

for general plantation programmes for Valparei and areas having similar eco-climates. The future selective breeding of *E. grandis* should utilize Paluma and other provenances as a source of breeding population for selections. The inferiority in performance of the Valparei local seed source may be due to inbreeding because the original population may have been established from seed from a small number of parent trees.

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Genetic Control of Fifth Year Traits in *Pinus patula* Schiede and Deppe

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Summary

Polycross, factorial and diallel mating designs were used in the genetic improvement programme for *Pinus patula* SCHIEDE and DEPPE in ZIMBABWE. Their function was to elucidate genetic structure and control in economically important traits, to investigate genotype-environment interaction, to identify the best general combiners and to provide information on the efficiency of mating and experimental designs. Productivity, stem straightness and crown traits were measured in the fifth year from planting in the field. Analysis of the data showed that all traits were under multigenic control with practically insignificant contributions from dominance, maternal or reciprocal effects. Family heritability estimates were highest for the branch traits (up to 0.85, 0.80, 0.91 and 0.91 for branch basal area, total number and number per whorl and internode length respectively) but also high for stem volume (up to 0.82) and moderate for stem straightness (up to 0.67). Genotype-environment (locality) interaction could be of practical value for stem volume but was absent for stem straightness and the branch traits. There was no genotype-year interaction. Sub-blocking made no practical contribution to the precision of ranking the families but use of the lattice design might mean that the same precision of comparison could be achieved for some traits in some environments with experimental plantings that were up to 25% smaller. The assumption of half-sib relationship within families in the polycross was shown to be valid and the test was an efficient one to rank parents for general combining ability. The only adverse genetic correlation was a positive one between the amount of sinuosity in the upper stem in the second year and stem volume in the fifth year. Otherwise there were very strong genetic correlations between height and diameter in the second year and the same traits in the fifth year (0.94 (s.e. 0.06) and 0.94 (s.e. 0.09) respectively); and the same applied to the branch traits, internode length and total number of branches (0.85 (s.e. 0.11) and 0.91 (s.e. 0.06) respectively). The conclusion is that in the fifth year after planting, there are still strong indications that substantial and rapid genetic gain should be available for *P. patula* through

early selection for general combining ability using conventional breeding methods.

Key words: Progeny tests, diallel, factorial mating design, polycross test, genetic correlations, juvenile-mature correlations, triple lattice design, genotype-environment interaction, general combining ability, specific combining ability.

Introduction

The genetic improvement programme for *Pinus patula* SCHIEDE and DEPPE in Zimbabwe (then Rhodesia) started in 1958. It included the use of polycross, factorial and reciprocal mating designs for progeny testing and estimating genetic parameters in the first generation of plus trees selected from unimproved plantations. The aim was to identify parents with high general combining ability (*gca*) and to provide genetic information on the local population (BURLEY *et al.*, 1966). Controlled crosses for this plan were completed in 1967 and progeny tests were planted between 1967 and 1972 (BARNES, 1973). Nursery assessments were made and the data analysed and published (BARNES and SCHWEPENHAUSER, 1978) as were the data from extensive assessments made at 1.5 years after planting in the field (BARNES and SCHWEPENHAUSER, 1979). In this paper we report on results of analyses of growth, stem and branch form traits measured at 4.5 years including estimates of juvenile-mature correlations.

Materials and Methods

The plus tree population, mating design, progeny test localities and environmental design of the experiments have been fully described previously (see BURLEY *et al.*, 1966; BARNES, 1973; BARNES and SCHWEPENHAUSER, 1978 and 1979). For easy reference the mating design is repeated here in *figure 1*. Basic environmental design was randomized complete block, with superimposed lattice at the principle localities, with three replications of 10-tree line plots at 2.44 m square spacing. The polycross (controlled crosses between the seed parent and a 20-pollen mix) was repeated over two years at two localities and in each case was a double triple lattice. The factorial (controlled crosses between 9 seed parents and 5 pollen testers) was planted at the same two localities in one year as single triple lattices. The diallel (controlled crosses among five parents with reciprocals but without selfs) was planted as

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an integral part of the factorial experiment at the two main sites and extended to two additional localities on its own.

