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przyrost wysokości polskich proveniencji świerka pospolitego (*Picea abies* [L.] KARST.) w Leśnym Zakładzie Doświadczalnym Siemianice. Sylwan 4: 31–35 (1987). — VAZHOV, V. I. and YAROSLAVCEV, T. D.: Zavisimost godichnogo prirosta dreviesnyh rastenij ot klimaticeskikh faktorov. Lesovedenie 6: 86–89 (1973). — WALTER, H. and LIETH, H.: Klimadiagramm — Weltatlas. Jena, VEB Gustav Fischer Verlag (1964).

## Preliminary Genetic Parameter Estimates for Some Wood Quality Traits of *Pinus caribaea* var. *hondurensis* in Queensland, Australia

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### Summary

Diametral increment cores were sampled from 27 open pollinated families to study juvenile wood characteristics in an 11 year old progeny trial of *Pinus caribaea* var. *hondurensis* planted at two locations. Heritabilities and phenotypic and genetic correlations were estimated for radial and height growth, stem straightness, and wood quality traits. Estimates of individual tree narrow-sense heritability for latewood percentage, compression wood percentage and basic density were consistent with those reported previously for *Pinus caribaea* and the southern pines, with values of 0.55, 0.02 and 0.62 respectively.

Spiral grain angles at growth rings 3, 5, 7 and 9 were measured using positive and negative signs to indicate direction of spiral for right hand and left hand spirals respectively. Heritabilities and phenotypic and genetic correlations were estimated both using and ignoring sign. Heritability estimates increased from 0.12 for ring 3 to 0.46 for ring 9 while those for radial standard deviation and mean absolute spiral grain were 0.24 and 0.28 respectively.

Heritability estimates for growth and straightness were consistent with those reported previously. Genetic correlations were relatively imprecise, but suggest an adverse correlation of radial growth with percent latewood and basic density. The results of subsequent studies are needed to clarify the relationship between growth and juvenile wood quality of *Pinus caribaea* var. *hondurensis* in Queensland and to extend this work to mature wood as material from older trials becomes available.

**Key words:** *Pinus caribaea* var. *hondurensis*, genetic parameters, wood quality.

### Introduction

*Pinus caribaea* MORELET var. *hondurensis* BARRETT and GOLFARI is the exotic plantation species of major importance in Queensland, Australia. The Queensland Forest Service (QFS) has established some 48 000 ha to date (Queensland Department of Forestry, 1989), to supply saw timber and pulpwood. Genetic improvement of the species, undertaken since the early 1960s, has emphasized growth, stem and crown quality, and windfirmness (NIKLES, 1973; WOOLASTON *et al.*, 1990). Candidate plus trees are screened for wood density, spiral grain, latewood percentage, fibre

length, compression wood percentage, micellar angle and mean ring width. About 10% have been rejected on the basis of aggregate wood quality score or specifically on the basis of high grain spirality.

Major studies estimating genetic parameters for growth, stem and branch quality, and windfirmness have been reported by DEAN *et al.* (1986) and WOOLASTON *et al.* (1990). Parameters for wood quality traits, other than basic density (KANOWSKI, 1986), have not been reported previously for *P. caribaea* var. *hondurensis* in Queensland although knowledge of these parameters is necessary for efficient breeding. This paper reports preliminary estimates for a sample of the Queensland breeding population of *P. caribaea* var. *hondurensis*. The material used is of the Belize, Mountain Pine Ridge provenance.

### Materials and Methods

#### Experimental design and management

Wood samples were taken from two trials in the Experiment 467 series of the QFS, which was replicated on eight sites in coastal Queensland. The families represented in the trials originated from open pollinated seed collected from first generation plus trees selected in Queensland plantations. Details of the two trial locations sampled for this study are presented in Table 1. The parameter estimates reported are based on 471 samples taken from twenty seven families (20 trees per family), all of which were represented at Cardwell and twenty of which were represented at Elliott River.

The trials were established in a randomised complete block design. Eight blocks were established at each site. Blocks were comprised of six units; each unit containing one tree of each family as a single tree plot. The tubed seedlings were planted at a spacing of 3.0 m x 3.4 m, and

Table 1. — Details of the experimental sites sampled.

