GENETIC AND SITE DIFFERENCES IN *PINUS RADIATA* INTERNODE LENGTH IN NEW ZEALAND

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EXECUTIVE SUMMARY

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Internode lengths of the second log were measured in progeny trials on nine sites across New Zealand with progeny of 8 to 20 breeding clones representing the range of genetic differences measured in each. There is a strong genetic, and site influence on internode length in the second log in *Pinus radiata.* Mean internode length (MIL) was significantly different among families and strongly correlated with the branch cluster frequency breeding value (brBV), although the relationship was different for families from different selection groups. The variance among families in MIL differed among sites, and was strongly correlated with the site MIL. Inclusion of a genetic component in internode length prediction models is important for sites with a high variance among families, and could be based on this relationship. Continued development of the brBV in order to enable prediction of internode length for families from different selection groups is suggested. This information will provide the basis for the genetic component of a model for predicting internode length of *P. radiata*, which also incorporates site characteristics, and growth parameters.

INTRODUCTION

Tree breeding research has shown that a considerable number of traits influencing tree quality can be manipulated to suit specific sites, management regimes, processing methods, and markets (Carson 1996). The tree breeding programme can produce planting stock (designer trees) with altered quality features such as branch diameter, internode length, stem straightness, and wood density. It is proposed that the New Zealand Tree Seed Certification will give seedlots separate ratings for growth rate, branch habit, straightness, Dothistroma resistance, and wood density.

Forest managers will need to make decisions relating to market supply and processing options on which seedlot of radiata pine to plant. To aid forest managers in making these decisions, the impact on tree characteristics of growing designer radiata pine breeds on different sites with different management needs to be modelled. The development of genetic gain modifiers relating to characteristics manipulated by the tree breeding programme will enable forest managers to make informed decisions regarding the management of new breeds of radiata pine. The ability to model these effects is essential because of the time it takes for radiata pine crops to mature and the need for yield and log quality information before rotation end.

Genetic gain modifiers have already been developed for predicting volume for improved *Pinus radiata* by quantifying differences in the rate of change in growth with time, using data from genetic gain trials. The effect of the tree breeding programme on branch habit has previously been studied in terms of differences among selection groups, across a number of sites (Carson & Inglis 1988; Woods & Carson 1988; Grace & Carson 1993). The impact on branch habit for individual families, however, has only been estimated, to date, in terms of a subjective scoring system. A national ranking of families for branch habit, has been obtained through the development of breeding values[1] (Kumar, *et al.* 1996), using the extensive amount of subjective data available from field progeny trials. This scoring system enables efficient, and effective ranking and selection of parents, but it is not known how well it quantifies absolute differences among improved breeds.

This study explores the possibilities for predicting internode length from breeding values for branch cluster frequency (Figure 1). The development of models which

[1]The breeding value judges the value of an individual in terms of the mean value of its progeny (Falconer, 1989).

predict the changes resultant from genetic selection will enable forest managers to evaluate the effect of different management strategies on improved material. Also the effect of using genetic material tailored for different end uses and sites can be analysed in financial terms.

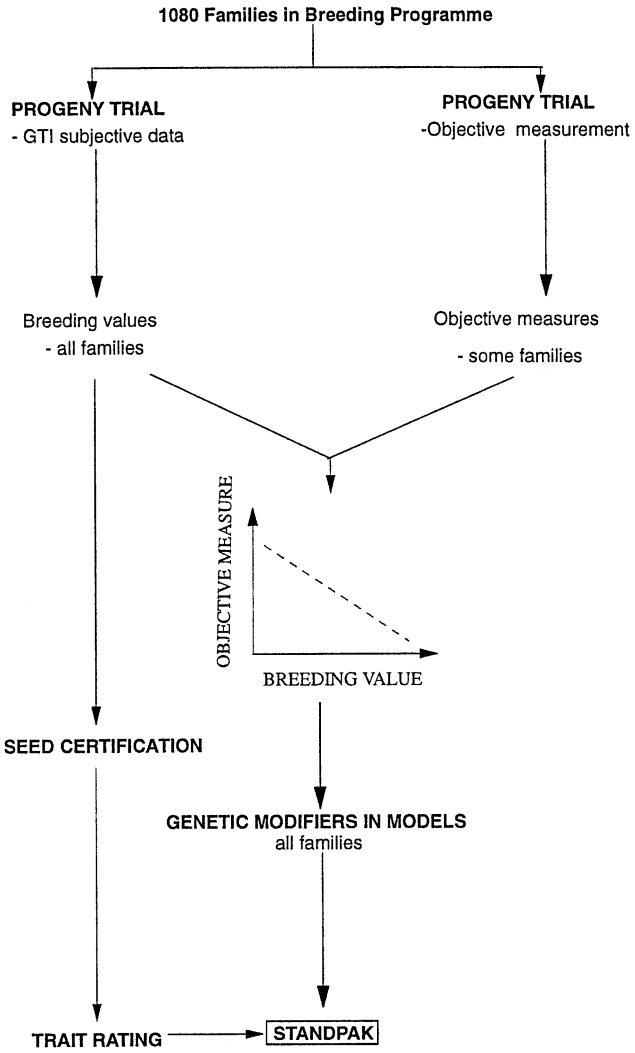

Figure 1: Project strategy for developing genetic gain modifiers for branch cluster frequency.

METHODS

Nine progeny trial sites were chosen to cover a range of latitudes, altitudes, and climates (Table 1 and Figure 2), as well as a range of genetic selection series and branch habit selection criteria.

