

### Transcriptional regulation of cell cycle genes during the temperature-modulated larch tree dormancy release and reactivation

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Dormancy release and reactivation of temperate-zone trees in spring involve the temperature-modulated expression of cell cycle genes. However, information on the detailed regulatory mechanism is limited. Here, we compared the transcriptome of stems of active and dormant larch trees, emphasizing the expression patterns of cell cycle genes and transcription factors, their relationships and responses to temperatures. The results showed that 12 cell cycle genes and 31 transcription factor, belonging to 17 families, were highly expressed in active stage, indicating regulatory relationships might exist between them. Bioinformatics analysis of the promoter sequences of 12 cell cycle genes suggested that they might be regulated by the transcription factors from 10 families. Altogether, 16 transcription factors from 7 families co-expressed with 12 cell cycle genes, and 73 regulations were predicted; while yeast one-hybrid assay showed that three regulations occurred between three transcription factors and two cell cycle genes. Last we measured their expression patterns during dormancy release and reactivation induced by temperatures naturally or artificially, and found that they almost had the same expression patterns, indicating that these regulatory modules functioned in the temperature-modulated dormancy release and reactivation of temperate-zone trees. These findings provide new insights into the links between the temperature signals and the expression of cell cycle regulators, helping to understand the temperature control of tree growth and development in the context of climate change.

### Genetic background hidden by methylation in hickory (*Carya cathayensis*) --- a view based on the construction of genetic and epigenetic linkage maps

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Recent studies have suggested epigenetic mechanism, one of which is DNA methylation, is involved in heterosis and apomixis in plant species. Hickory (*Carya cathayensis*), a woody nut species quite different from its relative pecan (*C. illinoensis*), has so far had no cultivar developed, presented a low DNA polymorphism by conventional molecular markers although propagated by seeding, but shown heterosis, apomixis and imprinted quantitative trait loci (iQTLs). To figure out the DNA methylation status in hickory, we analyzed the cytosine methylation pattern of two mapping populations resulting from reciprocal crosses between a hickory tree and a pecan cultivar "Mahan" using MSAP (methylation-sensitive amplified polymorphism) markers. With the locus information from MSAP, both non-methylation loci (NML) or methylation sensitive loci (MSL), and that from other molecular markers such as RAPD, ISSR and SRAP markers on the same mapping populations, we constructed a genetic and an epigenetic maps in hickory. Our results show that the epigenetic map (7742.3 cM) was doubled as compared with the genetic map (3580.2 cM) either in terms of the total length of linkage groups or in terms of the number of molecular markers. In addition, makers from MSAP, either NML or MSL, accounted for a large percentage of the total markers used and MSAP markers were often clustered in each of linkage groups. The results reveal that the hickory genome is highly methylated and DNA methylation might play an important role in this species, which has survived from global cooling in the late Tertiary.

## C2II: EUCALYPT PLANTATIONS

### Density and stomatal dimensions of contrasting *Eucalyptus* clones of across a climatic gradient

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The species of the *Eucalyptus* genus are widely used in forest plantations, representing economic importance for Brazil. However, little is known about the physiological processes that control their growth, and how these processes are governed by genetic and climatic factors. Therefore, the objective of this study is to characterize the density and dimensions of the stomata of different species of the *Eucalyptus* genus, and to evaluate the plasticity of these variables across a strong climatic gradient in Brazil. The experimental sites are part of the TECHS-IPEF Cooperative Research Program, located in SC, PR, SP, MG (from latitude 17° to 27° South). The clones evaluated are pure or hybrid of the following species: *E. urophylla*, *E. grandis*, *E. camaldulensis*, *E. saligna*, *E. benthamii*, *E. dunnii*. Histological blades of abaxial and adaxial leaf surfaces were prepared from leaves of three trees of each clone at each site, and the images analyzed in an optical microscope. The study is under development, and the studied clones have not been evaluated yet at all sites. However, previous results show that the clones differ in the occurrence of stomata in the leaf sides. Among the six clones, three showed stomata at both sides of the leaves, and the other three clones only on the abaxial side. The stomatal density is also different among clones, ranging from approximately 200 to 500 stomata per mm<sup>2</sup>. The stomatal characteristics are important to understand the physiological response of the trees and how they may be related to the adaptation of these clones to different climates.

### Coppice potential of 16 different species of *Eucalyptus* after an eight-year rotation.

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The adoption of coppice is a commonly used management in different regions of Brazil for plantations of *Eucalyptus*, which requires less investments. However, there are variations in the ability of each genotype to emit sprouts, and higher yields can be obtained by changing the genetic material. The objective of this study was to evaluate the coppice potential of 16 *Eucalyptus* genotypes of different species, (14 clonal and 2 seed origin). The experiment is located in the area of the EUCFLUX-IPEF Cooperative Research Program, in the state of São Paulo, Brazil. The following variables were evaluated at 100 days after harvest of an eight-year rotation of the 16 genotypes: number of shoots per stump, total height, and basal diameter of the three main shoots. Twelve genetic materials showed one or two shoots per stump, and the three clones, with higher development in height and diameter, showed 3 or more shoots per stump. The best shoots of the best clones presented total height of approximately 1 m and average base diameter of 8 cm. The genotypes with the highest number of shoots also presented

better development in height and basal diameter. The 3 less developed genotypes presented mean basal diameter of less than 3 cm and average height of 40 cm for the three main shoots. The results show the clone/species coppice potential, which is important to move forward with coppicing techniques. Future studies will be conducted to evaluate the productivity physiology of these genetic materials.

