

The Potential of Acoustics to Determine Family Differences for Wood Quality in a Loblolly Pine (*Pinus taeda* L.) Trial

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Abstract: Acoustics have been used to determine wood quality attributes in both standing timber and sawn lumber. Sonic transmission data are collected non-destructively and can act as a surrogate for stiffness, they are directly related to modulus of elasticity (MOE) and closely related to differences in microfibril angle (MFA). Together with wood density, MFA and MOE are the most important wood characteristics that affect solid wood properties.

Breeding and selection for desirable wood properties will be a key factor in determining the global competitiveness of the forest industry in the United States. Breeders of loblolly pine (*Pinus taeda* L.) have been able to select for differences in wood specific gravity, MOE and MFA based on data collected from wood increment core samples. The use of acoustics in determining wood quality has merit in that it requires no direct wood sampling. However, before differences in acoustic transmission can be used in a breeding program, a number of questions need to be answered. Are there differences in transmission of sufficient magnitude and repeatability to allow heritable differences to be detected among families? How large a component is genotype by environment interaction? Is the equipment robust enough to be used by field crews and can data be collected efficiently?

To answer these questions, the Southern Institute of Forest Genetics in collaboration with the Western Gulf Forest Tree Improvement Program collected acoustic velocity data using the Fakopp Stress Wave Timer in three control-pollinated loblolly pine progeny tests established by International Paper Company in southeast Texas. Sampled trees were disease free and without forks. Acoustic velocity was measured at two radial directions on each tree over a length of 1.2 m spanning breast height. Measurements were averaged for each tree. Variance components were estimated for each location using the software packages DIALL and DIALLC. Then single location heritabilities were calculated. Heritabilities for the averaged acoustic velocity were moderate yet large enough to be useful in an applied breeding program. Phenotypic correlations among these traits were small, but positive suggesting that selection for growth and stiffness can be done simultaneously. Field protocols, however, need to be further refined to avoid data outliers and to arrive at easier methods of collecting observations on the large numbers of trees required to estimate parental breeding values.

Keywords: Acoustics, sonic velocity, wood quality, stiffness, MOE, MFA
Loblolly pine, *Pinus taeda* L.

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INTRODUCTION

Acoustics have been used to determine wood quality attributes in both standing timber and sawn lumber (Brashaw and others, 2005; Grabianowski and others, 2006; Joe and others, 2004). Sonic transmission data are collected non-destructively and can act as a surrogate for stiffness. They are directly related to modulus of elasticity (MOE) and closely related to differences in microfibril angle (MFA) (Lindstrom and others, 2002). Together with wood density, MFA and MOE are the most important wood characteristics that affect solid wood properties. Whereas density determines the quantity of wood in a given volume, acoustic velocity with its inherent relationship with MFA can determine wood quality (Chauhan and Walker, 2006).

Breeding and selection for desirable wood properties will be a key factor in determining the global competitiveness of the forest industry in the United States. Breeders of loblolly pine (*Pinus taeda* L.) have been able to select for differences in wood specific gravity, MOE and MFA based on data collected from wood increment core samples (Isik and others, 2005). The use of acoustics in determining wood quality has merit in that it requires no direct wood sampling. Reasonable correlations have been found when comparing the acoustic velocity of standing trees and the mean stiffness of dried lumber cut from those trees (Chauhan and Walker, 2006). Associations between acoustic measurements taken in the outermost wood and from whole stems suggests that estimates of outerwood MOE are completely representative of whole stem MOE (Lassere and others, 2007).

This study was undertaken to develop answers to the following questions:

1. Are there differences in transmission of sufficient magnitude and repeatability to allow heritable differences to be detected among families?
2. How large a component is genotype by environment interaction?
3. Is the equipment robust enough to be used by field crews and can data be collected efficiently?

MATERIALS AND METHODS

The Southern Institute of Forest Genetics in collaboration with the Western Gulf Forest Tree Improvement Program (WGFTIP) collected acoustic velocity data in three six-year-old control-pollinated loblolly pine progeny tests established by International Paper Company in southeast Texas (Figure 1). Two of the tests contained three diallels from two different breeding groups, while the third had only a single diallel from each of the breeding groups. All tests were completely randomized single-tree plantings established on an 8' X 8' spacing with 40 replications. Survival, growth and form data were collected in all tests at the end of the fifth growing season (Table 1).



