Conference. Joint meeting of working parties on breeding theory, progeny testing and seed orchards. Williamsburg, Va., USA, 12 to 19 October, 1986. 298 (1986). —— NIKLES, D. G., HAYDOCK, K. P. and RATCLIFFE, D.: Four-and-a-half-year results of an international progeny trial of *Pinus caribaea* var. *hondurensis* BARRETT and Golfari in Australia and Fiji. In: E. G. NIKLES, J. BURLEY and R. D. BARNES (Eds.). Progress and problems of genetic improvement of tropical forest trees. Department of Forestry, Queensland, Australia, and Commonwealth Forestry Insritute, Oxford, UK. 1: 281—299 (1978). —— WOOLASTON, R. R., KANOWSKI, P. J. and NIKLES, D. G.: Genetic parameters for *Pinus caribaea* var. *hondurensis* in coastal Queensland, Australia. Silvae Genetica 39: 21—28 (1990).

Genotype-Environment Interactions in Pinus caribaea var. hondurensis in Queensland, Australia

II. Family x Site Interactions

By R. R. WOOLASTON[1]), P. J. KANOWSKI[2]) and D. G. NIKLES[3])

Queensland Forest Service, Indooroopilly,
Queensland, 4068, Australia

(Received 14th January 1991)

Summary

Family x site interactions were investigated in a large open pollinated progeny test of *Pinus caribaea* var. *hondurensis* planted at eight coastal sites in Queensland. Families were classified into populations according to their origin and were measured approximately six years after planting. Of the 210 families in the experiment, 85 were involved in this study, representing the three largest populations. Between-site genetic correlations for straightness score were high (average 0.83) compared with those for diameter (0.59). Diameters at the northern-most site were poorly correlated genetically with those at other sites (average 0.39) and this may have been due to heavy grass competition. Had individual selection been based at this site for planting at any of the other sites, the estimated genetic gain would have been only 29% to 57% as efficient as a selection programme based at the plantation site. Similarly, a selection programme based at any of the other sites would have been only 25% to 45% effective in improving diameter at the northern site. No one site was consistently superior as a selection site.

With the possible exception of the northern-most site, family x location interactions were not of sufficient magnitude to justify the formation of sub-populations for each latitudinal region. Selection index calculations indicated that for the purposes of estimating breeding values pertaining to the entire plantation, there is little need to establish more than three replicates of a progeny test.

Key words: *Pinus caribaea* var. *hondurensis*, genotype-environment interaction, genetic parameters, breeding strategy.

Introduction

The 50 000 ha of *Pinus caribaea* MORELET var. *hondurensis* BARRETT and GOLFARI (Pch) plantations in Queensland span a wide latitudinal range and include a variety of soil types (WOOLASTON et al., 1991). Historically, the Pch breeding population has been replicated in a variety of sites to safeguard against losses from localized phenomena such as cyclonic winds and to allow a flexible response to any important family x environment interactions. As part of a major review of the Pch breeding strategy in Queensland (KANOWSKI and NIKLES, 1988), an assessment of the importance of family x site interactions was necessary.

In a companion paper, WOOLASTON et al. (1991) found that the populations into which the Queensland Pch families are grouped appeared to rank similary across all sites examined. However interactions must also be examined at the family level, to determine the relevance of progeny tests at any particular site to the overall breeding programme. As the progeny tests also serve as source of selections for the ensuing generation, the likely effects of interactions on individual selection are also of interest.

An informative method for interpreting interactions was devised by FALCONER (1952) and applied to tree breeding by BURDON (1977, 1979), whereby performance at each site is treated as a separate, genetically correlated trait. Although an individual tree can obviously be planted at only one site, this methodology allows one to estimate the genetic correlation between its performance at that site and its performance at another site, had that same tree been planted there. Using conventional selection index theory, genetic gains from individual selection can be predicted from the genetic variance — covariance matrix. Similarly, gains can be predicted when individual selection is augmented by family information from any site, or when family information is used in a progeny test. With appropriate economic weights, gain can be predicted at any or all plantation sites, depending on the breeding objective. Sites which are not representative of the target plantation locality can be accorded an economic weighting of zero. As a refinement of this approach, economic weights can be defined according to the degree to which each test site reflects the characteristics of the plantation site.

