Honours project at the University of Tasmania, Hobart

Comparative genomic analysis of flowering-related genes in eucalypts

Flowering time is an important transition involving complex genetic pathways mainly characterised in annual plants. Genes in these pathways have been identified in the *Eucalyptus grandis* genome but comparative studies among phylogenetically divergent eucalypts will provide novel insights into the evolution of diverse developmental responses in this important group.

In collaboration with researchers at Southern Cross University (Lismore), this project will capitalise on the recently constructed genome sequence in the eucalypt genus *Corymbia*. Gene family / comparative genomics analyses will be undertaken which will improve the draft annotation of the *Corymbia* genome.

The **Eucalypt Genetics Group at UTAS**, led by Profs Potts and Vaillancourt, has a world-class interdisciplinary research programme that investigates the evolutionary and ecological forces that shape diversity in *Eucalyptus*.

The group consistently publishes in high impact journals, with recent publications in *Nature*, *New Phytologist* and *Molecular Biology and Evolution*.

The group collaborates with other universities and research institutions in Australia and internationally that can bring other skills to a supervisory team.

Learn more at [www.eucalyptgenetics.com](http://www.eucalyptgenetics.com)

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