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Resolution of disease epidemiology and detection of genetic and genotypic diversity in Australian populations of myrtle rust

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Progress Report (PBSF018)

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1. Executive Summary

This project aims to catalyse the development of diagnostic resources to distinguish different strains of myrtle rust, and to determine whether sexual reproduction has occurred in the population of myrtle rust in Australia. We have completed the first milestone of the project, to provide DNA from the South African strain of myrtle rust to researchers in the United States. We have progressed the second aim by testing whole genome amplification kits on single rust pustules (successfully), collection of pustules and signing a contract with the Australian Genome Research Facility. We have provided new knowledge to the scientific community as a result of PBSF funding, published in the European Journal of Plant Pathology (https://doi.org/10.1007/s10658-019-01903-y).

2. Introduction

A **very high priority** in the Myrtle Rust Action Plan is to prevent arrival of new strains of *Austropuccinia psidii* (Objective 5.1). Our collaborators in the United States, led by Ned Klopfenstein, are developing much-needed, high-throughput sequencing tools to distinguish strains of myrtle rust.

A **high priority** in the Myrtle Rust Action Plan is to monitor the population of *Austropuccinia psidii* in Australia for changes (Objective 5.3). These changes can arise from either introduction of new genetic diversity (incursions of new strains), or by mutation and sexual reproduction in the current genotype (currently considered clonal in Australia).

3. Aim

1. Foster collaborations between researchers from Australia, the USDA (United States of America), Scion (New Zealand) and FABI (South Africa), and provide DNA of *Austropuccinia psidii* from South Africa to determine genetic loci that distinguish strains of myrtle rust.
2. Determine the disease cycle of *A. psidii* in Australia through study of sexual reproduction.

4. Methods/Process

1. Extract genomic DNA from South Africa and send to the USDA team (Obj1).
2. Test efficacy of whole-genome-amplification kits to amplify DNA from single pustules (Obj2).
3. Amplify single pustules collected over three years for genotyping by sequencing (Obj2).
4. Test for evidence of recombination or clonality to determine disease cycle and epidemiology (Obj2).

5. Achievements, Impacts and Outcomes

The first objective is partially complete, with provision of DNA of the South African strain to our collaborators in the United States, confirmed on the 5th of August 2020 (milestone 1).

We published a paper in the course of our research on sexual reproduction of myrtle rust in New Zealand and South Africa (https://doi.org/10.1007/s10658-019-01903-y). This research supports our hypothesis that myrtle rust will reproduce sexually in Australia, and changes an assumption in the community that *A. psidii* is clonal in invasive populations.

We have collected most of the pustules needed for our analysis of ~200 individuals from the Tallebudgera valley. Sampling will finish in the next few months. Our colleagues in New Zealand have successfully tested whether whole genome amplification can be used on single pustules of myrtle rust. Based on their knowledge,

we have ordered amplification kits, and signed a contract with AGRF to use genotyping by sequencing for our population study. We expect to have genotypic data before the end of the year to resolve whether sexual reproduction occurs in Australia.

6. Discussion and Conclusion

7. Recommendations

9. Appendices, References, Publications

McTaggart AR, du Plessis E, Roux J, Barnes I, Fraser S, Granados GM, Ho W, Shuey LS, Drenth A. 2020. Sexual reproduction in populations of *Austropuccinia psidii*. European Journal of Plant Pathology 156: 537–545.

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