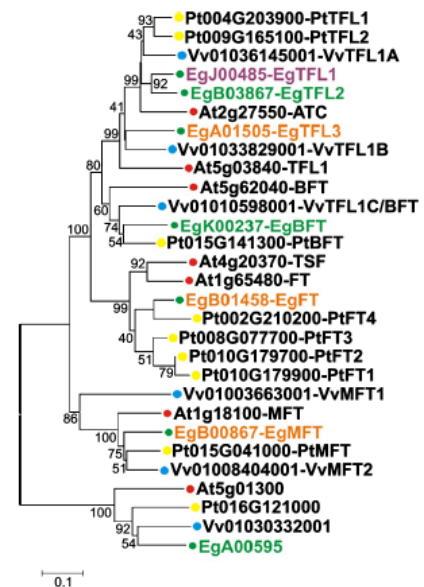


Comparative genomic analysis of flowering-related genes in eucalypts



- Latest genomic data
- Study iconic eucalypts
- Internationally recognised research groups

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.



Phylogenetic relationships among different plant members of the *FLOWERING LOCUS T* gene family (Vining et al 2015. The floral transcriptome of *Eucalyptus grandis*. *New Phytol.* 206, 1406-1422.)

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

For more information about this project please contact:



Dr. Jules Freeman
Jules.Freeman@utas.edu.au



Dr. Rebecca Jones
Rebecca.Jones@utas.edu.au



Prof. Rene Vaillancourt
Rene.Vaillancourt@utas.edu.au