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QUALITY CHARACTERISTICS
FOR USE IN STANDPAK
— A PRELIMINARY ANALYSIS**

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FOREST & FARM PLANTATION MANAGEMENT COOPERATIVE

EXECUTIVE SUMMARY

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In order to enable forest managers to evaluate the effect of different management strategies on improved genetic material, and also to explore the financial effects of using genetic material tailored for different end uses and sites, genetic gain modifiers for branch habit, stem straightness and malformation need to be included in STANDPAK. In order to estimate these genetic gain modifiers from the subjective scores used by Genetics and Tree Improvement (GTI) to score branch habit, stem straightness and malformation, a relationship needs to be developed between the GTI subjective scores and quantitative measures of log quality characteristics. This preliminary study aims to explore the relationship between GTI branch scores and sweep scores, as characterised by national breeding values (NBV), and mean internode length (MIL), mean internode index (MIX) and sweep. In exploring these relationships a secondary aim of this study is to develop suitable methods of assessment of branch habit and stem straightness for use in this project.

Trees of 35 families from the GTI breeding programme were measured from two progeny trials at both Woodhill and Kaingaroa forests for internode lengths, stem straightness and malformation. The relationships between MIL, MIX, and sweep and their respective NBV were explored graphically and in analyses of variance. The results of these analyses indicate that there is a good relationship between MIL and MIX and a branching habit NBV. Separate relationships are needed for the two forest sites due to the different branching habit apparent at each of the sites. Comparison of the relationship of NBV to MIL for the first and second logs showed there was a different relationship between NBV and MIL for the first and second log for trees in Woodhill but not for trees in Kaingaroa. The results of this preliminary study provides suggestions for areas of future work, in particular the need to explore the variation in MIL and stem straightness within a region and the relationship of NBV to MIL for the first log. Based on the sweep data collected thus far there is no clear relationship between stem straightness NBV and sweep. The results of analysis suggest the relationship between stem straightness NBV and sweep will need to be further explored, in particular there is a need to supplement the data set with more, highly swept trees. The poor relationship between stem straightness NBV and sweep may also be due to inaccuracies in the method used to measure sweep. Further work will need to be carried out to assess the appropriateness of different methods of sweep assessment for use in this project.

OBJECTIVES

1. To develop a system to predict the effect of genetic changes in log quality for improved radiata pine families or seedlots.
2. To evaluate field measurement techniques for assessing log quality characteristics in progeny trials.

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. To this end the tree breeding programme can produce planting stock (designer trees) with altered quality features such as branch size, 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 (G), branch habit (B), straightness (S) and wood density (D).

The different radiata pine breeds may respond differently to specific site and management options. Forest managers will need to make decisions relating to market supply and processing options based on how the different seedlots of radiata pine respond to differing sites and management. To aid forest managers in making these decisions, the impacts of growing designer radiata pine breeds for different characteristics needs to be modelled. The inclusion of genetic gain modifiers relating to characteristics manipulated by the tree breeding programme in STANDPAK will enable forest managers to make informed decisions regarding the management of new breeds of radiata pine. The ability to model these effects in STANDPAK 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 included in STANDPAK for *Pinus radiata* basal area and height growth (Carson, *et al.* 1990; Carson *et al.* (in prep)). This has been possible because the impact of the breeding programme on tree growth has provisionally been quantified in terms of diameter and height growth in genetic gain trials. The impact of the tree breeding programme on branch habit, sweep and malformation however, has only been estimated in terms of a subjective scoring system. This scoring system has enabled relatively quick and low cost information for the ranking and selection of parents, but is not satisfactory for quantifying absolute differences among improved breeds.

Towards establishing a national ranking of families for branch habit, malformation and stem straightness research in other programmes is concerned with the development of breeding

values¹ (Carson, *et al.* in prep.¹). These breeding values are being calculated for all parents in the breeding population, for each log quality trait, using the extensive amount of subjective data available from Genetics and Tree Improvement (GTI) field progeny trials.

This study aims to complement the development of breeding values by producing genetic gain modifiers related to the breeding values (Figure 1). These genetic gain modifiers for mean internode length (MIL), mean internode index² (MIX), stem straightness, malformation and density are to be included in STANDPAK. The inclusion of these modifiers in STANDPAK will enable forest managers to evaluate the effect of different management strategies on improved material, and also the effect of using genetic material tailored for different end uses and sites can be analysed in financial terms.

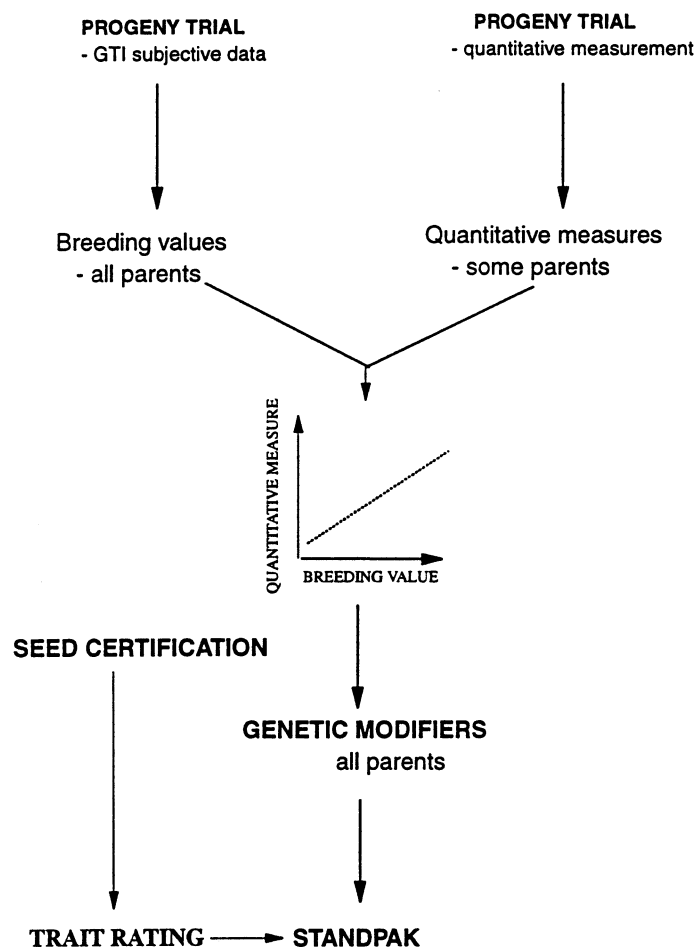


Fig. 1: Project strategy for developing genetic gain modifiers.

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

²mean internode index (MIX) is $\frac{\sum (\text{internode lengths} > 0.6\text{m})}{5.5\text{m}}$.

In order to develop the appropriate genetic modifiers there is a need to obtain quantitative measures of branch habit, stem straightness, malformation and wood density for each parent in the breeding programme across New Zealand. Quantitative measurement of internode length, stem straightness and malformation are needed as GTI has not taken direct quantitative measures of these characteristics in their progeny trials. If there is a relationship between the breeding values, based on GTI subjective scores, and quantitative measures, actual values could be predicted by STANDPAK by genetic gain modifiers. Based on the established relationships quantitative measures of MIL, MIX, stem straightness and malformation may be predicted from the subjective scores for each family in the GTI breeding programme.

The general steps involved will be:

- Develop and refine field measurement techniques for obtaining objective measures related to economic worth of log quality characteristics from progeny trials. Initially research will focus on internode length and stem straightness.
- Characterise the genetic variation in each log quality trait over a range of forest sites in New Zealand by measuring a representative sample of families in different progeny tests using objective measurement techniques. Develop relationships between subjective scores and objective measurement so that objective measurements can be predicted for any family or seedlot that has been ranked using the subjective scoring system.

This preliminary study focuses on sites which have extreme internode lengths so that the relationship between mean internode length (MIL) and mean internode index (MIX), and branch score across sites can be established. The information gathered will act as a precursor to more intensive measurement of sites across New Zealand. This initial study is also designed to determine the appropriateness of measurement techniques for malformation, stem straightness and internode length so they may be modified for the future work involved in the study.

