glen House, Inverness, Scotland, UK

^f Faculty of Arts and Sciences, Department of Environmental and Health Studies, University of South-Eastern Norway, N-3800, Bø i, Telemark, Norway



Beaver reinforcement options for Knapdale

- 1 ● Norway population
- 2 ● Knapdale population
- 3 ● Tayside population
- 4 ● Beaulieu population
- 5 ● Wildwood Trust
- 6 ● Derek Gow Consultancy
- 7 ● Bavaria population



Several genetic clusters of beavers in Eurasia

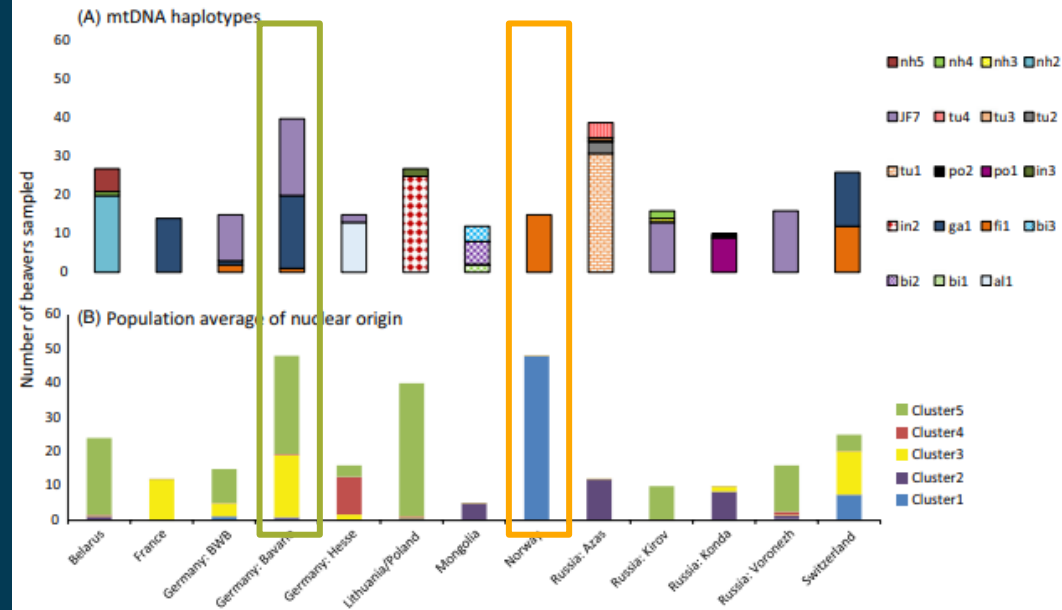
Norwegian beavers show relatively low genetic diversity

Bavarian beavers are a mixture of other populations and show relatively high genetic diversity

ORIGINAL ARTICLE

Nuclear and mitochondrial genetic structure in the Eurasian beaver (*Castor fiber*) – implications for future reintroductions

Helen Senn,¹ Rob Ogden,¹ Christiane Frosch,² Alena Syručková,³ Roisin Campbell-Palmer,¹ Pavel Munclinger,³ Walter Durka,⁴ Robert H. S. Kraus,² Alexander P. Saveljev,⁵ Carsten Nowak,² Annegret Stubbe,⁶ Michael Stubbe,⁷ Johan Michaux,⁸ Vladimir Lavrov,⁹ Ravchig Samiya,¹⁰ Alius Ulevicius¹¹ and Frank Rosell¹²

