

Conservation Genomic Management for Endangered Species Breeding Programmes

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Project summary

Genomic data have the potential to improve retention of genetic diversity in wildlife conservation breeding programmes. This project combines theoretical models with xdata to develop novel approaches in conservation genetics.

Background

Ex-situ management, including captive breeding, plays a vital role in the conservation of endangered and threatened species (McGowan et al., 2017). As with animal production, conservation breeding programmes require careful management to minimise the loss of genetic diversity and prevent inbreeding. Within intensive breeding systems, such as zoos, this has traditionally been achieved at an individual level using information from pedigrees to minimize kinship, with DNA markers occasionally used to fill pedigree gaps (Fienieg & Galbusera, 2013). However, it has been demonstrated that higher levels of genetic diversity can be retained in breeding programmes through the use of genomic data to determine optimal contributions from individual animals within a breeding system (de Cara *et al.* 2011). Furthermore, extensive breeding strategies, which bridge the gap between intensive individual-based programmes and management of natural populations, are increasingly recognised as playing an important role along a conservation breeding continuum, both for wildlife and rare livestock breeds. Extensive systems that lack pedigree data rely instead on group management models to maximise genetic diversity, but these are underdeveloped and untested in non-model species. This situation creates an exciting opportunity to conduct fundamental research to underpin the transfer of genomic data into population genetic management and applied conservation breeding strategies. This project will deliver the science necessary to develop evidence-based solutions for the international conservation community for implementation across a range of taxa and management scenarios.



Key research questions

1. How do models based on genomic data perform relative to existing theoretical approaches for maximizing the retention of diversity in conservation breeding programmes?
2. How can optimal contribution models be extended from intensive breeding systems to extensive group management?
3. Is it possible to derive a general framework that enables the routine implementation of genomic management in endangered species breeding programmes?

Methodology

This project will combine the use of simulations and empirical genomic data from livestock and zoo populations to test models of optimal genomic contribution across a range of breeding strategies. We will first use the novel breeding software, Alphamate (Gorjanc & Hickey 2018), to explore how pedigree data and genome-wide molecular markers compare in minimizing loss of genetic diversity between generations. This will inform the development of pedigree-free methods for group management. Next, we will examine how measures of genomic diversity vary across different populations and species, and how marker number and sample size affect

our level of confidence in these results. Optimal models will be validated with existing and novel datasets to help improve breeding strategies across key management scenarios, from intensive pairwise breeding to extensive metapopulation management. The project will be undertaken in collaboration with the CASE partner, EAZA, and with a complimentary project under development at the University of Antwerp, Belgium, with which strong collaborative links are in place.

Year 1. Research training. Familiarisation with existing datasets, software and comparative population genetic analysis. Experimental design and initial exploration of datasets. One-month placement at EAZA to introduce the student to institutional captive breeding programmes.

Year 2. Production and analysis of comparative data to address primary research questions. One-month placement at EAZA to present and discuss findings and plan subsequent research.

Year 3. Development and testing of a general framework that enables research outputs to be incorporated into population management by the conservation community. One-month placement at EAZA to facilitate knowledge exchange.

CASE partnership: European Association of Zoos and Aquariums (EAZA)

The student will spend a minimum of three months at EAZA headquarters, working in the Population Management Centre, based at Artis Zoo in Amsterdam, The Netherlands.

Training

A comprehensive training programme will be provided comprising both specialist scientific training and generic transferable and professional skills. This project offers a wealth of opportunities for the student to gain experience in using genomic data for informing wildlife and livestock management. The student will benefit from training in genomics, bioinformatics, population genetics and science communication and will be able to take advantage of the international collaborative links of supervisors in both livestock and captive breeding programme communities. The studentship will be based at the Royal (Dick) School of Veterinary Studies and the Roslin Institute, world leading centres in the analysis of molecular data from wildlife and livestock. The lead supervisor, Dr Rob Ogden, has extensive experience in transferring genome-wide technologies from agriculture and veterinary medicine to wildlife conservation projects. Co-supervisor Professor John Hickey holds a chair in Animal Breeding at the Roslin Institute, has extensive expertise in animal genetics and has developed methods for optimising selection and mate allocation in animal breeding programmes. The project CASE sponsor, EAZA, is the membership organisation of the leading zoos and captive breeding institutes in Europe and the Middle East, operating a dedicated population management unit that oversees all endangered species breeding programmes in the region.

Requirements

We seek a bright and motivated student with a background in conservation genetics, evolutionary biology, bioinformatics or population biology. Previous experience working with genomic data would be advantageous, as well as experience in programming in a language such as R, Python or UNIX, however, full training will be provided.

Further Reading

McGowan PJK, Traylor-Holzer K & Leus K (2017). Guidelines for determining when and how ex situ management should be used in species conservation. *Cons. Letters*, 10, 361-66

Fienieg ES & Galbusera P (2013). The use and integration of molecular DNA information in conservation breeding programmes: a review. *JZA* 1(2):44–51.

De Cara MA, Fernández J, Toro MA & Villanueva B (2011). Using genome-wide information to minimize the loss of diversity in conservation programmes. *J Anim Breed Genet.* 128:456–464.

Gorjanc G & Hickey JM (2018). AlphaMate: a program for optimising selection, maintenance of diversity, and mate allocation in breeding programs. *Bioinformatics.* 34(19):3408–3411.