Region	Forest	Compt	Experiment	Breeding Series	Breeding Goal	Planted	Families Measured	Control Seedlots
Auckland sands	Woodhill		diallel	850	multinodal	1975	10	Kaingaroa bulk
	Woodhill		polycross	850	multinodal	1975	20	Southland "850" SO Canterbury "850" SO Gwavas "850" SO Kaingaroa bulk
Central NI	Kaingaroa	1350	OP	268	multinodal	1969	9	"850" SO (R68/A1)
	Kaingaroa	905	diallel	850	multinodal	1975	10	Kaingaroa bulk
	Kaingaroa	905	OP	870	uninodal	1972	9	Kaingaroa bulk
	Kaingaroa	327	diallel	850	multinodal	1975	10	Kaingaroa bulk
	Kaingaroa	327	polycross	850	multinodal	1975	20	Southland "850" SO Canterbury "850" SO Gwavas "850" SO Kaingaroa bulk
	Awahohonu		diallel	850	multinodal	1975	10	Kaingaroa bulk
Nelson	Golden Downs		diallel	850	multinodal	1975	10	Kaingaroa bulk
	Golden Downs		polycross	850	multinodal	1975	20	Southland "850" SO Canterbury "850" SO Gwavas "850" SO Kaingaroa bulk
Canterbury	Eyrewell		diallel	850	multinodal	1975	10	Kaingaroa bulk
	Eyrewell		polycross	850	multinodal	1975	20	Southland "850" SO Canterbury "850" SO Gwavas "850" SO Kaingaroa bulk
West Coast	Mawheranui		diallel	850	multinodal	1975	10	Kaingaroa bulk
Southland	Taringatura		diallel	850	multinodal	1975	10	Kaingaroa bulk

Table 1: Trial locations by region, and breeding programme purpose of trials.

Figure 2: Locations of trials measured in this study for internode length.

Four different progeny trial designs and three selection series are represented in the measurements; the "850"[2] diallel, the "850" polycross, the "268" open-pollinated (OP), and the "870" uninodal OP trials. The "870" uninodal OP trial represents intensive selection for long internode trees, while the other series were selected for multinodality (Table 1). Although the "850" diallel and the "850" polycross both represent groups of clones selected in 1950, the clones represented in the "850" diallel were selected in the Central North Island with multinodality especially emphasised, while the clones in the "850" polycross were selected primarily in the South Island with much less emphasis on short internode length. The progeny trials are "common garden" experiments comparing progeny of different plus trees.

While the "850" diallel trial covers a wide range of sites, the "850" polycross trial, and "870" uninodal OP trials have a wider range of genetic material on fewer sites (Table 1). The "850" diallel, has a half diallel crossing design which involves five sets of five parents crossed in all combinations (without selfs or reciprocals) giving a total of 10 different full-sib[3] families per diallel. In each of the six replicates, five trees of each of the 50 parental crosses were randomly planted in non-contiguous plots. The "850" polycross trial is a randomised block design of 101 clones with 10 replications in a 'sets-in-replications' design, with five half-sib[4] progeny per clone, per replication planted as non-contiguous plots. The "268" OP progeny test is a 'sets-in-replicates' design, with five 10-tree-row plots per family with 580 "268" clones represented in the trial. The "870" uninodal OP progeny test is a 'sets-in-replicates' design with 104 "870" clones each represented by seven 5-tree-row plots.

All of the progeny trials were assessed at age eight for branch cluster frequency[5]. These data, and data from other progeny trials have been combined into national breeding values for branch cluster frequency (brBV) using best-linear prediction (BLP) techniques (Kumar *et al.* 1996). Ten families were selected from the "850" diallel trial, twenty families from the "850" polycross trial, eight from the "268" OP, and nine families from the "870" uninodal OP trial to cover the range of brBV in each trial series from multinodal to uninodal, with an emphasis on the extremes. Breeding

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[2] The number "850" is a prefix number denoting a particular series of clone. The first digit in the clonal series number refers to the regional origin of the clone (8 signifies collections carried out by FRI, not necessarily within one conservancy). The second two digits refer to the year of selection, in this, case 1950 (Vincent & Dunstan, 1989).

[3] full-sib families are those for which both parents are common, and therefore known.

[4] half-sib families are those for which one parent is common, and therefore, only the mother is known.

[5] The branch cluster frequency score is a subjective score from 1 to 9 based on the number of branch clusters per year, where 1 = extremely uninodal, 9 = extremely multinodal (Carson 1991) for multinodal breeds, and 1 = extremely multinodal, 9 = extremely uninodal, for uninodal breeds.

values ranged from -2.67 to 1.63 in the "850" diallel trial, from -1.82 to 1.40 in the "850" polycross trial, from -0.89 to 1.02 in the "268" OP trial, and from -1.13 to 1.20 in the "870" uninodal trial. The families chosen also met a threshold of acceptability for diameter, and malformation. This meant families likely to have "crop" trees, ie., trees of crop standard which are "relatively straight, non-malformed dominants" were selected for measurement. Trees to be measured were selected from trial maps; if any of these proved not to be crop trees then replacement trees were selected in the field. At each trial site, at least one control seedlot, usually a bulk unselected seedlot from Kaingaroa Forest, was also measured (Table 1), and included in all analyses.

Measurement Technique and Data Analysis

Each tree was assessed for the following characteristics:

- diameter at breast height (1.4 m);
- pruned height;
- internode lengths in the branched section of the stem up to the first branch cluster above 12 m.

The height of the base and top of each branch cluster was measured from a 0.2 m stump height using a height pole, to an accuracy of ±0.05 m (Figure 3). Each branch cluster was measured, starting with the base of the first branch cluster in the branched section of the stem, up to the top of the second log. A stem cone cluster was measured as the end of an internode, even if the stem cone cluster had no branches associated with it. When two or more branch clusters occurred close together and there was no discernible internode the branch clusters were counted as one (Figure 4). Mean internode length (MIL) for a 5.5 m log from 6.3 to 11.8 m on the stem was calculated from these measurements.

