

## NERC DTP Studentship projects at Queen Mary University of London

**Project title:** Rewilding and Natural Flood Management

**Supervisor(s):** Gemma Harvey ([g.l.harvey@qmul.ac.uk](mailto:g.l.harvey@qmul.ac.uk) QMUL Geography), Alex Henshaw (QMUL Geography), Stewart Clarke (National Trust)

**CASE Partner:** National Trust

**Project description:** Over the last decade, the UK has experienced some of the most significant and extreme flood events of the last 100 years, and predicted changes in precipitation are expected to increase the frequency and costs of flooding. New approaches to managing flood risk are required, and there is increasing emphasis on Natural Flood Management (NFM) whereby natural processes are used to reduce the risk of flooding and coastal erosion. NFM has been identified as a core element of the UK government's new 25-year environment plan to mitigate the effects of flooding. Alongside this, a radical new approach to land management is emerging that has the potential to deliver significant changes to hydrological processes over large spatial scales. Rewilding is a conservation approach focusing on landscape-scale restoration of ecosystems and reinstating natural processes. It can include, but is not limited to, the reintroduction of missing keystone species (cattle, ponies, deer, pigs, beavers). These ecosystem engineering animals can generate significant landscape-scale changes in vegetation structure. Increasingly, the debate about rewilding in the UK recognises the potential for different degrees of 'wildness' from a more hand-off approach to land management through to allowing nature to take over. It is likely that we begin to see many different approaches across this gradient with NFM being a major driver. Combining novel remote sensing methods and plot-scale experimentation, this PhD will seek to characterise vegetation changes for different rewilding settings and trajectories and determine how they modify key hydrological processes. These analyses will inform the development of decision-support tools for modelling rewilding impacts in the context of NFM.

**Case Partner and contribution:** The PhD will be undertaken in partnership with the National Trust. The National Trust is an independent charity dedicated to environmental and heritage conservation and is the largest membership organisation in the UK. The National Trust is a major landowner and has recently embarked upon a programme of catchment management projects 'Riverlands'. This programme will see the Trust expand its work on NFM and explore new models for land management and hence this research is very timely. It supports a wide-ranging programme of research to collect evidence needed to deliver internationally renowned conservation; to inform decision making; and to help people understand more about and be inspired by the properties and land in its care. Collaboration will centre around the use of field sites on National Trust land and co-development of land management planning tools. There will be an opportunity to work closely with National Trust staff and share research findings with the Trust and its partner organisations for example through the Catchment Based Approach.

**Project title:** Microplastic-sediment interactions (MiPSi)

**Supervisor(s):** Kate Spencer ([k.spencer@qmul.ac.uk](mailto:k.spencer@qmul.ac.uk) QMUL Geography), Geraldene Wharton (QMUL Geography)

**CASE Partner:** Deltares

**Project description:** The accelerating global release of microplastics (mP) into the aquatic environment seems inevitable, with long-term consequences for water quality and biodiversity. Managing plastics in the environment and ensuring effective intervention policies and practices requires an understanding of mP source, transport and fate. Whilst much has been reported on the occurrence of mP in environmental media (e.g., surface waters, sediment, soils) and potential uptake and impacts on aquatic biota (Woodall et al., 2014; Ivar do Sul & Costa, 2014), virtually nothing is known of their wider impacts on ecosystem functioning, particularly outside the marine environment.

mP are hydrophobic, yet once they enter the aquatic environment they are quickly colonized by microbial biofilm and interact with fine minerogenic suspended sediment, forming mP-aggregates in the water column. The overall aim of this PhD is to understand how mPs modify the flux of suspended sediment, and associated carbon, nutrients and pollutants to the marine environment. We will focus on understanding how mPs associate with sediment and how mP modify the settling characteristics of suspended sediments as they transition from fresh to saline water conditions (i.e. estuaries and deltas). The PhD will be conducted with project partners, Deltares, who are currently working on heavily mP-polluted sediments (8% vol) from the Rhine Delta and Port of Rotterdam. There will be an opportunity to spend 3 months at Deltares' research facilities in Delft, Netherlands where you will focus on learning techniques to understand fine sediment dynamics and transport.

