

Genetic resistance to fungal diseases of barley



Project description

Net and spot forms of net blotch are globally significant diseases that are widespread across Australia. With a predisposition to overcoming fungicide controls, these diseases have become challenging to manage as most barley cultivars are susceptible to either one or, more often, both forms of net blotch.

The primary objective of this project is characterising new resistance genes in barley from diverse germplasm as well as through mutagenesis. In addition, our researchers seek to understand their mode of action, the host-pathogen genetic interactions, and pathotype specificity. This will guide how best to deploy new resistance genes and assist breeders in improving cultivar performance and reducing control costs for growers.



Key achievements

To inform screens for resistance, our team monitors the current disease populations for changes in population structure, genetic diversity, and virulence both in Australia and internationally.

Our team have identified barley landraces with good levels of resistance to both net and spot forms of net blotch. Large doubled haploid barley populations combined with genotyping-by-sequencing is used to locate resistance genes.

We have expertise in complementary techniques for investigating host resistance including gene expression, proteomics and cytology.

Our group has an established record in pathogen genomics, as well as developing transformation protocols that are invaluable for studying disease virulence and corresponding resistance genes.

Our team

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