

## **Genome-wide association study of myrtle rust (*Austropuccinia psidii*) resistance in *Eucalyptus obliqua* (subgenus *Eucalyptus*)**

### **ABSTRACT**

Myrtle rust (caused by *Austropuccinia psidii* Beenken) is exotic to Australia, yet specific resistance is present in a range of naïve myrtaceous host plants. Resistance to myrtle rust is primarily quantitative in nature and controlled by multiple interacting loci. We undertook a genome-wide association study (GWAS) to discover relationships between nuclear genomic sequence variation and multiple aspects of resistance to *A. psidii* in *Eucalyptus obliqua*, a representative species from subgenus *Eucalyptus*. Sequence variation was assessed with respect to numeric severity, binary symptomatic, hypersensitive, and pustulation responses to inoculation of seedlings with *A. psidii*. A total of 1.13 million, single-nucleotide polymorphisms (SNPs) were tested for association with the rust resistance responses of 637 phenotyped *E. obliqua* seedlings, each from different, single mother tree seedlots. Thirty-three highly significant SNP-trait associations were detected, of which 26 associated with the binary symptomatic/asymptomatic response to *A. psidii*. Comparison of the genomic position of these SNPs with rust resistance loci (Ppr1-5), previously reported in species from subgenus *Symphyomyrtus*, suggested that several were positioned near the major Ppr1 locus and other Ppr loci. This study provides the first integrated genomic view of *A. psidii* resistance across the *Eucalyptus* subgenera and provides the foundation for discovering key resistance genes for use in marker-based resistance breeding.