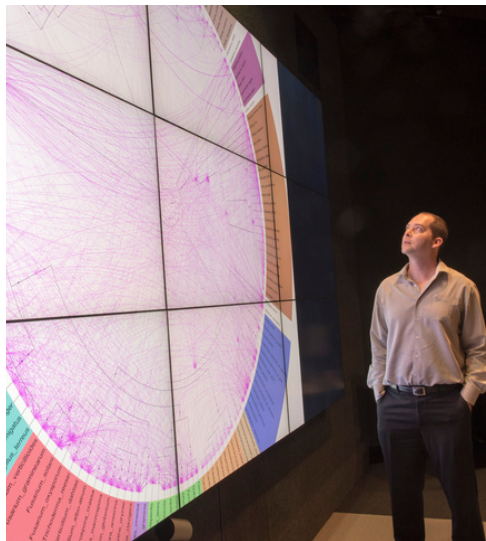
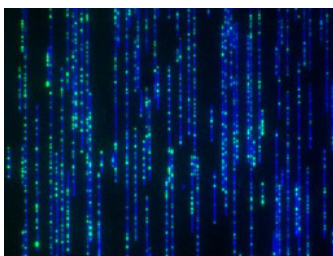
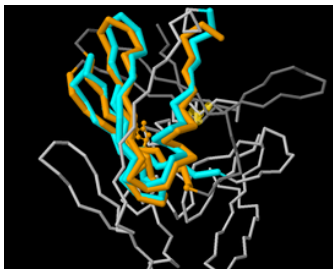


Advanced bioinformatic approaches

Project description

Molecular plant pathology has been intrinsically linked with genomics and bioinformatics since the mid-2000s, beginning with the establishment of genomic resources for key pathogen species.

Our bioinformatic specialists will focus on improving effector prediction and exploring applications of novel informatics to breeding for biotic stress, providing improvements to breeders for disease resistance and genomic selection experiments. The project will also look at developing a pan-genomic pathogenicity screening toolkit to profile disease risk and screen for effector profiles and fungicide resistance across regional populations in Australia.



Key achievements

Challenging an established dogma of plant pathology, a new data-driven method for predicting pathogen trophic types (whether they are biotrophs feeding off living cells, necrotrophs that kill host cells, or other types) from basic fungal genome data was developed ([DOI:10.3389/fmicb.2019.03088](https://doi.org/10.3389/fmicb.2019.03088)). Through this study, the team has proposed a rethink of traditional trophic classifications based on their new method.

Development of several new methods for improved prediction of fungal effectors: Predector for gene properties ([DOI:10.1038/s41598-021-99363-0](https://doi.org/10.1038/s41598-021-99363-0)), RemEff for predicting structural homology with known effectors ([DOI:10.1099/mgen.0.000637](https://doi.org/10.1099/mgen.0.000637)) and other 3D protein structure-based methods ([DOI:10.3390/ijms24076262](https://doi.org/10.3390/ijms24076262); [DOI:10.1007/s12033-023-00703-4](https://doi.org/10.1007/s12033-023-00703-4)). With effectors being proteins secreted by plant pathogens that help them to infect specific plant host species or varieties, this information can be used to counter their disease impact through molecular diagnostics or to enhance breeding for disease resistance.

Our team

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New pan-genome-based approaches for analysing virulence and fungicide-resistance data across large populations and regions are being developed which may enable new and information-rich ways to monitor the incidence of spread of disease sub-types and provide region-specific disease management support.

