

BBSRC Research Experience Placement Studentship

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| Title of Project | Genetics of wheat blast resistance |
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Wheat blast is a destructive disease of wheat in Brazil and other countries of South America. In 2016, it appeared in Bangladesh causing devastation, and the following year it spread to India. The major wheat belts of India and China have warm, wet climates that enable proliferation of this disease making it a potential threat to food security in this region.

The causal agent of wheat blast is the fungus *Magnaporthe oryzae* pathovar *tritici* (to differentiate it from the type causing rice blast – also a devastating disease). Both the rice and wheat pathovars exhibit a ‘race structure’, i.e. they can infect some varieties while others remain resistant. Whether a particular wheat or rice cultivar is resistant depends on the race attacking it. Many (but not all) resistance genes in rice have been shown to encode NLR intracellular immune receptors. We have demonstrated that the same situation exists in wheat (given the race structure of the *tritici* pathovar).

We have a set of contemporary strains of the wheat blast pathogen and have developed high throughput seedling and detached head-based wheat blast assays. We have a configured diversity panel of the D genome donor to wheat (*Triticum tauschii*) which we have shown to contain functional wheat blast NLR resistance genes.

Our close collaborators have previously developed NLR resistance gene enrichment sequencing (RenSeq) to selectively sequence the NLR repertoire of the wheat genome, thus reducing the cost and computational challenge of scrutinizing the ~2600 NLRs in wheat. Very recently, they coupled RenSeq to association genetics on a diversity panel of the wild diploid wheat *Triticum tauschii*. The resulting application, AgRenSeq, allowed them to discover and clone, in a matter of months, three stem rust resistance genes.

Using the AgRenSeq analytical pipeline we have identified several resistance genes that function against individual strains of wheat blast.

The wild ancestors of domesticated wheat (such as *T. tauschii*) represent a rich source of genetic variation with huge potential for improving disease resistance. Deploying this genetic diversity into elite, cultivated wheat by traditional breeding takes many years for just a single resistance gene. However, using the AgRenSeq pipeline enables the rapid acceleration of breeding by producing so-called ‘perfect’ markers for use in marker-assisted selection programmes. Most importantly, perfect markers allow breeders to combine resistances to maintain durability of disease resistance and avoid the boom-bust cycles of the past

This project will involve the screening of the *T. tauschii* diversity panel with a new isolate of wheat blast to identify NLR genes conferring resistance against this isolate. The project will involve a broad range of techniques including microbiology, plant production and pathology experiments and bioinformatics analysis.

The project addresses the BBSRC priority area of Food Security.