Fungicide resistance characterisation and monitoring



Project description

As fungicide resistance continues to emerge in Australia, our researchers are working to monitor its spread and enhance our understanding of the underlying mechanisms of fungicide resistance. By building on previous research, our team aims to produce better, faster, and more affordable methods of monitoring this issue and continue to develop new ways to characterise the resistance and assess potential genes involved in fungi acting as inhibition targets.

This improved understanding of fungicide resistance hopes to arm the industry with targeted response capacity and improved management advice for growers.







Our team

Leader:

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Key achievements

We responded rapidly to a recent wheat powdery mildew outbreak, by working with agronomists and pathologists to identify Qol (Quinone outside Inhibitors, Group 11) fungicide resistance and DMI (Demethylase Inhibitors, Group 3) fungicide resistance in regions of South Australia, Victoria, NSW and Queensland. Mutations associated with resistance to DMIs were found to be widespread across all monitored regions. Mutations associated with resistance to Qols were also detected in all regions, including Oueensland where it has not been identified until now.

For net form net blotch, we characterised the genomic region where target gene Cyp51A1 duplications occurred, and discovered that Cyp51A1 is in a highly dynamic repeat-rich sub-telomeric region of the *Pyrenophora teres f. teres* genome. This finding will help improve the accuracy of effective monitoring of populations carrying this resistance mechanism.

We identified many fungicide resistance mechanisms over past few years. We used this information to develop phenotypic and molecular quantification tools for the screening of field samples, in-field resistance analysis, and to release resistance management advice on the use of DMI, SDHI and Qol fungicides across the Australian grains industry.







