



## Plant cell wall plasticity in response to environmental cues

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### Scientific objectives

**Plasticity of plant cell walls** is studied in plants in response to environmental abiotic stress as well as in the context of application as bioenergy resources. Studies are being performed on two dicots *Arabidopsis thaliana* a model plant and *Eucalyptus* a woody plant of high economic interest both for pulp and bioenergy.

**Plant primary cell walls** are mainly composed of polysaccharide polymers, such as cellulose, hemicellulose and pectins, and proteins. Their composition and structure vary during development and in response to environmental constraints. Proteins are major actors of cell wall plasticity by playing roles in polysaccharide assembly and remodelling as well as in signaling. The project will be focused on the search of the function of cell wall proteins possibly involved in these processes such as peroxidases (Francoz *et al.* 2015, *Phytochemistry* 112:15), proline-rich proteins (Hijazi *et al.* 2014, *Front Plant Sci* 5:395) and lectins/lectin receptor kinases (Jamet *et al.* 2008, *Proteomics* 8:893). In particular, germination is chosen as a physiological process requiring specific cell wall modifications for critical processes such as mucilage secretion (Francoz *et al.* 2015, *Trends Plant Sci* 20:515) or radicle protrusion. Pyrenean ecotypes are studied for possible adaptation to low temperature conditions. Phenotyping, genetics, transcriptomics and proteomics experimental approaches are combined to understand the function of these proteins in cell wall plasticity.

We are also studying the plasticity of the **lignified secondary cell walls** of *Eucalyptus* trees in response to environmental cues (cold, drought and mineral nutrition) (Camargo *et al.* 2014, *BMC Plant Biol* 14:256; Ployet *et al.*, in preparation). Thanks to the availability of the *Eucalyptus grandis* genome (Myburg *et al.* 2014, *Nature* 510:356), we have performed genome-wide analyses of several transcription factor families (Soler *et al.* 2014, *New Phytol* 206:1364; Hussey *et al.* 2015, *New Phytol* 206:1337; Yu *et al.* 2014, *PLoS One* 9:e108906; Yu *et al.* 2015, *Plant Cell Physiol* 56:700; Cao *et al.* 2015, *PLoS One* 10:e0121041; Li *et al.* 2015, *Genome Biol Evol* 7:1068) and eleven lignin gene families (Carocha *et al.* 2015, *New Phytol* 206:1297). By combining comparative phylogeny and large scale expression analyses in a vast array of tissues and organs under different conditions, we have identified very promising candidate genes for the regulation of wood formation in *Eucalyptus* at the cross talk between development and stress conditions. In the frame of the Plant KBBE project “Tree For Joules” (<http://tfj.lrsv.ups-tlse.fr/>), whose main goal is to optimize wood properties for bioenergy production, we have undertaken the functional characterization of more than ten candidate genes in *Arabidopsis* and poplar transgenics as well as in transgenic *Eucalyptus* hairy roots (Plasencia *et al.* 2015, *Plant Biotech J* doi: 10.1111/pbi.12502). The characterization of the most promising genes and lines is ongoing at the histochemical, biochemical levels (structure, composition, saccharification potentials) and transcriptomic levels. We are also studying more in depth some MYB factors by identifying their direct targets as well as their interacting partners.

### TULIP MTR

This project is part of **MTR1** entitled: “*Organism - abiotic environment interactions (the scale of the sole organism)*”, where the interactions between one organism and its environment (habitat and social context) are considered. Researches in developmental biology and interactions between the organism and environmental factors will be developed with a special focus on cell wall remodelling.

**ETPs involved in the project: 5 (Researchers/Professors/Assistant-Professors)**