METHOD

PROGENY TRIAL SELECTION

In this study trees were measured from the 1975 "850"³ polycross and 1975 "850" disconnected diallel. These GTI progeny trials were established to estimate the general combining abilities of the parents planted into the first seed orchards. The polycross trial design is a randomised complete block of 4 family sets in 10 replications' of a 'sets-in-replications' design, with five half-sib⁴ trees per seedlot per replication planted as non-contiguous plots. The diallel trial design involves each cell containing 5 parents crossed in all combinations giving a total of 10 different families. In each of six replicates, five trees of each of these 10 full-sib⁵ family and six trees of unselected Kaingaroa bulk seedlot (R69/65) were randomly planted at a 5 x 5 m spacing.

These trials were chosen for this assessment because they provide a coverage of New Zealand wide sites. Use of both the diallel and polycross was necessary as the polycross has a wide range of genetic material while the diallel covers a wide range of sites (Table 1).

Disconnected diallel	Polycross trial
Woodhill	Woodhill
Maramarua	Maramarua
Kaingaroa Cpt 905	
Kaingaroa Cpt 327	Kaingaroa Cpt 327
Awahohonu	
Ruatoria	
Golden Downs	Golden Downs
Mawhera	
Eyrewell	Eyrewell
Berwick	Berwick
Taringatura	

Table 1. Sites covered by the 1975 "850" polycross and disconnected diallel progeny trials.

³ The number "850" is a prefix number denoting a particular series 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).

⁴ half-sib families are those for which one parent is common.

⁵ full-sib families are those for which both parents are common.

A final crop stocking trial was established in the polycross in 1986 to study the effect of early⁶ and late⁷ thinning to different stockings on genetically improved material. Trees in this study were selected from the unthinned (600 N/ ha) plots except for two plots at Woodhill where trees had to be selected from plots thinned to 400 N/ ha. These plots were 4/2 which received a late thinning to 400 N/ ha and 1/4 which received an early thinning to 400 N/ ha. The selection of trees from plots at 400 N/ ha should not affect MIL or MIX estimates compared with estimates of these parameters from the unthinned stands. Stocking has not been found to significantly influence MIL or MIX on forest sites (Woods and Carson, 1988; Tombleson, Grace and Inglis, 1990; Grace and Carson, 1992; Knowles and Kimberley, 1992).

SITE SELECTION

The progeny trials in Kaingaroa and Woodhill forests were chosen for their strongly contrasting branch habits. Woodhill on low fertility sands has short tree MIL's (Carson and Inglis, 1988). Kaingaroa is a more fertile site and so has longer tree MIL's than Woodhill (Carson and Inglis, 1988).

LOCATION	ALTITUDE (m)	ASPECT	SLOPE (°)	SOIL AND SITE PREPARATION
Woodhill	20	west	3-12	Sand, stabilised with marram and lupin. Rows crushed by bulldozer before planting.
Kaingaroa	560	west	2-7	Pumice soil, manuka, Douglas fir and radiata crushed and burned before planting

Table 2. Site details for the Woodhill and Kaingaroa polycross and disconnected diallel.

FAMILY SELECTION

20 families were chosen from the polycross plus 4 controls; Southland orchard (Amberley), Canterbury orchard (Amberley), Gwavas orchard and Kaingaroa bulk unselected. 10 families were chosen from the disconnected diallel plus 1 control (unselected bulk material). Families were selected on the basis of the following characteristics which were checked in the GTI database:

⁶ Early thinning was carried out immediately following final pruning.

⁷ Late thinning was carried out 3 to 4 years following final pruning.

- The families had to be represented at all sites covered by the polycross and diallel trials, with at least 10 "crop" trees at each site;
- The 20 families needed to cover the range of GTI branch scores, ie., highly multinodal to more uninodal, with an emphasis on the extremes of branch habit (Figure 2). Selection was made on the basis of an estimated national breeding value (NBV) for branching habit for the parents in the progeny trials studied. An estimated NBV is being used prior to the calculation of actual NBV by GTI. The estimated breeding value for a parent was defined as the standardised mean of the GTI branch scores, calculated by:

$$\text{estimated parental BV for a site} = \frac{\text{parental mean branch score} - \text{site mean branch score}}{\text{site standard deviation of branch score}}$$

For the full-sib progeny in the disconnected diallel the breeding values for the progeny are the average of the two parents breeding values. For the half-sib progeny in the polycross the breeding values are the same as those calculated for the progeny's mother.

The estimated NBV for each parent was derived by averaging the site breeding values for each parent across the sites. Selection of parents on the basis of their estimated national breeding value was used because each parent's MIL and MIX will eventually be related to their associated NBV derived from a wider range of GTI trials (Carson, *et al.*, 1995). It is this relationship that will allow a parent's MIL and MIX to be derived from the parental NBVs which are to be calculated by GTI.

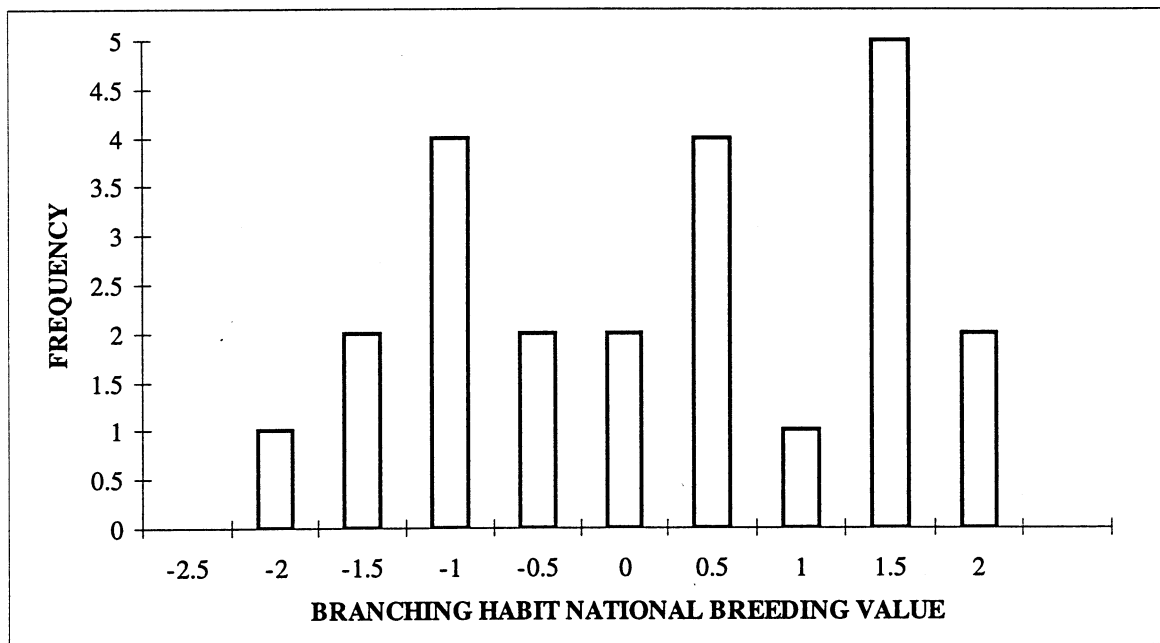


Fig. 2. Range of estimated national breeding values (NBV) covered by the families selected for measurement in this study.

- The families chosen meet a threshold of acceptability for diameter, straightness 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. Malformation, particularly ramicorns and forking influence branching habit. Longer internodes tend to occur on stem sections adjacent to ramicorns and forks (Woods, 1988; Carson and Inglis, 1988).

For each family, at each site, 10 trees were selected for measurement. Trees to be measured were selected in the office, if any of these proved not to be crop trees then replacement trees were selected in the field.

MEASUREMENT

Each tree was assessed for the following characteristics:

- diameter at breast height;
- pruned height;
- whorl count in pruned section;
- internode lengths up to the first whorl above 12 m;
- butt log sweep(5 sweep classes);
- malformation (type and height of occurrence);

- stem cone whorls (height of occurrence);
- 48 tree heights per site;
- branch score (GTI scoring);
- straightness score (GTI scoring);
- malformation score (GTI scoring).

Internode Lengths

Internode lengths on the branched section of the stem (the second log from 6 m to 12 m) were measured using a height pole. The base and top of each whorl was measured to ± 0.05 m (Figure 3). Each branch whorl was measured from a 0.2 m stump height up to the base of the first whorl above 12 m. A stem cone whorl was measured as the end of an internode, even if the stem cone whorl had no branches associated with it. When 2 or more whorls occurred close together and there was no discernible internode the whorls were counted as one (Figure 4). This method of internode length measurement was used because the use of a height pole allows quick measurement of whorl heights while maintaining reasonable accuracy (Turner, 1995). Measurements were made to ± 0.05 m as this was a realistic level of accuracy of measurement while still ensuring that the subtle differences in branching habit between families could be identified by statistical analysis. The stem from 0.2 to just above 12 m was measured to cover the first and second logs. Internode length for these logs has a strong influence on management and processing options.