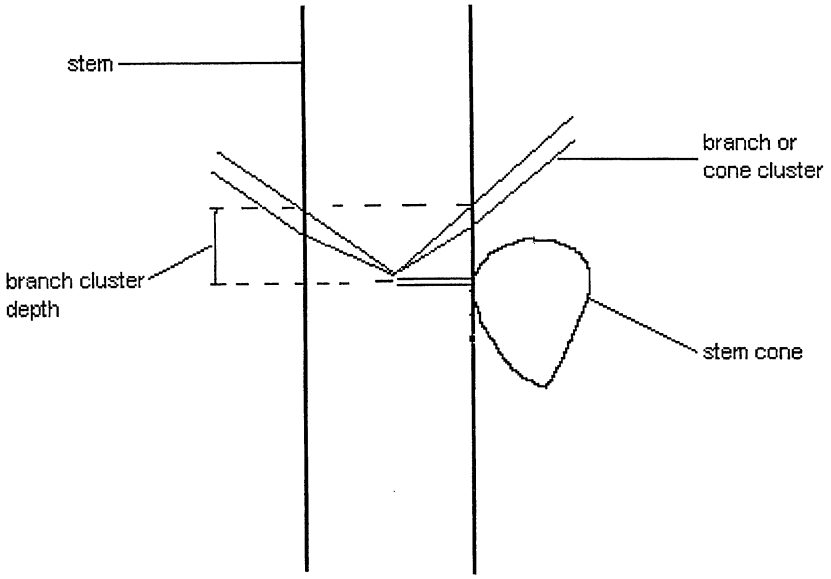

Figure 3: Branch cluster depth illustrated. Source: Woods and Carson (1988).

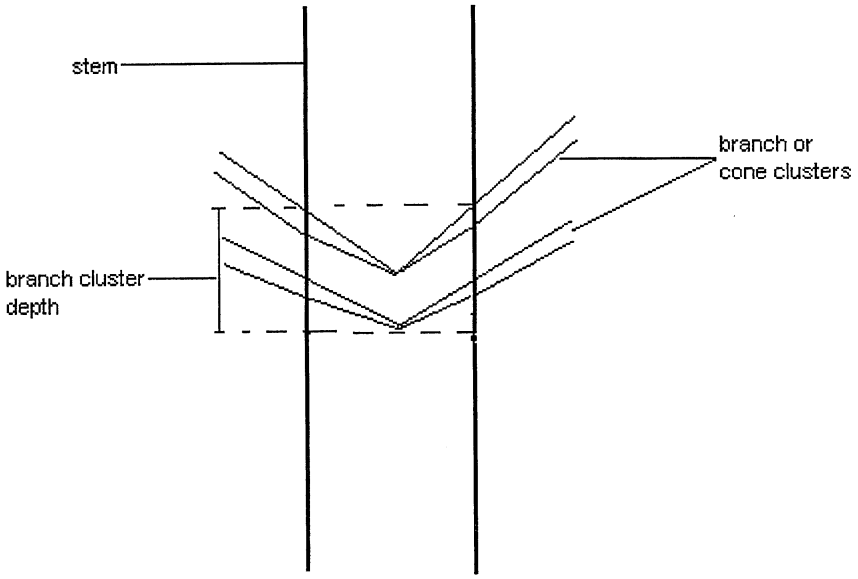

Figure 4: Branch cluster depth for close branch clusters. Source: Woods (1988).

Two sets of analysis of variance (ANOVA) were performed in order to examine genetic differences in MIL, and the relationship of MIL and brBV. The sets of ANOVA essentially differed in the statistical treatment of brBV. The first set of ANOVAs included brBV as a class variable (Appendix I), therefore, each brBV acts as a family identifier. In these analyses, brBV is treated as a random effect, to allow inferences about the effect on MIL in the total breeding population. The second set of ANOVAs included brBV as a covariate, and therefore, are similar to a simple linear regression analysis. These ANOVAs are provided in the main body of the report. In

addition, tests for quadratic relationships between brBV and MIL were made using simple linear regression techniques (Appendix III). In all these analyses the average brBV of full-sib families was used for the "850" diallel, and the maternal brBV only was used for half-sib families. Also the ANOVA with brBV used as a covariate was repeated for Central North Island sites with the maternal and paternal brBV taken into account for half-sib families. This required estimation of the average performance of the fathers, with a brBV of 0.52 for fathers in the "850" polycross (the average brBV of the fathers in the pollen mix), and -0.96 for the "268" OP, and "870" uninodal OP trials (the brBV for the bulk unselected seedlot, G. Vincent pers. comm.). Genotype x environment interaction in MIL was examined by calculating pair-wise correlation of average family MIL at different sites (Appendix II).

RESULTS

Family Differences in MIL

Differences in average MIL among families in the "850" diallel, "850" polycross trials, and the "870" uninodal OP trial were significant, but differences among families in the "268" OP trial were not (Appendix I). Where the same families occurred on multiple sites, differences in MIL among sites were highly significant and the interaction of families and sites was highly significant. Changes in the rankings of families, or differences in the variance in MIL among families for each of the sites can lead to differences of this type. The correlations of family mean MIL between sites (Appendix II) are similar to those observed for other progeny trials (Kumar *et al.* 1996), suggesting that the changes in family rankings for MIL between sites are not important for achievement of maximum genetic gains, as has been concluded before (Carson 1991). There is, therefore, a reasonable indication that the significant interactions are due largely to differences in the variance of MIL on different sites.

Site Differences in MIL

Site mean MIL for trials with multinodal selection groups ranged from 0.61 to 0.32 m (Table 2). Differences in mean MIL among sites for the "850" diallel trials, and "850" polycross trials (Appendix I), where the same families were planted on each site, were large, and are similar to differences in site mean MIL identified in previous studies (Carson & Inglis 1988; Woods & Carson 1988; Tombleson *et al.* 1990; Grace & Carson 1993).

Table 2: Summary statistics for brBV, MIL, and the regression of brBV on MIL by trial.

