Project 3.4b – Project Executive Summary

Comparative genomics of Puccinia psidii

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A comparative genomics approach is being used to examine strains of *Puccinia psidii* that differ in host range. A specimen from *Psidium guajava*, collected from the same location as the type specimen, has been designated as an epitype and a strain established from it. Urediniospores have been multiplied and DNA extracted and sent to the Australian Genomic Research Facility for Illumina sequencing. Additional strains were made from collections from *Psidium guineense*, *Eugenia uniflora*, *Eucalyptus grandis* and *Eucalyptus grandis* x *E. urophylla*, DNA extracted and sent for sequencing. Sequences will be aligned to the myrtle rust genome sequenced by Tan et al, and additional mate pair libraries from Australian strains will be sequenced to improve the assembly.

The Final Report for this project is not available as manuscripts describing this work are in preparation. For further information, please contact Lead Researcher Dr Morag Glen Morag.Glen@utas.edu.au