Deltares are an independent research institute for applied water research specializing in coastal and delta systems. They provide fundamental science expertise in the fields of coastal systems, sediment transport modelling and coastal management and host state-of-the-art large-scale flume and wave basin facilities, and well-equipped sediment and soil laboratories for applied research and sample characterisation. They have an excellent track record in translating science into real-world management solutions, delivering high-impact science, and successfully managing major projects (including running very large EU-funded pure and applied science projects).

**Policy Impact of Research:** Improved understanding of how microplastics are transported from catchment to coast will have impacts for compliance with Water Framework Directive, whilst an understanding of how different types of plastic impact wide ecosystem functioning can inform the development of new intervention policies on plastic reduction.

**Project Title:** Quantification of the impact of changing vegetation on hillslope sediment transport  
**Supervisor(s):** Stuart Grieve ([s.grieve@qmul.ac.uk](mailto:s.grieve@qmul.ac.uk)) QMUL Geography, Emily Lines (QMUL Geography)

**Project description:** Hillslope sediment transport exists on a continuum from the gradual downslope motion of particles, termed soil creep, to catastrophic shallow landslides and debris flows. In upland, forested landscapes trees and other vegetation play a vital role in the modulation of these processes, with root growth and tree throw driving soil creep, whilst reducing landslide hazard through an increase in soil cohesion. There is growing evidence that the structure and dynamics of forests are changing as a consequence of climate change, alongside changes to forest structure driven by changing forest management practices. Consequently, it has become increasingly important to understand the implications these large scale changes in forests will have on both fine scale sediment transport and slope stability.

This project will integrate forest structural analysis using terrestrial laser scanning (TLS), with topographic analysis from airborne LiDAR and ecological and landscape evolution modelling to constrain the key factors which influence hillslope sediment transport at short (minutes to hours) to long (millennial) timescales. The analysis of TLS data to quantify tree structural properties such as branching, leaf area, crown density, biomass and neighbourhood interactions, will build on techniques developed by current PhD student Harry Owen (cohort 3). Analysis of airborne LiDAR data will be performed using LSDTopoTools (<http://LSDTopoTools.github.io>), a state of the art software package developed at QMUL in collaboration with colleagues from Edinburgh, Glasgow and Durham Universities. Full training in all of these methods, alongside opportunities to collaborate with other users of LSDTopoTools, will be provided to the successful student.

**Policy Impact of Research:** In the UK, a significant amount of forested land lies upslope of infrastructure (rail lines, roads, power lines), and it is therefore vital to understand the implications of changing forest dynamics on slope stability.

**Project Title:** Investigating the impacts of drought on Spanish forests using terrestrial laser scanning  
**Supervisor(s):** Emily Lines ([e.lines@qmul.ac.uk](mailto:e.lines@qmul.ac.uk) QMUL Geography)

**Project Description:** Evidence for the impact of climate change on the structure and function of forests across the world is growing. Of particular concern is the growing frequency and severity of droughts in some regions, which can cause crown dieback and ultimately tree mortality. Resilience to, and recovery rates from drought are uncertain and the legacy effects of droughts on individual tree and whole-forest structure may be long lasting.

This project will undertake research into the impacts of historical droughts on tree morphology and stand structure in Spain, a highly biodiverse region where drought is a major control of ecological processes. Under climate change, Spain is predicted to become hotter and drier, so the resilience of Spanish forests to withstand or adapt to this future is a key research question. In this project the student will investigate the impact of drought on the morphology of a range of key species using terrestrial laser scanning (TLS), a technology capable of reconstructing three-dimensional properties of trees to very high accuracy. The project will assess long-term impacts of historical drought and ecological 'memory' using plots with known drought histories, quantifying impacts on tree structural properties such as branching, leaf area, crown density, biomass and neighbourhood interactions. Building on techniques developed by current PhD student Harry Owen (cohort 3), the student will work closely with Spanish ecologists in Madrid and undertake fieldwork to collect new data using this novel technology.

