

Decoding the genome of *Eucalyptus grandis*, the most widely planted hardwood in the world

Native from Australia, the genus *Eucalyptus* encompasses more than 700 species. With 20 million hectares of industrial plantations, *Eucalyptus* (mainly *E. grandis* and *E. globulus* species) are the most planted hardwoods in the world mainly for the production of pulp and paper. With the increasing need for renewable energy to replace fossil resources in a sustainable way, the use of *Eucalyptus* lignocellulosic biomass is an attractive alternative for the production of second-generation biofuels.

The LRSV team « Functional Genomics of *Eucalyptus* » is a founding member of the international consortium "EUCAGEN" which brought the project to sequence the genome of *Eucalyptus grandis*, efforts rewarded by its publication in *Nature* in 2014. Several members of LRSV participated to the assembly and annotation and are co-authors of this paper (Myburg & al., 2014).

Taking advantage of the availability of the *E. grandis* genome, the GFE team characterized eleven families of genes involved in the lignin biosynthetic pathway (Carocha & al., 2015) as well as four families of transcription factors such as the MYB (Soler & al., 2015), NAC (Hussey & al., 2015), Aux/IAA (Yu & al., 2015) and ARF (Yu & al., 2014) families. Altogether five papers published or in press, including three companions papers in the special issue of *New Phytologist* dedicated to the *E. grandis* genome. The combination of phylogenetic studies with large-scale expressional analyzes revealed the presence of "woody-specific" and "Eucalyptus-specific" clades and have further offer a very promising candidate genes for the regulation of wood formation in *Eucalyptus*.

Twenty of these candidate genes are being functionally characterized in the frame of the Plant KBBE project Tree For Joules coordinated by the LRSV team, whose main goal is to optimize wood properties for bioenergy production

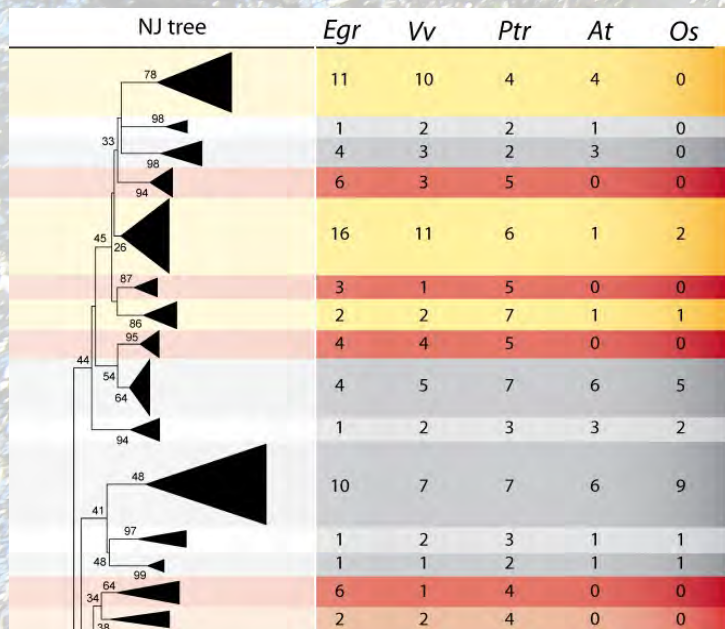


Fig. : Part of neighbour-joining phylogenetic tree including proteins from *Eucalyptus grandis* (Egr), *Vitis vinifera* (Vv), *Populus trichocarpa* (Ptr), *Arabidopsis thaliana* (At) and *Oryza sativa* (Os). Subgroups in general expanded in woody species are highlighted in yellow, whereas subgroups preferentially found in woody species are highlighted in red.