



## W287

## Increase In Efficiency Of Genomic Selection Using Epistatic Interactions and Detection Of Candidate Genes For Rust Resistance In Eucalyptus

Date: Sunday, January 13, 2013

Time: 10:40 AM

Room: Sunrise

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The Rust disease caused by *Puccinia psidii* has a broad hosts range in the *Myrtaceae* family and is one of the main diseases in Eucalyptus plantations. Furthermore, the fungi has recently invaded Australia, imposing a significant risk to the native Australian ecosystem which has the *Myrtaceae* as the country's dominant plant family. Given the long generation cycle of a tree-breeding program, genomic tools such as Genomic Selection (GS) can accelerate the development of resistant or tolerant trees and potentially identify candidate genes involved in the genetic defense mechanism. We applied a novel joint approach of defining GS models for phenotype prediction and detecting regions that contain candidate genes underlying resistance. We used a hybrid *Eucalyptus* population of 476 individuals from 56 families. The GS model was fit under a hierarchical Bayesian approach with 2733 DArT markers that were physically mapped onto the *Eucalyptus* genome and predicted 44% of the disease phenotype (78% of the breeding value). Three regions on pseudo-chromosome 3 and one region on pseudo-chromosome 8 were detected as candidates from an association analysis and explained respectively 11%, 8%, 1.2% and 4% of the phenotypic variation. The association was further validated in BAMD (Bayesian Association with Missing Data) software correcting for family structure. When a new genotypic file was created based on the pairwise interaction of the most significant candidates with all the other markers, the GS model was enhanced in 27%. We hypothesize that this increase is due to epistatic effects and the contribution of genes that were not detected in the additive model.

[Back to: Forest Tree](#)

[<< Previous Abstract](#) | [Next Abstract >>](#)

[Home/Search](#)

[Browse by Day](#)

[Browse by Type](#)

[Author Index](#)

[Exhibitor Index](#)

[Poster Categories](#)

[Personal Scheduler](#)

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