Yueqi Zhang

Biography

Yueqi obtained her Bachelor of Biotechnology with first class Honours degree at the Australian National University. She joined the multi-national biotechnology company Epoch Life Science (USA) subsidiary Taihe Biotech (Beijing) Corp. Ltd and made contributions to international endeavours on crop improvement, medical research and environmentally friendly chemical productions. She has been a PhD student in the Batley lab since October 2017 researching the identification and characterisation of resistance genes in canola against blackleg disease using a wide range of genetic, transcriptomic, genomic, flow cytometry and microscopy technologies.

Research Interests

Crop genetics and genomics, Disease resistance genes, Plant-pathogen interactions, Chromosomal flow cytometry and Microscopy

Current Projects

**Identification of qualitative disease resistance genes in canola against blackleg**

**Evolutionary and comparative analysis on gene relatives of qualitative disease resistance genes**

**Development of genetic markers for the identified qualitative disease resistance gene for durable management**

**Development of protocol for isolating single chromosomes in canola for sequencing**

**Summary**

The Brassica genus contains many agriculturally important oilseed crops and vegetables. Canola (*Brassica napus*) is one of the most important oilseed crops worldwide. Canola production in Australia, Europe and North America is threatened by blackleg disease, caused by the fungal pathogen *Leptosphaeria maculans*. The deployment of qualitative disease resistance genes is the most effective and sustainable approach in controlling the disease. Identification and cloning of qualitative resistance gene candidates is therefore crucial for understanding the gene-for-gene interactions in the pathosystem which will facilitate sustainable management of the disease. Efforts in building multiple genome assemblies of *B. napus* and its progenitors *B. rapa* and *B. oleracea*, coupled with genome-wide prediction of resistance gene analogs in several *B. napus* assemblies, have greatly facilitated the identification of candidate genes that are associated with disease resistance phenotypes. The aim of this research was to identify and characterise a cluster of qualitative resistance genes, *Rlm3-Rlm4-Rlm7-Rlm9*, located on *B. napus* chromosome A07. Firstly, strong candidates for *Rlm3, Rlm4* and *Rlm7*, located within the candidate regions defined by published genetic markers, were identified through sequence comparison of resistance gene analogs between resistant and susceptible cultivars obtained from Nanopore, next generation sequencing and Sanger sequencing approaches. Secondly, the gene relatives for *Rlm3, Rlm4, Rlm7* and *Rlm9* at syntenic genomic regions in two *B. rapa*, two *B. oleracea* and eight *B. napus* assemblies were identified and compared, to provide insights on the evolution and functions of the genes. Domains and amino acids that are related to the interactions with the corresponding virulence proteins were characterised. Thirdly, PCR screening markers were designed to target unique sequences in the candidate *Rlm3*, candidate *Rlm4*, candidate *Rlm7* and *Rlm9* genes, in order to develop reliable, high-throughput genetic screening markers to complement phenotypic screening. All current and past Australian commercial cultivars were screened with the markers and their blackleg resistance gene complement was identified. Lastly, we aimed to establish a protocol for flow sorting single chromosomes for canola, in order to characterise genetic variations on a specific chromosome of interest in diverse Brassica germplasm and Brassica wild relatives. The highest mitotic index and metaphase index were achieved for the first time in canola. However, persistent issues of metaphase chromosome clumps hindered the flow sorting of single chromosomes, which needs to be overcome as technologies advance.

**Why my research is important**

The identification of the qualitative resistance genes, and molecular and evolutionary characterisation of the gene families, and genetic screening markers have laid the foundation for a revolutionary understanding on the blackleg pathosystem as well as informing more durable management of the precious limited resistance resources worldwide. The first single chromosome isolation protocol in canola paved the way for chromosome genomics in Brassica crops which would facilitate ongoing crop improvements given predicted global population growth and climate change.

Publications

**Yueqi Zhang**, David Edwards & Jacqueline Batley. 2020. Comparison and evolutionary analysis *Brassica* Nucleotide Binding Site Leucine Rich Repeat (NLR) genes and importance for disease resistance breeding. The Plant Genome, pp. e20060-e20060. <https://acsess.onlinelibrary.wiley.com/doi/full/10.1002/tpg2.20060>

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**Yueqi Zhang**, William Thomas, David Edwards & Jacqueline Batley. 2020. Frontiers in dissecting and managing *Brassica* diseases: from SNP based genome wide association with RGA gene repertoires to building pan-RGAomes, The International Journal of Molecular Sciences, , vol 21, no. 23, pp.8964. <https://www.mdpi.com/1422-0067/21/23/8964>

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Anna Nowicka, Martin Kovacik, Barbara Tokarz, Jan Vrana, **Yueqi Zhang**, Dorota Weigt, Jaroslav Doležel & Ales Pecinka. 2020. Dynamics of endoreduplication in developing barley seeds. Journal of Experimental Botany, vol 72, pp 268-282. <https://academic.oup.com/jxb/article-abstract/72/2/268/5917133>

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