					MIL				Regression of brBV and MIL				
						Family Mean							
Region	Forest	Compt	Experiment	Series	Mean	Min	Max	Stdev	R^2	slope	probability	intercept	probability
Auckland sands	Woodhill		diallel	850	0.32	0.18	0.63	0.0851	0.45	-0.024	0.0230	0.32	0.0001
	Woodhill		polycross	850	0.34	0.18	0.62	0.0846	0.43	-0.029	0.0002	0.34	0.0001
Central NI	Kaingaroa	1350	OP	268	0.54	0.25	1.63	0.2329	0.08	-0.028	0.4410	0.54	0.0001
	Kaingaroa	905	diallel	850	0.48	0.24	1.30	0.1700	0.83	-0.053	0.0001	0.48	0.0001
	Kaingaroa	905	OP	870	0.64	0.33	1.55	0.2712	0.64	-0.146	0.0055	0.68	0.0001
	Kaingaroa	327	diallel	850	0.52	0.22	1.80	0.2175	0.77	-0.068	0.0004	0.51	0.0001
	Kaingaroa	327	polycross	850	0.56	0.25	1.80	0.2290	0.53	-0.083	0.0001	0.54	0.0001
	Awahohonu		diallel	850	0.46	0.25	0.95	0.1301	0.76	-0.039	0.0005	0.46	0.0001
Nelson	Golden Downs		diallel	850	0.53	0.28	1.90	0.2697	0.66	-0.094	0.0024	0.51	0.0001
	Golden Downs		polycross	850	0.61	0.26	1.90	0.2741	0.59	-0.102	0.0001	0.59	0.0001
Canterbury	Eyrewell		diallel	850	0.38	0.21	0.83	0.1144	0.51	-0.027	0.0138	0.38	0.0001
	Eyrewell		polycross	850	0.41	0.22	1.32	0.1531	0.56	-0.059	0.0001	0.4	0.0001
West Coast	Mawheranui		diallel	850	0.47	0.26	0.90	0.1292	0.47	-0.039	0.0192	0.48	0.0001
Southland	Taringatura		diallel	850	0.53	0.23	1.55	0.2546	0.69	-0.084	0.0014	0.52	0.0001

Relationship of MIL to Breeding Values

There is a significant linear relationship between brBV and MIL for the "850" diallel and "850" polycross trials (Table 3 and Table 4), and for the "870" uninodal OP trial (Table 5 and Table 6) but not for the "268" OP trial (Table 2).

Table 3: ANOVA of second log MIL for the "850" diallel trials with brBV as a covariate.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	7	4.25	0.61	23.09	0.001
brBV	1	4.59	4.59	174.51	0.001
LOCATION*brBV	7	1.05	0.15	5.68	0.001
ERROR	874	22.99	0.03		

Table 4: ANOVA of second log MIL for the "850" polycross trials with brBV as a covariate.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	3	10.54	3.51	103.02	0.001
brBV	1	4.19	4.19	122.93	0.001
LOCATION*brBV	3	0.68	0.23	6.66	0.002
ERROR	941	32.10	0.03		

Table 5: ANOVA of second log MIL for multinodal trials within the Central North Island (excluding the "870" uninodal trial), with brBV as a covariate.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	4	0.72	0.18	4.86	0.0007
brBV	1	1.44	1.44	38.65	0.0001
LOCATION*brBV	4	0.27	0.07	1.80	0.1279
ERROR	655	24.34	0.037		

Table 6: ANOVA of second log MIL for all trials within the Central North Island (including the "870" uninodal trial), using brBV as a covariate.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	5	2.97	0.59	14.59	0.0001
brBV	1	2.47	2.47	60.76	0.0001
LOCATION*brBV	5	0.62	0.12	3.05	0.0098
ERROR	756	30.72	0.04		

The relationship between brBV and MIL is linear for the most part, however, there is some suggestion of a quadratic relationship at the "850" diallel trials on South Island sites with higher average MIL (Appendix III). No strong conclusions regarding the curvilinear relationship may be drawn, however, due to the small number of families measured in these trials.

Differences Among Sites

Differences among sites of the "850" diallel trials (Table 3), and "850" polycross trials (Table 4), were large even when the effect of brBV was taken into account as a covariate. Differences in MIL among sites with multinodal families in the Central North Island region were significant (Table 5), although differences among site means within a region were smaller than the differences between regions (Table 2). The significant LOCATION*brBV term suggests, the slope of the relationship between brBV and MIL, as well as the level of the relationship, differs by site. This is illustrated by different slopes of the trend lines of family MIL on brBV for the "850" diallel, and the "850" polycross trial sites (Table 2, Figure 5 and Figure 6). The differences in the slope of the regressions at different sites also represent differences in variance among family means.