In this paper we use this methodology to estimate the relevance of genotype x environment interactions to both individual selection and progeny tests and consider the implications for the breeding programme.

Materials and Methods

The progeny tests on which these analyses were based are part of the Experiment 567 series of the Queensland

---

[1]) Present address: CSIRO Pastoral Research Laboratory, Armidale, NSW 2350, Australia

[2]) Present address: Oxford Forestry Institute, University of Oxford, Oxford OX1 3RB, England

[3]) Queensland Forest Service, PO Box 631, Indooroopilly, Queensland, 4068, Australia

Table 1. — Total number of families in each population in these analysis.

Set	Population	Seed source	Origin	Number of families
1	1	ortet	Queensland plantations	37
2	5	ramet	Queensland plantations	24
2	6	ramet	Congo plantations	24

Table 2. — Details of relevant progeny trials in the series.

Site name	Code	Set	Latitude and Longitude	Elevation a.s.l. (m)	Annual rainfall (mm)	Establishment date
Cardwell Ridge	cr	1,2	18° 15' S 145° 55' E	20	2122	February 1980
Byfield Ridge	br	1,2	22° 50' S 150° 45' E	50	1625	March 1980
Byfield Swamp	bs	1,2	22° 50' S 150° 45' E	50	1625	March 1980
Wongi Swamp	ws	1,2	25° 27' S 152° 35' E	35	986	March 1980
Tuan Swamp	ts	1	25° 38' S 152° 47' E	20	1393	March 1980
Toolara Ridge	tr	1,2	25° 53' S 152° 50' E	50	1369	April 1980
Glasshouse Swamp	gs	1,2	26° 48' S 153° 05' E	10	1590	July 1980
Glasshouse Ridge	gr	1,2	27° 05' S 153° 05' E	20	1337	May 1980

Forest Service. The composition, location, design and assessment of these tests were described by Woolaston et al. (1990). Only a summary is presented here.

The 210 open pollinated families in this experiment comprise eight populations, each population representing a particular seed source. In the field, populations were grouped into three sets according to origin. For the analyses reported here, only two sets are included (*Table 1*), as the third had not been measured at a sufficient number of sites at the time of analysis. This grouping of families into sets enabled each test to be kept to a tractable size (where a test is defined as a set established at a particular location). The experiment was planted in 1980 and replicated at eight locations in coastal Queensland. All eight set 1 tests and seven of the set 2 tests were sufficiently developed to be included in these analyses.

Details of the tests included in these analyses are presented in *table 2*. Each test was established in a randomized complete block design. Blocks contained six trees from each family arranged in single tree plots, with eight blocks at all sites except Glasshouse Ridge, which contained only four blocks.

Although heights were measured at some sites, they are not included in these analyses, as they were highly correlated with diameter and were not recorded at all sites (Woolaston et al., 1990).

Statistical Methods

When population x site interactions are negligible, family means can be adjusted for population effects and adjusted family means can then be pooled for correlation analysis. However in the presence of significant population x site interactions, pooling will lead to incorrect estimates of within-population genetic correlations. Under these circumstances, correlations must be calculated within each population. As shown in the companion paper (Woolaston et al., 1991), these interactions were significant, so it was decided to estimate correlations within those populations that provided the most complete representation of families over the availables sites: population 1 (Queensland open pollinated ortets, or Qld opo) in set 1 and populations 5 (Queensland open pollinated ramets, or Qld opr) and 6 (Congo opr) in set 2.

Pairwise correlations between least-squares family means from different sites were calculated, and between-site genetic correlations were derived from these using equation 5 of Burdon (1977):

(Equation 1)

$$rg_{xy} = r_{xy}/(h_{fx} \cdot h_{fy})$$

where rg_{xy} is the genetic correlation between environments x and y

r_{xy} is the correlation between family means at x and y

h_{fx} and h_{fy} are the square roots of the heritabilities of family means at x and y.

