TRAVEL, CONFERENCE or SCIENTIFIC EXCHANGE REPORT 2018

Part 1 - Summary Details

Please use your TAB key to complete Parts 1 & 2.

CRDC Project Number: RRDP1723

Project Title: Managing *Verticillium* risk for cotton

Project Commencement Date: 14/07/1 **Project Completion Date: 06/08/18**

CRDC Research Program: Industry

Part 2 – Contact Details

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Part 3 – Travel, Conference or Scientific Exchange Report

(Maximum two pages)

1. A brief description of the purpose of the travel.

The purpose of travel was to attend and present posters at two international conferences, the International Mycological Congress 11 (IMC 11) and the International Congress of Plant Pathology 2018 (ICPP 2018), and to do a lab exchange in Dr Libo Shan's lab at Texas A&M university.

2. What were the:

a) major findings and outcomes

The first week was spent attending IMC11 In San Juan Puerto Rico, a conference focused on all aspects of mycology. There were quite a few talks relevant to my work, particularly those that examined taxonomy and evolution. Some highly interesting symposia I attended included "evolutionary genomics" and "integrative approaches to understand the ecology and evolution of fungi". Notable talks in these symposia were on codon bias and gene flow, which are features that can be examined when looking at genomes within populations, and methods or suggestions on the best ways to examine these features – useful as I am examining genomes. Another symposia, "Metagenomics: Whole fungal genomes from complex samples", included a talk on using nanopore MinION longread sequences. This was especially interesting as this is the method that I have been using for my genome sequences, so I could compare and contrast which programs he used for assembling and annotating genomes. Following this talk was a presentation on a program called Scgid. Scgid is software designed to sort and identify sequences belonging to different isolates from a mixed sample. Although it is probably not specific enough yet to identify different isolates within the species level, programs like this could be useful for getting an idea of the diversity of microbes within a soil sample. As the costs of sequencing continue to fall sequencing farm soil samples will become more common. The presenter of this talk indicated that although it currently works quite well they are continuing to work on improving Scgid, so this could be some software to keep in mind for the future.

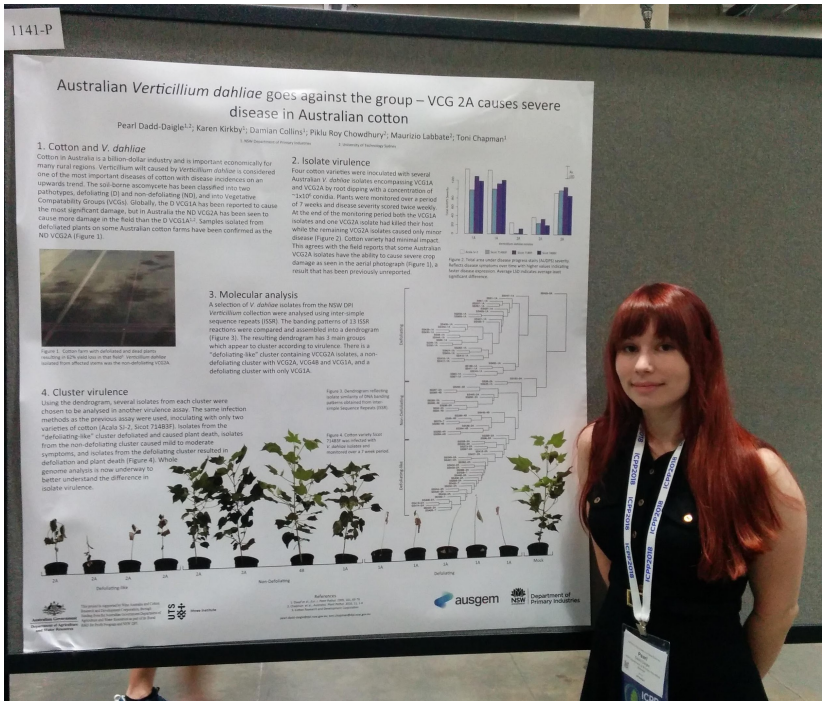
There was also an interesting comment at the end of one of the keynote talks. Dr Priscilla Chaverri gave a talk on the evolution of protective mutualism in plant-fungal endosymbiosis, and when giving examples at the end of her talk mentioned that commercial endophytes have been shown to reduce fusarium growth when applied to crops. This could be an interesting area to explore in regards to not only *fusarium*, but *V. dahliae* and cotton. The great symposia continued with talks on fungal pan-genomes. These included many useful suggestions for programs and pipelines to follow when examining common features like chromosomes, and secondary metabolites in pan-genomes, as well as recommendations for how to filter sequences to get the most accurate gene predictions. My poster presentation was well received and I had many people ask me to explain my research in more detail. Overall this was a great conference and well worth attending particularly for the amount of information I gathered on the many tools and techniques to use when analysing fungal genomes and populations.