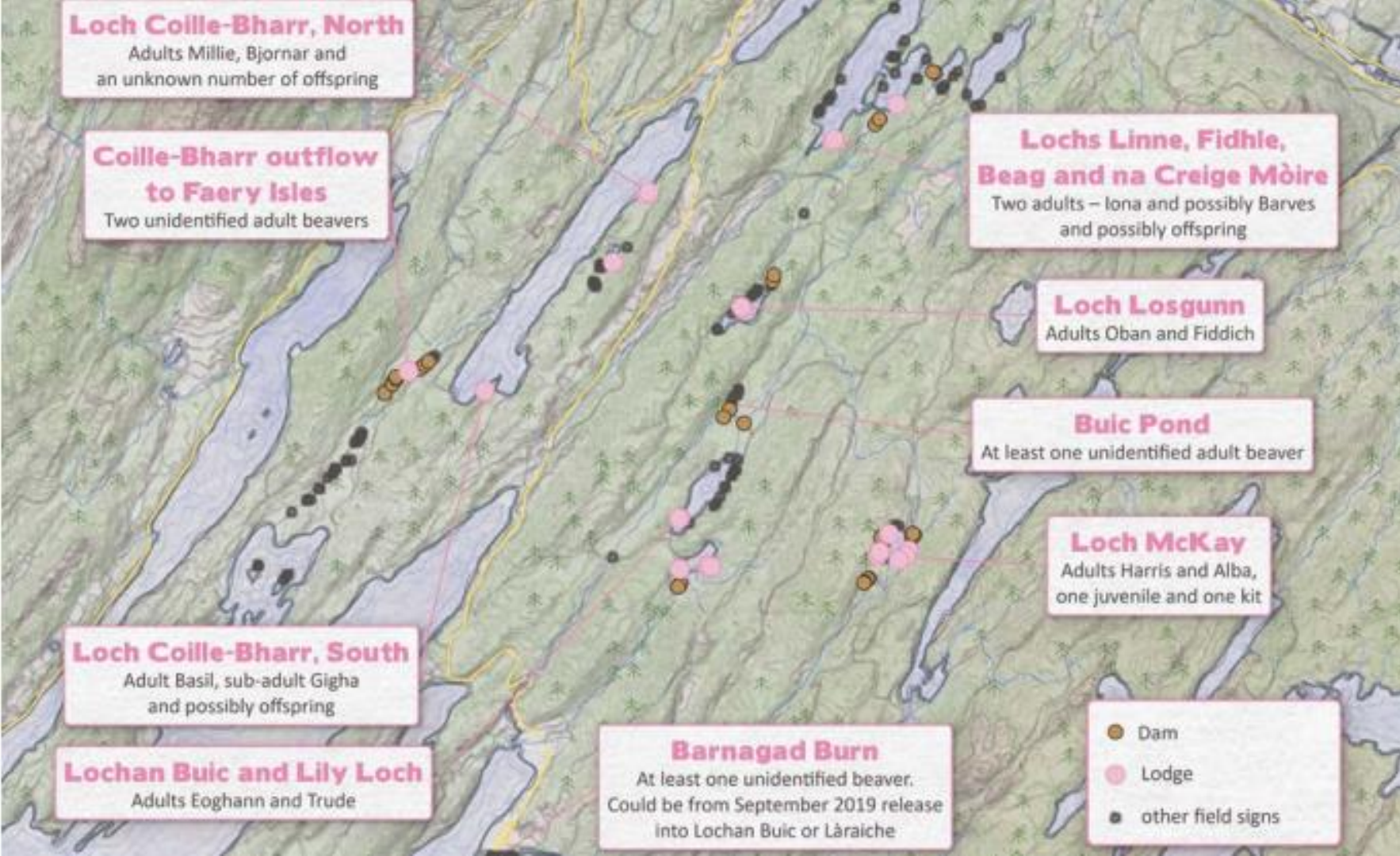


Scottish Beavers reinforcement

2017-2020



21 "Bavarian" beavers translocated to Knapdale from Tayside, River Beauly, wildwood, and Derek Gow Consultancy



The genetic legacy of the first successful reintroduction of a mammal to Britain: Founder events and attempted genetic rescue in Scotland's beaver population

Helen R. Taylor¹ | Jean-Marc Costanzini^{1,2} | Kara L. Dicks² | Helen V. Senn^{1,2} | Sarah Robinson⁴ | Gill Dowse⁴ | Alex D. Ball²

¹Field Conservation, Royal Zoological Society of Scotland, Edinburgh, UK

²WildGenes Laboratory, Royal Zoological Society of Scotland, Edinburgh, UK

³Microbiology and Infection Control, Aberdeen University Hospital, Ochs, Norway

⁴Scottish Wildlife Trust, Edinburgh, UK

Correspondence

Helen R. Taylor, Field Conservation, Royal Zoological Society of Scotland, Edinburgh, UK.
Email: h.taylor@rzs.org.uk