**Policy Impact of Research:** Climate change impacts on forests as a natural resource is a critical issue in Spain and this project will provide outputs that can be used to understand the impact on biodiversity and to manage and conserve forests in the future.

**Project Title:** Past intermediate and deep ocean circulation during sustained periods of warmth  
**Supervisors(s):** Heather Ford ([h.ford@qmul.ac.uk](mailto:h.ford@qmul.ac.uk) QMUL Geography)

**Project Description:** The ocean is absorbing much of the heat and carbon dioxide emissions related to human caused climate change, but the long-term impacts on heat transport, carbon cycling and deep ocean circulation are poorly understood. Looking at past warm periods such as the Last Interglacial (125,000 years ago) and other “Super-Interglacials” where global temperatures are estimated to be 0.5 to 1.5°C warmer than today may provide insight into how the ocean accommodates heat and carbon. This project will use a suite of locations in the Atlantic and/or Pacific to characterize and map intermediate and deep water masses and ocean circulation.

This project necessitates a multi-proxy approach including stable isotopes ( $\delta^{13}\text{C}$ ,  $\delta^{18}\text{O}$ ), minor (Mg/Ca, temperature) and trace elements (B/Ca,  $[\text{CO}_2]$ ) and trace isotopes (ENd). The project can be tailored to focus on regional (e.g. North Atlantic, Southern Ocean) or basin-wide reconstructions of ocean circulation depending on the research interests of the student.

**Policy Impact of Research:** As the ocean is a large part of the climate system, being able to constrain the ocean’s long-term response to future climate change on a variety of time scales has significant economic and societal impacts.

**Project Title:** Functional genomics of olfaction in an echinoderm

**Supervisor(s):** Maurice Elphick ([m.r.elphick@qmul.ac.uk](mailto:m.r.elphick@qmul.ac.uk) QMUL SBCS), Yannick Wurm (QMUL SBCS)

**Project Description:** The sense of olfaction enables animals to detect, recognise and respond to chemicals in their environment, which is critical for survival and reproduction. A key breakthrough in our understanding of the mechanisms of olfaction was the discovery of a large family of genes that encode G-protein coupled odorant receptors in humans and other vertebrates, which was recognised in the award of the 2004 Nobel Prize for Physiology or Medicine. Subsequently, it has been discovered that different families of genes have evolved as mediators of olfaction in other taxa; e.g. in arthropods two families of genes encoding ion channels mediate olfaction. Therefore, characterisation of odorant receptors in a variety of phyla is now needed if we are to understand the evolution of mechanisms of olfaction.

The aim of the project proposed here will be to address this objective by analysing the molecular mechanisms of olfaction in an animal that occupies an “intermediate” phylogenetic position with respect to vertebrates and arthropods – the starfish *Asterias rubens* (phylum Echinodermata). Informed by analysis of genome sequence data, we have recently identified several candidate odorant receptor genes in *A. rubens* and the proposed project will build upon these preliminary findings to investigate the mechanisms of olfaction by addressing the following objectives:

**Objective 1 (year 1):** Genome-wide discovery of odorant receptor genes in *A. rubens* – Informed by the complementary expertise of the Wurm and Elphick in comparative genomics, a detailed analysis of *A. rubens* genome sequence data generated by the Sanger Institute will be performed to identify candidate odorant receptor genes. By analysing gene number, structure, synteny and phylogenetics, important new insights into the evolution of odorant receptor genes in starfish and other echinoderms will be obtained.

**Objective 2 (year 1-2):** Mapping odorant receptor gene expression in starfish “noses” – Located at the tips of each of the five arms of starfish is a terminal tentacle with associated sensory organs, which include an optic cushion and flaps of tissue known as lappets, which are the presumptive olfactory organs or “noses”. Transcriptome sequencing and mRNA *in situ* hybridisation methods will be used to identify putative odorant receptor genes that are expressed by cells located in sensory (olfactory) organs located at the tips of starfish arms.

