

B2t: NOVEL ADVANCES IN GENOMICS AND TREE BREEDING FOR SUSTAINABLE FORESTS

The variation of genotypes in natural forest populations: an important variable to precision silviculture

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The term precision silviculture can mean the selection of individuals of a species in a natural population with characteristics suitable for a particular purpose of use. As each individual of the population occupies a specific site, in addition to the soil variables, it is fundamental to genotype characterization to identify genotype environment interactions. To access of DNA of each individuals, we adapted a method of extraction of the genomic DNA of these samples. An improved protocol for the isolation of DNA from sapwood of *Astronium fraxinifolium* Schott, *Cariniana legalis* (Mart.) Kuntze, *Pterocarpus rohrii* Vahl, *Handroanthus serratifolius* (Vahl) S.Grose, *Astronium graveolens* Jacq., *Cedrela odorata* L., *Lecythis pisonis* Cambess., *Manilkara salzmanii* (A.DC.) H.J.Lam., *Handroanthus riocordensis* (A.H.Gentry) S.O.Grose, native species of Mixed Ombrophilous Forest is described. The isolated DNA is suitable for RAPD and SSR for DNA analysis. Different DNA protocols were examined to determine which might yield DNA from sapwood of the studied species. The protocols tested were Cationic hexadecyl trimethyl ammonium bromide (CTAB), CTAB modified, and the commercial kits Quiagen® - DNeasy Plant Mini Kit, MoBio®, Noren Biotek® and Himedia®. None of these protocols produced yielded DNA suitable purity for RAPD analysis. We established a new procedure involving CTAB protocol varying the incubation time and the concentration of proteinase K, denominated CTAB modified. The recovery of DNA with an average yield of 20 and 100 µL of sapwood samples, using protocol CTAB modified.

Evaluation of growth traits as selection indicators for *Phyllostachys pubescens* seedlings in radiation-induced breeding programs

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Deriving novel germplasm of the bamboo *Phyllostachys pubescens* from tradition approaches to plant breeding is problematic, due to its indeterminate growth, however radiation-induced breeding represents a potential solution. Here, seeds of *P. pubescens* were radiation-treated with 60 Co γ-ray irradiation, from which 16 superior seedlings were screened and planted in an experiment from 2011 to 2017 and found variation in the traits among the phenotypes within and across years, and principal components analysis showed that growth of the phenotypes was more accurately described using a combination of growth traits, rather than a single trait. Using our trait analysis, we found that growth in a phenotype derived from seed irradiated with 10 Gy of 60 Co γ-ray irradiation was superior; these results supported a previous study of growth of this phenotype in an afforestation experiment. This study provides a feasible method and foundation for the selection and screening of superior *P. pubescens* genotypes in radiation-induced breeding programs.

Ecology and evolution of a tree species challenged by dual threats

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We are studying the ecological and evolutionary processes affecting the geographical distribution of southwestern white pine (SWWP; *Pinus strobiformis*), an important tree species of the Southwestern USA and Mexico. Southwestern white pine viability is threatened by changing climate and an invasive tree disease, white pine blister rust (caused by the fungal pathogen, *Cronartium ribicola*). Rapid climate change is negatively affecting SWWP by increasing heat and drought stress, and thus challenging its ability to adapt. White pine blister rust causes extensive tree decline and mortality, including in SWWP. The dual threats of climate change and invasive species make forecasting future tree distributions at continental scales an urgent challenge. The goal of our project is to determine how gene movement among populations, adaptation to disease and drought, heritable changes beyond DNA mutations, and a changing environment interact to govern the success of SWWP. We are utilizing and developing tools to help forecast and manage the future of the species, including those from genomics, common gardens, tree disease resistance testing, engineering and technology innovation to measure drought tolerance and physiological response. Results will be synthesized and included in cutting-edge landscape genomics models to meet our overarching goal. We will present our framework and current project status, including results. Completed products include development of landscape genomic models, a species distribution model incorporating climate change, and adaptive trait, phenotype plasticity and genomic variation analyses. Continuing work incorporates these aspects in addition to transgenerational plasticity research and a genome-wide association study.

Artificial neural networks for predicting the genetic value of *Eucalyptus* progenies

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