In the fifth year, crown competition in *P. patula* starts to cause branches in the lower whorls to become moribund and pruning becomes necessary for access and for restriction of the knotty core in the basal log. It was therefore the last stage at which crown characteristics could be measured on that part of the stem that has the highest value. The opportunity was taken at this assessment to make detailed branch measurements as well as assessing the usual characteristics of height, diameter and stem straightness. No thinning or pruning was carried out in the trials before assessment and all traits were measured on all 10 trees in each plot. The branch traits were assessed in only one triple lattice in each year, at each locality. The measured and derived traits are described in table 1.

The generalized form of the fully random models of the analyses of variance and covariance, the statistical procedures and the genetic interpretation of the results have been given previously (BARNES, 1973; BARNES and SCHWEPENHAUSER, 1978 and 1979, *q.v.*). The genetic correlations were estimated from the maternal parents component in the analysis of covariance.

		Pollen parent code number							
		MP	5	25	14	20	31	44	51
Seed parent code number	14	P				R	R	R	R
	20	P				R		R	R
	31	P				R	R		R
	44	P				R	R	R	
	51	P	F	F		RF	RF	RF	R
	1	P	F	F	F	F	F		
	2	P	F	F	F	F	F		
	7	P	F	F	F	F	F		
	15	P	F	F	F	F	F		
	26	P	F	F	F	F	F		
	27	P	F	F	F	F	F		
	32	P	F	F	F	F	F		
	48	P	F	F	F	F	F		
	6	P							
	12	P							
	16	P							
	30	P							
	34	P							
	52	P							
	63	P							
	5	P							
	17	P							
	19	P							
	21	P							
	25	P							

P — polycross test planted 1967/1968 and 1968/1969
 F — factorial test planted 1968/1969
 R — reciprocal test planted 1968/1969

Figure 1. — Mating designs for *Pinus patula* progeny tests.

Results and Discussion

Analyses of variance for selected 4.5-year-old traits in the polycross, factorial and diallel are given in tables 2, 3 and 4 respectively. The data are for the contribution of each source to total variation and the total variance itself; this, with the degrees of freedom, makes it possible for the reader to construct an approximation to the complete analysis of variance table. Negative estimates have been entered as zero. Significance of the F-test for families in the analysis of variance for individual localities is also shown for the polycross and factorial tests. Other statistics given for these two tests are family means, ranges, standard errors, coefficients of variation, repeatabilities over localities and years, heritabilities, blocking efficiencies and Spearman's rank correlation coefficients for adjusted and unadjusted means.

Genetic, genotypic and phenotypic correlations between fifth-year traits are given in table 5 and those between nursery and fifth and second and fifth year traits in tables 6 and 7 respectively. In each of these tables, those genetic correlations where the standard errors are approximately a third or less of the size of the correlation coefficient itself, and therefore likely to be of practical significance, are highlighted. All these correlations are based on the experiments at Martin. Early bird damage in the Stapleford trial resulted in irregularities that were thought to have caused erratic correlation coefficients with large standard errors.

Analyses, means, heritabilities and correlations are based on the randomized complete block design. Means adjusted by using the sub-blocking information from the triple lattice design have been used to rank families and parents for second generation selections but here it is simpler to indicate the value of the triple lattice design through the blocking efficiency term and to use variance components for construction of genetic parameters unconfounded with the environmental correlations of the lattice design (BARNES, 1973).

Genetic control of traits

The polycross test showed all eight traits to be under a high degree of *gca* control with family variance statistically highly significant and family heritabilities over localities and years ranging from 0.58 for height (HGT5) to 0.85 for branch basal area (BBA5). Parental variances were not as high in the factorial test except for internode length (AIL5) and number of branches (B/H5). With more trees to represent each parent, the factorial should be more precise but there were 24 parents represented in the polycross as opposed to 2 sets, 1 of 9 and 1 of 5, in the factorial, and it is likely that this lack of agreement was due to a sampling effect and the greater variation in the polycross families reflected in the sizes of the coefficients of variation shown in tables 2 and 3. Internode length and total branch number were under particularly strong genetic control. Specific combining ability (*sca*) effects were virtually absent in both the factorial and diallel tests as were maternal and reciprocal effects in the diallel.