**Objective 3 (year 2-3):** Identification of pheromone receptors in starfish - Here the student will focus in on a more specific objective of identifying odorant receptors involved in starfish reproduction. Release of eggs or sperm in starfish is triggered by a relaxin-like gonadotropic peptide (RGP) and we have recently discovered that RGP is expressed by cells located in the lappets of the terminal tentacles (Lin et al. 2017a). Our hypothesis is that activation of pheromone receptors co-expressed with RGP triggers the release of RGP to induce spawning. The objective here will be to identify receptors that are activated by chemicals (pheromones) released with eggs or sperm by conspecifics when they spawn and to accomplish this the student will repurpose an *in vitro* cell-based assay that we have used successfully to identify ligands for G-protein coupled neuropeptide receptors (Tian et al., 2016). Then use of double mRNA *in situ* hybridisation will enable identification of pheromone receptors that are co-expressed with RGP.

**Project Title:** Sex, death and extinction: testing the role of harvesting and sexual selection in determining adaptation

**Supervisor(s):** Rob Knell ([r.knell@qmul.ac.uk](mailto:r.knell@qmul.ac.uk) QMUL SBCS)

**Project Description:** Sexual selection is important in determining the outcome of population-level processes such as speciation, adaptation and extinction. Of particular importance is the role of sexual selection in driving adaptation to changing environments. Strong sexual selection leads to reproductive skew in favour of a few “high quality” males, or, in sex role reversed species, females. When the environment is changing this leads to faster adaptation because those males which are well adapted to the new environment obtain a disproportionate number of matings, leading to faster spread of their genes and a reduced risk of extinction (Martínez-Ruiz and Knell 2017 and references therein). Research at QMUL indicates that human activity can disrupt these processes because human harvesters such as trophy hunters specifically target male animals with exceptionally large antlers, horns, or other secondary sexual traits. A new model (Knell and Martínez-Ruiz 2017) shows that the removal of small numbers of the best ornamented males can reverse the adaptive benefits of sexual selection and cause extinction. This important result arises because rather than those individuals with the ‘best’ genes acquiring the majority of the matings, ensuring rapid spread of adaptation through the population, these high-quality individuals are instead removed, substantially lowering the adaptive capacity of the population.

This is clearly an important result with the potential to influence wildlife management worldwide. Thus far, however, we only have data from one simulation model to help us understand the effect of selective harvest on populations experiencing environmental change. For this studentship I propose a combination of laboratory experiments and further modelling to allow us to test these ideas empirically and to explore the relationship between selective harvest and population responses to changing environments in more realistic settings.

**Testing the effect of selective harvest on responses to changing environments.**

We propose to empirically test the effect of removing large, well ornamented males using a well-established model laboratory system, namely the stalk-eyed fly, *Teleopsis dalmanni*. Stalk-eyed flies are strongly sexually selected, and the length of the eyestalks is known to be strongly condition dependent. We will expose replicated laboratory populations of *T. dalmanni* to directional environmental change in two forms: firstly increasing temperature and secondly increasing concentrations of copper in their food, and impose harvesting regimes of varying selectivity, ranging from random removal of individuals of both sexes to highly selective removal of the males with the longest eyestalks only. Comparing the adaptive responses of these populations using measures including size, longevity, fecundity and egg to adult survivorship will allow us experimentally to quantify the effect of selective harvest of males with large sexual ornaments when a population is exposed to continuous environmental stress.

**Project Title: Big data evolutionary genomics of social insects.**

**Supervisor(s):** Yannick Wurm ([y.wurm@qmul.ac.uk](mailto:y.wurm@qmul.ac.uk), QMUL SBCS)

**Project description:** We have two main lines of research.

**Genetics of social behaviour.** Social animals exhibit a broad range of behaviors, and some theoretical understanding exists of the tradeoffs between different forms of social organisation. However, we know little about the genes and processes underpinning social organisation or how it evolves. The diversity of social behaviors across the 20,000 species of ants represents a unique opportunity to empirically understand the mechanisms and tradeoffs involved in social change. We use highly molecular approaches, including genomics and bioinformatics but also potentially behavioural or field work to address major questions about social evolution. We aim to generate exciting new insights into genes and processes underpinning a major social transition, with implications on understanding evolution of complex phenotypes.