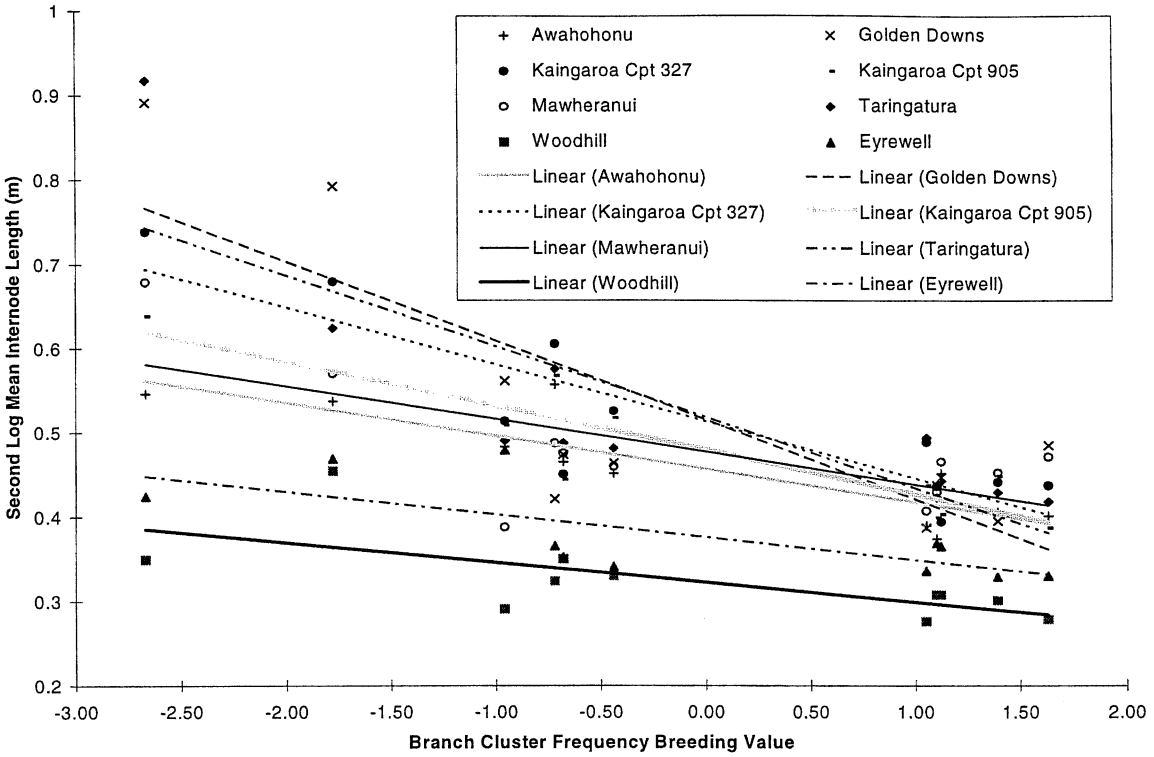

Figure 5: Second log MIL against brBV, with trend lines fitted using simple linear regression for the "850" diallel trial sites.

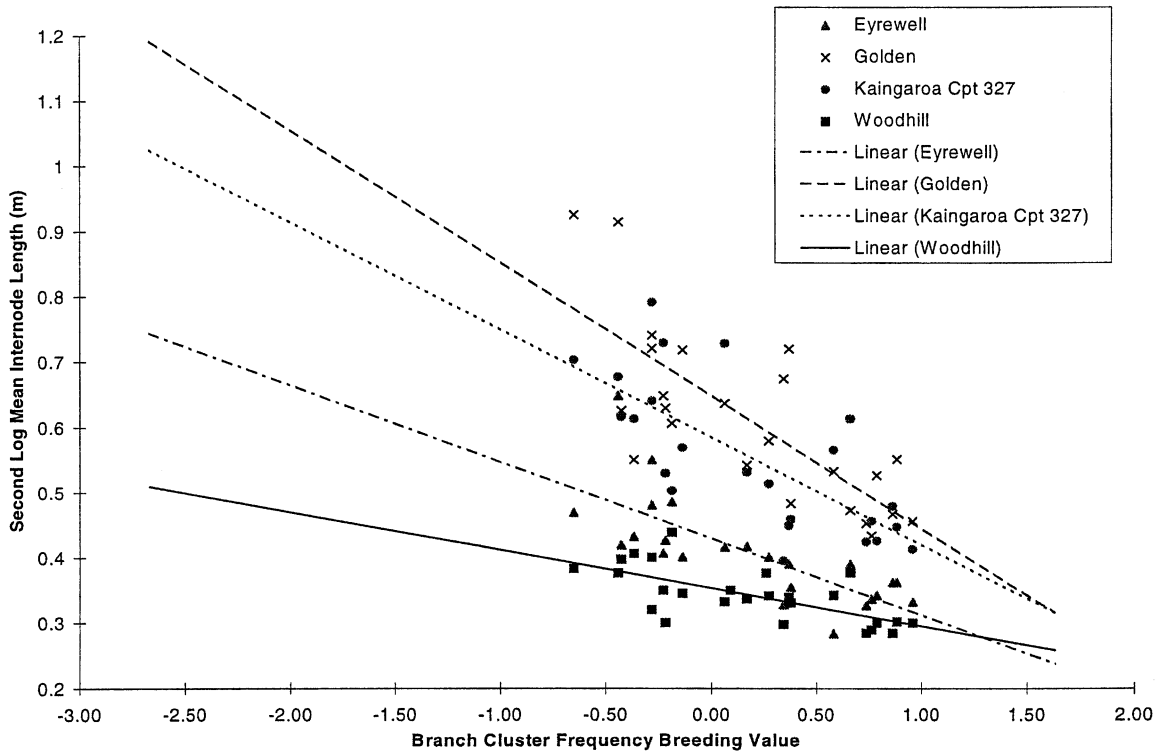

Figure 6: Second log MIL against brBV, with trend lines fitted using simple linear regression for the "850" polycross trial sites.

Differences Among Selection Groups

With brBV defined as only the maternal brBV for the polycross families, the slope of the relationship of brBV and MIL for the "850" polycross and "850" diallel trials across sites, did not differ between trial designs, but was significantly different among locations (see TRIAL DESIGN*brBV and LOCATION*brBV interactions, respectively, Table 7 and Figure 7). Average MIL, however, differed between the "850" diallel and "850" polycross trial designs, shown by the significant TRIAL DESIGN effect (Table 7), even when the effect of brBV was taken into account as a covariate.

