RESEARCHER PROFILE

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RESEARCH AREA

Genetic composition of fungal pathogens that are harming cotton

Tell us a bit about yourself?

I was born and raised in a mountainous town of Greece. After my bachelor studies in the city of Thessaloniki, I moved abroad (to Europe and Australia) in order to study the genetics of pathogenic microorganisms including plant pathogenic fungi.

What research have you previously been involved with?

Biology was my primary area of interest starting as a university student. Having studied virology during my Master's degree and fungal plant pathogens for many years during my PhD, I have always worked on the microorganism/fungal genetic diversity, plant-pathogen interactions, and migration patterns of such fungi across plant hosts and populations. Most recently, I had been working with the powdery mildew causal agents of some grasses like wheat, and other crops.

What excites you about working in the Australian cotton industry?

Understanding more about the cotton fungal pathogens as cotton is a widely grown crop, used in many parts of Australia, across various states, climates and geographic regions, would be an incredible privilege. Thus, it is very exciting to collaborate with cotton farmers and pathologists in order to gain insight into the epidemiology and impact of these fungal pathogens on cotton and be able to help them with more resources for these pathogens to understand fungicide resistance and virulence patterns, supporting more informed choices.

What do you like to do when you're not researching?

Usually, I enjoy being creative by either writing fiction, singing, or watching films, while on occasions I like to appreciate nature, by exploring my surroundings, swimming in the sea or just lying on the ground.

PROJECT OVERVIEW

ACDC Project B1.3: Monitoring pathogen genetic diversity and B1.4: Reference genome for cotton pathogens

Explain your current research project

We are currently working to better understand the genetic composition of fungal pathogens that are harming cotton; either species with higher impact (Tier 1) or emerging ones (Tier 2).

Why is it important?

Genomic tools and resources play a key role in understanding how important and emerging pathogens evolve in order to try and predict how, when and where they could become a bigger problem in the near future, reducing the risk of an upcoming epidemic. Furthermore, genomic resources can lead to quick development of markers for molecular diagnostics that may identify virulent ('aggressive') strains of these fungi in order to understand the gravity of their impact. Using this information, we can also better comprehend the mechanics of pathogen resistance to fungicides.

What does your current project aim to do?

One project aims at creating reference genomic resources for Australian fungal isolates for important (Tier 1) and emerging (Tier 2) pathogens. Moreover, the objective of another project is to use fungal populations and their genetics in order to understand their genomic composition, diversity and potential impact, while also identify genes of interest (e.g. fungicide resistance or virulence related genes).

What does it involve?

Firstly, it involves the use of one or a couple of fungal isolates per species of importance to create higher quality Australian reference genomes, and then, multiple isolates per region to create population genomic datasets. This can be achieved with the help of the ACDC collection of fungal isolates by isolating samples of interest. Then, extraction of their DNA and outsourcing for DNA sequencing will produce genomic data that will be crucial in studying their genomes. Finally, extensive bioinformatic analyses will take place using computer software and manual data processing to study and compare these genomes, populations and species.

How will this work benefit Australian cotton growers and industry?

These projects can have numerous results with multiple benefits. Pathologists will be able to better identify and characterize fungal species and virulent strains. Additionally, identification of fungal isolates (and populations) that are more virulent and have specific genes that make them infect specific varieties could better inform farmers on the choice of certain varieties or rotation crops used in their fields/regions. Similarly, understanding genes of fungicide resistance, could help with a better use of fungicides.

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