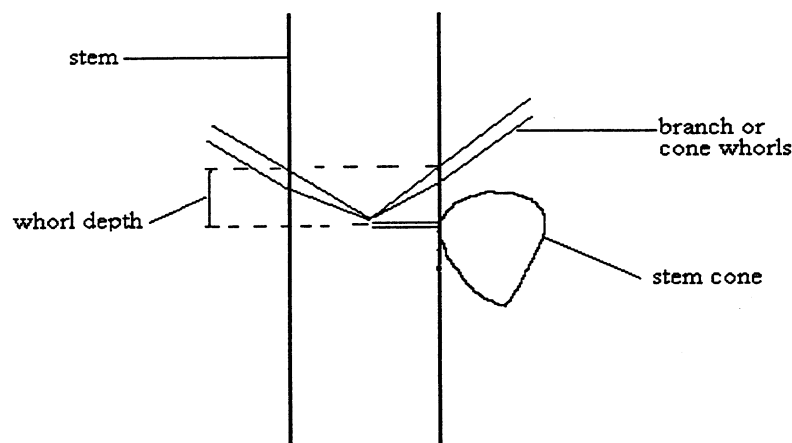


Fig. 3: Whorl depth illustrated. Source: Woods and Carson (1988).

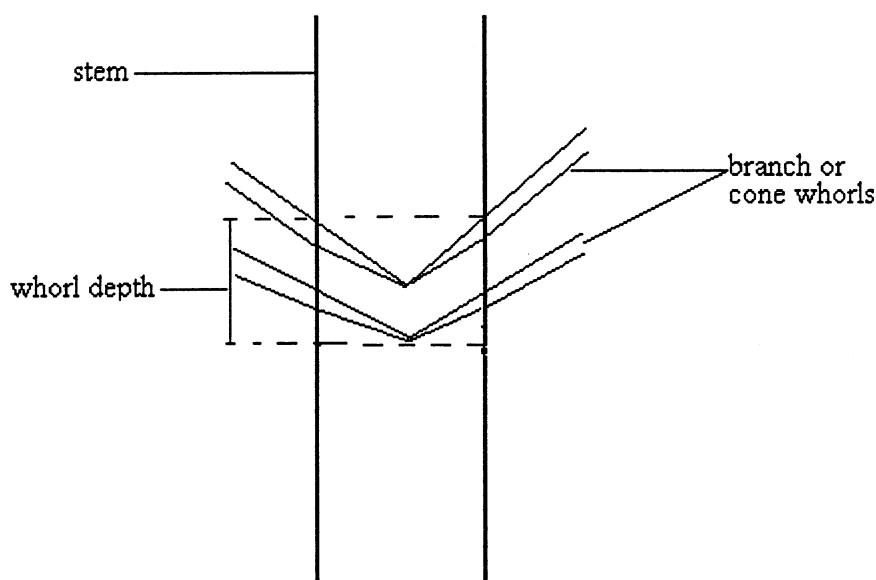


Fig. 4. Whorl depth for close whorls. Source: Woods (1988).

Whorl counts were used to estimate MIL in the pruned section of the stem. This method was used as it was felt direct measurement of internode lengths with the height pole would not achieve any greater level of accuracy due to the lack of branches to accurately measure the whorl base and top. The whorl count method is also quick and provides a good estimate of MIL (Woods, 1988; Woods and Carson, 1988; Turner, 1995).

Stem Straightness

The sweep measurement technique is based on work by Gralleis and Klomp (1982) and West and Kimberley (1991). West and Kimberley (1991) carried out an assessment of sweep on trees which had just received a high prune, ie., trees younger than those assessed in this study. 4 sweep measurement techniques, straight edge, harp, height pole and s-gauge, were tested. They found the height pole to be the best method. While the height pole is not as accurate as the harp or the straight edge its ease of use meant the height pole could be used to measure sweep 50% faster than the harp or s-gauge and considerably more rapidly than the straight edge. The relative rankings of the 4 methods in terms of estimates of mean are given in Table 3. The straight edge method is assumed to be 100% accurate

METHOD	MEAN SWEEP (cm)
Straight edge	6.2
Harp	6.0
Height pole	5.8
S-gauge	4.6

Table 3. Estimated mean sweep by four methods of sweep assessment. The actual sweep is 6.2 cm. Source: West and Kimberley (1991).

The ability of the harp, height pole and s-gauge to estimate stem straightness for a range of levels of sweep was checked by West and Kimberley (1991). The harp, height pole and s-gauge all have a tendency to overestimate sweep when trees have < 4 cm sweep and underestimate stem straightness on trees with sweep > 10 cm

West and Kimberley (1991) had 3 sweep classes when using the height pole to assess stem straightness in terms of deviation expressed as a proportion of stem diameter at point of maximum sweep. These sweep classes are:

- 0 - diameter/4;
- diameter/4 - diameter/2;
- $>$ diameter/2.

These sweep classes were considered to be the minimum range that was practical to measure with the instruments tested. The height pole is reasonably accurate at differentiating trees into these 3 categories.

Based on this work by West and Kimberley (1991) and Grallelis and Klomp (1982) a method of sweep assessment was devised. Stem sweep was measured over a 6.0 m log length using a height pole at right angles to the plane of maximum sweep. The centre to centre method described by Grallelis and Klomp (1982) was used (Figure 5). The 5 sweep classes are:

- 0 - no sweep;
- 1 - $<$ diameter/ 8;
- 2 - $<$ diameter/ 4;
- 3 - $<$ diameter/ 2;
- 4 - $>$ diameter/ 2.

The height of maximum sweep was also measured to enable a measure of sweep in terms of mm/ m in the 6 m log (Figure 5).

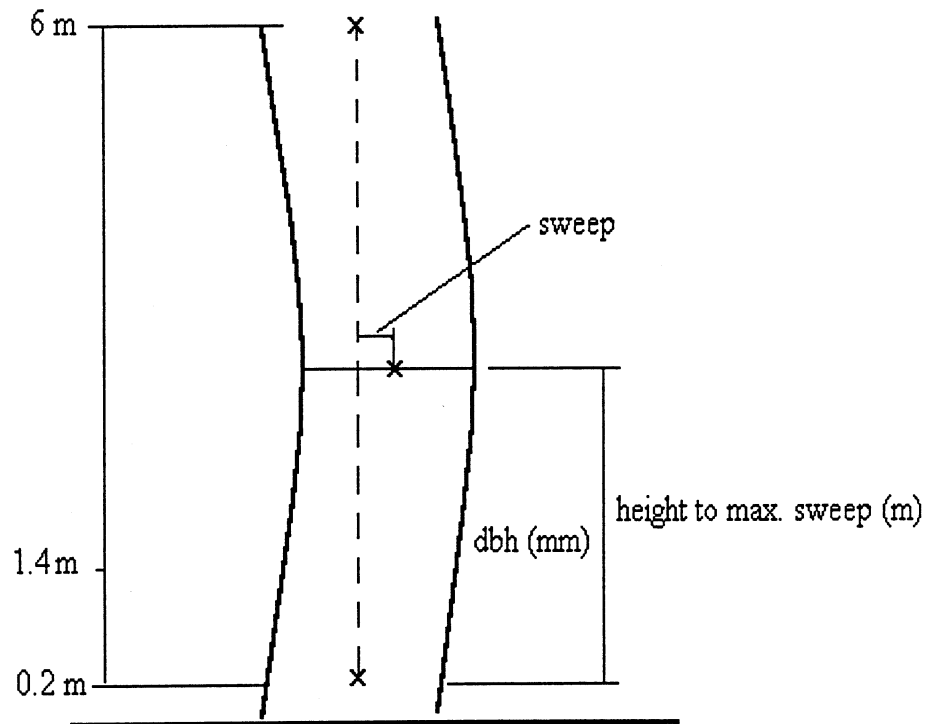


Fig. 5. The centre to centre method of sweep measurement. Source: Grallelis and Klomp, 1982.