The heritabilities of family means in *equation 1* were calculated using the formula given in Falconer, (1967, *Table 13.3*):

(Equation 2)

$$h^2_f = h^2 (1 + (n-1)r)/(1 + (n-1)t)$$

where h^2_f is the heritability of family means

h^2 is the individual heritability

n is the family size

r is the coefficient of relationship (assumed to be 0.25 for half-sibs)

t is the correlation of phenotygic values of members of the families.

The efficiency of individual selection at site x for planting at environment y relative to both selection and planting at y is given by the standard formula for indirect selection (*equation 19.7*, Falconer, 1967), assuming equal selection intensities:

(Equation 3)

$$\text{Efficiency} = rg_{xy}\, h_x/h_y$$

where rg_x is the genetic correlation between environments x and y

h_{xy} and hy are the square roots of the individual heritabilities at x and y.

The heritabilities substituted in *equations 2* and *3* were those estimated for each site by Woolaston et al (1990).

Selection index calculations for the accuracy of progeny tests were made using the procedure described by Cunningham (1969). For the gain calculations, a breeding objective of improving diameter was assumed, with improvement at all sites equally important. This assumption corresponds closely to the current breeding objective for Pch in Queensland, which is to maximize growth while at least maintaining stem straightness (Kanowski and Nikles, 1988). Genetic parameters from set 1 were used and each progeny test was assumed to contain 48 trees per family. When the accuracies of progeny tests planted at two or more sites were compared, it was assumed that the tests were planted in separate latitudinal regions, as shown in *table 2*, viz 18^0, 22^0 or 25^0 to 27^0 S.

Table 3. — Between-site genetic correlation estimates for diameter (above diagonal) and straightness (below diagonal) in Queensland open pollinated ortet families.

Trial	br1	bs1	cr1	gr1	gs1	tr1	ts1	ws1
br1		0.76	0.49	0.75	0.88	0.82	0.82	0.84
bs1	0.49		0.27	0.28	0.54	0.65	0.85	0.59
cr1	0.44	0.88		-0.04	0.21	0.06	0.31	0.58
gr1	0.75	1.00	0.79		0.79	0.89	0.74	0.46
gs1	0.83	0.94	0.85	0.96		0.76	0.60	0.54
tr1	1.00	1.00	0.81	0.69	0.92		0.68	0.50
ts1	-	-	-	-	-	-		0.98
ws1	0.38	0.81	0.81	0.86	0.92	0.83	-	

Table 4. — Between-site genetic correlation estimates for diameter (above diagonal) and straightness (below diagonal) in Queensland open pollinated ramet families.

Trial	br2	bs2	cr2	gr2	gs2	tr2	ws2
br2		1.00	0.36	1.00	1.00	0.95	0.81
bs2	0.73		0.52	1.00	1.00	1.00	0.90
cr2	1.00	0.54		0.54	0.63	0.60	0.37
gr2	0.93	0.90	0.97		0.67	0.95	0.80
gs2	1.00	0.73	1.00	1.00		0.90	0.97
tr2	-	-	-	-	-		0.84
ws2	0.89	0.67	1.00	0.88	1.00	-	

Table 5. — Between-site genetic correlation estimates for diameter (above diagonal) and straightness (below diagonal) in Congo open pollinated ramet families.

Trial	br2	bs2	cr2	gr2	gs2	tr2	ws2
br2		0.82	0.46	0.45	0.19	0.53	0.57
bs2	0.58		0.52	0.53	0.59	0.77	0.91
cr2	1.00	1.00		0.19	0.46	0.31	0.53
gr2	0.80	0.59	0.93		0.89	0.47	0.84
gs2	1.00	0.58	1.00	0.74		0.71	0.75
tr2	-	-	-	-	-		0.83
ws2	0.97	0.44	1.00	0.78	0.91	-	

Results

Genetic correlations

Estimates of between-site genetic correlations are shown in *tables 3, 4* and *5*. In these tables, estimates that were greater than unity (and thus theoretically impossible) are reported as 1.00. The number of pairs of families varied from 26 to 35 for Qld opo, 19 to 23 for Qld opr and 22 to 24 for Congo opr.

In Qld opo families (*Table 3*), estimates for between-site genetic correlations for diameter ranged from —0.04 to 0.98. Correlations involving the Cardwell site (cr1) were generally lower than other correlations. On average, genetic correlations for straightness were higher than for diameter, varying from 0.38 to 1.00, and with no obvious trends in the size of the estimates.