Table 7: ANOVA of second log MIL for the "850" diallel and "850" polycross trials on four common sites with brBV as a covariate.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	3	10.97	3.66	115.87	0.0001
TRIAL DESIGN	1	0.42	0.42	13.28	0.0003
LOCATION*TRIAL DESIGN	3	0.18	0.06	1.89	0.1295
brBV	1	6.48	6.48	205.23	0.0001
LOCATION*brBV	3	1.37	0.46	14.44	0.0001
TRIAL DESIGN*brBV	1	0.09	0.09	2.91	0.0880
ERROR	1392	43.93	0.03		

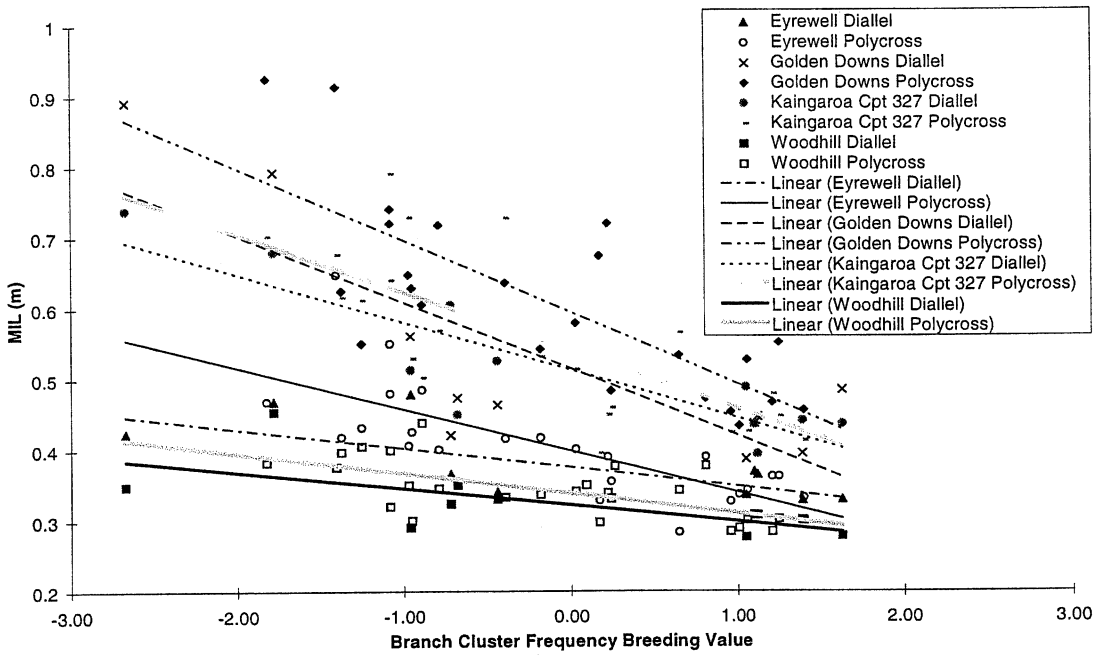

Figure 7: Second log MIL against brBV with trend lines fitted using simple linear regression for the "850" diallel and "850" polycross trials.

For Central North Island multinodal trials, when brBV was defined as only the maternal brBV for the "850" polycross and OP trials, similar slopes in relationships between brBV and MIL were suggested by the non-significant LOCATION*brBV effect for the analyses (Table 5 and Figure 8). The slope of the relationship between brBV and MIL for the "870" uninodal OP trial, however, is significantly different from the other trials measured in the Central North Island, as suggested by the significant LOCATION*brBV term in the ANOVA when the "870" uninodal OP trial is included with the other Central North Island sites (Table 6 and Figure 8).

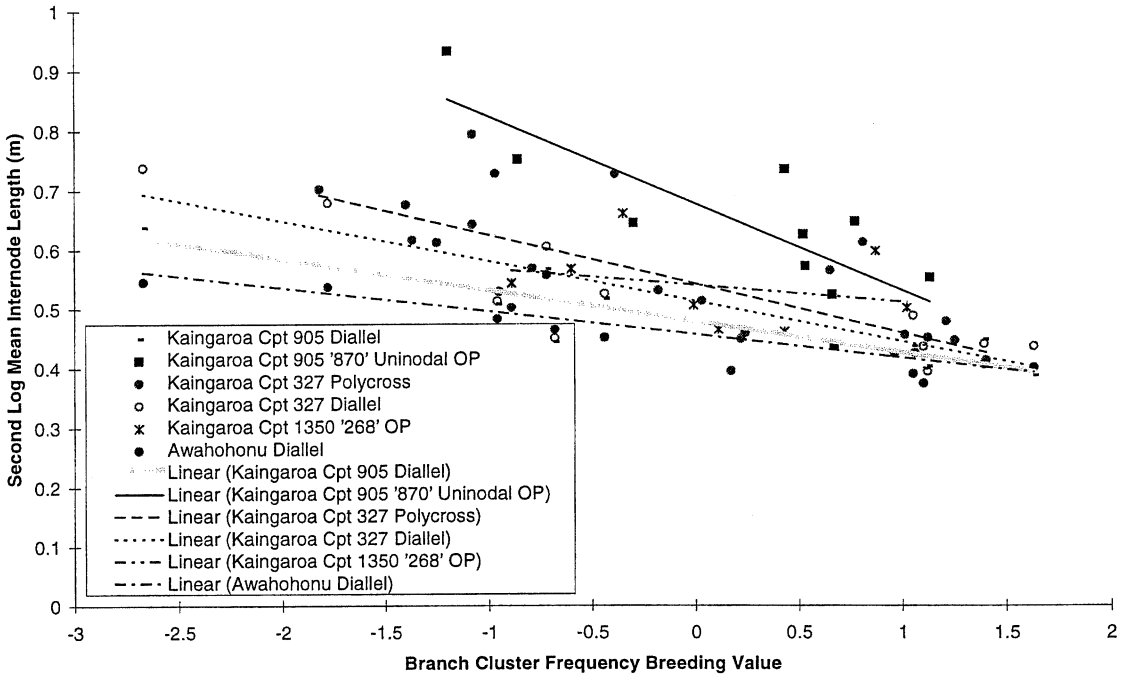

Figure 8: Second log MIL against brBV, with trend-lines fitted by simple linear regression, for all trials within the Central North Island.

When the paternal contribution to brBV was taken into account for OP and "850" polycross trials, the relationship of brBV and MIL was significantly different for multinodal trials in the Central North Island (Table 8) with the relationship for the "850" polycross trial being different from that of the "850" diallel, and "268" OP trials (Figure 9).

