Principal Supervisor: Eamonn Mallon (Genetics)

Co-supervisor: Shaun Cowley (Molecular and Cell Biology)

PhD project title: Uncovering intergenerational epigenetics in the bumblebee using whole genome bisulfite sequencing

University of Registration: University of Leicester

**Project outline**

1. **Project outline describing the scientific rationale of the project**

This project will establish an insect model for intergenerational epigenetic inheritance by studying parent of origin allele specific methylation in the bumblebee *Bombus terrestris*, an important European, pollinator species. This extends the host lab's discovery of monoallelic methylation in this species. Bees are a good model for understanding the effects of methylation on complex traits because they have small, sparsely methylated genomes, and because genetically identical individuals exhibit large differences in behaviour and longevity which are thought to be epigenetically controlled.

The proposed project will use next generation sequencing and reciprocally crossed bumblebee colonies to follow the dynamic methylation patterns as passed from parents through gametes to offspring in bumblebees in order to establish the basis for a model for intergenerational epigenetic inheritance. In addition to our results being published in high impact journals, they will establish a model system to study the role of methylation in social evolution and complex behaviours.

**Objectives**

- We will analyse BS-seq libraries of mother queens and father males and their reciprocally produced offspring colonies in order to identify genes that show parent of origin allele specific methylation.
- We will analyse BS-seq libraries of gametes in order to confirm that these parent of origin epigenetic marks are passed through the gametes.
- We will analyse BS-seq libraries of single lineages of reproductive worker, their eggs, their sons and the sons' sperm in order to elucidate the DNA methylation dynamics during epigenetic reprogramming from gamete to adult.

This project will establish an insect model for intergenerational epigenetic inheritance by studying parent of origin allele specific methylation in the bumblebee *Bombus terrestris*, an important European pollinator species. By analysing BS-seq libraries for parents, gametes and offspring in reciprocal colonies we will be able to identify genes where the methylation pattern of the offspring rely on which parent the given allele came from (parent of origin allele specific methylation). This type of parental imprinting, despite being predicted to exist, is yet to be discovered in this or any other social insect.

Epigenetics is the study of heritable changes in gene expression that do not involve changes to the underlying DNA sequence. Social hymenoptera (ants, bees, and
wasps) are important emerging models for epigenetics. This is due to theoretical predictions for a role for the epigenetic phenomenon, genomic imprinting in their social organisation, the recent discovery of parent-of-origin allele specific expression in honeybees, and data showing a fundamental role for methylation, an epigenetic marker, in social insect biology. Genomic imprinting is allele specific expression in diploid individuals, where expression is dependent on the sex of the parent from which an allele was inherited. In mammals and flowering plants, genomic imprinting is often associated with methyl groups attached to DNA (DNA methylation) passed from parents to offspring.

DNA methylation is involved in controlling reproductive behaviour in the bumblebee. The Mallon lab found methylation differences between the genomes of reproductive workers and non-reproductive workers. In the same paper, they found workers whose genomes had experimentally altered methylation were more likely to develop ovaries compared with control workers. They have also found that monoallelic methylation is linked with monoallelic expression in some bumblebees genes. Genomic imprinting in mammals usually involves monoallelic methylation and monoallelic expression.

**Relevant BBSRC Strategic Research Priority:** Food security

Techniques that will be undertaken during the project.

The PhD student will carry out all experiments and bioinformatic analysis under the guidance of the supervisory team. They will be provided with training in R, a powerful and increasing popular statistical programming language, Python, a general-purpose, high-level programming language widely used in bioinformatics, molecular biology, BS-seq, anatomical dissection and neuroanatomy, and bee husbandry as required.

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