The following week I went to Texas A&M university in College Station to visit Dr Libo Shan's laboratory. I was given a tour of the building by Kevin Cox, a PhD student in the lab studying bacterial blight of cotton. He showed me around the numerous growth chambers, indoor glasshouses and laboratory facilities they had there, and introduced me to the many people working in the lab. Fortunately for me Dr Terry Wheeler had sent several *V. dahliae* isolates taken from American cotton plants with defoliating symptoms to Dr Shan's lab. Using materials that were graciously provided by Dr Shan I was able to spend my time in the lab extracting DNA from these isolates and run a PCR to confirm that the extractions had worked properly. I have brought this DNA back from Texas to be included in my molecular work to see how Australian isolates compare to the American isolates. Not only was it great being able to extract this DNA, but it was interesting to see how different labs perform standard experiments. Never before had I seen an agarose gel poured just onto a small

glass sheet. It seemed quite useful though as it dried almost instantly and used a lot less agarose than the gels we make, perhaps a method to use in our lab.

The final week was in Boston for ICPP 2018, a conference all about plant pathology. During this conference I shared a room with Shelby Young, a masters students from Texas who I met previously when she was in Narrabri working with Dr Karen Kirkby. ICPP 2018 was another interesting conference with symposia on interactions between endophytes and pathogens and microbial interactions and resilience for plant health. One particularly good talk in these sessions was by Professor Greg Sword looking at beneficial fungal endophytes in cotton. He has found that not only do fungal endophytes help improve drought resistance in cotton, they also help to increase plant defense responses to insects. A second interesting talk was looking at the populations of *V. dahliae* in potatoes, with emphasis on asymptomtic groups. They found that asymptomatic *V. dahliae* clusters in VCG 4B and that other crops used for rotation act as reservoirs for these 4B isolates. They are going to be looking into using these asymptomatic isolates as endophytes to take up the niche that the pathogenic varieties would otherwise invade. It was also interesting listening to talks on remote sensing. The photographic capability of drones to take extremely high resolution images of farms and the accompanying software to identify plant diseases from these photos was very impressive.

There were also some good genetics talks at this conference as well. The sequence-based taxonomy for plant pathogens symposium included a talk that focused on the importance of sequencing individual isolates not just environmental samples, as you can't understand the "big data" if you don't have the information about many of the organisms that would be sequenced in an environmental sample. Other talks looked at how horizontal gene transfer drives evolution of pathogencity by the uptake of virulence plasmids, and another the best way to approach fungal taxonomy arguing that using the "RDP classifier" is much better than ITS of fungal LSU regions. I found that presenting my poster at this conference was useful as I had people suggest several areas to look at. One person suggested I look into the nematode *Pratylenchus penetrans* as it has been shown to increase *Verticillium* susceptibility of host plants, and another person suggested that maybe I should see whether any mycoviruses are helping to drive *V. dahliae* virulence. Again, this conference was very useful to attend as I was able to learn a lot of new information about plant pathology and can apply this to my own work.



b) other highlights

Aside from the knowledge gained at these conferences and the lab exchange, the most important thing was probably the connections made. At IMC11 I made several friends based in different laboratories in America. Denny Wang is based in Wisconsin and is studying population genetics. He suggested useful websites that have free workshops to help me learn certain tools for the analysis of my genomes and has kindly offered to assist me if I have any questions. David studies in California and works on *Fusarium* and *Verticillium* in cotton. He is a useful person to know as he may be able to assist with future molecular analysis of American *V. dahliae* if we have any further questions sparked from the DNA I have brought back. We now also have improved relationships with the people at Texas A&M and could potentially work on a collaborative project in future. At ICPP 2018 I was able to strengthen my relationship with Shelby Young and she will collaborate on a paper that I am in the process of writing. Shelby was also able to introduce me to many students that she knew through the American Phytopathological Society. I was also able to meet with Dr Robert Nichols from Cotton Inc. Shelby and I went to lunch with him where we had the opportunity to discuss our projects and further the relationship with Cotton Inc. I also made several friends with people who work in indirectly related fields such as José García who studies potatoes in West Virginia. As potatoes are a host for *V. dahliae* he could be a useful connection if we want to branch out into looking at the connection between *V. dahliae* and its virulence on different plants to better understand the pathogen.

Please email your report 30 days after travel/conference to: research@crdc.com.au