Table 8: ANOVA of second log MIL for multinodal trials within the Central North Island (excluding the "870" uninodal trial), with brBV as a covariate, and brBV defined as the paternal contribution as well as the maternal for polycross and OP trials.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	4	1.53	0.38	10.29	0.0001
brBV	1	0.92	0.92	24.62	0.0001
LOCATION*brBV	4	0.78	0.19	5.23	0.0004
ERROR	655	24.34	0.037		

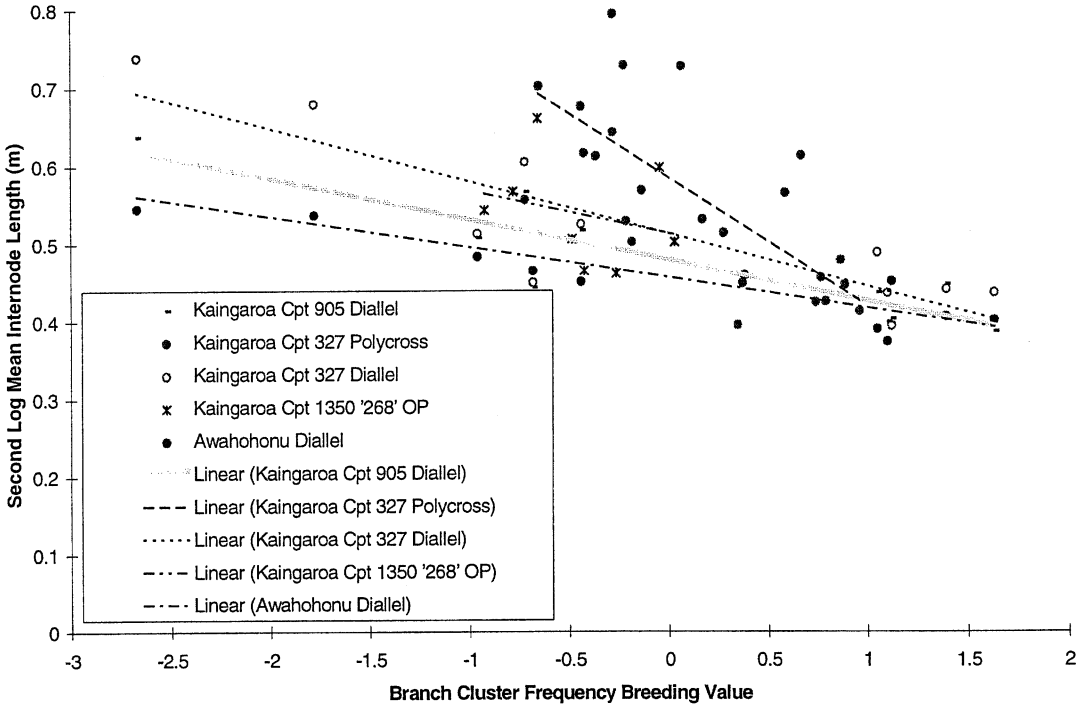

Figure 9: Second log MIL against brBV including the paternal contribution, with trend-lines fitted by simple linear regression, for the "850" diallel, "850" polycross, and "268" trials within the Central North Island.

Relationship of Site MIL and Variance Among Families

The site mean MIL was highly correlated with variance among families in mean MIL ($R^2 = 0.82$) (Figure 10), suggesting that sites with a high mean MIL have a large variance among families in mean MIL.

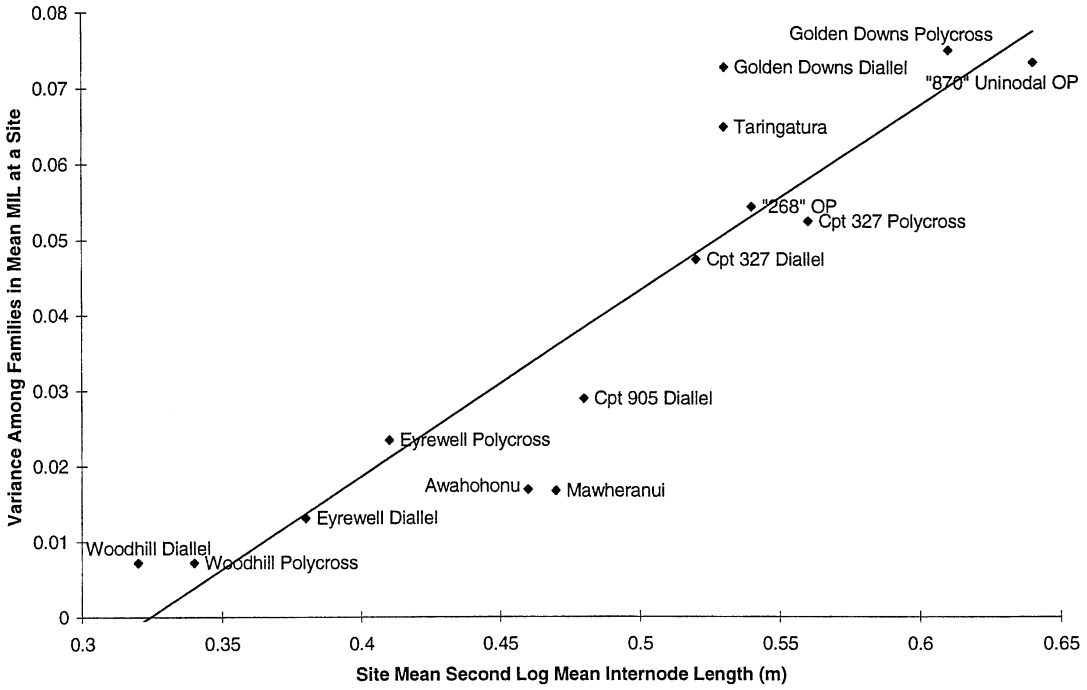

Figure 10: Site mean MIL against variance among families in mean MIL at a site.