As with Qld opo families, correlations for diameter in Qld opr families in volving the Cardwell site (cr2) were generally lower than other correlations (*Table 4*). Similarly, genetic correlations for straightness showed no clear trends but were generally higher (range 0.54 to 1.00) than those for diameter (0.36 to 1.00).

Genetic correlations in Congo opr families also showed the same trends for diameter, with correlations involving the Cardwell site being lower than average (*Table 5*). Again, the genetic correlations for straightness were generally higher (range 0.44 to 1.00) than those for diameter (0.19 to 0.91).

Efficiency of individual selection

The efficiencies of selecting for diameter at one site and planting in another are shown in *table 6*. Comparable efficiencies for straightness are shown in *table 7*. For purposes of brevity, only marginal means are tabulated for Qld opr and Congo opr families. With the exception of comparisons involving br1, estimated efficiencies in Qld opo families were higher for straightness than for diameter (*Tables 6* and *7*). In almost all instances it would have been less efficient to select at a site other than the site of planting. This was the case in 55 of the 56 combinations for diameter and 34 of 42 combinations for straightness (*Tables 6* and *7*). No one site appeared to be superior as a selection site for both diameter and straightness. Efficiencies involving diameter at the Cardwell site generally appeared lower than those involving other sites, although this was not the case for straightness. If progeny were to be planted at the Cardwell site (cr1), then selection for diameter at another site is only 25% as efficient as selection at Cardwell itself, on average. Similarly, if selection for diameter was based at Cardwell for planting elsewhere, the efficiency is poor (29% versus 50% to 73% for other sites).

For Qld opr families, there was also a tendency for efficiencies to be higher for straightness than for diameter (*Tables 6* and *7*), but the trend was less consistent than for Qld opo families. In 32 of the 42 combinations, selection for diameter was less efficient at a site other than the planting site, as was the case with 21 of the 30 combinations for straightness. Again Cardwell appeared to be an inefficient site to select for diameter if planting is to be on another site, an average of 57% versus 82% to 89% for other selection sites. If selection for diameter was based at another site for planting at Cardwell, the efficiency was also poor, at 45% versus 73% to 97% for other planting sites.

In Congo opr families, estimates of the efficiency of selection for diameter at a site other than the planting site were all less than or equal to 1.00. For straightness, this was also the case for 22 of the 30 combinations.

Accuracy of progeny tests

The accuracy of progeny tests at one, two or three sites relative to tests in each of the eight sites are shown in *table 8*.

Index calculations summarized in *table 8* indicate that a single progeny test at one site will give 47% (cr1) to 93% (br1) of the accuracy expected when all eight sites are used. Part of the reason that these figures are less that 100% is that a smaller number of trees are involved when only one site is used. Had it been possible to plant 384 (= 8 x 48) trees from each family at each site to equal the total number when all sites are used, the theoretical accuracies increase slightly to a range of 49% (cr1) to 103% (br1). Combinations of two test sites, with each in a different latitudinal region, were 73% (cr1 and bs1) to 96% (br1 and ts1) as accurate as testing in all eight sites. Similarly, combinations of three test sites were 88% (cr1, bs1 and ws1) to 97% (cr1, br1 and ts1) as accurate as eight test sites (*Table 8*). The relative accuracies shown in *table 8* are also applicable to the value of half-sib information in a combined selection index.

Discussion

Despite the fact that straightness is a subjectively assessed trait and it was scored by at least four separate teams, family rankings in this trait were less affected by environment than were rankings for diameter. This result is similar to that reported for *Pinus radiata* D. Don by Johnson et al. (1988). The majority of between-site genetic correlation estimates for straightness were above 0.8. At this level, very few changes in family rankings would be expected between sites. Many of the estimates for diameter were also high. Bearing in mind the sampling errors of such estimates and that the average would be biased down slightly by forcing the parameters to be in the permissible space, most of the correlations were within an operationally acceptable range. As pointed out by Matheson and Raymond (1984), the genetic correlation between performance at a particular site with that at an adjacent site is not likely to be perfect, nor is the correlation with performance from plantings in other years at the same site.

