
Quantitative Genetics and Tree Breeding

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Genetic variation in second generation *Pinus elliottii* var. *Elliottii*

Ananda Virginia de Aguiar¹, Wesllen Schuhli Kieras¹, Mayte Sampaio Cesário da Silva¹, Wanderley dos Santos², Jarbas Y. Shimizu³, Mario Luiz Teixeira de Moraes², Valderês Aparecida de Sousa¹

¹Embrapa Forestry, Brazil, ²Universidade Estadual Paulista Júlio de Mesquita Filho, São Paulo, Brazil,

³Autonomous Research

Presenter's email: ananda-virginia.aguiar@embrapa.br

Genetic parameters were estimated for growth traits in *Pinus elliottii* var. *elliottii* second generation half-sib families. Twenty five families harvested from a first generation seed orchard established in Colombo, PR, Brazil, were used in the study. The experiment was established in a randomized complete block design with thirty two replications of single plant plots. Height and dbh (diameter at breast height) were measured four years after planting. Deviance analysis and genetic parameter estimations were performed by using the best linear unbiased predictor (BLUP) and the residual maximum likelihood (REML) methods. A highly significant family variation in growth traits was detected. Narrow-sense individual heritabilities were estimated at 0.32, 0.14 and 0.37 for total height, dbh and volume, respectively. Average family heritability estimates ranged from 0.54 to 0.76 in dbh and volume, respectively. These results show promising perspectives to obtain substantial genetic gain, especially in wood volume growth, through either individual or family selections.

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Phytopathology of a quantitative trait: identification of potential resistance mechanisms to *Didymascella thujina* in *Thuja plicata*

Juan A. Aldana¹, John Russell², Barbara J. Hawkins¹

¹Centre for Forest Biology, University of Victoria, Victoria, British Columbia, Canada, ²British Columbia Ministry of Forests and Range, Cowichan Lake Research Station, British Columbia, Canada

Presenter's email: jaldana@uvic.ca

Thuja plicata (western redcedar, WRC) is one of the most valuable trees in British Columbia due to the durability, dimensional stability and beauty of its wood. WRC is prone to infection by the foliar fungus *Didymascella thujina* (Cedar Leaf Blight, CLB), an airborne disease that is especially problematic in forest nurseries. Early studies with CLB in Europe noted that another species in the genus, *Thuja standishii*, was completely resistant to the blight, and that hybrids of the two species were equally resistant to the blight. However, all WRC trees studied were susceptible but with varying amounts of the disease between individual trees. More recently, the British Columbia Ministry of Forests, Lands and Natural Resource Operations research staff have shown quantitative variation among iWRC populations and families in CLB disease symptoms and that such potential quantitative resistance is significantly related to population or family origin. Trees originating in either drier, hotter or colder ecosystems tend to exhibit more disease symptoms than those from humid, cool environments.

Most studies on CLB have focused on chemical methods to control the disease, but little research exists on the underlying resistance or tolerance mechanisms. Our objective is to examine the histological characteristics of WRC that may be related to CLB resistance or tolerance. Two groups of WRC F₁ families, one that exhibited less disease symptoms and the other more, were assessed for stomatal density, epidermis thickness, leaf thicknesses, cuticle thickness, and lignin and flavonoid deposition by using compound-specific stains and a combination of light and fluorescence microscopy techniques. Preliminary analysis of the data depicts differences among families in cuticle thickness, lignin and flavonoid deposition. Cuticles were thicker in families exhibiting more disease symptoms, which may