Genotype-environment interaction — (*gei*)

Genotype-locality interaction effects were statistically significant for stem volume (VOL5) and one or other of its components (HGT5 and CAQ5) in all three tests and could be of practical significance as, on the average, they accounted for a share of the variance equivalent to a third or a half of that contributed by *gca*. Genotype-

Table 1. — Descriptions of measured and derived traits.

TRAIT	DESCRIPTION	UNIT
Nursery traits		
CON	Number of cotyledons at 6 weeks	count
COL	Average length of cotyledons at 3 months	mm
NH12	Total seedling height at 12 months	cm
1.5-year-old-traits		
HT12	Height to leader bud minus post-planting	m
CAQ2	Circular area of stem at a quarter of total height	cm ²
VOL2	Total stem volume - (total height x CAQ x VFF)	dm ³
SIN2	Stem sinuosity index - (assessed on that part of the stem between the leader tip and the third whorl of branches from the tip) - (category 1 = slight deviation to 3 = severe deviation, multiplied by the frequency of deviations in the category, summed for the tree and subtracted from 20 so that the less the sinuosity of the stem the higher the numerical value)	index
BD12	Total branch x-sectional area in that whorl contributing most to crown	cm ²
BL12	Total branch length in that whorl contributing most to crown	m
BA12	Average branch angle (90° = 10.0) in that whorl contributing most to crown	9°
AIL2	Average internode length - (excludes that section between the ground and the first whorl)	cm
ABW2	Average number of branches per whorl - (based on total number of branches on the tree)	number
B/H2	Number of branches per metre of height - (total number of branches/total height)	number
4.5-year-old traits		
HGT5	Total height	m
CAQ5	Circular area of stem at breast height (1.3 m)	cm ²
VOL5	Total stem volume over bark - (total height x CAQ x 0.45)	dm ³
STR5	Stem straightness rating - (category 1 best to 7 = worst; subtracted from 8 so that the straighter the stem the higher the numerical value) (Barrett and Mullin, 1968)	rating
BBA5	Total branch basal area of 2 whorls nearest breast height	cm ²
AIL5	Average internode length (for lower 10 whorls)	m
B/H5	Branches per metre run of stem (for lower 10 whorls)	number
ABW5	Average number of branches per whorl (for lower 10 whorls)	number

locality effects were virtually absent for the branch traits. The polycross test showed genotype-year interaction effects to be absent. The highly significant locality-year interaction effects were no doubt due to the variation of climatic and cultural influences being between years within localities.

Sub-blocking

The almost perfect reproduction of ranking of the unadjusted by the adjusted means indicate that the triple lattice design was not of practical use. However, the blocking efficiencies for the productivity traits in both the polycross and the factorial were high enough to indicate that had the experiments been of the order of 25% smaller, they would have achieved the same degree of precision in assessing these traits as in the randomized complete block.

Mating design

An essential assumption underlying the validity and practical use of the polycross test is that the families consist of half-sibs. Doubts have frequently been express-

ed however as to how randomly the male parent population is sampled when a mixed pollen is applied even when the female strobilus is isolated. It is thought that viability differences between pollens (even when their contribution to the mix is in proportion to their viability as assessed in a sucrose solution), pollen competitive ability and genetic preference could cause this assumption to be invalid through unequal sampling of the pollen parents by the individual seed parents.

In the data presented here, the similarity of heritability estimates from variances estimated from the polycross and factorial tests suggest that the underlying assumption of a half-sib relationship in the polycross families is valid.

A more practical way of testing the validity of this assumption is to compare the ranking of parents by the two tests. The ranking for internode length (AIL5) of parents common to the polycross and factorial by the 2 tests is shown in *table 8*. This trait was chosen because of its high heritability and low *gel* which should ensure that the ability of the polycross to repeat the ranking by the factorial can be expressed as freely as possible from

Table 2. — Analyses of variance of fifth-year traits in the *Pinus patula* polycross tests at Stapleford and Martin planted in 1967 and 1968.