In general, correlations were higher than those reported by Johnson et al. (1988) and similar in magnitude to the earlier reports for Pch by Eisemann and Nikles (1983). The most notable exceptions were the correlations involving the Cardwell tests. In the early years after planting, these tests were heavily infested with blady grass (*Imperata cylindrica* var. *major* (Nees) C. E. Hubbard) and we expect that this has probably influenced the results. The families that excelled at Cardwell were probably those that could compete under adverse conditions. There is insufficient information in these data to indicate whether or not the same rankings would apply in the absence of strong competition from blady grass. However, the fact that neither Nikles et al. (1978) nor Eisemann and Nikles (1983) found that families behaved appreciably differently at Cardwell suggests that blady grass may indeed have had an effect on these particular tests. It is interesting to note from Woolaston et al. (1990) that the heritability of diameter at Cardwell was higher than at any of the other sites. This reinforces the need to treat performance at each site a trait correlated with that at others, and to look beyond the heritability estimate as an indicator of a site's relevance to the breeding programme.

Table 6. — Efficiency of selection for diameter at environment X for performance at environment Y for trials involving families from Queensland open pollinated ortets, with marginal means. Mean correlations are also shown for families from Queensland and Congo open pollinated ramets.

Selection Site (X)	Planting Site (Y) br	bs	cr	gr	gs	tr	ts	ws	Population means Qld opo	Qld opr	Congo opr
br		0.82	0.44	0.71	0.82	0.75	0.81	0.75	0.73	0.82	0.48
bs	0.71		0.22	0.25	0.47	0.55	0.78	0.49	0.50	0.89	0.66
cr	0.55	0.33		-0.04	0.22	0.06	0.34	0.58	0.29	0.57	0.46
gr	0.79	0.32	-0.04		0.78	0.86	0.78	0.44	0.56	0.83	0.57
gs	0.94	0.62	0.20	0.80		0.74	0.64	0.52	0.64	0.84	0.56
tr	0.90	0.77	0.06	0.92	0.78		0.73	0.49	0.66	0.89	0.61
ts	0.83	0.93	0.28	0.71	0.56	0.63		0.88	0.69	-	-
ws	0.94	0.71	0.58	0.49	0.56	0.51	1.09		0.70	0.84	0.79
Mean Qld opo	0.81	0.64	0.25	0.55	0.60	0.59	0.74	0.59			
Mean Qld opr	0.89	0.97	0.45	0.83	0.94	0.86	-	0.73			
Mean Congo opr	0.53	0.73	0.37	0.56	0.64	0.60	-	0.70			

Table 7. — Efficiency of selection for straightness at environment X for performance at environment Y for trials involving families from Queensland open pollinated ortets, with marginal means. Mean correlations are also shown for families from Queensland and Congo open pollinated ramets.

Selection Site (X)	Planting Site (Y) br	bs	cr	gr	gs	tr	ts	ws	Population means Qld opo	Qld opr	Congo opr
br		0.51	0.40	0.72	0.73	1.00	-	0.36	0.62	0.89	0.85
bs	0.47		0.75	0.91	0.78	0.95	-	0.72	0.76	0.73	0.68
cr	0.49	1.03		0.85	0.83	0.90	-	0.85	0.83	0.72	0.79
gr	0.78	1.20	0.73		0.87	0.72	-	0.84	0.86	1.01	0.83
gs	0.95	1.13	0.87	1.06		1.05	-	0.98	1.01	0.98	0.88
tr	1.00	1.05	0.73	0.66	0.81		-	0.78	0.84	-	-
ts	-	-	-	-	-	-		-	-	-	-
ws	0.40	0.91	0.77	0.88	0.86	0.88	-		0.78	1.04	0.97
Mean Qld opo	0.74	0.98	0.70	0.84	0.80	0.92	-	0.76			
Mean Qld opr	0.94	0.71	1.14	0.88	0.93	-	-	0.77			
Mean Congo opr	0.90	0.61	1.24	0.72	0.82	-	-	0.70			

Table 8. — Accuracy of progeny tests at one, two or three sites relative to progeny tests at each of the eight sites. The relative accuracies are also applicable to the value of halb-sib information in a combined selection index. A breeding objective of improving diameter at all sites is assumed.