The height pole was used because while being 50% faster than the harp and s-gauge it is still reasonably accurate. The use of the height pole for internode length measurement meant that stem straightness could be assessed as internode length measurements were made, resulting in further time savings over the other sweep measurement techniques. It was decided to expand the number of sweep classes to 5, with more emphasis on the lower levels of sweep. The focus on the lower levels of sweep was needed as "crop" trees were chosen for measurement. These trees have only minor levels of sweep. Stem straightness was measured for the first 6 m of the stem as this section of stem is normally pruned. Level of sweep in the pruned log is an important influence on log value (West and Kimberley, 1991). This measurement will only give an indication of the level of sweep by family because only "crop" trees with low levels of sweep were selected for measurement.

48 trees at each site, 24 from the diallel and 24 from the polycross were measured for total tree height using a Suunto. This information was used in a taper function to enable stem straightness to be expressed in terms of mm/ m.

Malformation

The method of malformation assessment is based on that developed by Grallelis and Klomp (1982). The work by Grallelis and Klomp (1982) was carried out in older crop stands containing higher levels of malformation than present in the GTI progeny trials studied. The method aims to quantify the main region of stem influenced by a malformation and the level of stem deviation that has occurred. Trees were visually assessed for type of malformation (Appendix I contains definitions of the malformation types). For each malformation the height the defect starts, and length of stem affected were measured using the height pole. The malformation was also assessed for level of stem deviation in relation to stem diameter:

- minor - defect core to $< D/2$;
- medium - $> D/2$ to $< D$
- major - $> D$.

Each of these malformation characteristics and combinations of characteristics will need to be correlated with the GTI malformation score to assess which components of malformation relate to the malformation score. By establishing which malformation characteristics are correlated with malformation score future assessments of malformation in the genetic gains study can be based on those specific characteristics. This aspect of the study is yet to be assessed.

In this preliminary study carried out in Kaingaroa and Woodhill forests malformation was measured on the basis of type:

- ramicorns;
- double leaders;
- multiple leaders
- kinks;
- wobble;

and height of occurrence only. As for sweep measurement, the measurement of malformation occurrence will only give an indication of the level of malformation by family because "crop" trees with low levels of malformation were selected.

ANALYSIS

INTERNODE LENGTH

The focus of the analysis is to establish the relationship between MIX and MIL, and the estimated national breeding value for branch score across the two sites in this study. MIX was calculated for a 5.5 m (6.3 m to 11.8 m) and MIL was calculated for the second log (6 m to the first whorl above 12 m). To check the relationship, MIX and MIL were plotted against estimated national breeding value and the significance of the relationship tested using analysis of variance. The analysis of variance included estimated NBV as a covariate, forest (Kaingaroa and Woodhill), experiment (diallel and polycross) and interaction effects. The analysis of variance was calculated without the control families. The relationship between MIL and MIX, and branch score (1984 assessment) was also analysed. The relationship between sweep and stem straightness score were also be analysed, using the same method as for MIL and MIX.

Whorl counts were used to estimate MIL in the pruned section based on the formula from Woods & Carson (1988),

$$MIL = \frac{l - (n * d)}{n + (I - 1)}$$

where MIL is mean internode length for the log length measured;

l is the length of stem or log being measured;

n is the number of branch and/ or stem cone whorls per length of stem or log being measured;

d whorl depth (based on tree average whorl depth in the section of stem measured with the height pole);

I is the number of times for each stem or log that the end of the indicated "log" does not coincide with a branch or stem cone whorl, ie., 0, 1, or 2.

STEM STRAIGHTNESS

To calculate sweep in terms of mm/ m, the stem diameter at the point of maximum sweep needed to be established. Using the heights of 48 trees (stratified by experiment type) from each site Petterson curves for Kaingaroa and Woodhill were produced (Appendix II). The Petterson curves enabled height to be estimated for all other trees measured based on dbh. Using estimated tree height and measured dbh, taper functions were used to predict the

diameter under bark at the height of maximum sweep. The Woodhill 370 N/ ha (tree taper table 326) and Kaingaroa Transition Crop (tree taper table 327) taper functions were used to estimate stem diameter at the point of maximum sweep (Eggleston, 1992).

RESULTS AND DISCUSSION

MEAN INTERNODE LENGTH

The large variation in tree MIL within a family is shown in Figure 5. The greater within family variation in second log MIL in Kaingaroa forest compared with Woodhill forest may be due to the greater range in MIL found at Kaingaroa.

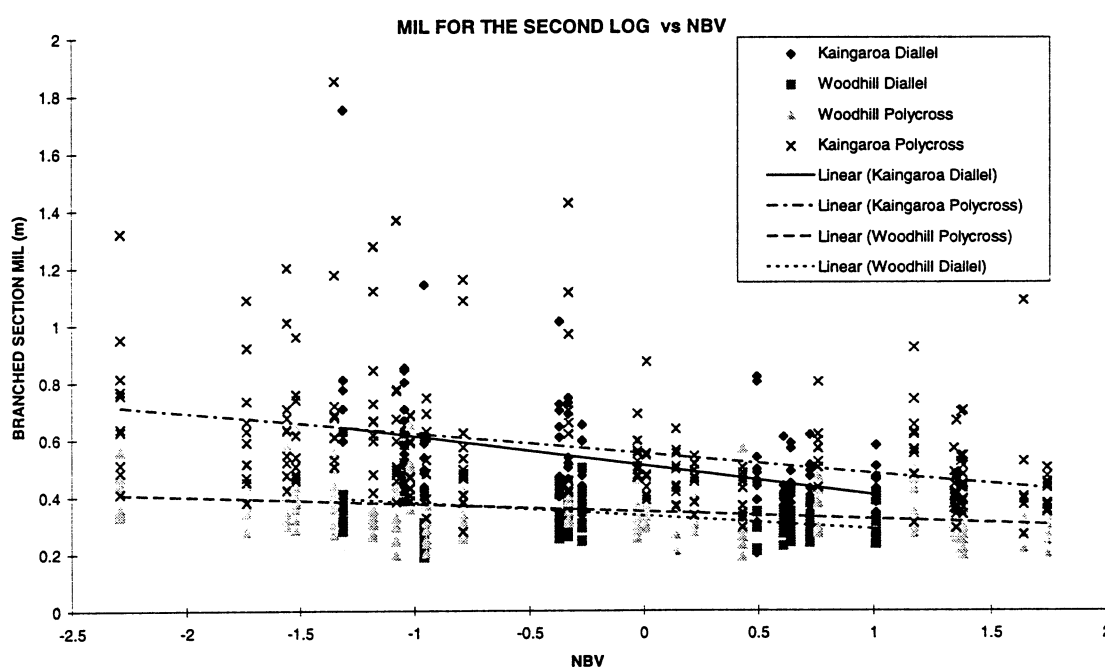


Fig. 5: Individual tree second log MIL vs estimated NBV by site and trial for Woodhill and Kaingaroa 1975 "850" polycross and disconnected diallel.

The relationship between branching habit NBV and MIL by site and trial is shown in Figure 6 and the analysis of variance results relating to these relationships are given in Tables 4 and 5. There is a significant difference in MIL between the GTI families measured in the study (Table 4). This difference creates the relationship between branching habit NBV and MIL. The greater the difference between the families the steeper the slope of the trend line. There is also a significant difference in MIL between Kaingaroa and Woodhill, which is likely to be due to site fertility differences (Carson and Inglis, 1988). There is also a significant difference in the slopes of the relationships between Kaingaroa and Woodhill (Table 5). This reflects the difference in variance of MIL for the two sites. Woodhill has less range of internode lengths

resulting in a shallower trend line. These results suggest separate models will be needed to predict MIL from NBV for Kaingaroa and Woodhill.

