Cambridge BBSRC DTP - Agriculture and Food Security sample projects

(Students are provided with a list of ~150 projects to select from, these are just a sample)

Rotation projects

Quantitative analysis of antimicrobial resistance in livestock

Department of Veterinary Medicine

There is an urgent need to rationalise the use of antibiotics in agriculture, with the dual requirement of protecting animal health and reducing antibiotic resistance. The first step is the accurate reporting of the prevalence of resistant strains of bacterial pathogens in farms. Diagnosis can be genetic (based on the presence of known mutations or genetic elements) or phenotypic (based on the measurement of minimum inhibitory concentration or MIC).

While diagnostic tools are becoming increasingly available and affordable, there remains a technical issue: susceptibility to antimicrobials is often a multi-factorial trait of bacterial strains which varies along a spectrum, yet it is ultimately reported as a binary trait (either resistant or susceptible).

This project will explore some of the statistical issues around the classification of bacterial isolates and the relationship between genotype and phenotype.

How slippery are trapping surfaces of pitcher plants?

Department of Zoology

Pitcher plants of the genus Nepenthes possess surfaces specialised for trapping, which are either covered by layers of epicuticular wax crystals on the inner pitcher wall, or by a regular hierarchy of cuticular ridges on the pitcher peristome. It is likely that both surfaces are optimised for insect capture.

Mechanisms explaining the slipperiness have been proposed for both surfaces, but insect attachment forces have so far only been quantified by simple traction tests. However, to assess the level of specialisation for pitcher plant surfaces, and to allow comparisons with other natural and synthetic substrates, reliable adhesion and friction measurements are needed that reflect the natural climbing conditions of insects.

We will perform sensitive force measurements on single adhesive pads of insects, under experimentally varied conditions similar those during natural climbing, and compare them with climbing tests and force measurements on whole insects.

Adhesive pads and surfaces will be studied after testing using SEM and checked for the presence of detached wax crystals. The approach will allow quantitative comparisons of naturally slippery plant surfaces with synthetic substrates, providing a critical step towards developing biomimetic anti-adhesive and insect-repellent surfaces.

Extracellular ATP signalling in plants

Department of Plant Sciences

Abiotic stress and pathogen attack cause an increase in extracellular ATP. This is now acknowledged as a signalling agent in plants, as it has been for decades in animals. However, the mechanism of signal transduction appears to be significantly different, starting with the plasma membrane receptor *(DORN1 in plants; Science 343,290)*. Activation of DORN1 causes an increase in cytosolic free calcium as a second messenger.

This project aims to identify the plasma membrane calcium channels that are responsible for that calcium increase by testing candidate Arabidopsis mutants expressing aequorin as a luminescent cytosolic free calcium reporter.

Mapping the protective proteins of bacteria spores

Department of Chemical Engineering and Biotechnology

Bacterial spores are seed-like cells that possess an astonishing degree of robustness – including the ability to survive immersion in boiling water – which is conferred upon them (in part) by their armor-like protein coats. In this rotation project we will continue to map out the location of important proteins in the coat, by building on the super-resolution microscopy methods which the two project supervisors jointly published in 2015 in the Biophysical Journal. Revealing the protein coat map will be useful in several branches of biotechnology. Key questions that this project will help to answer are:

1. What are the outermost protein layers of the coat? The outermost proteins may be involved in the adhesion of spores to (say) stainless steel surfaces in the food processing industries, and detailed knowledge of these proteins is important in designing cleaning methods. These proteins may also be accessible to chemical tests for contamination.
2. It is often important to completely decontaminate food processing equipment, or even a person (say, prior to surgery). Existing biocides that can kill spores are generally very aggressive chemicals. We want to find out which layers of the spore coat are affected by new biocides, and mapping out the structure of live and decontaminated spores will reveal this.
3. Can our method for mapping the spore coat, using quantitative image analysis methods, be made faster? How many different proteins (with different fluorescent colours) can be mapped simultaneously? Only low-risk strains of spores will be handled in the rotation project.

Domestication of the African vine *Cryptolepis sanguinolenta* for cultivation by smallholder African farmers

National Institute of Agricultural Botany (NIAB)

Cryptolepis sanguinolenta is an African vine found across tropical regions of Africa, from Ghana to Tanzania. *C. sanguinolenta* is extensively used in Ghana in local herbal remedies to treat malaria. Currently *C. sanguinolenta* is collected from the wild, being dug up for its roots, where most of the anti-malaria active ingredient, cryptolepine is found. Consequently the plant is becoming harder to find and threaten with eradication from the wild.

This project is part of a collaboration with Dr Naalamle Amissah at the Uni. of Ghana, Legon, Ghana (www.niabinternational.org). Dr. Amissah maintains a collection of *C. sanguinolenta* plants held at the Uni. of Ghana, the roots of which will be assayed for their cryptolepine content at NIAB in an established HPLC assay. The cryptolepine levels will be analysed alongside morpho-agronomic characteristics collected by Dr. Amissah as part of a programme to select the best genotypes for domestication and subsequent release as varieties.

Further work, which will form part of a 3 year PhD programme, will include generation of RADseq data on this *C. sanguinolenta* collection, and regression analysis of the cryptolepine and morpho-agronomic phenotypes against the genotypic marker data to identify the underlying genes responsible for the selected domestication traits.

During a sabbatical at NIAB Dr. Amissah identified a tissue culture media that significantly enhanced cryptolepine production in callus. Plants regenerated from this callus are maintained at NIAB. These plants have an enhanced sap colouration (wild-types are mainly yellow, while callus-derived plants are mainly red).

The rotation project will also assess cryptolepine levels in the roots of these callus-derived plants to determine whether enhanced sap colouration translates into higher levels of cryptolepine in the roots. Further work will determine whether this somaclonal variation is transferrable through subsequent generations, or is purely epigenetic.