Figure 1. Natural distribution of loblolly pine in the western Gulf region. Progeny test locations are marked with ▲.

Table 1. Summary statistics of fifth-year survival, growth and form in the study tests. Straight score is a relative assessment of straightness on a scale of 1-4, with 1 being very crooked and 4 being very straight. Tests with average straightness score 2.5 for this trait.

Test	County	N	Survival (%)	HT (m)	DBH (cm)	Vol/tree (dm ³)	Straight Score	Forks (%)
1	Cherokee	46	87.8	5.9	9.0	11.6	2.6	7.2
2	Trinity	46	95.1	5.6	8.5	10.8	2.6	7.9
3	Polk	33	74.3	5.0	7.9	6.6	2.4	10.2

Acoustic time of flight (ToF) was measured at two radial directions on each tree over a length of 1.2 m centered at breast height using a Fakopp Wave Stress Timer (also known as a Tree Sonic). Sampled trees were from a single diallel that was common to all three tests. They were disease free and without forks. Time data were the average of three separate taps on the uppermost transducer. These data were converted to velocity using a time correction factor and formula provided by FAKOPP. Modulus of elasticity (MOE) was calculated using the formula:

$$MOE = \rho V^2$$

where ρ = green density and V is the velocity of sound. Since apparent wood density at fiber saturation point is theoretically a constant, V^2 is considered a surrogate for dynamic longitudinal MOE (Huber and others, 2007). MOE values for each tree were analyzed separately for each face and as an average of the two (aveMOE). A subsample of trees from each test was cored for specific gravity determination using the maximum moisture method.

Variance components at each location were estimated for ToF, velocity, MOE and aveMOE using the software packages DIALL and DIALLC (Schaffer and Usanis, 1968), where family sums of squares are partitioned into estimates of general (GCA) and specific combining abilities (SCA). Negative variance estimates were assumed to be zero. Narrow-sense heritabilities were calculated for all traits at each location using the following formula:

$$h^2 = 4 \sigma^2_{GCA} / [2\sigma^2_{GCA} + \sigma^2_{SCA} + \sigma^2_{GE} + \sigma^2_r + \sigma^2_e],$$

where GE denotes the GCA by replication (r) interaction effect.

Data for aveMOE were pooled across locations and variance components estimated using the methods of Johnson and King (1998). Overall narrow-sense heritability was calculated using the previous formula and full-sib family heritability was calculated using the formula:

$$h^2 = 2\sigma^2_{GCA} / [2\sigma^2_{GCA} + \sigma^2_{SCA} + \sigma^2_{GE/s} + \sigma^2_r/lr + \sigma^2_e/lrn],$$

where s = number of test sites, r = number of test replications and n = number of sample trees. Phenotypic correlations among the growth, specific gravity and acoustic traits were estimated as product-moment correlations using PROC CORR in SAS (SAS 1985).

RESULTS AND DISCUSSION

Data for all acoustics variables were statistically significant in each of the individual tests. Individual site narrow-sense heritability estimates ranged from 0.18 to 0.49 for ToF, from 0.25 to 0.47 for velocity, from 0.27 to 0.46 for individual MOE estimates and from 0.31 to 0.44 for aveMOE (Table 2). The estimates for MOE are not very different from those observed in standing slash pine at age eight (Huber and others, 2007). The estimates for tests 1107 and 1109 were lower than those from test 1108 possibly due to outliers in the data sets for these two tests. However, removal of these outliers did not result in vastly different heritability estimates for any of the acoustic traits. In addition, correction for sample day was attempted with the data from test 1107, but resulted in little change in the estimates.

Table 2. Narrow-sense heritability estimates for each of the acoustic traits by radial direction ('Side') and test. aveMOE is the average of individual side MOE.