Funding information

Peoples Postcode Lottery

Abstract

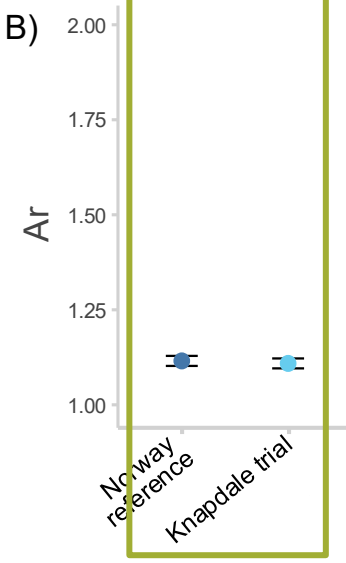
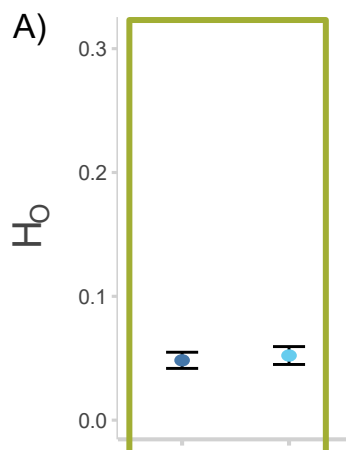
Conservation translocations often inherently involve a risk of genetic diversity loss, and thus loss of adaptive potential, but this risk is rarely quantified or monitored through time. The reintroduction of beavers to Scotland, via the Scottish Beaver Trial in Knapdale, is an example of a translocation that took place in the absence of genetic data for the founder individuals and resulted in a small and suspected to be genetically depauperate population. In this study we use a high-density SNP panel to assess the genetic impact of that initial translocation and the effect of subsequent reinforcement translocations using animals from a different genetic source to the original founders. We demonstrate that the initial translocation did, indeed, lead to low genetic diversity ($H_e = 0.052$) and high mean kinship ($KING\text{-}robust = 0.159$) in the Knapdale population compared to other beaver populations. We also show that the reinforcement translocations have succeeded in increasing genetic diversity ($H_e = 0.196$) and reducing kinship ($KING\text{-}robust = 0.028$) in Knapdale. As yet, there is no evidence of admixture between the two genetic lineages that are now present in Knapdale and such admixture is necessary to realise the full genetic benefits of the reinforcement and for genetic reinforcement and then rescue to occur; future genetic monitoring will be required to assess whether this has happened. We note that, should admixture occur, the Knapdale population will harbour combinations of genetic diversity not currently seen elsewhere in Eurasian beavers, posing important considerations for the future management of this population. We consider our results in the wider context of beaver conservation throughout Scotland and the rest of Britain, and advocate for more proactive genetic sampling of all founders to allow the full integration of genetic data into translocation planning in general.