Location	Latitude/ longitude	Elevation a.s.l. (m)	Annual rainfall (mm)	Establishment date (mo/yr)	Sampling date (mo/yr)
Cardwell	18°15'S 145°55'E	20	2122	3/72	11/82
Elliott River	25°01'S 152°19'E	50	1019	3/72	3/83

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the trials were unthinned when sampled. The sampling strategy was designed to be balanced across families, blocks, and locations. Although complete balance was not possible in practice, there were few missing samples.

#### Field Methods

One unit from each of the eight blocks on each site was sampled. An additional unit was sampled from a further four randomly chosen blocks. This sampling strategy yielded twelve trees per family at each site. However, four units at the Elliott River site were excluded from the study because of severe butt sweep resulting from wind damage. Uncharacteristically small, damaged and/or severely mis-shapen trees were excluded from the study. Where a representative of the desired family was not available in the selected unit, a substitute from the closest possible unit within the same block was chosen.

Data recorded for each sample tree were diameter over bark at 1.3 m above ground (DBHOB), tree total height, and bole straightness scored on a points scale from 1 (crooked) to 6 (straight).

A twelve millimetre diametral increment core of wood was removed from the inter-whorl closest to 1.0 m above ground level for assessment of wood properties. This wood sample was obtained as either a single core bored from bark-to-bark through the pith, or as two bark-to-pith cores taken at 180°. Core sampling was at right angles to the lean of the tree or to the prevailing wind direction if no lean was detectable. All samples were sealed in plastic bags and frozen until assessed in the laboratory.

Grain angle at the cambial layer was recorded in the field through a bark window cut immediately adjacent to the core sampling point. The methods described by HARRIS (1984) were used.

#### Laboratory Methods

Basic density was measured as the ratio of oven dry weight to maximum saturated volume for individual cores using the principles of the method reported by HEINRICH and LASSEN (1970). Where radial core samples were taken, the data from the two cores were averaged to yield a mean value for the tree (with due weighting for volume differences).

Latewood percentage was estimated by lineal measurement of latewood using a 10x eyepiece graticule. It was calculated as a proportion of diametral distance without volumetric weighting.

Prior to spiral grain and compression wood measurement each moist diametral wood core was cut into radial samples. All radial core samples were planed transversely to flat, approximately parallel upper and lower surfaces. Final machined thickness was about seven millimetres.

To assess compression wood a sector (originating at the pith) was drawn on the machined surface of each core from pith to cambium. The core was then placed on a light box and the proportion of the sector affected by compression wood obtained by dot grid count. Results from the radial cores of each tree were averaged to give the compression wood percentage reading for that tree.

Grain angles were measured at the last formed latewood of growth rings 1,3,5,7 and 9 with spirality direction indicated by assigning a negative sign to left handed angles and a positive sign to right handed angles following the convention reported by HARRIS (1989). However, results

from ring 1 were not used due to a large number of missing values which arose mainly in single bark to bark sample cores which had not passed through the pith. In these samples accurate identification of ring 1 can be difficult or the size of the sample at this point becomes impractical to process. The mean grain angle for the whole tree was calculated as the mean of the absolute growth ring angles, ignoring differences in sign. Standard deviation of the spiral grain values across growth rings 3,5,7 and 9 was calculated as a measure of the within tree variability of spiral grain.

Mean ring width was determined as the mean radial distance divided by the number of annual growth rings identified in the sample.

#### Statistical Analyses

Data were pooled across the two sites and analysed by the method of least squares (HARVEY, 1960). It was necessary to logarithmically transform compression wood percentage data prior to analysis.

The model fitted is described by equation (1):

$$y_{ijm} = \mu + f_i + b_j + e_{ijm} \quad (1)$$

where  $y_{ijm}$  is the observation on tree  $m$  of family  $i$  in unit  $j$ ;

$\mu$  is the overall mean;

$f_i$  is the effect of family  $i$ ;

$b_j$  is the effect of unit  $j$ ;

$e_{ijm}$  is the normally and independently distributed random deviation of tree  $m$  of family  $i$  in unit  $j$ , with a mean of zero.

For the purposes of estimating between-family variances, this simplified model is equivalent to fitting the terms in equation (1) plus additional effects due to site and the interaction of sites and families. In this simplified model, variation due to sites is partitioned into the unit effect, and variation due to the family  $\times$  site interaction is contained in the error term. Variance components were estimated from the analysis of variance by equating the appropriate mean squares to the expectations shown in Table 2.