SOURCE OF VARIATION	DF ¹	TRAIT CODE							
		STEM				BRANCH			
		HGT5	CAQ5	VOL5	STR5	BBA5	AIL5	B/H5	ABW5
Families (F)	23	2***	4***	3***	1***	2**	3***	8***	4***
Localities (C)	1	17	6	10	9	17	19	0	33***
Years (Y)	1	0	0	0	16	0	0	1	4***
Lattices (L)/C/Y	4	0	0	1	0	—	—	—	—
Replications (R)/L/C/Y	16	3***	3***	3***	1***	2***	2***	1**	1**
C x Y	1	17***	14***	17***	4***	4*	5**	7***	0
F x C	23	2***	1**	2**	0	1	1	0	1
F x Y	23	0	0	0	0	0	0	2	0
F x C x Y	23	0	0	0	0	0	0	1	1
F x L in C in Y	92	0	0	0	0	—	—	—	—
Residual (π)	436	3	4	4	3	1	1	1	0
Trees in plots (T)	5017	56	68	61	65	72	68	79	57
TOTAL VARIANCE		1.328	1019	228.8	0.6249	95.42	3.61⁻³	12.26	0.7485
SIGNIFICANCE OF F TEST FOR FAMILIES AT SEPARATE ENVIRONMENTS COMBINED OVER YEARS									
Martin		***	***	***	**	**	**	**	**
Stapleford		***	***	***	**	**	***	***	**
MEANS, RANGES, STANDARD ERRORS, COEFFICIENTS OF VARIATION AND REPEATABILITY OVER ENVIRONMENTS AND YEARS									
Overall	- mean	7.7	92.1	33.1	4.2	20.1	0.29	16.2	4.5
	- range - from	7.2	78.3	27.2	4.1	17.0	0.26	13.7	4.0
	- to	8.2	107.3	39.2	4.5	23.1	0.30	18.5	4.9
	- s.e.	0.07	2.15	0.97	0.05	0.83	28.62 ⁻²	0.31	0.06
Martin	- mean	8.2	100.3	37.9	4.42	17.0	0.27	16.2	4.2
	- s.e.	0.10	3.07	1.46	0.07	1.08	7.1 ⁻³	0.47	0.08
	- CV(%) indiv. tree	12.5	32.5	40.7	15.9	40.3	19.8	23.4	14.6
Stapleford	- mean	7.3	83.8	28.4	4.0	23.2	0.31	16.3	4.9
	- s.e.	0.10	3.01	1.29	0.07	1.27	6.9 ⁻³	0.41	0.09
	- CV(%) indiv. tree	13.0	32.0	40.4	19.6	43.7	16.2	19.4	16.0
Repeatability of ♀ parents	- Re	0.49	0.74	0.67	1.00	0.56	0.73	0.99	0.92
over environments	- rs	0.27	0.63	0.56	0.52	0.36	0.57	0.76	0.64
over years	- Ry	1.00	0.98	0.98	0.85	1.00	0.87	0.84	0.96
	- rs	0.82	0.84	0.85	0.47	—	—	—	—
HERITABILITIES									
Localities combined	- family	0.58	0.77	0.72	0.67	0.85	0.68	0.80	0.76
	- tree	0.13	0.20	0.18	0.06	0.09	0.17	0.35	0.23
Martin	- family	0.83	0.83	0.82	0.37	0.74	0.71	0.65	0.77
	- tree	0.27	0.26	0.27	0.04	0.29	0.20	0.27	0.29
Stapleford	- family	0.83	0.82	0.81	0.62	0.61	0.78	0.79	0.73
	- tree	0.26	0.27	0.27	0.08	0.10	0.27	0.47	0.27
EFFICIENCY OF TRIPLE LATTICE DESIGN									
Mean blocking efficiency (%)	Martin	108	103	105	106	109	101	108	103
	Stapleford	143	134	139	108	105	112	105	102
rs of adjusted & unadj. family means	over environment and yrs	0.96	0.97	0.99	0.99	0.97	0.98	1.00	0.99

1) Degrees of freedom for all branch traits were 8, 276 and 2509 for replications, residual and trees-in-plots respectively.
 Re and Ry — intra-class correlations
 ra — Spearman's rank correlation

within plot and *gei* effects. Data in the table show that the polycross repeated the ranking by factorial very closely. The assumption of half-sib relationship i.e. random matings within the polycross family is therefore likely to be valid.