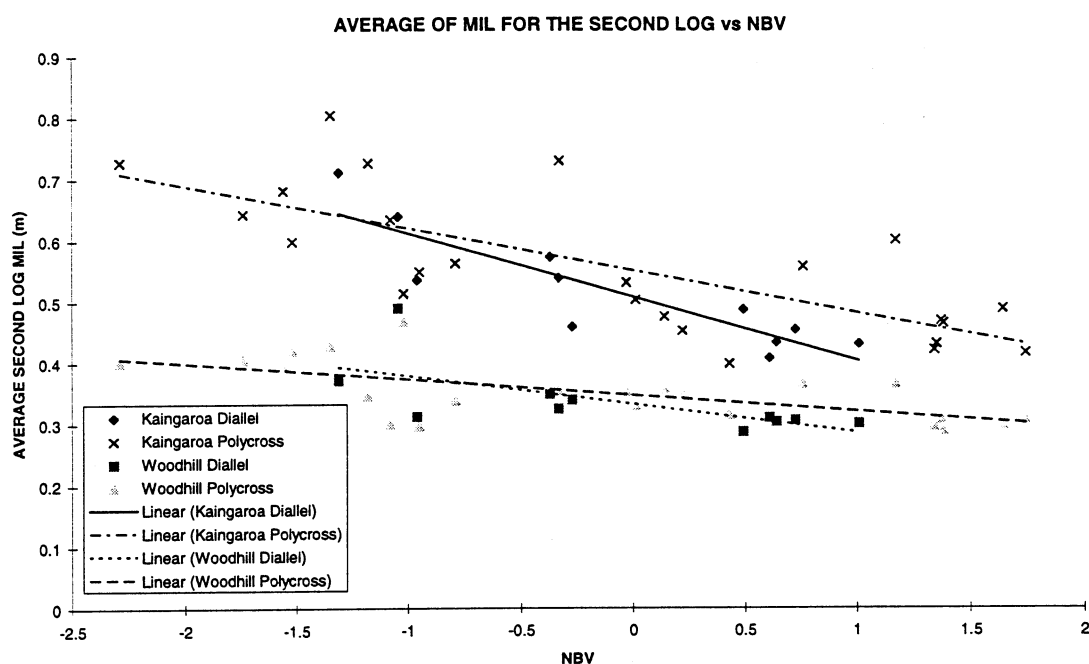


Fig 6. Average family second log mean internode length vs estimated NBV by site and trial for Woodhill and Kaingaroa 1975 "850" polycross and disconnected diallel.

Dependent Variable: SECOND LOG MIL

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
FOREST	1	4.43	4.43	253.95	0.0001
EXPT	1	0.13	0.13	1.09	0.3060
FAMILY(EXPT)	28	3.36	0.12	5.62	0.0001
FOREST*EXPT	1	0.03	0.03	1.31	0.2527
FOREST*FAMILY(EXPT)	28	1.19	0.04	1.99	0.0021
ERROR	521	11.13	0.02		

Table 4: Analysis of variance relating second log MIL to forest, family and experiment effects. FOREST is Woodhill or Kaingaroa, EXPT is the polycross or the disconnected diallel, and FAMILY are the GTI breeding program families measured in this project.

Dependent Variable: SECOND LOG MIL

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	1.88	1.88	84.04	0.0001
FOREST	1	4.74	4.74	212.39	0.0001
EXPT	1	0.13	0.13	5.82	0.0162
FOREST*EXPT	1	0.03	0.03	1.18	0.2782
NBV*FOREST	1	0.24	0.24	10.72	0.0011
NBV*EXPT	1	0.11	0.11	4.98	0.0260
NBV*FOREST*EXPT	1	0.01	0.01	0.28	0.5962
ERROR	573	12.79	0.02		

Table 5: Analysis of variance relating second log MIL to forest, branching habit national breeding value and experiment effects. FOREST is Woodhill or Kaingaroa, and EXPT is the polycross or the disconnected diallel.

MEAN INTERNODE INDEX

The large variation in tree MIX within a family is shown in Figure 7. There is a larger variation in tree MIX than for second log MIL.

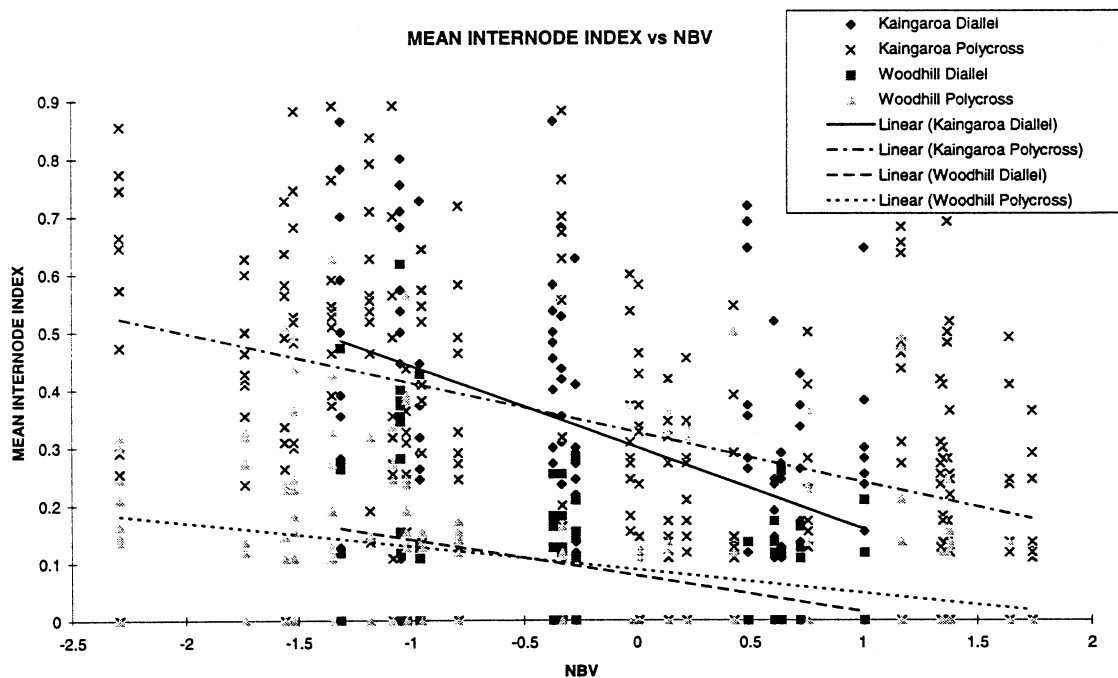


Fig. 7: Individual tree MIX vs estimated NBV by site and trial for Woodhill and Kaingaroa 1975 "850" polycross and disconnected diallel.

The relationship between branching habit NBV and MIX by site and trial is shown in Figure 8 and the analysis of variance results relating to these relationships are given in Tables 6 and 7. The results of these analysis are similar to those for MIL, however, there is a greater level of unexplained variation in estimated MIX than for MIL. Table 7 indicates there is a significant difference in the relationships between NBV and MIX between the two trials measured in this project.

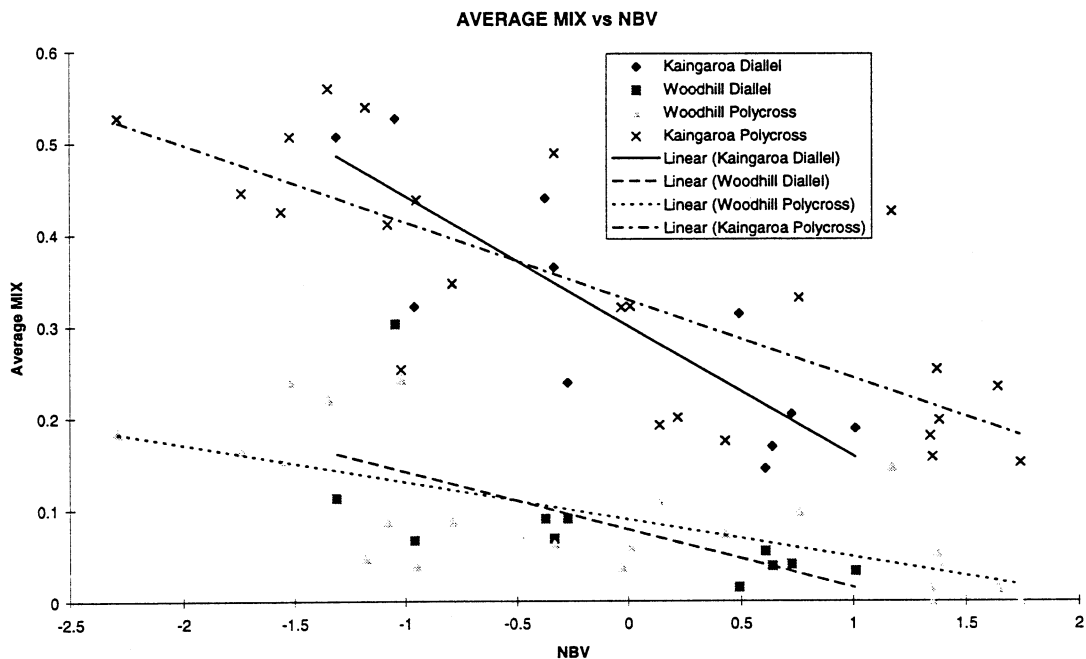


Fig 8. Average family mean internode index vs NBV by site and trial for Woodhill and Kaingaroa 1975 "850" polycross and disconnected diallel.