Table 2. — Expected mean squares for analyses of variance.

Source of variation	Degrees of freedom	Expected mean squares
Family	26	$\sigma_e^2 + 12.9\sigma_f^2$
Unit	19	not relevant
Within unit	425	$\sigma_e^2$

where  $\sigma_f^2$  is the variance component due to families;

$\sigma_e^2$  is the variance component due to random error.

The progeny within each family were assumed to be half sibs, and narrow sense heritabilities on an individual tree basis were estimated according to equation (2):

Table 3. — Site means, pooled means and standard deviations, and individual tree narrow-sense heritability estimates for selected wood and growth traits.

Trait	Cardwell mean	Elliott River mean	Pooled mean	Standard deviation	Heritability ± standard error
DBHOB (cm)	19.07	19.07	19.07	2.55	0.43 ± 0.16
Height (m)	15.37	12.76	14.50	1.86	0.25 ± 0.13
Straightness	2.21	1.37	1.93	0.81	0.22 ± 0.12
Latewood percentage	17.36	11.14	15.28	5.71	0.55 ± 0.19
Compression wood percentage	7.53	8.72	8.48	6.07	0.02 ± 0.07
Basic density (kg/m <sup>3</sup> )	442.19	421.45	435.28	34.79	0.62 ± 0.20
Mean radial ring width (mm)	8.33	8.04	8.23	1.19	0.29 ± 0.14
Spiral grain (including sign) (°)					
– ring 3	-5.12	-2.28	-4.18	2.99	0.12 ± 0.10
– ring 5	-3.97	-1.59	-3.18	3.03	0.30 ± 0.14
– ring 7	-2.75	-0.56	-2.02	3.13	0.36 ± 0.15
– ring 9	-2.15	-0.75	-1.68	3.04	0.46 ± 0.17
Spiral grain (ignoring sign) (°)					
– ring 3	5.18	2.70	4.35	2.72	0.10 ± 0.09
– ring 5	4.23	2.30	3.59	2.54	0.27 ± 0.13
– ring 7	3.40	2.00	2.93	2.29	0.25 ± 0.13
– ring 9	3.11	1.67	2.63	2.27	0.27 ± 0.13
– radial standard deviation	2.03	1.47	1.84	1.01	0.24 ± 0.12
– radial mean	3.98	2.17	3.38	2.04	0.28 ± 0.14

$$h^2 = 4\sigma_f^2 / (\sigma_e^2 + \sigma_f^2) \quad (2)$$

where  $h^2$  is the estimate of individual tree narrow-sense heritability;

$\sigma_f^2$  is the variance component due to families;

$\sigma_e^2$  is the variance component due to random error.

Following COTTERILL (1987), the resulting individual tree narrow-sense heritability estimates are appropriate to data adjusted for unit (and site) effects, as there is no variance due to units (and therefore sites) in the denominator of equation (2). Similarly, the inference population is one which is planted at both sites, as the denominator

of equation (2) contains variance due to the interaction of families and sites.

Standard errors were estimated according to SWIGER *et al.* (1964). Genetic correlations were estimated from additive genetic variances and covariances according to HAZEL *et al.* (1943), and the standard errors of these correlations according to TALLIS (1959).

### Results and Discussion

Means, standard deviations, estimates of heritabilities and their standard errors are presented in Table 3.

Estimates of phenotypic and genetic correlations, and standard errors of the latter, are presented in Tables 4 and 5.

#### Heritability estimates

The heritability estimates presented in Table 3 suggest that basic density and latewood percentage are strongly inherited; DBHOB, height, straightness, ring width and spiral are moderately so; and compression wood percentage is under little additive genetic control.

Heritability estimates for basic density, latewood percentage, spiral grain and ring width are of the order expected from studies of these traits in the southern pines (ZOBEL and TALBERT, 1984; ALLEN, 1985; MEGRAW, 1985). The high heritability estimated for basic density is consistent with the individual tree broad-sense heritability estimate previously reported for *P. caribaea* var. *hondurensis* in northern Queensland by KANOWSKI (1986).

It should be noted that the parameter estimates reported here are based on relatively few samples because the determination of wood quality characteristics is slow and expensive. They should be treated cautiously until confirmed by further work which is currently underway. Also, the age of the trial material when sampled means that the wood samples were representative of juvenile wood

Table 4. — Genetic (top right) and phenotypic (bottom left) correlations, with standard errors of each genetic correlation in parentheses.