Genetic correlations

The correlations among fifth-year traits are given in

table 5. The significant (shaded) genetic correlations indicated as expected that trees with large diameters were tallest but also that the large trees had fewer branches. There were no genetic correlations between nursery and fifth-year traits with small enough standard errors to draw comment except that greater nursery height (NH12) was associated with fewer branches per whorl in the fifth year (ABW5). By the second year in the field,

Table 3. — Analyses of variance of fifth-year traits in the *Pinus patula* factorial progeny tests based on unadjusted means at Stapleford and Martin.

SOURCE OF VARIATION	DF	TRAIT CODE							
		STEM				BRANCH			
		HGT5	CAQ5	VOL5	STR5	BBA5	AIL5	B/H5	ABW5
PERCENTAGE CONTRIBUTION TO TOTAL VARIANCE AND SIGNIFICANCE OF THE F TESTS ON THE MEAN SQUARES FOR COMBINED ENVIRONMENTS									
Localities (c)	1	59**	38***	47***	25*	10**	14*	17***	0
Paternal parents (p)	4	0	5*	3	0	3	11**	19**	12*
Maternal parents (m)	8	1	1	1	1*	3	7**	7*	2
m x p	32	1	0	0	0	0	0	0	0
p x c	4	1	1*	1*	1*	0	0	0	1*
m x c	8	1	1	2**	0	2**	0	2**	1
m x p x c	32	2*	2*	1*	0	1	0	1*	0
Residual (π)	252	4	4	4	4	2	6	1	3
Trees in plots (T)	2377	32	47	39	68	80	64	52	80
TOTAL VARIANCE		2.012	1359	367.3	0.4452	64.07	2.8 ⁻³	10.31	0.3896
SIGNIFICANCE OF F TESTS FOR SEPARATE LOCALITIES									
Martin - paternal parents (p)		**	***	***		***	***	***	***
- maternal parents (m)		***	***	***		***	***	***	***
m x p		*				*		*	
Stapleford - paternal parents (p)			**	*	***	**	***	***	***
- maternal parents (m)			**	**	***	***	***	***	**
m x p		***	**	**		*	*	*	
MEANS, RANGES, STANDARD ERRORS, COEFFICIENTS OF VARIATION AND REPEATABILITY OVER LOCALITIES									
Overall - mean		8.1	98.0	37.1	4.0	19.4	0.30	14.9	4.4
- range 5 ♀ parents - from		7.9	86.6	32.2	3.9	17.6	0.28	13.0	4.1
- to		8.2	110.2	42.3	4.0	20.8	0.32	16.4	4.7
- s.e.		0.05	1.50	0.74	0.03	0.34	2.3 ⁻³	0.11	0.03
- range 9 ♀ parents - from		7.9	88.8	32.9	3.9	18.0	0.28	13.4	4.3
- to		8.5	106.7	41.4	4.1	22.2	0.33	16.4	4.6
- s.e.		0.07	2.02	0.99	0.04	0.45	3.1 ⁻³	0.15	0.04
Martin - mean		8.9	114.3	46.5	4.2	17.6	0.32	13.9	4.3
- s.e.		0.08	2.19	1.17	0.05	0.35	3.1 ⁻³	0.13	0.03
- CV(%) indiv. tree		10.7	27.8	35.4	13.7	33.5	15.1	18.1	12.1
Stapleford - mean		7.3	81.6	27.6	3.7	21.2	0.29	15.9	4.5
- s.e.		0.07	2.06	0.90	0.04	0.59	3.3 ⁻³	0.18	0.05
- CV(%) indiv. tree		11.9	31.8	39.3	15.6	42.7	18.1	20.5	15.9
Repeatability of ♀ parents - Re		0.63	0.90	0.76	0.76	1.00	1.00	1.00	0.83
over environments - rs		0.60	0.58	0.58	0.60	0.63	0.82	0.82	0.63
HERITABILITIES									
Localities combined - family		0.33	0.62	0.53	0.38	0.64	0.91	0.90	0.80
- tree		0.08	0.20	0.17	0.04	0.13	0.42	0.63	0.27
Martin - family		0.57	0.77	0.76	0.11	0.61	0.88	0.91	0.78
Stapleford - family		0.12	0.28	0.23	0.62	0.65	0.71	0.89	0.76
EFFICIENCY OF TRIPLE LATTICE DESIGN									
Mean blocking efficiency (%) - Martin		149	106	112	111	101	120	105	104
- Stapleford		122	129	134	105	100	109	100	110
rs of adjusted & unadjusted means		0.95	1.00	1.00	1.00	1.00	1.00	1.00	0.98