One site	Gain	Two sites		Gain	Three sites			Gain
br1	93%	br1	gr1	94%	cr1	br1	gr1	96%
bs1	65%	br1	gs1	94%	cr1	br1	gs1	94%
cr1	47%	br1	tr1	95%	cr1	br1	tr1	96%
gr1	72%	br1	ts1	96%	cr1	br1	ts1	97%
gs1	79%	br1	ws1	95%	cr1	br1	ws1	95%
tr1	80%	bs1	gr1	88%	cr1	bs1	gr1	96%
ts1	79%	bs1	gs1	86%	cr1	bs1	gs1	87%
ws1	83%	bs1	tr1	84%	cr1	bs1	tr1	92%
		bs1	ts1	82%	cr1	bs1	ts1	86%
		bs1	ws1	88%	cr1	bs1	ws1	88%
		cr1	br1	93%				
		cr1	bs1	73%				
		cr1	gr1	88%				
		cr1	gs1	86%				
		cr1	tr1	90%				
		cr1	ts1	84%				
		cr1	ws1	83%				

Averaged across the three populations and both traits, Wongi swamp (ws) appeared be the most efficient site at which to practise individual selection (85%) if progeny were to be planted at another site. Cardwell (cr) was the least efficient (61%). Byfield ridge (br) and Glasshouse swamp (gs) appeared to be the least sensitive to off-site selection (average 79% efficient) and Cardwell the most sensitive (69%). Perhaps more notable than these differences in average efficiency was the fact that no one site was consistently superior.

We conclude from calculations similar to those summarized in *table 8* that, for the purposes of estimating breeding values, there is little need to establish more than three replicates of a progeny test of Pch in Queensland. These results would also apply to other populations characterized by similar genetic parameters. The genetic information gained from three test sites may be less than that gained from eight test sites (average 93%, *Table 8*), but less than 40% of the resources are required to achieve this figure. Although this experiment has contributed greatly to our knowledge of genetic parameters and genotype-environment interactions, there would appear to be scope in future experiments for reducing the number of test sites. The breeding strategy for Pch in Queensland (Kanowski and Nikles, 1988) proposed a reduction in the number of test sites, in accordance with these results.

With the possible exception of the Cardwell site, family x location interactions were not sufficient magnitude to justify the formation of sub-populations for each latitudinal region. Studies on more recently established tests should indicate whether the apparently severe interactions involving diameter at the Cardwell site are a general phenomenon or whether this study describes an unusual situation brought about by early grass infestation.

Acknowledgements

The tests on which these analyses are based are part of the research programme of the Queensland Forest Service. We thank the many staff of the Tree Breeding Section for their tireless work in establishing, maintaining and assessing the tests and processing the data. We also thank the Conservator of Forests for permission to publish these results.

References

Burdon, R. D.: Genetic correlation as a concept for studying genotype-environment interaction in forest tree breeding. Silvae Genetica 26: 168—175 (1977). —— Burdon, R. D.: Generalisation of multi-trait selection indices using information from several sites. New Zealand J. Forest Science 9: 145—152 (1979). —— Cunningham, E. P.: The relative efficiency of selection indices. Acta Agriculturae Scandinavia 19: 45—48 (1969). —— Eisemann, R. L. and Nikles, D. G.: Population-environment interactions in *Pinus caribaea* var. *hondurensis* in Queensland and elsewhere and their implications for local and regional breeding programmes. Pap. to XV Pacific Science Congress, Dunedin, New Zealand, 1 to 11 February, 1983. 26p. (1983). —— Falconer, D. S.: The problem of environment and selection. The American Naturalist 86: 293—298 (1952). —— Falconer, D. S.: Introduction to Quantitative Genetics. Oliver and Boyd, London 365p (1967). —— Johnson, R., Volker, P. and Pederick, L.: Proc., 10th Meet. Res. Work. Group No. 1, Aust. For. Council, Gympie, Queensland, 30 October to 4 November 1988. 187—190. (1988). —— Kanowski, P. J. and Nikles, D. G.: A summary of plans for continuing genetic improvement of *Pinus caribaea* var. *hondurensis* in Queensland. Paper to IUFRO Meeting: Breeding Tropical Trees. Pattaya, Thailand. 28 November to 2 December 1988. 18p. (1988). —— Matheson, A. C. and Raymond, C. A.: The impact of genotype x environment interactions on Australian *Pinus radiata* breeding programs. Australian Forest Research 14: 11—25 (1984). —— Nikles, D. D., Haydock, K. P. and Ratcliffe, D.: Four-and-a-half-year results of an international progeny trial of *Pinus caribaea* var. *hondurensis* Barrett and Golfari in Australia and Fiji. In: D. G. Nikles, J. Burley and R. D. Barnes (Eds.). Progress and problems of genetic improvement of tropical forest trees. Department of Forestry, Queensland, Australia, and Commonwealth Forestry Institute, Oxford, UK. 1: 281—299 (1978) —— Woolaston, R. R., Kanowski, P. J. and Nikles, D. G.: Genetic parameters for *Pinus caribaea* var. *hondurensis* in coastal Queensland, Australia. Silvae Genetica 39: 21—28 (1990). —— Woolaston, R. R., Kanowski, P. J. and Nikles, D. G.: Genotype-environment interactions in *Pinus caribaea* var. *hondurensis* in Queensland, Australia. I. Population x site interactions. Silvae Genetica 40 (1991).