TRAIT †	DBHOB	HEIGHT	S'NESS	% LW	% CW	BD	RW	SGSD	Mean SG
DBHOB	–	.24 (.30)	.13 (.33)	–.54 (.24)	.52 (1.01)	–.72 (.21)	.92 (.05)	–.45 (.31)	–.05 (.32)
Height	.56	–	–.01 (.38)	–.22 (.30)	2.05 (2.96)	.02 (.31)	.21 (.33)	–.10 (.37)	–.16 (.35)
S'ness	.13	.18	–	–.61 (.27)	1.31 (2.00)	–.38 (.30)	.27 (.34)	–.78 (.32)	.42 (.34)
% LW	–.14	.10	.02	–	.80 (1.35)	.62 (.16)	–.76 (.24)	.60 (.25)	–.42 (.28)
% CW	.16	.16	.07	.02	–	.15 (.78)	.41 (.96)	–.04 (.94)	–.28 (.96)
BD	–.16	.10	–.03	.56	.15	–	–.81 (.23)	.36 (.29)	.17 (.29)
RW	.91	.60	.19	–.18	.17	–.18	–	.69 (.32)	–.01 (.34)
SGSD	–.13	–.03	–.01	.12	.02	.07	–.14	–	–.23 (.35)
Mean SG	.06	–.06	.03	–.06	.03	.04	.07	.12	–

†) DBHOB = Diameter at breast height over bark. S'ness = Straightness. % LW = Latewood percentage. % CW = Compression wood percentage. BD = Basic density. RW = Mean radial ring width. SGSD = Radial standard deviation of spiral grain angles across growth rings 3, 5, 7 and 9. Mean SG = Mean of the absolute values of spiral grain angles at growth rings 3, 5, 7 and 9.

Table 5. — Genetic (top right) and phenotypic (bottom left) correlations for: spiral grain ring values using direction of spirality, spiral grain standard deviation and mean of spiral grain absolute ring values ignoring spirality direction (with standard errors of each genetic correlation in parentheses).

TRAIT †	SG3 (+/-)	SG5 (+/-)	SG7 (+/-)	SG9 (+/-)	SGSD	Mean SG
SG3 (+/-)	—	.92 (.16)	.82 (.23)	.68 (.28)	.03 (.48)	-.82 (.63)
SG5 (+/-)	.67	—	.96 (.06)	.75 (.16)	.37 (.34)	-.93 (.40)
SG7 (+/-)	.54	.75	—	.92 (.07)	.53 (.27)	-.96 (.37)
SG9 (+/-)	.41	.56	.73	—	.59 (.24)	-.79 (.33)
SGSD	-.36	.02	.27	.36	—	-.23 (.35)
Mean SG	-.71	-.77	-.75	-.68	.12	—

†) SG3 (+/-), SG5 (+/-), SG7 (+/-), SG9 (+/-) = Spiral grain angle at growth rings 3, 5, 7 and 9 respectively with sign used to denote spirality direction. SGSD = Radial standard deviation of the spiral grain values across growth rings 3, 5, 7 and 9. Mean SG = Mean of the absolute values of spiral grain angles at growth rings 3, 5, 7 and 9.

only. Further work on these trials will be needed at a later age to provide older samples for mature wood investigation. However the narrow-sense estimates presented here for wood quality traits are the best available for *P. caribaea* var. *hondurensis*. The estimates for DBHOB, height and straightness do not differ significantly from those in the larger study of growth parameters reported by WOOLASTON *et al.* (1990).

#### Genetic correlations

The genetic correlations between latewood percentage, basic density and either DBHOB or ring width suggest that increased radial growth results from an increased proportion of relatively lower density earlywood. The adverse genetic correlation between DBHOB and basic density is a source of concern. It is much more strongly adverse than that reported by KANOWSKI (1986), who found essentially no genetic relationship between growth and wood density in a full-sib study. However, the different findings may reflect a higher component of non-additive variance in the material of this present study; such discrepancies are not unexpected between estimates made from different trials on different sites (COTTERILL and DEAN, 1990). The conflicting evidence from these two studies means that clarification of the genetic relationship between growth and wood quality traits of *P. caribaea* var. *hondurensis* in Queensland must await the results of additional studies currently underway. Without substantial confirmation of this relationship from additional studies, it would seem premature to significantly amend the current tree breeding strategy because of adverse findings from one trial, even though these findings raise significant concerns.