Re — intra-class correlation coefficient
rs — Spearman's rank correlation

however, there was a number of well-defined genetic correlations with the fifth-year traits (Table 7). All 3 productivity traits (HGT, CAQ and VOL) in the second year were good predictors of each other in the fifth. Sinuosity (SIN2) in the second year was associated with large volume (VOL5) trees that had few branches (B/H5)

in the fifth year. Average internode length (AIL2). Average branches per whorl (ABW2) and number of branches (B/H2) were accurate predictors of the same characteristics in the fifth year even though these traits were assessed over a very much greater length of stem on the older trees.

Table 4. — Analyses of variance of fifth-year traits in the *Pinus patula* diallel progeny tests at Stapleford, Martin, Bende and Nyangui.

SOURCE OF VARIATION	DEGREES OF FREEDOM	TRAIT CODE							
		STEM				BRANCH			
		HGT5	CAQ5	VOL5	STR5	BBA5	AIL5	B/H5	ABW5
Localities (c)	3	63.4***	24.2***	40.0***	27.6**	15.9***	12.0***	15.9***	3.3
Replications in c	8	0.6**	1.9***	1.5***	2.9***	0	1.4***	0.7	3.2**
General (g)	4	1.7*	8.3	5.3**	0.5	2.8**	9.1**	6.8**	1.1
Specific (s)	5	0.5	0.7	0.3	1.3*	0.4	1.3*	0	0.9
Maternal (m)	4	0.1	0	0	0.1	0	0	0.2	0.4
Reciprocal (r)	6	0	0.4**	0.1	0.1	0	0	0.1	0.4
g x c	12	1.0*	1.7	1.7**	0	1.0*	1.0*	0.5	0.9
s x c	15	0	0	0	0.9	0	0	0	0.4
m x c	12	0.2	0.4	0.4	0	0.1	0	0.1	0.3
r x c	18	0	0	0	0.1	0	0	0	0
Residual in c	152	4.6	6.6	5.6	2.1	2.1	3.9	1.7	2.1
Trees in plots	2144	27.9	55.7	45.0	64.5	77.7	71.2	74.1	87.2
TOTAL VARIANCE		1.620	1022	272.0	0.4711	69.6	0.0022	6.946	0.3842
Heritability - family		0.54	0.77	0.75	0.16	0.64	0.90	0.85	0.28
- individual tree		0.19	0.45	0.36	0.03	0.13	0.42	0.32	0.05

Table 5. — Genetic, genotypic and phenotypic correlations between selected fifth-year traits in the factorial test at Martin.

		HGT5	CAQ5	VOL5	STR5	BBA5	AIL5	B/H5	ABW5
		GENETIC CORRELATION (STANDARD ERROR)							
HGT5	GENOTYPIC/PHENOTYPIC CORRELATION		0.77 (0.15)	0.88 (0.08)	0.14 (0.63)	-0.50 (0.31)	0.62 (0.22)	-0.58 (0.24)	-0.05 (0.38)
CAQ5		0.74 0.75		0.98 (0.01)	0.40 (0.57)	-0.41 (0.34)	0.47 (0.28)	-0.63 (0.22)	-0.51 0.31
VOL5		0.84 0.85	0.99 0.98		0.36 (0.58)	-0.43 (0.33)	0.53 (0.25)	-0.63 (0.22)	-0.38 (0.34)
STR5		0.31 0.27	0.16 0.23	0.21 0.25		-1.49 (0.82)	-0.80 (0.59)	0.20 (0.60)	-1.32 (0.78)
BBA5		-0.16 0.21	0.28 0.14	0.18 0.04	-0.41 -0.31		0.16 (0.36)	0.14 (0.36)	0.62 (0.27)
AIL5		0.54 0.57	0.67 0.62	0.67 0.63	-0.03 -0.08	0.42 0.20		-0.91 (0.06)	0.02 (0.36)
B/H5		-0.57 -0.52	-0.78 -0.70	-0.77 -0.69	-0.13 -0.02	-0.30 -0.17	-0.94 -0.91		0.39 (0.31)
ABW5		-0.44 -0.19	-0.74 -0.52	-0.72 -0.48	-0.32 -0.18	-0.02 0.09	-0.57 -0.32	0.81 0.68	

Table 6. — Genetic, genotypic and phenotypic correlations between nursery and fifth-year traits at Martin.