Dependent Variable: MEAN INTERNODE INDEX

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
FOREST	1	7.59	7.59	276.40	0.0001
EXPT	1	0.04	0.04	0.18	0.6731
FAMILY(EXPT)	28	5.75	0.21	7.48	0.0001
FOREST*EXPT	1	0.001	0.00	0.06	0.8068
FOREST*FAMILY(EXPT)	28	1.68	0.06	2.18	0.0005
ERROR	524	14.39	0.03		

Table 6: Analysis of variance relating the MIX to forest, family and experiment effects.

Dependent Variable: MEAN INTERNODE INDEX

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	3.28	3.28	110.07	0.0001
FOREST	1	6.90	6.90	231.55	0.0001
EXPT	1	0.03	0.03	1.03	0.3095
FOREST*EXPT	1	0.0005	0.0005	0.017	0.8959
NBV*FOREST	1	0.37	0.37	12.43	0.0005
NBV*EXPT	1	0.27	0.27	9.04	0.0028
NBV*FOREST*EXPT	1	0.05	0.05	1.78	0.1832
ERROR	576	17.15	0.03		

Table 7: Analysis of variance relating MIX to forest, branching habit national breeding value and experiment effects.

FIRST LOG BRANCHING HABIT

The distribution of internode lengths along the tree stem (Figure 9) shows that the first log (0.2 to 6.3 m) is likely to have a shorter MIL than the second log (6.3 to 12 m) (Turner, 1994 & Grace and Carson, 1992). This difference in internode lengths between the first and second logs may mean a separate model needs to be developed to relate NBV to MIL and MIX for the first log. All the trees measured in this preliminary project were pruned so only a rough estimate of MIL for the first log could be made based on whorl counts. The information gathered will, however, provide an indication of the extent to which there is a difference in the relationship between NBV and MIL for the first and second logs.

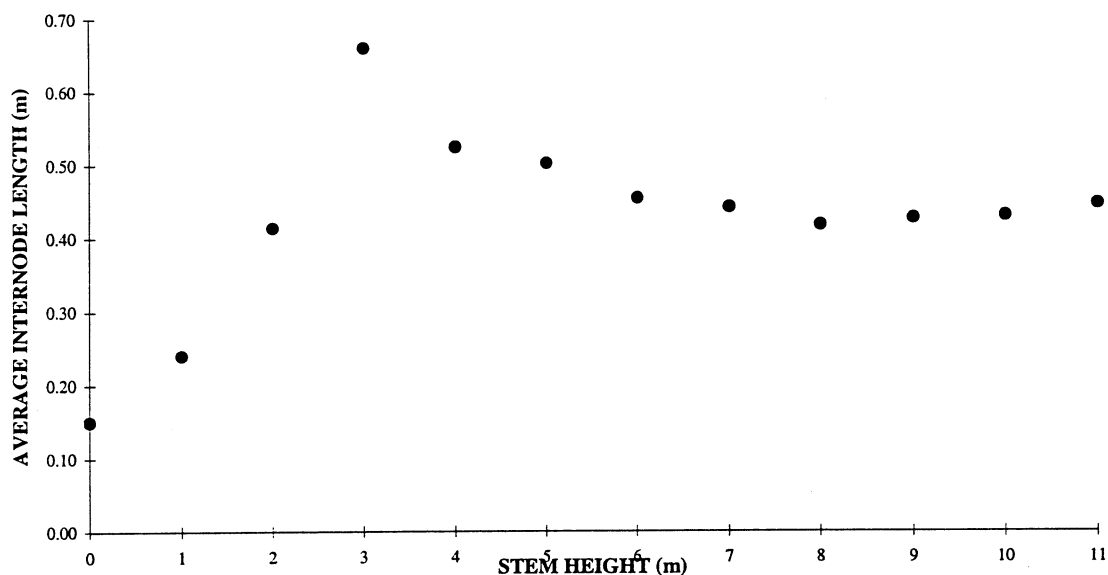


Fig. 9: Distribution of mean internode lengths over the stem length, by 1 m height classes, for "850" series improved material. Source: Turner, 1994.

The plots of MIL for the branched and pruned sections of the stem against NBV for Kaingaroa and Woodhill forest (Figures 10 and 11) indicate there is a difference in MIL for the pruned and branched section of trees at Woodhill forest, but that this is not the case for trees at Kaingaroa forest. These results are verified by the analysis of variance (Tables 8 and 9) which shows there is a significant difference in MIL estimate between the first and second log for Woodhill, but not for Kaingaroa forest. For Kaingaroa forest the second log MIL is greater than the pruned section MIL, whereas the opposite is the case for Woodhill.

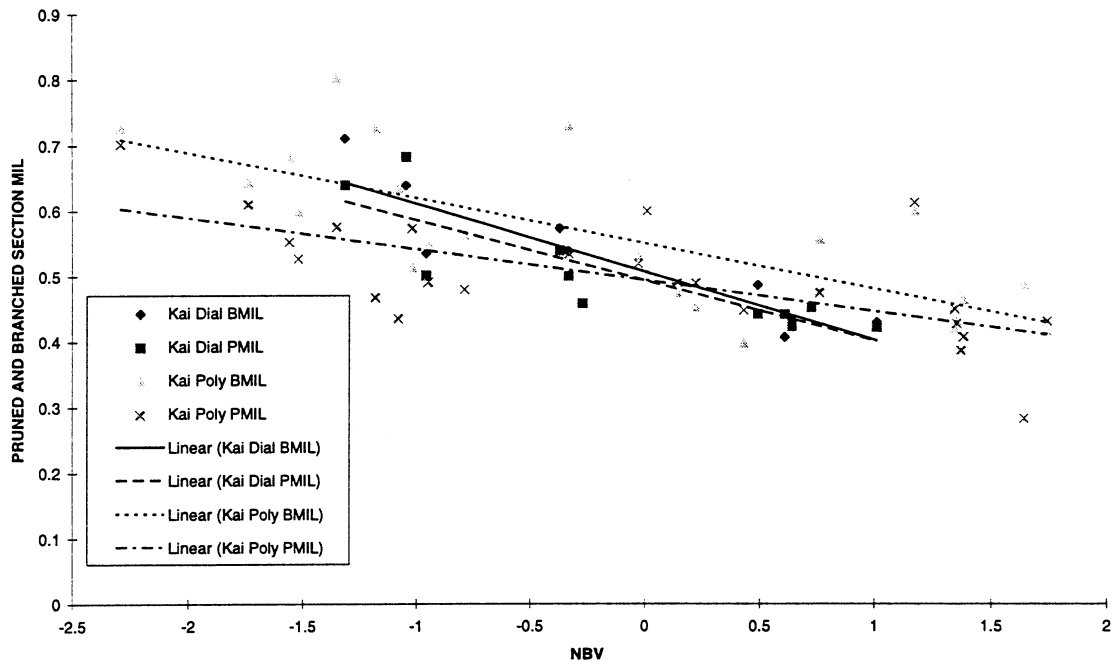


Fig. 10: The relationship of NBV to second log MIL and pruned section MIL for the Kaingaroa diallel and polycross.

