Plant physiological responses to fungal diseases

Centre for Crop and Disease Management

GRDC GRAINS RESEARCH & DEVELOPMENT CORPORATION

Curtin University

Project description

We have well-established techniques to visualise the movement of a fungal pathogen within plant tissues. We also have improved our ability to characterise host resistance and susceptibility genes that are key to disease resistance. However, we are still building the foundation knowledge to define the spatially resolved molecular interactions between host and pathogen and impact on plant physiology at the point of infection, tissue recovery post-disease disruption and plant's ability to tolerate disease pressure.

To address this we are applying phenotyping, "omic" and novel data analytic approaches to resolve complex traits pertaining to disease tolerance and tissue recovery. Continued exploration of the physiological responses in infected crops aims to unlock new knowledge for breeders develop crops with increased performance.

Our team

Project Lead:
Fatima Naim
fatima.naim@curtin.edu.au
@FatiNaim
Google Scholar

Researchers:
Mark Gibberd
Lilian Sanglard

Students:
Meg Willans
Yutathkarn Coles
Jade Davis
Ciara Gifford

Key achievements

We have leveraged off new skills and in-house expertise to develop a suite of novel tools and techniques and collaborations to enable investigation of physiological responses of crops to diseases pre- and post-fungicide treatment in wheat. The collaborations include the NCRIS-funded facility, the Australian Synchrotron with competitive funding that enabled the use of highly sought X-ray fluorescence microscopy (XFM) and Infrared microscopy (IRM) beamlines, opening new horizons to understanding plant diseases.

Our high-resolution nutrient mapping of infected leaves is the first reported use of the synchrotron based XFM instrument to study the physiological impacts of plant diseases. The XFM and IRM imaging datasets have enabled studies of nutrient re-distribution in diseased leaves. This work has added another layer of investigation to characterise complex traits, and optimisation of these experiments has provided our team with meaningful data that can be applied to various other studies.

We have applied rigorous experimental design, phenotyping and gene expression analyses to define the impact of fungal pathogen on the green asymptomatic region surrounding diseased symptomatic region. A combination of microscopy and transcriptomic data was used to show that Ca is uniquely manipulated by fungal pathogen, leaving the disease susceptible and wheat desensitised to further attacks.