		NURSERY TRAITS					
		CON		COL		NH12	
		GENETIC CORRELATION (AND STANDARD ERROR) GENOTYPIC AND PHENOTYPIC CORRELATIONS					
FIFTH YEAR TRAITS	HGT5	-0.42 -0.40	(0.33) -0.27	-0.20 0.03	(0.44) 0.10	0.09 -0.03	(0.38) -0.04
	CAQ5	-0.59 -0.31	(0.27) -0.30	0.41 0.22	(0.39) 0.21	0.58 0.40	(0.29) 0.25
	VOL5	-0.58 -0.37	(0.27) -0.33	0.27 0.19	(0.41) 0.19	0.45 0.30	(0.32) 0.18
	STR5	-1.01 -0.51	(0.62) -0.32	0.30 0.19	(0.74) 0.15	1.00 -0.11	(0.75) -0.10
	BBA5	0.03 0.08	(0.40) 0.04	0.42 0.28	(0.41) 0.17	-0.22 0.53	(0.37) 0.28
	AIL5	-0.02 -0.04	(0.37) -0.03	0.30 0.23	(0.40) 0.16	0.29 0.40	(0.33) 0.28
	B/H5	0.07 0.10	(0.36) 0.05	-0.44 -0.24	(0.36) -0.20	-0.59 -0.39	(0.25) -0.36
	ABW5	0.30 0.19	(0.37) 0.08	-0.50 -0.21	(0.36) -0.21	-0.79 -0.26	(0.17) -0.34

Conclusions

General conclusions of practical significance that can be drawn from the analyses of fifth year traits in these *P. patula* progeny tests are:

- 1) family heritabilities are high for all stem and crown characteristics assessed, especially for the branch number and distribution traits;
- 2) *sca*, maternal and reciprocal effects are of no practical significance;
- 3) genotype-locality interaction effects in productivity traits may be pronounced enough to be of use; they are absent in the branch traits;
- 4) there is no genotype-year interaction;
- 5) incorporation of sub-blocking in the environmental design of the tests may make it possible to reduce the size of the experiment by thirty per cent without sacrificing precision in ranking the parents;
- 6) the assumption of a half-sib relationship within the polycross test is valid and the mating design is precise in ranking parents;
- 7) there is a positive genetic correlation between one year

Table 7. — Genetic, genotypic and phenotypic correlations between second-year and fifth-year traits at Martin.