### Changes in biomass production after windstorms in *Eucalyptus grandis* x *Eucalyptus urophylla* hybrids / Alterações na produção de biomassa de híbridos de *Eucalyptus grandis* x *Eucalyptus urophylla* danificados por vendavais

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As florestas plantadas do gênero *Eucalyptus* estão expostas à ação dos fatores abióticos do ambiente, que muitas vezes as causam danos e geram reduções em sua produtividade. Nos últimos anos tem-se intensificado as observações de danos por vendavais em plantios clonais de *Eucalyptus*, principalmente em idades mais jovens, preocupando a silvicultura nacional. O presente estudo buscou quantificar as perdas médias na produção de árvores de 7 anos de idade decorrentes de danos anteriores por vento na idade de 2 anos. Foram selecionados 3 talhões de híbridos de *E. grandis* x *E. urophylla* que apresentassem árvores normais (retas e sem danos) próximas a árvores danificadas pelo vento e que permaneceram vivas até a idade final, tipicamente arqueadas e com a presença de brotações ao longo do fuste. Quantificou-se, para cada talhão, um número de 4 árvores médias arqueadas pelo vento e 2 árvores médias normais, medindo-se sua biomassa recém abatida do fuste, separando-a nos sortimentos de celulose (acima de 8 cm de diâmetro com casca), resíduo (entre 2 e 8 cm com casca) e total (somatório dos anteriores). A biomassa média, respectivamente para os sortimentos de celulose, resíduo e total, foi de 411, 19 e 430 kg/árvore para as árvores normais e de 193, 61 e 254 kg/árvore para as árvores arqueadas. Isto corresponde a uma diminuição de 53% na madeira antes destinada a celulose e um aumento de 231% na quantidade de resíduo gerada, ocasionada pelas brotações ao longo dos fustes arqueados. A biomassa fresca total foi reduzida em 41%.

### Changes in heartwood/sapwood ratio in *Eucalyptus urophylla* due to soil water deficit

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Different heartwood/sapwood proportions affect wood use and quality. With forest plantation expansion, clones tend to decrease their ideal phenotypic expression due to the occupation of areas with different edaphoclimatic conditions from locations they were developed. The aim of the study was to compare the heartwood/sapwood ratio (C/A) of eucalyptus wood in contrasting soil water deficit conditions (SWD) across Brazil latitudinal gradient. One wood disc at DBH was sampled from seven *Eucalyptus urophylla* trees at age of 6 years for C/A quantification at 10 sites of the TECHS-IPEF Cooperative Research Program. Heartwood delimitation was visual, by the color difference. The discs were scanned and total heartwood area values were obtained by image analysis system. The sites were separated into 3 groups. Those with the highest latitudes, Botucatu/SP and Buri/SP (SWD: 106 mm year<sup>-1</sup>) presented the highest C/A values, 2.3 and 1.8, respectively. The sites Estrela do Sul/MG, Guanhães/MG, Rio Verde/GO and Três Lagoas/MS, located at medium latitudes, formed the second group with means of C/A: 1.1 and SWD of 367 mm year<sup>-1</sup>. The group with the lowest C/A mean (0.6) belonged to sites of the highest values of SWD (534 mm year<sup>-1</sup>) and lower latitudes, Peixe/TO, Urbano Santos/MA and Eunápolis/BA, and also Belo Oriente/MG. The C/A ration decreased with the increase of the SWD and decrease of the latitude, demonstrating that SWD conditions the response of tree to heartwood production.

### Growth and distribution of fine roots in clonal *Eucalyptus* plantations under contrasting climate

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The main function of fine roots is to provide water and nutrients, therefore, understanding their growth in depth, and distribution over the soil layers is crucial to understand soil water dynamics and nutrients uptake by forest plantations. The objective of this study is to quantify biomass of fine roots ( $\leq 2$  mm) in different species of *Eucalyptus* on contrasting climatic conditions. Fine roots were sampled at the age of 3 years, on four genotypes (*E. urophylla*, *E. urophylla* x *E. grandis*, *E. grandis* x *E. camaldulensis* and *E. urophylla* x *E. brassiana*) at two sites (Bocaiúva-MG and Telêmaco Borba-PR) of the TECHS-IPEF Cooperative Research Program, with deep Oxisols and mean annual precipitation of 850 and 1750 mm, respectively. On the drier site, fine roots were shallower, with the distribution of their biomass on the top 3 meters ranging from 58 to 91% among clones. The wetter site showed deeper fine roots with the distribution of their biomass on the top 3 meters ranging from 60 to 82%. On both sites, the hybrid *E. urophylla* x *E. grandis* showed the shallower fine roots, contrasting with *E. grandis* x *E. camaldulensis* and *E. urophylla* x *E. brassiana*, that showed similarly deeper roots. Studies currently under development are focusing on understanding the relations among fine roots, aboveground growth, wood production, soil water use at different soil layers, and tolerance capacity of these clones to water stress.

### Optimal temperatures for growth of contrasting *Eucalyptus* species in Brazil

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The genetic improvement of *eucalyptus* has evolved in the development of genotypes, but we still need more information on the genotype-environment interaction. Understanding the interactions between forest plantation and climate is mandatory for predicting the impacts of climate change on terrestrial ecosystems, and assessing the adaptation and vulnerability of tree species. In this context, potential genotypes were planted at 6 experimental sites, from the South to North of Brazil. We measured the CBH every 15 to 30 days of 9 genotypes (6 trees per genotype) planted in 3 x 3 m spacing, from 2012 to 2018. Finally, two destructive samplings were performed in the middle and at the end of the rotation (2014 and 2018, respectively). Meteorological data of each site was used