Test	Side 1			Side 2			aveMOE
	ToF	V ²	MOE	ToF	V ²	MOE	
1107	0.23	0.26	0.27	0.23	0.30	0.32	0.31
1108	0.49	0.47	0.45	0.41	0.39	0.37	0.44
1109	0.41	0.45	0.46	0.18	0.25	0.27	0.40

In the combined analysis family differences for aveMOE were significant but the interaction between families and sites was non-significant. The estimate of narrow-sense heritability was quite high at 0.94. The estimate of full-sib family heritability was also quite high at 0.97. GCA effects accounted for 16 percent of the total variance for aveMOE. With the large number of replications sampled in this study, the non-genetic components were only a small contributor to the total variance.

Family-mean phenotypic correlations among the growth traits, wood specific gravity and aveMOE were all positive (Table 3). However, the correlations between diameter and specific gravity and between volume and average MOE, while positive, were not significantly different from zero. The correlation between wood specific gravity and average MOE was also positive.

Table 3. Family-mean phenotypic correlations between growth, wood specific gravity and average MOE. Phenotypic correlations significant at $P < 0.01$ in bold.

Trait	DBH	VOL	SPGR	aveMOE
HT	0.72	0.83	0.18	0.23
DBH		0.96	0.08	0.18
VOL			0.23	0.12
SPGR				0.27

CONCLUSIONS

The ultimate goal is to incorporate stiffness along with breeding values for volume, straightness, and wood specific gravity into a sawlog index for ranking candidates for inclusion in seed orchards. Results from this study suggest that acoustics may play a valuable role in the development of an additional wood quality selection trait. Family differences for all variables were statistically significant. Average MOE had moderate but positive correlations with growth variables, suggesting that simultaneous selection for growth and wood quality may be possible. However, to simultaneously improve volume growth and MOE, selection must be made first for specific gravity.

There was no significant genotype by environment interaction. However, this was not unexpected given the relatively small distance between tests. Single-location individual heritabilities for the averaged acoustic velocity were moderate and large enough to be useful in an applied breeding program. However, field protocols need to be further refined to avoid data outliers and to arrive at easier methods of collecting observations on the large numbers of trees required to estimate parental breeding values.

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LITERATURE CITED

- Brashaw, B.K., R.J. Vatalaro, J.P Wacker, and R.J. Ross. 2005. Condition assessment of timber bridges: 2. Evaluation of several stress-wave tools. USDA Forest Service, Forest Products Laboratory General Technical Report 160. Madison, WI. 11p.
- Chauhan, S.S. and J.C.F.Walker. 2006. Variations in acoustic velocity and density with age, and their interrelationships in radiate pine. *For. Ecol. and Manage.* 229:388-394.
- Grabianowski, M., B. Manley and J.C.F. Walker. 2006. Acoustic measurements on standing trees, logs and green lumber. *Wood Sci. Technol* 40: 205-216
- Huber, D., L. Parisi, G. Powell and X. Li. 2007. Cooperative Forest Genetics Research Program 49th Annual Progress Report. 22p.
- Isik, F., B. Li and B. Goldfarb. 2005. Genetic Variation in MFA, MOE and wood density among clones of *Pinus taeda* L. *Proc. Of the 287th South. For. Tree Improv. Conf.*, p. 95.
- Joe, B., R. Dickson, C. Raymond, J. Ilic and C. Matheson. 2004. Prediction of *Eucalyptus dunnii* and *Pinus radiata* timber stiffness using acoustics. RIRDC Publication No. 04/013. 121 p.
- Johnson, G.R., and J.N. King. 1998. Analysis of half diallel mating designs: 1- A practical analysis procedure for ANOVA approximation. *Silv. Gen.* 47: 74-79.
- Lassere, J.-P., E.G Mason and M. S. Watt. 2007. Assessing corewood acoustic velocity and modulus of elasticity with two impact based instruments in 11-year-old trees from a clonal-spacing experiment of *Pinus radiata* D. Don. *For. Ecol. And Manage.* 239: 217-221.
- Lindstrom, H., P. Harris and R. Nakada. 2002. Methods of measuring stiffness of young trees. *Holz als Roh- und Werkstoff* 60. pp. 165-174

SAS Institute Inc. 1985. SAS[®] Language Guide for Personal Computers, Release 6.03 Edition. SAS Institute Inc., Cary, NC, 558 pp.

Schaffer, H.E. and R.A. Usanis. 1968. General least squares diallel analysis. Department of Genetics, North Carolina State University, Raleigh.