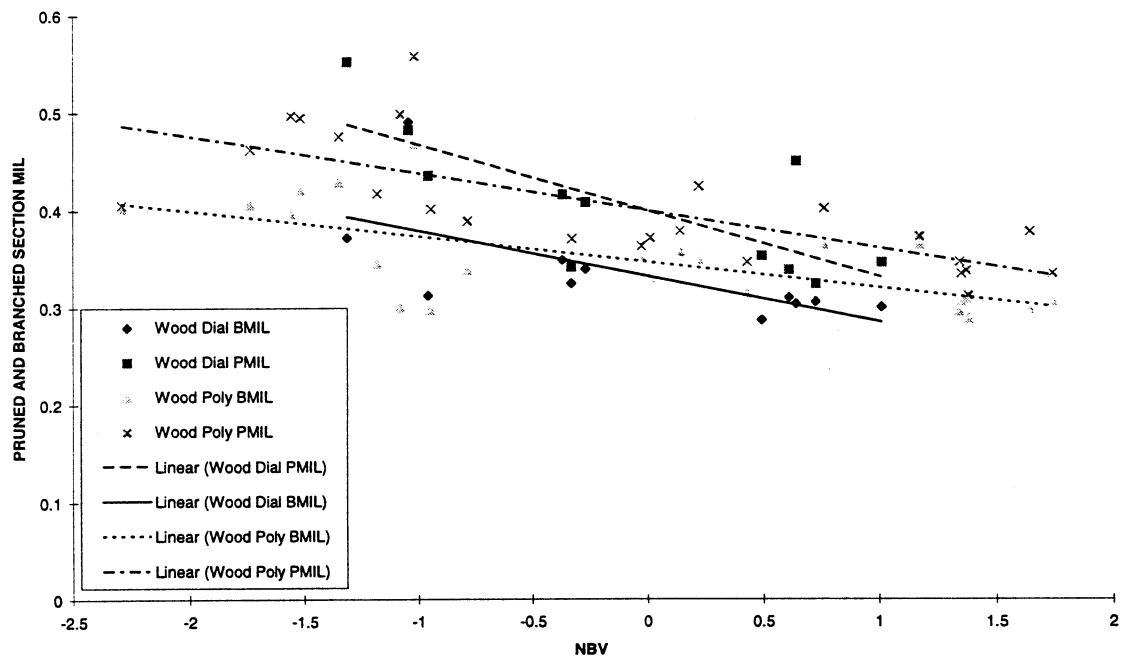


Fig. 11: The relationship of NBV to second log MIL and pruned section MIL for the Woodhill diallel and polycross.

Dependent Variable: MEAN INTERNODE LENGTH

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	2.99	2.99	91.66	0.0001
LOG	1	0.14	0.14	4.42	0.0360
EXPT	1	0.08	0.08	2.53	0.1121
EXPT*LOG	1	0.06	0.06	1.74	0.1880
NBV*LOG	1	0.02	0.02	0.71	0.4010
NBV*EXPT	1	0.23	0.23	7.19	0.0076
NBV*EXPT*LOG	1	0.00	0.00	0.14	0.7129
ERROR	574	18.73	0.03		

Table. 8: The analysis of variance for the relationship of NBV to second log MIL and pruned section MIL for the Kaingaroa diallel and polycross. LOG is first and second logs

Dependent Variable: MEAN INTERNODE LENGTH

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	0.95	0.95	84.11	0.0001
LOG	1	0.36	0.36	32.04	0.0001
EXPT	1	0.01	0.01	0.54	0.4624
EXPT*LOG	1	0.01	0.01	1.24	0.2659
NBV*LOG	1	0.01	0.01	0.97	0.3254
NBV*EXPT	1	0.08	0.08	7.50	0.0064
NBV*EXPT*LOG	1	0.00	0.00	0.14	0.7092
ERROR	565	6.37	0.011		

Table. 9: The analysis of variance for the relationship of NBV to second log MIL and pruned section MIL for the Woodhill diallel and polycross.

These results suggest the need for separate models relating sweep NBV and sweep for first and second logs will need to be assessed for each site.

STEM STRAIGHTNESS

The sampling of trees for exploring the relationship between sweep NBV and stem straightness was biased towards less swept trees. This biased sample set has resulted in there being no clear relationship between sweep NBV and stem straightness (Figure 12). This lack of a clear relationship is further emphasised by stem straightness NBV and family not being statistically significant effects in the analysis of variance (Tables 10 and 11). The analysis of variance results indicate that for the data measured in this preliminary analysis, family is not a

significant influence on tree sweep, however, there are significant differences in levels of stem straightness between forests and trials. The differences between forests is likely to relate to the differences in site fertility, with the more fertile Kaingaroa site having a greater incidence of swept trees. The differences between trials may relate to the differences in initial stockings. The polycross was established at 600 N/ ha while the diallel was established at approximately 1250 N/ ha, and was thinned to 625 N/ ha.

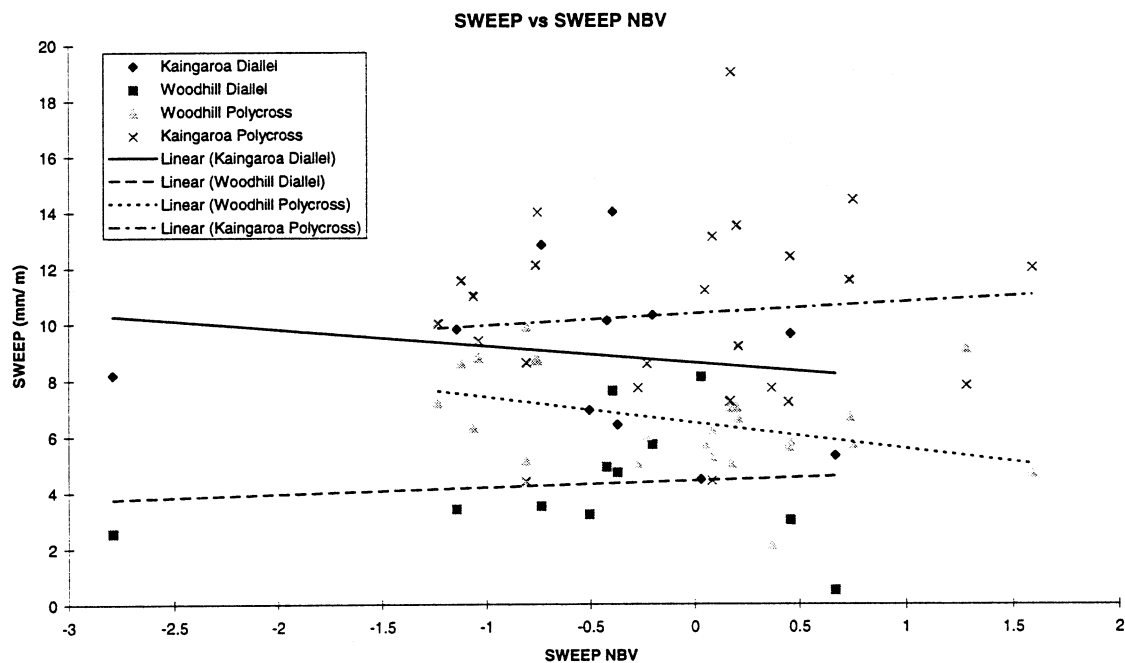


Fig 12. Stem straightness vs sweep NBV by site and trial for Woodhill and Kaingaroa 1975 "850" polycross and disconnected diallel.

Dependent Variable: SWEEP

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
FOREST	1	3369.79	3369.79	42.39	0.0001
EXPT	1	690.72	690.72	9.54	0.0046
FAMILY(EXPT)	28	2031.42	72.55	0.91	0.5970
FOREST*EXPT	1	6.27	6.27	0.08	0.7789
FOREST*FAMILY(EXPT)	28	1622.04	57.93	0.73	0.8452
ERROR	521	41416.63	79.49		

Table 10: Analysis of variance relating the stem straightness to forest, family and experiment effects.

Dependent Variable: SWEEP

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	5.69	5.69	0.07	0.7876
FOREST	1	2976.77	2976.77	37.99	0.0001
EXPT	1	641.13	641.13	8.18	0.0044
FOREST*EXPT	1	2.46	2.46	0.03	0.8595
NBV*FOREST	2	62.23	31.12	0.79	0.3732
NBV*EXPT	1	56.50	56.50	0.72	0.3962
NBV*FOREST*EXPT	1	67.51	67.51	0.86	0.3537
ERROR	572	44823.94	78.36		

Table 11: Analysis of variance relating stem straightness to forest, branching habit national breeding value and experiment effects.

The relationship between external sweep and pith sweep, which relates to juvenile sweep, was explored graphically to ascertain how strongly the external sweep measured at age 20 may relate to the juvenile sweep which was scored by GTI at age 8. A database of 814 records from cross sectional analysis of logs (C.L. Todoroki, pers. comm.) was used to produce Figure 13. The plots suggest there is a good relationship between juvenile and external sweep, therefore, the poor influence of national breeding value for sweep on stem straightness at age 20 is probably not due to the sweep measured at age 20 bearing little similarity to the juvenile sweep scored at age 8 by GTI.

