

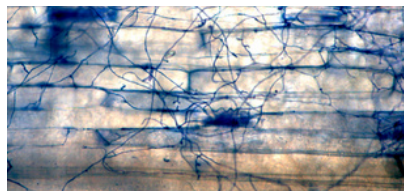
Effector and co-infection biology

Project description

Breeding for fungal disease resistance in wheat can be difficult due to co-infecting pathogens and variations in fungal effector gene properties. These factors allow fungal pathogens to rapidly overcome host disease resistance.

Parastagonospora nodorum and *Pyrenophora tritici-repentis* are fungal pathogens that cause septoria nodorum blotch (SNB) and yellow spot (YS) of wheat, respectively. We are developing methods to quantify and discriminate these pathogens in the SNB-YS disease complex and identifying genes that dictate these co-infection dynamics. We are also using pull-down methods to identify signal transduction pathway components that are associated with effector regulation in *P. nodorum*. In addition, we have projects on understanding the role of epigenetic regulation in the pathogenicity *P. nodorum* on wheat, identification of powdery mildew resistance in wheat and proteomic analysis of the dieback pathogen *Phytophthora cinnamomi*.

Revealing new aspects of pathogen interaction and effector biology can open avenues for the improvement of existing disease control strategies being used by growers.



Our team

Project Lead:

Kar-Chun Tan

 kar-chun.tan@curtin.edu.au

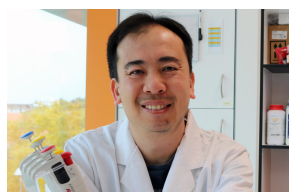
 [@karchuntan](https://twitter.com/karchuntan)

 [Google Scholar](#)

Researchers:

Callum Verdonk

Leon Lenzo



Students:

Shota Morikawa

Ancy Tony

Anjana Sharma

Key achievements

We have identified several 'molecular switches' that turn effector genes on and off in *P. nodorum* and *P. tritici-repentis*. The significance of this is that we can use the knowledge to look for novel effector and pathogenicity genes controlled by these 'switches'.

Our recent study on effector epistasis in septoria nodorum blotch (SNB) of wheat ([DOI: 10.1371/journal.ppat.1010149](https://doi.org/10.1371/journal.ppat.1010149)) recommended to breeders that the effector sensitivity *Snn1* gene be removed to further improve SNB resistance in Australian wheat.

We have developed a sensitive and reference-free fungal biomass quantification assay to 1. Rapidly discriminate and quantify the contribution of *P. nodorum* and *Ptr* on field-infected wheat and 2. Determine that a major effector gene in *P. nodorum* exhibits both 'selfish' and 'altruistic' characteristics during strain versus strain co-infection.