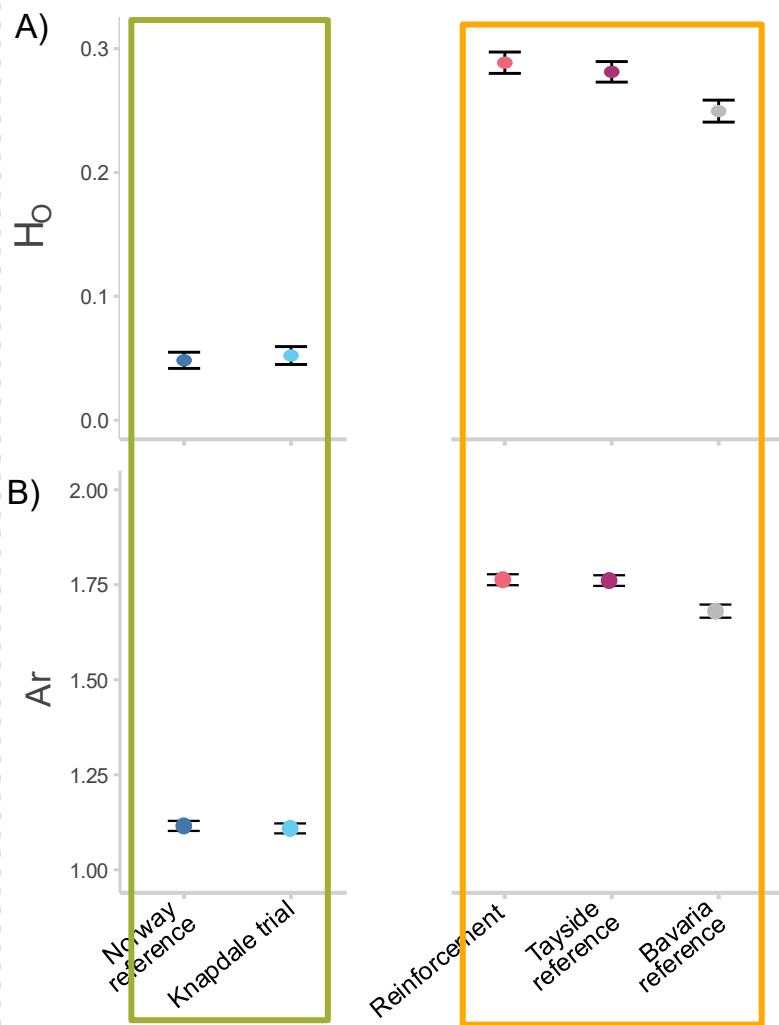
KEYWORDS

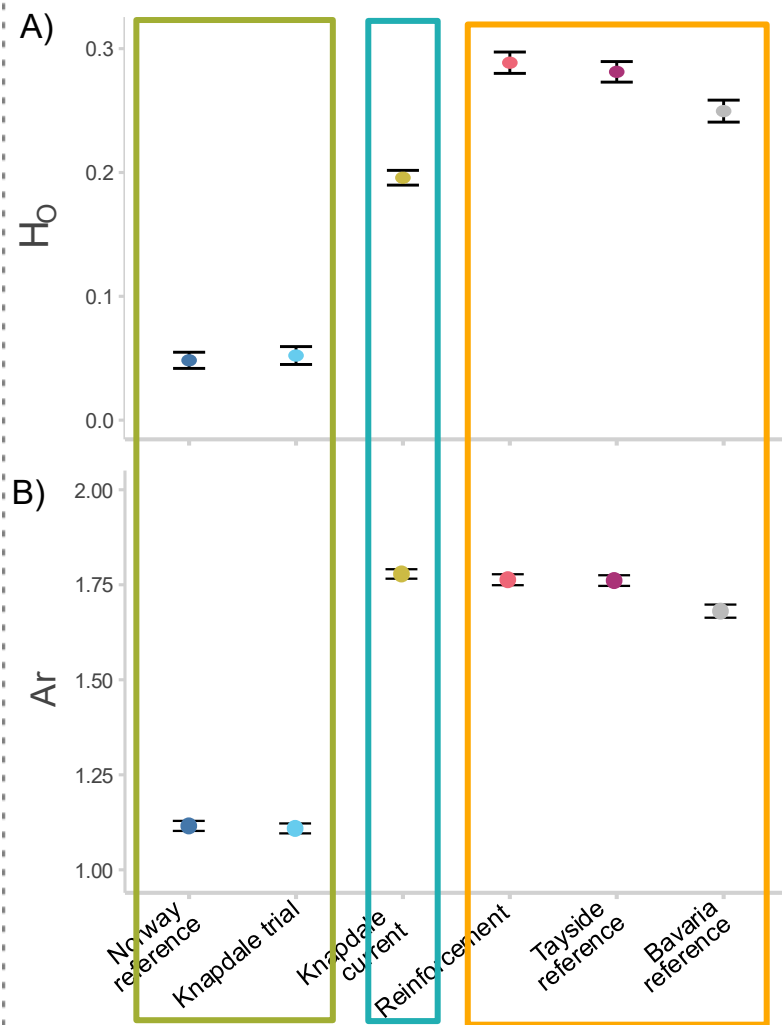
conservation, genetic rescue, mammal, reintroduction, relatedness, translocation