		SECOND YEAR TRAITS									
		HTI2	CAQ2	VOL2	SIN2	BDI2	BLI2	BAI2	AIL2	ABW2	B/H2
		GENETIC CORRELATION (AND STANDARD ERROR) GENOTYPIC AND PHENOTYPIC CORRELATIONS									
FIFTH YEAR TRAITS	HGT5	0.94 (0.06) 0.75 0.80	0.81 (0.17) 0.64 0.69	0.81 (0.14) 0.65 0.72	-0.42 (0.31) -0.23 -0.21	-0.30 (0.39) -0.27 -0.15	0.20 (0.43) -0.35 -0.10	0.48 (0.30) 0.36 0.35	0.50 (0.28) 0.22 0.33	-0.08 (0.37) -0.44 -0.20	-0.49 (0.28) -0.36 -0.36
	CAQ5	0.85 (0.11) 0.82 0.82	0.94 (0.09) 0.87 0.81	0.90 (0.08) 0.88 0.86	-0.70 (0.21) -0.56 -0.46	-0.02 (0.41) 0.04 0.02	0.09 (0.45) -0.26 -0.14	0.40 (0.32) 0.33 0.28	0.43 (0.30) 0.51 0.49	-0.54 (0.30) -0.61 -0.46	-0.54 (0.26) -0.69 -0.62
	VOL5	0.92 (0.06) 0.84 0.85	0.96 (0.09) 0.85 0.80	0.92 (0.07) 0.86 0.85	-0.63 (0.24) -0.49 -0.41	-0.09 (0.40) -0.04 -0.04	0.12 (0.44) -0.32 -0.16	0.42 (0.31) 0.35 0.31	0.46 (0.29) 0.45 0.46	-0.42 (0.52) -0.62 -0.44	-0.55 (0.26) -0.64 -0.58
	STR5	0.75 (0.59) 0.01 0.12	0.93 (0.59) 0.10 0.23	0.73 (0.57) 0.03 0.18	-0.14 (0.63) 0.10 0.02	0.03 (0.71) -0.22 -0.17	0.56 (0.81) -0.35 -0.18	0.68 (0.61) -0.06 0.06	-0.19 (0.62) -0.20 -0.19	-0.23 (0.66) -0.23 -0.06	0.08 (0.62) 0.06 0.12
	BBA5	-0.64 (0.29) 0.07 -0.03	-0.66 (0.36) 0.34 0.17	-0.53 (0.33) 0.28 0.12	0.18 (0.37) -0.46 -0.23	0.29 (0.39) 0.62 0.45	-0.31 (0.45) 0.32 0.21	-0.65 (0.24) -0.30 -0.36	-0.04 (0.39) 0.58 0.34	-0.21 (0.37) 0.04 0.03	-0.06 (0.38) -0.54 -0.38
	AIL5	0.58 (0.25) 0.42 0.48	0.34 (0.37) 0.57 0.49	0.50 (0.28) 0.58 0.54	-0.68 (0.21) -0.59 -0.49	0.17 (0.38) 0.29 0.22	0.31 (0.39) -0.14 -0.02	-0.16 (0.35) -0.13 -0.06	0.85 (0.11) 0.79 0.77	-0.44 (0.30) -0.57 -0.44	-0.92 (0.07) -0.92 -0.86
	B/H5	-0.68 (0.21) 0.47 0.48	-0.51 (0.32) -0.61 -0.51	-0.66 (0.22) -0.62 -0.55	0.87 (0.11) 0.56 0.52	-0.13 (0.38) -0.16 -0.18	-0.24 (0.40) 0.33 0.16	0.04 (0.36) -0.04 0.00	-0.81 (0.13) -0.68 -0.67	0.63 (0.23) 0.76 0.67	0.91 (0.06) 0.90 0.89
	ABW5	-0.41 (0.38) -0.46 -0.27	-0.62 (0.35) -0.54 -0.33	-0.58 (0.31) -0.54 -0.34	0.57 (0.27) 0.32 0.29	0.14 (0.41) 0.13 0.02	0.23 (0.45) 0.56 0.37	-0.27 (0.36) -0.19 -0.14	0.03 (0.38) -0.28 -0.18	0.62 (0.23) 0.88 0.82	0.18 (0.36) 0.61 0.50

Table 8. — Ranking of the 8 common female and 5 common male parents for average internode length (AIL5) by the factorial (F) and polycross (P) tests at Stapleford (A) and Martin (B) separately and combined.

Parent	Test					
	A		B		A + B	
	F	P	F	P	F	P
8 common ♀ tested against 5♂						
1	5	8	7	7	7	8
7	3	2	3	3	3	3
15	1	3	1	1	1	2
26	8	7	7	4	8	6
27	4	4	4	5	4	4
32	6	5	6	8	5	7
48	7	6	5	6	6	5
51	2	1	2	2	2	1
5 common ♂ tested against 9♀						
5	2	2	1	1	1	1
14	4	5	3	5	4	5
20	1	1	2	3	2	2
25	3	3	4	2	3	3
31	5	4	5	4	5	4

height in the nursery and tree size in the fifth year; 8) height, diameter and volume in the second year are excellent genetic predictors of the same traits, and of each other, in the fifth year; 9) the branch number and distribution traits in the fifth year can be accurately predicted from assessments in the second year.

These results indicate high heritability of economically important traits, considerable genetic variation and generally favourable genetic, including juvenile-mature, correlations. Substantial and rapid gain should therefore be achievable for *P. patula* through conventional breeding strategies with early selection for *gca*. It is emphasized, however, that the tests are only in their fifth year which is about one third of a pulpwood and only one sixth of a current sawlog rotation.

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