



PROJECT TITLE: Sexual selection, mating systems and speciation: testing a novel

hypothesis using genomic data

DTP Research Theme(s): Living World

Lead Institution: University of Bath

CASE Partner: BGI (Beijing Genomics Institute)

Lead Supervisor: Prof Tamas Szekely, Milner Centre for Evolution, University of Bath Co-Supervisor: Prof Michael Bruford, Cardiff School of Biosciences, Cardiff University

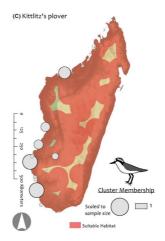
Co-Supervisor: Dr Araxi Urrutia, Milner Centre for Evolution, University of Bath

Co-Supervisor: Prof Guojie Zhang, Beijing Genomics Institute, China

Project Enquiries: T.Szekely@bath.ac.uk



The monogamous Madagascan plover has highly structured breeding population



The polygamous Kittlitz's plover has unstructured population and males and females disperse in search of mates

## **Project Background**

Sexual selection is usually viewed as an engine of speciation, although recent works by our group show that this textbook example of speciation is not correct. Working in Madagascar, we found that the monogamous Madagascan plovers that return to breed to the same place year after year, so that they exhibit highly structured populations whereas polygynous Kittlitz's plovers seek out mates in distant breeding locations that lead to mixing the breeding gene pool over large geographic distances. Our more recent work across 6 monogamous and 4 polygamous shorebirds confirmed these patterns since in polygamous species that are under strong sexual selection the adults move between breeding sites to find mates. By moving, they blend the gene pool which reduces the diversification between geographically different breeding populations. In contrast, adults in monogamous species find mates more easily and thus move less resulting in greater isolation between breeding sites and the accumulation of higher genetic differences between the populations over time.

# **Project Aims and Methods**

The objective of this NERC DTP Studentship is to test whether sexual selection leads to reduced geographical diversification using Arctic shorebirds as model organisms. Shorebirds (sandpipers, plovers and allies) are highly suitable for this project: they exhibit one of the highest variations in the intensity of sexual selection as represented by monogamous, polygynous and polyandrous matings. By collecting DNA from different species that nest over large geographic areas, we will compare for the first time the genetic structure of populations between monogamous and polygamous shorebirds that may breed 1000s of km apart. To compare these populations, we will apply genome wide sequence analyses and a novel transcriptome-based methodology developed by our group to assess genetic diversity and population structuring. Transcriptome sequencing will allow independent molecular assessment of the extent of sexual selection complementing behavioural and morphological assessments as well as identifying selected molecular functions. Such an integrated and systematic approach has never been attempted before to assess the impacts of sexual selection on wild bird populations.







The student will have substantial freedom setting up his/her own research hypotheses and designing the tests of these hypotheses using a combination of fieldwork, behavioural observations and advanced genomics. Our group has established collaborations with scientists in Arctic regions, so that the student will benefit from working with these colleagues in some of the most exotic and remote habitats in the world.

### **Candidate Requirements**

We are seeking candidates with strong interest in evolution, behaviour and conservation genetics/genomics. Excellent quantitative skills are required to perform data analyses and run mathematical simulations, and stamina and curiosity to carry out fieldwork in harsh environments. Innovative thinking and ability to solve problems on the spot will be necessary to draw links between disparate sources of data. The student will join three internationally leading research teams, and will benefit from our extensive network of collaborators, students and conservationists.

#### **CASE Partner**

BGI is a world-leader in genomics and bioinformatics (https://www.bgi.com/global/) and they produce cutting edge scientific results by carrying out large-scale analyses as part of BIG DATA biology. BGI will provide unique services and facilities for the NERC project. BGI is a global genomics organization that offers the widest range of sequencing services available today, with applications in human, plant and animal, and microbial research. They provide innovative, affordable, and reliable solutions for virtually any genomic challenge. Their facilities feature the industry's latest next-generation sequencing technologies and quality management systems. Thus, the NERC DTP project offers great learning opportunities from a leading industrial organisation.

#### **Training**

This project will provide unique combination of cutting-edge skills since the successful candidate will gain expertise in fieldwork (that includes behavioural monitoring, trapping and bird ringing) and key laboratory techniques (microdissection, RT-PCR, in situ hybridization, bioimaging). In addition, there will be strong training in bioinformatics including RNA seq quality check, transcriptome annotation and differential gene expression analyses. From a wider perspective, the GW4+DTP also provides enhanced training opportunities in research and transferable skills.

Collaboration with an international team of students and scientists will be a major feature of this project and attending meetings and conferences overseas will be essential aspects of the studentship. The project will lead to a well-rounded expertise in behaviour, ecology & conservation with special emphasis on using genomic approaches.

### References / Background reading list

- 1. Eberhart-Phillips, L. J et al. 2015. Contrasting genetic diversity and population structure among three sympatric Madagascan shorebirds: parallels with rarity, endemism, and dispersal propensity. *Ecology and Evolution* 5: 997-1010.
- 2. D'Urban Jackson, J. et al. 2017. Polygamy slows down population divergence in shorebirds. *Evolution* 71: 1313-1326.
- Pan S, et al. 2017. Population transcriptomes reveal synergistic responses of DNA polymorphism and RNA expression to extreme environments on the Qinghai-Tibetan Plateau in a predatory bird. *Molecular Ecology* 26, 2993–3010.
- 4. Kubelka, V. et al. 2018. Global pattern of nest predation is disrupted by climate change in shorebirds. *Science* (in press).

## **Useful links**

Enquiries relating to the project should be directed to the lead supervisor (see email address above for Project Enquiries). Enquiries relating to the application process should be directed to doctoraladmissions@bath.ac.uk

In order to apply, you should select the relevant University of Bath PhD online application form found here: <a href="https://www.bath.ac.uk/study/pg/applications.pl">https://www.bath.ac.uk/study/pg/applications.pl</a>. When completing the form, please state in the 'Finance' section that you wish to be considered for GW4+ DTP funding and quote the project title and lead supervisor's name in the 'Your research interests' section.

Further information about the application process may be found here: http://www.bath.ac.uk/topics/postgraduate-research/

The application deadline is 1600 hours GMT Monday 7 January 2019 and interviews will take place between 4 and 15 February 2019. For more information about the NERC GW4+ DTP, please visit <a href="https://nercgw4plus.ac.uk">https://nercgw4plus.ac.uk</a>.