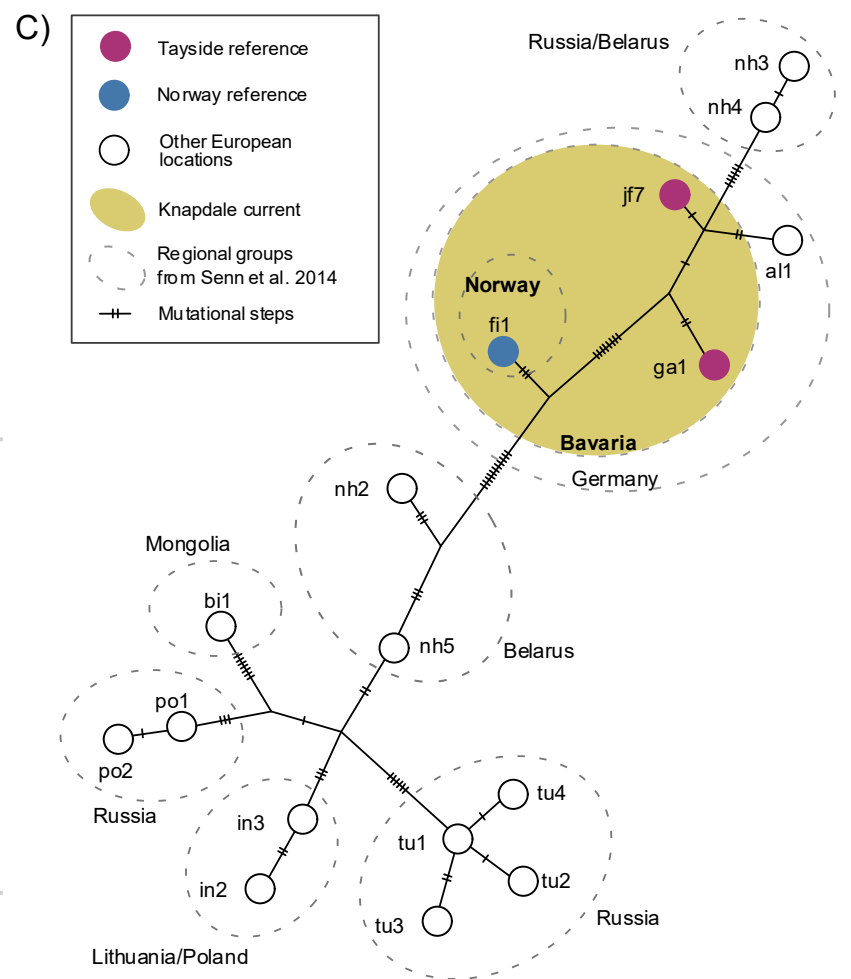
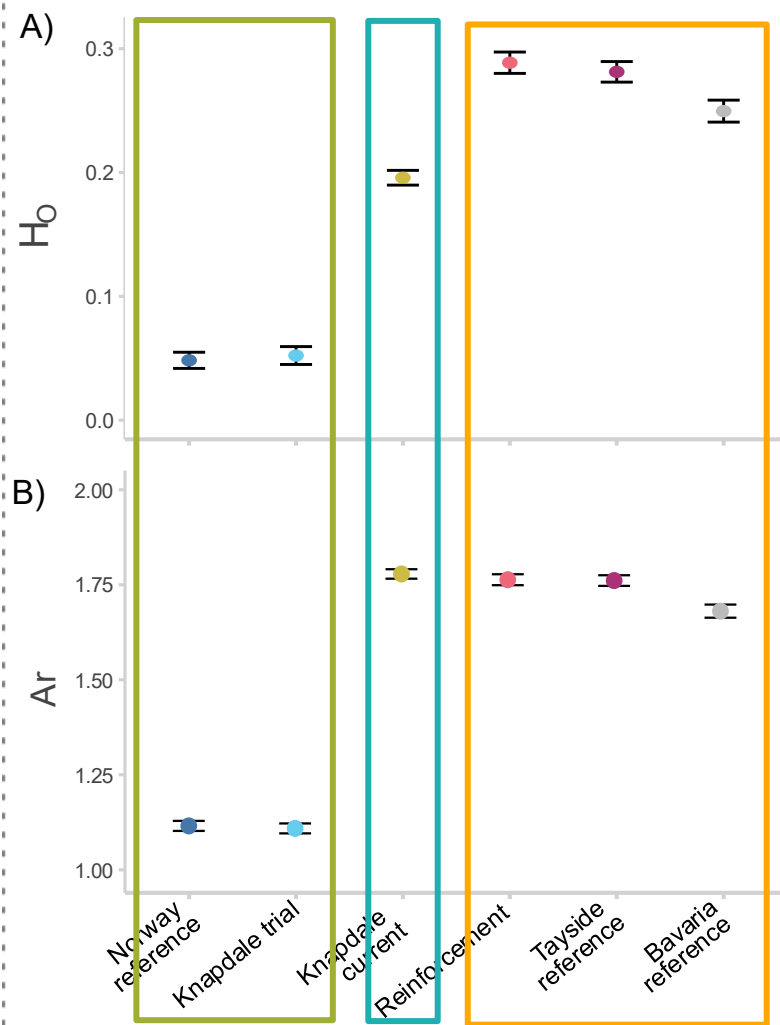
DNA from:

- 29 beavers from Norway
- 11 Norwegian beavers translocated to Knapdale
- 17 beavers from Bavaria
- 22 beavers from Tayside
- 19 "Bavarian" beavers translocated to Knapdale
- 6 beavers born in Knapdale