Genetic Parameters for Wood and Growth Properties in Araucaria cunninghamii

By K. J. Harding[1]) and R. R. Woolaston[2])

Queensland Forest Service, 80 Meiers Road,
Indooroopilly, 4068, Queensland, Australia

(Received 16th January 1991)

Summary

All available information on genetic variation in wood properties of Queensland hoop pine is drawn together and examined. Results come from two half-sib progeny trials and one full-sib progeny trial, all about 15 years old.

Previously reported parameter estimates, from an earlier wood study on one of the half-sib progeny trials containing 25 families, were supported with new results from 22 families of which 17 were unrelated to the families in the earlier trial. Pooled narrow-sense heritability estimates obtained from the combined data of the two half-sib progeny trials were 0.60 for basic density, 0.19 for per cent compression wood, 0.36 for mean spiral grain, 0.17 for diameter and 0.58 for straightness. Approximate standard errors of the four estimates ranged from 0.10 to 0.16. Heritability of grain spirality at six equally spaced points from pith to bark averaged about 0.20 but peaked at 0.35 (approximate s.e. = 0.12) for the third sampling point from the pith, where average spirality was greatest.

Selection procedures that emphasize growth and straightness and ignore wood quality traits are likely to increase basic density, decrease spiral grain and lead to a small increase in compression wood. Improvements in spiral grain and compression wood can be ensured by further selecting plus tree candidates for these wood traits. However, genetically controlled increases in density can probably only be restricted by decreasing the rate of improvement in straightness.

Estimation of non-additive or dominance variance, by comparing the components of variance of the full-sib and half-sib results, was not successful. Negative estimates of dominance variance for compression wood and mean spiral grain, as well as high standard errors associated with all estimates, call into question the value of this technique. It should be further examined in a larger data set, representing larger numbers of families, to better test its validity.

Offspring-parent regressions suggest that screening plus trees for basic density and spiral grain could be effective in providing a genetic ranking for these parameters, even though the plus trees may be of different ages and growing in different environments.

Key words: Araucaria, heritability, correlation, growth, straightness, wood properties.

Introduction

Hoop pine (*Araucaria cunninghamii* Aiton ex D. Don) is noted for its high quality timber (Smith, 1980) suited for veneer, joinery, particle board and structural products (Dean *et al.*, 1988). However, for practical reasons, little emphasis has been placed on wood properties for first- and second-generation plus tree selections as part of a hoop pine breeding programme in south-east Queensland, Australia. Rather, selection has focussed on improving growth rate and tree form (Nikles *et al.*, 1988), with a second-stage screening to eliminate trees with undesirable grain spirality. No changes in basic density have been

---

[1] Currently at: Department of Forestry, North Carolina State University, Box 8002, Raleigh, NC 27695-8002, USA

[2] Now at: CSIRO Pastoral Research Laboratory, Private Bag, P.O., Armidale, 2350, NSW, Australia