Principal Supervisor: Prof Ed Louis

Co-supervisor: Dr James Higgins

**PhD project title:** Analysis of cross kingdom natural variation of meiosis genes in yeast and Arabidopsis accessions

University of Registration: Leicester

**Project outline**

1. Project outline describing the scientific rationale of the project (max 4,000 characters incl. spaces and returns)

In sexually reproducing organisms, meiotic crossing over ensures that offspring inherit a unique combination of alleles that can be selected on by evolution. A large population of Arabidopsis ecotypes and yeast isolates have been collected and sequenced from different ecological niches. These strains exhibit sequence divergence that has originated either by genetic drift or through selection due to environmental pressures. Preliminary data has shown that divergence of such strains becomes particularly important in hybrids where the sequence divergence inhibits proper recombination. Recombination rates vary across the genome and between individuals in such populations which can impact fertility. Among different populations of the brewers’ yeast (*Saccharomyces cerevisiae*), recombination rates and fertility are similar. However, some hybrid crosses between populations exhibit significant reductions in recombination rates, and in one case a significant effect on fertility. Among ecotypes of *Arabidopsis thaliana*, there is variation in recombination rates. In both Arabidopsis and yeast, there is genetic variation in the known genes involved in meiotic recombination, in particular the ZMM genes, and these genes are conserved. Preliminary data indicate genetic interactions between variants are responsible for the reduced recombination in yeast while variation in some of these genes correlates with the recombination rate differences in Arabidopsis. The comparative genomics of recombination rates between yeast and Arabidopsis will inform evolutionary biologists and ecologists about a fundamental aspect of adaptation to different niches – that is how does recombination rate and its variation affect adaptation to different niches and will also provide important information on the control of recombination rate in hybrids, both between different isolates of the same species but also between closely related species. This has potential applications in improving fertility in crops, many of which are hybrids, as well as facilitating crop improvement through introgression in breeding strategies.

**Year 1:** Use a bioinformatics approach to identify natural variation in ZMM genes for Yeast populations and Arabidopsis ecotypes. Clone genes and transfer into isogenic backgrounds to determine effect on recombination using tetrad analysis. Cross different lines to obtain various allelic combinations of ZMM proteins as well as into marker strains.

**Year 2:** Use cytological techniques in Arabidopsis, and next generation sequencing on yeast tetrads, to characterise the frequency and distribution of recombination events. Based on the hypothesis that ecotypes have evolved in relation to their environment, analyse recombination in selected accessions with a range of temperatures.

**Year 3:** Model data for effect of allelic variation on crossover interference. Use reporter lines to determine strength of inter-homolog bias. Perform further analysis of material generated in the first two years.
Relevant BBSRC Strategic Research Priority: Food security

Techniques that will be undertaken during the project.

Quantitative genetic analysis; bioinformatic comparative genomics; cytological analysis of recombination proteins using widefield and confocal fluorescence microscopy; and molecular biology techniques including PCR, cloning, sequencing and Western Blots.

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