**Molecular diagnostics for pollinator health.** Effective pollination is crucial for the stability of the ecosystem, and for crop productivity. Governments had approved what they thought were "safe" levels of pesticides. But in fact, the pesticides are generic neurotoxins: they reduce the learning abilities, dexterity, foraging ability and ultimately survival of pollinators who consume nectar or pollen. As a result, several commonly used pesticides have now been banned. However, the problem may just have been shifted: we lack a good way of understanding whether authorised pesticides are better.

Thus there is an urgent need for approaches that are more powerful/sensitive. The 50,000-fold drop in the cost of DNA sequence over the past 10 years has completely changed medical research and practice. Inspired by the changes, we are developing high-resolution molecular diagnostics approaches for pollinator health – these are poised to fundamentally change for the better how research on pesticides is performed and the mechanisms through which such crop chemicals are evaluated by regulatory agencies.

**Context.** We collaborate extensively with relevant national and international partners and stakeholders. There is some flexibility in adapting the project to the students' interests and background.

The student will receive extensive **training** in big data bioinformatics, phylogenomics, data visualisation, and experimental research approaches in evolution and genomics. Furthermore, they will receive hands-on training in interdisciplinary project management, communicating science in writing and verbally, including by presenting at workshops and conferences.

**Project title:** Targeting interventions in outbreaks of sexually transmitted infections

**Supervisor(s):** Steven Le Comber ([s.c.lecomber@qmul.ac.uk](mailto:s.c.lecomber@qmul.ac.uk) QMUL SBCS), Rob Knell (QMUL SBCS)

**CASE Partner:** Barts Health NHS Trust

**Project Description:** Sexually transmitted infections (STIs) are a major problem around the world, with 499 million new cases diagnosed worldwide in 2008; in England alone there were 450,000 new cases in 2012<sup>1,2</sup>. Spatial analysis of STIs is increasingly important as cases tend to be highly clustered and mapping them forms the basis for decisions on where to focus interventions. The WHO suggest that practitioners ask patients where they first met their recent partners to ‘help direct prevention efforts to epidemiologically important hotspots’<sup>3</sup>. Here, we test whether geographic profiling (GP) can identify specific sites for community level public health interventions without expensive and time-consuming interviews. GP was developed in criminology to prioritise large lists of suspects in cases of serial crime. It uses locations of crime sites to create a probability surface that is overlaid on the study area to produce a geoprofile. Geoprofiles allow police to prioritise investigations by checking suspects associated with locations in descending order of their height on the geoprofile<sup>4</sup>. GP is highly successful in criminology, and is used by law enforcement worldwide. This success has led to its application to epidemiology, identifying disease sources from the addresses of infected individuals (eg identifying vector breeding sites during an outbreak of malaria in Cairo)<sup>5</sup>. Pilot studies with Chelsea & Westminster NHS Trust suggest that GP can be highly effective in identifying hotspots of STI transmission, and it is this work that we extend here. This project asks if GP can locate places people meet sexual partners and contract STIs. This will help identify locations that are important for STI transmission so that prevention programs can be targeted to these. We ask (1) if maps produced by GP can improve the performance of questionnaires/interviews; (2) if GP can remove the need for questionnaires/interviews; (3) if socioeconomic/demographic information can improve model performance. Methodology The GP model is well established and runs in the open-source software. Patient data will be made available from Chelsea & Westminster and Barts NHS trusts. The model will use as input the postcodes of patients diagnosed with STIs (the project has passed C&W ethical review) to identify sites where sexual partners have been met. The study that will form the first 2 chapters of the thesis has 3 phases. Phase 1 follows current best practice in that participants (excluding decliners) are given questionnaires asking where they have met recent partners. In Phase 2, Cohort 1 is divided into two groups. A control group (Group 1) is interviewed as normal, while in a second group (Group 2) interviews are supplemented with GP hotspot maps. Simultaneously, Cohort 2 is recruited, and participants given the questionnaire alone (the control group, Group 3) or the questionnaire plus GP map from Cohort 1 (Group 4). In Phase 3, GP of the full data set (Groups 1-4) will be used to see how well the model can identify locations highlighted in the questionnaire/interviews using addresses alone.