DISCUSSION AND CONCLUSION

These data suggest that in order to obtain accurate predictions of MIL a genetic effect should be incorporated into planning models, particularly on sites which have large mean MIL. The use of the relationship between site MIL and variance in MIL among families in predicting the magnitude of genetic differences in MIL for a site should be explored. The development of useful predictors of internode length in radiata pine also requires the prediction of regional or site effects.

It appears that breeding values for branch cluster frequency of clones from different selection groups have different relationships with MIL, and adjustment of MIL for brBV did not remove these differences among selection groups. These differences may in part be due to the original subjective measurement of the branch cluster frequency of the different selection groups being made using different 1 to 9 scales, ie., the branch cluster frequency of a 5 in the "850" polycross is not equivalent to that of a 5 in the "850" diallel, or a 5 in the "870" uninodal OP trial. The adjustment of

brBV for the paternal contribution also leads to differences in the slope of the relationship between brBV and MIL between selection groups. Differences in MIL among clones in different selection groups, therefore, may not be adequately reflected by branch cluster frequency breeding values, although comparisons within selection groups should be valid. Further development of brBV may therefore be desirable in order to put selection groups on the same footing and enable comparison of internode length performance between these groups.

Future Work

1. Develop model to predict site internode length. This process will begin with the testing of a model for internode length prediction developed by Grace & Carson (1993) using data collected in this study;
2. Develop model to predict variance among families on a particular site and the relationship of brBV and internode length;
3. Validation of the predictive model for internode length using new data;
4. Integration of the internode length prediction model into STANDPAK. This will allow forest growers, woodlot owners, and consultants to explore the potential end products of different seedlots under different regimes on a particular site, and to evaluate the financial effect of using genetic material with different quality characteristics;
5. Exploration of the site and genetic differences in the variance in MIL within families.

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Appendix I: Analysis of Variance With brBV as a Class Variable

Table 1: ANOVA of second log mean internode length (MIL) for the "850" diallel trials with branch cluster frequency breeding value (brBV).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	7	4.47	0.64	16.29	0.0001
brBV	10	5.46	0.55	13.97	0.0001
LOCATION*brBV	70	2.75	0.04	1.54	0.0038
ERROR	802	20.39	0.03		

Table 2: ANOVA of MIL for the "850" polycross trials.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	3	11.12	3.71	78.22	0.0001
brBV	24	5.33	0.21	4.57	0.0001
LOCATION*brBV	69	3.29	0.05	1.44	0.0130
ERROR	851	28.14	0.03		

Table 3: ANOVA of MIL for the "850" polycross and "850" diallel trials on four common sites.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
LOCATION	3	11.45	3.82	62.17	0.0037
TRIAL DESIGN	1	0.38	0.38	1.57	0.2228
LOCATION*TRIAL DESIGN	3	0.18	0.06	1.24	0.2997
brBV(TRIAL DESIGN)	34	8.38	0.25	5.07	0.0001
LOCATION*brBV(TRIAL DESIGN)	96	4.77	0.05	1.63	0.0002
ERROR	1267	38.65	0.03		

Table 4: ANOVA of MIL for the "870" uninodal OP trial in Kaingaroa Forest Compartment 905.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
brBV	9	1.77	0.20	3.18	0.0021
ERROR	93	5.73	0.06		

Table 5: ANOVA of MIL for the "268" OP trial in Kaingaroa Forest Compartment 1350.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
brBV	9	0.33	0.04	0.65	0.7488
ERROR	86	4.83	0.06		

Appendix II: Site Correlations for Mean Internode Length

Table 1: Correlation (r) matrix for family mean MIL for each of the "850" diallel trial sites.

Location	Awahohonu	Eyrewell	Golden Downs	Kai 327	Kai 905	Mawhera	Taringatura	Woodhill
Awahohonu	1.00	0.61	0.65	0.81	0.88	0.65	0.73	0.63
Eyrewell		1.00	0.73	0.60	0.59	0.33	0.49	0.53
Golden Downs			1.00	0.83	0.74	0.85	0.85	0.67
Kaingaroa Cpt 327				1.00	0.95	0.79	0.90	0.64
Kaingaroa Cpt 905					1.00	0.71	0.86	0.58
Mawheranui						1.00	0.89	0.62
Taringatura							1.00	0.48
Woodhill								1.00

Table 2: Correlation matrix for family mean MIL for each of the "850" polycross trial sites.

Location	Eyrewell	Golden Downs	Kaingaroa Cpt 327	Woodhill
Eyrewell	1.00	0.73	0.61	0.55
Golden Downs		1.00	0.58	0.43
Kaingaroa Cpt 327			1.00	0.60
Woodhill				1.00

Appendix III: Test for Curvilinear Relationship Between brBV and MIL

Table 1: Level of significance of the quadratic term ($brBV^2$) in the model of mean MIL by family and site against brBV for the "850" diallel trial sites.

Location	Pr > F for brBV	Pr > F for $brBV^2$	
Awahohonu	0.0010	0.7466	*ns*
Eyrewell	0.0206	0.9461	*ns*
Golden Downs	0.0001	0.0013	*s*
Kaingaroa Cpt 327	0.0003	0.1035	*ns*
Kaingaroa Cpt 905	0.0002	0.5201	*ns*
Mawheranui	0.0014	0.0031	*s*
Taringatura	0.0001	0.0015	*s*
Woodhill	0.0326	0.9560	*ns*

Table 2: Level of significance of the quadratic term ($brBV^2$) in the model of mean MIL by family and site against brBV for the "850" polycross sites

Location	Pr > F for brBV	Pr > F for $brBV^2$	
Eyrewell	0.0001	0.3410	*ns*
Golden Downs	0.0001	0.3280	*ns*
Kaingaroa Cpt 327	0.0001	0.6194	*ns*
Woodhill	0.0003	0.7561	*ns*