



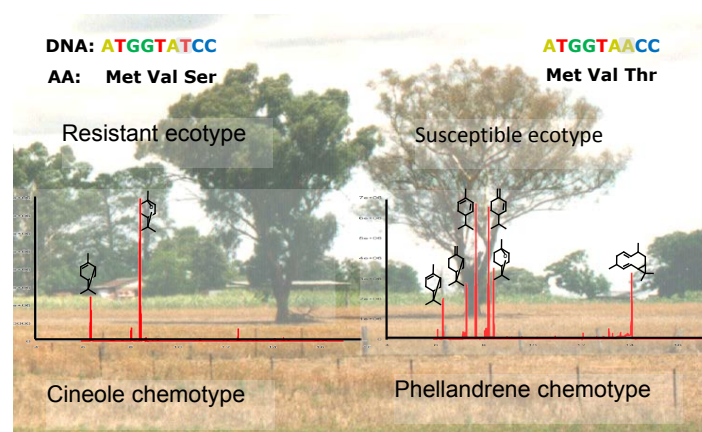
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Genetic control of quantitative and qualitative variation of plant secondary metabolites in Australian Myrtaceae

Thursday 17 October 2013 1pm

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Gould Seminar Room (Rm 235) Gould Building (Bldg. 116), Linnaeus Way, ANU



Variations in plant secondary metabolites (PSMs) have profound influence in mediating the interactions between plants and animals. The variation within a species can occur on a number of scales including qualitative variation within a single tree canopy (mosaic trees), or between neighbouring trees and quantitative variation across the landscape. How this variation arises and is maintained has been of wide interest to ecologists and to date, most research has focused on resource availability via environmental variation.

However, the heritability of variation in some

PSMs is high ($h^2 > 0.7$) suggesting that genetic control of variation is significant. Here I describe a number of studies that elucidate the genes that underlie some of this variation.

Variation in the qualitative profile of foliar terpenes in both *Eucalyptus* and *Melaleuca* is due to genomic presence/absence patterns and/or transcriptomic control of a large gene family (113 members in *Eucalyptus grandis*) called terpene synthases. These genes encode enzymes that use common intermediates (geranyl pyrophosphate or farnesyl pyrophosphate) to produce a large variety of mono- and sesquiterpenes, which have profound effects on plant-herbivore interactions. Quantitative variation in terpenes in *Eucalyptus globulus*, *E. loxophleba* and *Melaleuca alternifolia* is partly due to single nucleotide polymorphisms in genes of the terpene biosynthetic pathway. Although as expected, each polymorphism explains only a small amount of phenotypic variation. Low levels of linkage disequilibrium in outcrossing forest trees limit the opportunities for genome-wide association studies for now, but identifying transcriptional regulators that control biosynthetic pathways of PSMs remains a high priority. These studies are the first to unravel the molecular basis of quantitative variations in ecologically important traits in Australian Myrtaceae.

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