## References

- 1 Public Health England. (2013). Shooting Up: Infections among people who inject drugs in the UK.
- 2 Public Health England. (2012). Sexually transmitted infections and chlamydia screening in England, 2012. Health Protection Report 7:23.
- 3 Steen., et al (2009). Bull. WHO 87:858-865.
- 4 Rossmo (2000) Geographic Profiling. CRC Press, New York.
- 5 Verity et al (2014). Methods in Ecol Evol 5:647–655.

**Project title:** Genomics of African indigenous cattle

**Supervisor(s):** Laurent Frantz ([laurent.frantz@qmul.ac.uk](mailto:laurent.frantz@qmul.ac.uk) QMUL SBCS), Chris Faulkes (QMUL SBCS), Steve Rossiter (QMUL SBCS)

**CASE Partner:** Silverstreet Capital

**Project Description:** Sub-Saharan Africa is home to a rich but poorly understood diversity of indigenous cattle breeds. Many of the region's ~150 indigenous breeds show unusual resistance to extremes of climate and disease, and these phenotypic traits are likely to become increasingly important in the face of climate change and mixing of stocks. Despite this, the genes and gene complexes that confer these traits are not known, and this is especially worrying given that many of these local cattle breeds are endangered, facing threats from uncontrolled crossbreeding, as well as from replacement by exotic yet ill-adapted European breeds. There is now an urgent need to identify and characterise the genomic diversity of African cattle, to better manage and retain genetic diversity and avoid the permanent loss of desirable traits. This information is not only of research interest: our nonacademic partner SilverStreet Capital has committed substantial funds so that our results can be quickly used to develop a genetic screening programme across the region, with potentially far-reaching impacts. SilverStreet capital focuses on investing in agriculture to improve livelihoods of rural African communities, and is exceptionally well-placed to achieve this goal. The goal of this PhD studentship project will be threefold:

**1. Generate genomic data for representative indigenous cattle breeds.** The student will have access to samples from multiple breeds from each of the four broad groups present, termed: Bos indicus (zebu), Bos taurus, sanga (B. taurus/B. indicus hybrids) and zenga (sanga/zebu backcross). With consumables funds contributed by our partner, the student will be able to generate genome-wide data for more than 200 samples. These will include those resident in Silverland Ranching farms, invested in by SilverStreet Capital, as well as those represented by >100 samples collected by collaborators Daniel Bradley (Trinity College, Dublin), and Olivier Hannote (University of Nottingham) [1], and Albano Beja-Pereira (University of Porto) [2]. We will also include trypanosome-tolerant breeds from tsetse fly infested areas. All data will be analysed using existing pipeline developed by supervisor Frantz (see publications list).

**2. Identify genes associated with particular adaptive traits so that these can be used for screening.** Recent advances in genomic-assisted breeding (genomic selection) in European breeds have demonstrated that it is now possible to use genomic tools to improve production in specific populations, while limiting inbreeding. Currently these genomic tools are only available for European populations, reflecting the relative lack of genomic research on indigenous African cattle despite their genetic diversity, and the potential socioeconomic importance of their traits. The student will perform analyses to quantify genetic diversity available in African cattle populations, and identify key genetic markers for disease, fertility and drought resistance in the genome of specific populations. Newly discovered markers will then be used to develop a screening panel (Affymetrix SNP array; see impact below). This genomic tool is necessary to pave the way for future genomic selection of cattle breeds in Africa.

**3 Perform genomic analyses to reconstruct the population histories of indigenous cattle breeds.** Genetically-varied African cattle breeds have evolved from a complex history of artificial and natural selection. The student will use genomic methods to reconstruct these processes. These analyses will be able to address key questions concerning African cattle, such as the origin and number of introductions of zebu cattle.

[1] Hanotte et al (2002) African pastoralism: genetic imprints of origins and migrations. *Science*, 296, 336-339. [2] Beja-Pereira et al (2006) The origin of European cattle: Evidence from modern and ancient DNA. *PNAS* 103, 8113-8118.