

research used shotgun cloning and specific gene cloning method to establish genomic library. The genomic library was successfully constructed using pGEM-T Easy vector in *E. coli* bacteria strain DH5 $\alpha$ , generating about 9 colonies by shotgun cloning method and sequences of sengon TI genes were obtained with sizes ranging from 107 to 308 bp. The sequences of the colonies had high similarity from nuclear, chloroplast and mitochondrial genomes of various tree species and TI sequences were similar to *Tamarindus indica*, *Glycine max*, *Populus trichocarpa* and *Populus nigra*, however those TI sequences had low E values.

### Studying ecophysiological patterns to improve the management of high-productivity *Eucalypt* plantations: the EUCFLUX project

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Global climatic changes may deeply affect the functioning of *Eucalyptus* plantations. It is therefore crucial to gain knowledge on the drivers of *Eucalyptus* productivity, carbon (C) allocation and resource-use efficiency in order to ensure a sustained productivity. These data are key to improve the productivity of *Eucalyptus* plantations and reduce their impacts on natural resources towards sustainable management. Building on the innovative results obtained in its first phase (2007-2017), the second phase of the EUCFLUX project, initiated in 2018, aims to enhance our knowledge on eucalypt plantations functioning at various spatiotemporal scales. The EUCFLUX study site is located on a commercial clonal plantation of ca 260 ha in Southern Brazil. The project will specifically 1) quantify the fluxes of energy, C and water along a complete rotation using the Eddy Covariance technique, girth inventories, litter and C content surveys and flux chambers; and assess the effects of forest plantations on soil water availability down to 10m and water table 2) use high-resolution dendrometers and anatomical analyses to study the determinism of growth 3) combine field data, high resolution remote sensing and modelling to upscale our knowledge of eucalypt functioning from site to regional scales and 4) compare the functional responses of more than 16 eucalypt genotypes (clonal and seed-origin) in a common-environment field trial, in order to evaluate the generality of the results obtained on the main clone, but also to evaluate how different are the functional responses of coppice and planted eucalypt trees.


### JERFs regulate intracellular K<sup>+</sup>/Na<sup>+</sup> balance in *Populus alba* × *P. berolinensis* under salt stress

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Maintaining K<sup>+</sup>/Na<sup>+</sup> balance in the cytoplasm is important for metabolism as well as salt resistance in plants. In this study, we monitored the growth (height and diameter) of *Populus alba* × *P. berolinensis* genotypes 9# and transgene 9# (ABJ01) carrying the JERF gene over 4 years. Expression of NHX1 and SOS1 which encode Na<sup>+</sup>/H<sup>+</sup> antiporters in the vacuole and plasma membranes were measured in leaves. Ion flux of Na<sup>+</sup>, K<sup>+</sup> and H<sup>+</sup> were measured in the root tip of seedlings stressed by 100 mM NaCl for 7 days, 15 days and 30 days. The results showed that transgenic genotype (ABJ01) grew faster than 9#, and ABJ01 displayed higher NHX1 and SOS1 expression in leaves than 9#. Root ion flux measurement revealed a higher Na<sup>+</sup> efflux and H<sup>+</sup> influx in ABJ01 than in 9#, but K<sup>+</sup> efflux was lower in ABJ01. The results suggest that salt stress induces NHX1 and SOS1 to a greater extent in the ABJ01 genotype, which up-regulate the Na<sup>+</sup>/H<sup>+</sup> antiporter to better maintain K<sup>+</sup>/Na<sup>+</sup> balance in the cytoplasm of this more salt resistant variety.

### Morphological dissection and cellular and transcriptome characterizations of bamboo pith cavity formation reveal a pivotal role of genes related to programmed cell death

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Pith cavity formation is critical for bamboo to overcome the bending force during fast growth, but the molecular mechanism is largely unknown. Multiple approaches were employed to study the biology of pith cavity formation, including anatomical dissection, mathematical modeling, and transcriptome profiling. We found that the corruption of pith tissue occurred sequentially and asymmetrically from the top-center of the internode down to the bottom, which might be caused by the combined effects of asymmetrical radial and axial tensile forces during shoot-wall cell elongation and spiral growth of bamboo internode. Programmed pith cell death manifested by TUNEL positive nuclei, DNA cleavage and degraded organelles, which was regulated by ethylene and calcium signaling pathway, ROS burst, cell wall modification, proteolysis, and nutrient recycle genes finally might be responsible for pith tissue corruption of *Pseudosasa japonica*. Although similar physiological changings and transcriptome profiles were found in other randomly selected bamboo species, different forming speed of pith cavity, which might be caused by different pith cells across the internode that negatively correlate with culm diameter was discovered. These findings provided a systematical view on the formation of the bamboo pith cavity and revealed that PCD plays an important role in the bamboo pith cavity formation.

### Douglas-fir seedlings in the Pacific Northwest: the genetics of drought adaptation

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Douglas-fir (*Pseudotsuga menziesii*) is a widely distributed, ecologically important, and commercially valuable tree species in North America. However, climate change is expected to adversely impact Douglas-fir trees, and assisted migration may become necessary to lessen the effects of climate change. Because