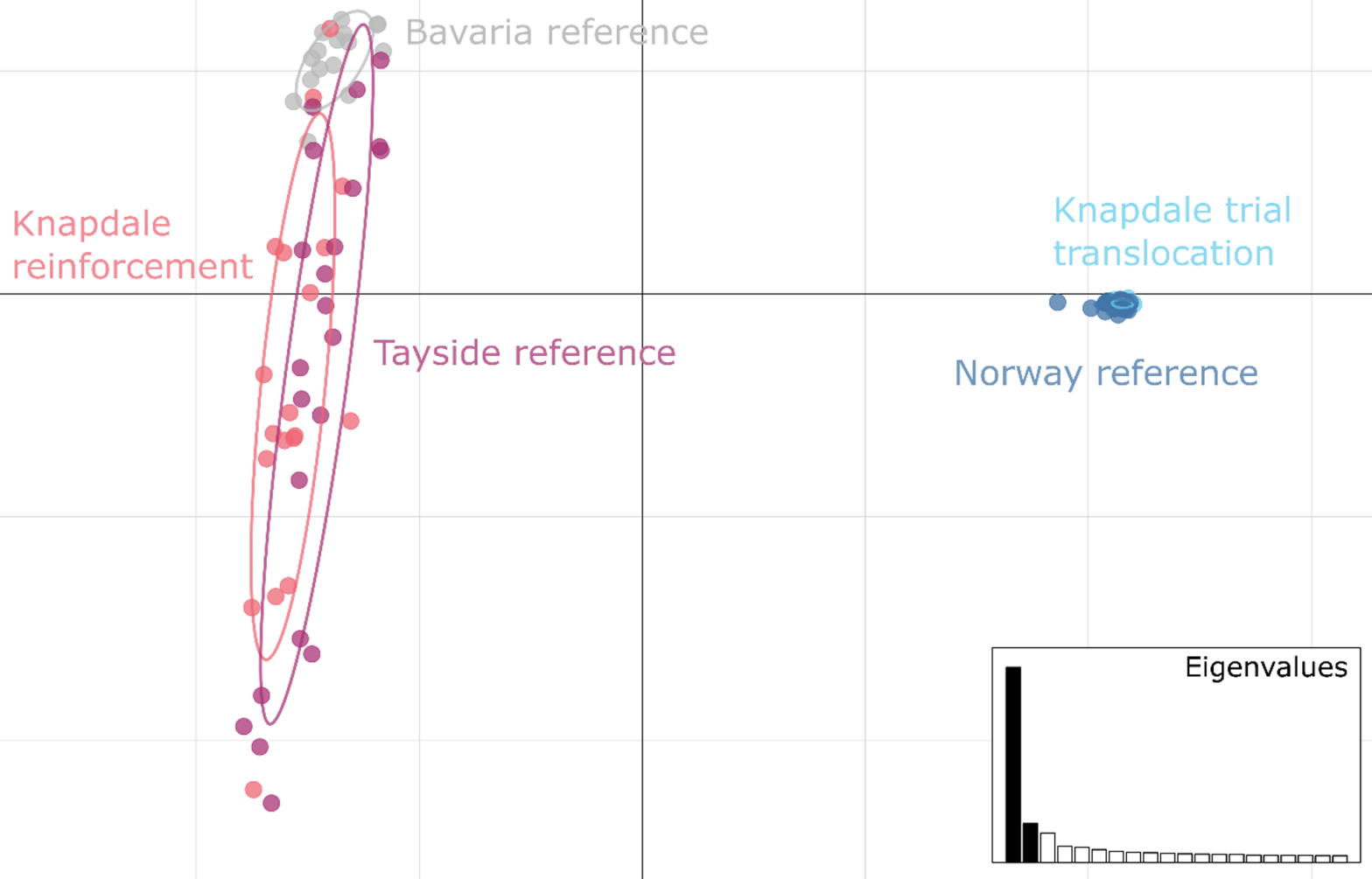






A)

d = 20



Knapdale's beavers in context

No mixing between “Bavarian” and Norwegian beavers at the end of the reinforcement

If mixing happens, Knapdale will have a different genetic profile to any Eurasian beaver population yet studied

Mixing would make Knapdale an important reservoir of genetic material – potentially useful for improving genetic diversity in wider Scottish and UK beaver population

Need for genetic monitoring and management in Knapdale



THE WILDLIFE CONSERVATION CHARITY



Scottish
Wildlife
Trust



Forestry and
Land Scotland
Coilltearachd agus
Fearann Alba



British beaver genetic work
continues!



Dr Heather Ritchie-Parker
RZSS WildGenes



Questions?

Dr Helen Taylor
Conservation programme manager

