

## Genetic Variation in Wood Quality (MOE) of Coastal Douglas-fir

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Douglas-fir (*Pseudotsuga menziesii*) is of economic importance for forest products industries in the western United States, New Zealand, and parts of Europe. Its primary uses are dimension lumber, piles, plywood and pulp, but it is found in many other solid and composite products as well. In almost all of these capacities, wood density is a good predictor of its economic value and/or its performance because of density's correlation with strength or pulp yield. Other traits, such as microfibril angle and tracheid length, also affect wood quality, but density has been the trait most examined because of its relative ease of measure and its adequacy as an index for other properties.

Genetic studies in the literature suggest that most of the variation found among trees for wood density is controlled genetically; heritability ( $h^2$ ) estimates for wood density in Douglas-fir range between 0.5 to greater than 0.9. Unfortunately, the reported genetic correlations between wood density and growth rate are strongly negative, ranging from -0.5 to -1.0 (Bastion et al. 1985, King et al. 1988, Vargus-Hernandez and Adams 1991, St. Clair 1994).

Because MOE is more important for utilization than is wood density per se, we decided to examine the genetic variation of MOE in coastal Douglas-fir indirectly with the Director HM-200 ® (Hitman). The Hitman measures the sound velocity through a log, which is highly correlated with dynamic MOE. Theoretically the relationship is:  $MOE = \text{green density} \times \text{velocity squared}$ ; see Andrews (2002) for more details.

### METHODS AND MATERIALS

Four 20-year-old progeny test sites were chosen from 10 potential sites in the 1<sup>st</sup> generation Nehalem breeding program (part of the Northwest Tree Improvement Cooperative). The average height of the four sites ranged from 15.4 to 16.5 m and average DBH ranged from 19.1 to 19.4 cm. This series of trials was designed as a reps-in-sets design that tested 10 sets of 40 families (a total of 400 families). Each set was established as three replications with 4 non-contiguous trees per replication (for a total of 12 trees per family per site). We chose a set (set 10) with a higher than average age-11 DBH heritability (0.22 vs. 0.13 for all sets) in order to gain more precise estimates of genetic correlations. The trials were designed so that diagonals could be removed and equal family representation would remain. We measured all trees in set 10 for DBH and selected the diagonals with the higher heritability to fell, thereby improving correlation estimates. One of the 40 families was a full-sib family and was dropped from the analyses, leaving 39 open-pollinated families.

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Felled trees were measured for total height. A 4m log was cut from the base of the tree and the sound velocity was obtained with the Hitman. A disk was cut at about 1.5 m and will be subjected to additional measurements. For this report, we are using sound velocity as a proxy for MOE.

Unbiased heritability estimates for height, DBH and sound velocity (“MOE”) were calculated with the formula:

$$\text{Heritability} = (3 \times \sigma^2_{\text{family}}) / (\sigma^2_{\text{family}} + \sigma^2_{\text{site-family}} + \sigma^2_{\text{rep-family(site)}} + \sigma^2_{\text{error}})$$

Additionally, cross-site family-means were calculated for age-20 variables (4 available sites), age-11 foliage traits (5 sites) and form traits (10 sites). BLUP estimates were used in place of family-means for height and diameter at age-11 (10 sites) and DBH at age-17 (5 sites). Correlations were calculated for all traits with sound velocity (“MOE”).

## RESULTS AND DISCUSSION

Heritability estimates are shown in Table 1. Heritability estimates for “MOE” were high at all four sites (0.39 to 0.84) and the unbiased heritability estimate calculated over all four sites was 0.49. In general, “MOE” had larger heritabilities than either of the growth traits (Table 1). The family-by-environmental variation for “MOE” was relatively small; it was only 16% of the family variation.

Table 1. Heritability estimates of age-20 variables for the felled trees.

Site	MOE (velocity)	DBH	Height
Over all sites	0.49	0.31	0.22
Coal Creek	0.58	0.29	0.00
Sarajarvae	0.84	0.40	0.00
Slick Rock	0.39	0.31	0.45
Vesper	0.60	0.69	0.58

When one considers tree averages, 75% of the variation in MOE in the region (for a given stand age) is found within stands, as opposed to 25% among stands (Johnson et al. 2005). Half of this within-stand variation is controlled by genetics; therefore, over a third of the variation in MOE in the region is impacted by our breeding programs.

The only statistically significant correlations of family means and “MOE” were with DBH, and they were negative (Table 2). This result suggests that selection for improved DBH will result in a decrease in MOE. Similar results are found in the literature for wood density. In bending data from 198 1×1×16 cm sticks (data not shown), the partial correlation coefficient of density and MOE ( $r = 0.46$ ) was larger than the partial correlation coefficient of microfibril angle (MFA) and MOE ( $r = -0.29$ ). Therefore, it was not totally unexpected that “MOE” followed the same pattern found for wood density.

Table 2. Family-mean / BLUP correlations with the family mean of sound velocity (“MOE”) and level of statistical significance (italicized and in parenthesis). BLUP estimates are for age-11 height and DBH (10 sites) and age-17 DBH (5 sites).

<u>Height</u>	$r_{\text{family mean}}$	<u>Form</u>	$r_{\text{family mean}}$
age-11	-0.13 ( <i>0.40</i> )	Forking	-0.06 ( <i>0.73</i> )
age-20	-0.02 ( <i>0.89</i> )	Ramicorns	0.10 ( <i>0.53</i> )
age-20*	-0.15 ( <i>0.35</i> )	Sinuosity	0.02 ( <i>0.91</i> )
<u>DBH</u>		<u>Foliage retention</u>	
age-11	-0.28 ( <i>0.08</i> )	(SNC)	-0.15 ( <i>0.35</i> )
age-17	-0.33 ( <i>0.04</i> )		
age-20	-0.16 ( <i>0.31</i> )		

\* using only the 2 sites with heritability > 0

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