The epigenetic fate of introgressed DNA in the wheat genome

Supervisory team:
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Collaborators: Prof Julie King (University of Nottingham)

Host institution: University of Bath

Project description:

Bread wheat (Triticum aestivum) is the source of 20% of all calories consumed worldwide. Understanding its biology and genetics is essential in developing a sustainable and productive agricultural landscape. Modern bread wheat derived from the hybridisation of the two cereal species (Aegilops tauschii and Triticum turgidum) approximately 10,000 years ago. The limited number of individuals involved in this hybridization, and subsequent inbreeding, mean that bread wheat has reduced levels of genetic diversity. This lack of diversity diminishes the ability of breeders to create cultivars able to respond to present and future environmental challenges. Introgression, the transfer of genetic material between related species, has been successfully exploited in breeding programs to overcome this bottleneck and expand the diversity of the bread wheat genome and to introduce agronomically beneficial traits. But how are introgressed genetic elements adapting to the host genome and why are some introgressions retained and others removed from the genome? These are the questions at the heart of this PhD project that combines functional wheat genomics with chromatin genetics and bioinformatics to provide a cutting-edge training experience for the next generation plant scientists.

As part of the project, the student will initially characterise the transcriptional activity of introgressions in established and newly created wheat accessions by RNA sequencing. Next, DNA methylation and histone H3K27me3 markings will be analysed by bisulfite sequencing and chromatin immunoprecipitation. Both epigenetic modifications are important mediators in the control of foreign genetic elements. These analyses will be accompanied by Hi-C experiments to study the integration of the introgressed segment into the 3D genome of the host. Together, these analyses will enable the student to define shared pattern in the genetic adaptation of introgressed segments. To analyse and evaluate the generated large-scale datasets the student will be trained in the application of advanced bioinformatic analysis pipelines of high-throughput data and essential coding skills.

The doctoral researcher will be based at the newly established Milner Centre for Evolution at the University of Bath and integrated into the wheat genomics group in Bristol and the BBSCR strategic programme ‘Designing Future Wheat’. A collaboration with the University of Nottingham will enable the student to visit the lab of Julie King and gain hands-on experience on wheat genetic manipulation. We are looking for an applicant who is curious to understand the fundamental biology behind a key technology in the modern breeding process.