If adverse correlations between these traits are confirmed, the breeding strategy for *P. caribaea* var. *hondurensis* in Queensland (KANOWSKI and NIKLES, 1988) would need to respond appropriately. Options available and considered for improving both wood density and growth rate in the presence of adverse correlations include: (i) the rapid introduction of the Guanaja population, which combines these characteristics (BARNES *et al.*, 1980) or (ii) the maintenance of separate high growth and high density

lines (as advocated for *P. radiata* by COTTERILL and CAMERON, 1984).

The negative genetic correlation between mean spiral grain and spiral grain ring values (Table 5) contrasts to the positive correlations between the ring values themselves. This change in sign of the correlation is a result of the individual ring values using direction of spirality (indicated by sign) whereas the mean spiral grain values are means of the absolute values of these individual ring values.

#### Spiral grain

Spiral grain angle in *P. caribaea* var. *hondurensis* characteristically changes sign (i.e. spirality changes direction) both within and between trees (QFS, unpublished; COWN *et al.*, 1981). The moderate to high phenotypic correlations between spiral grain measures (Table 5) indicate that within a tree, spirality in adjacent rings tends to be similar. This is supported by the observation that within a tree, the majority of measures are within two degrees of the radial mean (the mean radial standard deviation is 1.84 degrees, Table 3). Nevertheless, changes in sign between one or more of the readings at growth rings 1, 3, 5, 7 and 9 were recorded in the majority of trees. A consequence of this is that average spiral grain may not necessarily be a reliable guide to a tree's utilisation potential because positive and negative values will cancel when averaged. When the mean is close to zero it also presents difficulties in determining whether correlations with other traits are favorable or unfavorable. A more informative trait is the mean spirality, ignoring the sign of each ring, and this is the definition implied in the ensuing discussion. Clearly, a low mean spirality is then desirable, especially if it accompanied by a low radial standard deviation.

If an index which gives equal weighting to diameter, height and straightness in used to select plus trees, the correlations in Table 4 indicate that the mean spiral grain will increase by a negligible amount and the radial standard deviation will decrease. Therefore, emphasis on these growth and form traits is not likely to lead to significant adverse changes in spiral grain. Should it be necessary to adopt a relatively quick and inexpensive

method of screening trees for spiral grain, the correlations in *Table 5* indicate that a single reading at the seventh ring will be almost as effective a selection criterion as would the mean of rings 3, 5, 7 and 9. A single measurement of spiral grain is desirable due to the time and cost incurred in obtaining additional readings.

In this study, heritability estimates for spiral grain considering spirality direction are higher than those for absolute spiral grain (*Table 3*). We suggest that this is because some real differences between families may be masked when sign is ignored. The standard deviations of the absolute spiral grain values are less, as expected due to elimination of the variation caused by changes in spirality direction between trees.

Investigation of the degree of genetic control over mature wood values of spiral grain in *P. caribaea* var. *hondurensis* should be given high priority as trials reach sufficient age (15 to 20 years) to allow sampling of representative mature wood. COWN *et al.* (1981) recorded some very high spiral grain values, in excess of 10 degrees, in the mature wood (more than ten growth rings from the pith) of Fijian *P. caribaea* var. *hondurensis* which could significantly affect its utilisation potential for sawn products.

Further work is also required to investigate the best approaches to collection, analysis and interpretation of spiral grain results for *P. caribaea* var. *hondurensis*. It is beyond the scope of this study to reliably define such methods but these will be examined in additional studies now in progress.

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## Stochastic Dominance as an Aid to Genetic Roguing

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#### Abstract

Stochastic dominance can be used as a screening technique to divide data distributions into efficient and inefficient sets. This dichotomous division is useful in deci-

sion making where choices involve keeping or discarding certain alternatives. The procedure takes into account all moments of the distributions and is therefore particularly suited to data which are nonnormally distributed.

Stochastic dominance was used to compare loblolly pine (*Pinus taeda* L.) progeny test results. Based on age-15 volumes, stochastic dominance was judged effective in identifying poor families as early as age 5. Advantages of stochastic dominance are its simplicity and the efficient sets resulting independently of statistical confidence levels.

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