PhD projects

Molecular Genetics of Communication in Arbuscular Mycorrhizal Symbiosis in Cereals.

Department of Plant Sciences

The arbuscular mycorrhizal (AM) symbiosis is a fascinating mutualistic interaction between roots of most land plants and fungi of the phylum of the Glomeromycota. The development of this life-long alliance starts with reciprocal recognition of both partners in the rhizosphere, reprogramming both symbionts for the anticipated association. Upon successful recognition the interaction proceeds towards extensive root colonization which culminates in the formation of fungal feeding structures, the arbuscules, inside root cortex cells. As the arbuscule develops, the plant cell dramatically increases membrane biogenesis to envelope the growing hyphal structure. Thereby a hugely enlarged membrane surface area is created between the two organisms that appears ideal for the exchange of signals and nutrients.

The nature and complexity of the establishment of AM symbioses must be the result of a well-orchestrated exchange of molecular signals. The nature of some of the signals has been discovered in recent years, providing a first insight into the type of chemical language spoken between the two symbiotic partners.

My laboratory takes genetics and lately advanced imaging approaches to elucidate the molecular mechanisms underpinning this apparently harmonious symbiosis. Some of our recent observations which have led us to propose fundamentally new communication mechanisms operating during this intimate plant-fungal partnership. PhD projects are available to investigate mechanism and evolution of the rhizosphere dialogue or the intracellular plant-fungal communication during arbuscular mycorrhiza establishment, and also to study the potential of AM fungi as biofertilizers in sustainable rice cultivation.

Examining CD8 T cell immune responses to viruses as a basis for developing new poultry vaccines

Department of Pathology

Chickens are a most important food source, but are beset by many pathogens, causing both animal diseases and human zoonoses such as avian influenza. Many poultry diseases are controlled primarily (and just barely) by extensive vaccination, but vaccine breakthroughs are frequent as the pathogens evolve to evade the immune response. In order to ensure food security (and for some pathogens, public health), there is a need to develop poultry vaccines that are sustainable in the long-term, based on a solid understanding of the biology of the immune response and host/pathogen interaction. In this project, we explore one crucial part of the immune response, particularly important for resistance to viral pathogens, based on CD8 T cell recognition of MHC class I molecules in chickens.

Objectives:

- Set up a simple non-transmission model for T cell responses to retroviral-induced tumours, using v-src plasmid transfection in B4/13 and B12 chickens, then testing in chickens with a variety of MHC haplotypes
- Relate MHC-binding and T cell epitopes to protection, starting with historic data of regression and progression in B2, B4/13 and B12 chickens, (PCR and sequence v-src cDNA from RSV infected cells, predict peptides using motifs, assess binding, make tetramers and stain for reactive T cells, assess whether nonbinding versus binding peptides protect by peptide vaccination)
- Isolate T cells from birds with tumours to examine function and clonality (in vitro assays such as proliferation, killing, next generation sequencing for T cell receptor), and to attempt culturing long-term populations or clones.

Testing new genomic methods to accelerate genetic gain for UK wheat improvement

National Institute of Agricultural Botany (NIAB)

This project is a public-private partnership to optimise the application of Genomic Selection (GS) for wheat breeding. It combines fit-for-purpose germplasm, emerging genotyping techniques, targeted, trait assessment and novel genomic selection strategies. This will provide marker information of immediate relevance to breeding as well as a resource-efficient platform for scaling the project's impact for future wheat improvement.

The PhD project will involve screening of three Oakley-derived, nested DH mapping populations for a number of agronomically significant target traits in key European wheat environments. Existing high-density phenotypic and sensor data will direct trait priorities.

The student will optimise the NIAB genotyping-by-sequencing bioinformatics pipeline using the soon-to-be released NRGene wheat whole genome assembly to produce SNP calls for the populations. QTL mapping will inform the development of high-throughput KASP markers for use in marker-assisted selection in partnership with RAGT Seeds Ltd who operate a fully integrated facility at Ickleton, Cambridge, which provides support for their entire European programme. This will offer the student an in depth understanding of the application of genomics in a commercial breeding programme.

The student will also develop and validate algorithms for GS of traits within and between the nested DH mapping populations. They will then test the extension of trait prediction into larger, more complex experimental populations of relevance to UK wheat improvement allowing value-added outcomes, including the NIAB Elite [BB/M008908/1] and Diverse MAGIC [BB/M011666/1] populations, and WISP Robigus-derived synthetic hexaploid wheat [BB/I002561/1] populations. They will have the opportunity to interact with a range of other industrial and academic partners in an exciting and emerging field of research and application.

Investigating the link between genome reduction and pathogenicity in a zoonotic pathogen

Department of Veterinary Medicine

Bacterial pathogens very often have smaller genomes and fewer genes than their nearest non-pathogenic relatives. This pattern applies in phyla as diverse as the Firmicutes, Tenericutes and Proteobacteria. However, despite much speculation, it remains unclear why this pattern holds. Streptococcus suis, a bacterium that is common in non-pathogenic forms, but which also causes serious diseases in pigs and humans is an ideal system in which to investigate this question.

Preliminary data show that S. suis has made several recent and independent transitions to pathogenicity, each associated with genome reduction, and that the gene loss is non-random, suggesting that the process might be predictable. Using samples of whole genomes from global S. suis populations, this project will produce the first large-scale tests of the various hypotheses linking genome reduction and pathogenicity using functional data and statistical approaches.

This project will also determine new potential vaccine candidates by identifying the genes that buck-the-trend of genome reduction.

Together, the proposed research will further our understanding of an important emerging pathogen, and of pathogenicity much more broadly.