Characterising the genes responsible for segregation distortion in wheat

Supervisory team:
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Project description:
Food security relies on the development of new varieties, with increased yield and/or increased resistance to biotic and abiotic stress. However, commercial breeding is a numbers game, the more progeny generated the greater the chance the breeder has of generating that rare future elite variety. Like the breeders of all commercial species, the efforts of wheat breeders are confounded by a phenomenon referred to as segregation distortion (SD). SD commonly occurs in mapping populations and is thought to occur due to the favourable transmission or selection of specific alleles during either meiosis or the subsequent selection of seed/seedlings via, for instance their growth characteristics. Unfortunately SD interferes with the breeding process as certain regions of the genome are either over or under represented in the progeny. The under or over representation of specific alleles means that more progeny than expected are required to be generated, resulting in wasted resources. Interestingly, SD also interferes with the construction of genetic maps and as a consequence markers showing distortion are often removed from the mapping process. As such understanding the genes that underpin SD is a neglected area but one that is of critical importance in the breeding process.

In this four year project you will work with the cereal functional genomics group at Bristol to characterise and clone regions of the wheat genome involved in SD. The Bristol group leads the world in wheat molecular marker technology and as such you will utilise the latest techniques such as high throughput genotyping, next generation sequencing and various bioinformatical procedures to characterise genomic regions identified in a number of wheat mapping populations. In addition, during your project you will have ample opportunity to interact with, and possibly influence the activities of, a range of international wheat breeders.