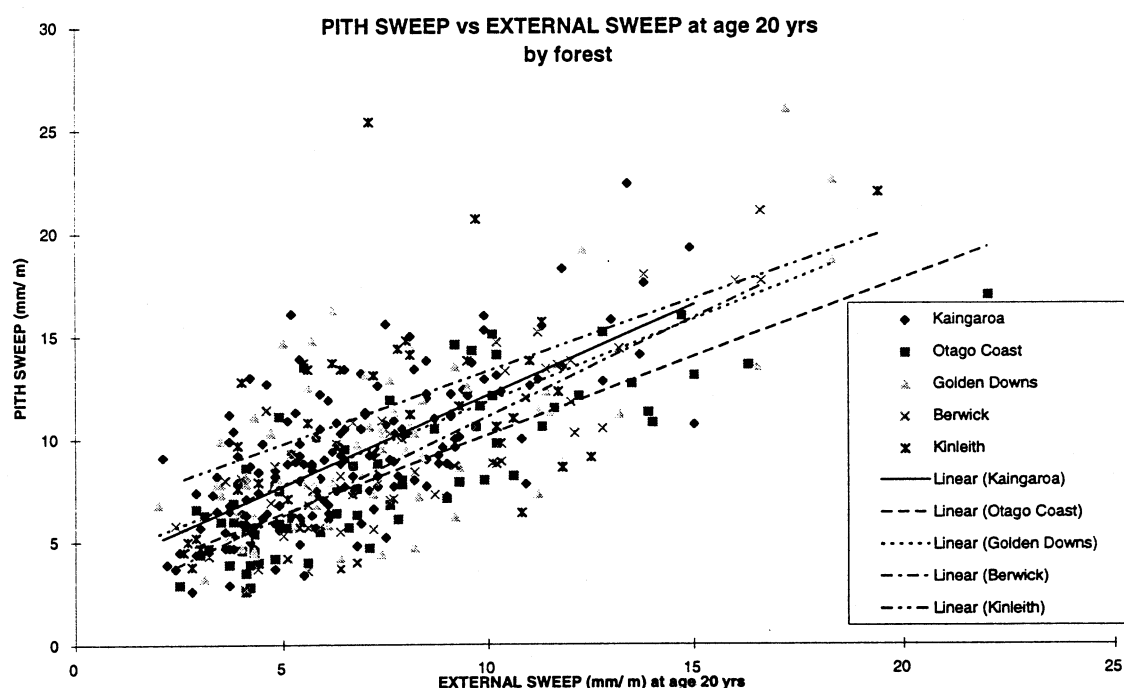


Fig. 13: Plot of pith sweep against external sweep at age 20 years by forest. The trend lines were fitted by simple linear regression.

To explore factors influencing the incidence of sweep analyses of variance relating sweep NBV to dbh and height of maximum sweep were carried out. The analysis of variance for stem straightness (Table 11) indicates sweep NBV is not significant in explaining the variation in sweep measured. The analysis of variance for diameter at 1.4 m (Table 12) indicates that sweep NBV is also not significant in explaining the variation in dbh measured. This suggests trees of different diameters are not more or less likely to be swept. The analysis of variance for height of maximum sweep (Table 13) also shows that sweep NBV is not significant in explaining the variation in height of maximum sweep. This suggests different families do not differ in the height at which maximum sweep occurs.

Dependent Variable: DBH

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	9037.26	9037.26	1.7274	0.1893
FOREST	1	584916.05	584916.05	111.7997	0.0001
EXPT	1	555059.09	555059.09	106.0929	0.0001
FOREST*EXPT	1	27213.44	27213.44	5.2015	0.0229
NBV*FOREST	1	32983.68	32983.68	6.3044	0.0123
NBV*EXPT	1	2360.05	2360.05	0.4511	0.5021
NBV*FOREST*EXPT	1	3013.05	3013.05	0.4511	0.4482
ERROR	573	2997833.33	5231.82		

Table 12: Analysis of variance relating dbh to forest, GTI trial, and sweep national breeding value.

Dependent Variable: HEIGHT OF MAXIMUM SWEEP

Source	DF	Type IV SS	Mean Square	F Value	Pr > F
NBV	1	133.73	133.73	0.3171	0.5736
FOREST	1	324.30	324.30	0.7689	0.3809
EXPT	1	1080.34	1080.34	2.5614	0.1101
FOREST*EXPT	1	112.14	112.14	0.2659	0.6063
NBV*FOREST	1	225.93	225.93	0.5357	0.4645
NBV*EXPT	1	174.81	174.81	0.4145	0.5200
NBV*FOREST*EXPT	1	332.01	332.01	0.7871	0.3753
ERROR	573	241681.29	421.78		

Table 13: Analysis of variance relating height of maximum sweep to forest, GTI trial, and sweep national breeding value.

FUTURE WORK

This preliminary analysis of internode length data for Woodhill and Kaingaroa suggests there is a need to further explore the within region influences, such as site fertility, climate factors, and altitude on tree internode length. This will determine the validity of a regional model for relating MIL and MIX to branch habit national breeding values (NBV).

The results so far also indicate that the prediction of mean internode length from national breeding values for the first log (0.2 to 6.0 m) may require a different predictive model to that developed for the second log. Development of a model relating NBV to first log MIL and MIX will require the measurement of unpruned trees in GTI progeny trials to gain an accurate estimate of first log branching habit.

The biased data set of stem straightness information may have resulted in the unclear relationship between sweep NBV and stem straightness. This indicates that there is a need for a more robust data set for sweep assessment. To this end the selection of several families from the 1975 "850" polycross and disconnected diallel with extreme sweep will be made and trees from these families measured at Kaingaroa and Woodhill. The method of stem straightness assessment is to be assessed to develop a more accurate and precise method.

CONCLUSION

This preliminary analysis of the relationship between branch habit NBV and MIL and MIX, for Woodhill and Kaingaroa forest indicates it is possible to predict MIL and MIX from GTI national breeding values. Separate models need to be developed for the two sites measured because of the differences in branch habit between Kaingaroa and Woodhill. Further work will be carried out within the Central North Island region to ascertain to what extent within region factors such as site fertility, climate and altitude influence branch habit, and therefore to what extent regional models relating MIL and MIX to NBV are valid. Models relating branch habit NBV to MIL in the first and second logs indicated there was a need for a separate model for the first and second log for trees in Woodhill forest but not for trees in Kaingaroa forest. The need for a separate model for the first and second logs suggests that measurements will need to be made of unpruned trees to ascertain a more accurate estimate of first log MIL. The relationship of sweep to stem straightness NBV is very poor, and suggests there is a need to further explore this relationship, by measuring trees from families with greater sweep than the families measured in this study.

The method of internode length measurement has proven to be suitable for gaining an accurate measure of MIL, and as such this method will be used in future studies. The poor relationship of sweep NBV to stem straightness may be due to inaccuracies in the method used to measure sweep. Work will need to be carried out to assess different methods of sweep assessment for suitability for use in this project.

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Hamish McElwee, and Stephen Wakelin provided invaluable assistance with the laborious task of field work. The authors are grateful to Carter Holt Harvey Forests and Forestry Corporation of New Zealand for allowing access to their forests. Christine Todoroki of FRI made available the data from cross sectional analysis of logs for the study of the relationship of pith sweep to external sweep.

REFERENCES

- Carson, M.J. and C.S. Inglis. 1988. Genotype and location effects on internode length of *Pinus radiata* in New Zealand. **New Zealand Journal of Forestry Science** 18(3). 267-279.
- Carson, M.J., R.D. Burdon, S.D. Carson, A. Firth, C.J.A. Shelbourne and T.G. Vincent. 1990. Realising genetic gains in production forests. Paper 3.1 in **Breeding and Genetic Resources: Proceedings, joint meeting of Western Forest Genetics Associates and IUFRO Working Parties S2.02.05, S2.02.06, S2.02.12, and S2.02.14 on Douglas fir, Contorta pine, Sitka spruce, and *Abies* spp.**, Olympia, Washington, August 1990.
- Carson, S.D., O. Garcia, J. Skinner and M.L. Kimberley (in prep.). Gain in improved radiata pine expressed as growth rate multipliers.
- Carson, S.D., S. Knowles, P.A. Jefferson and C.B. Low. (in prep.¹). Toward a matrix of breeding values: comparison of the average performance of radiata pine selection series.
- Carson, S.D., M.J. Carson, G.G. West, J.C. Grace, T.G. Vincent, P.A. Jefferson, and B.R. Manley. 1995. A strategy for efficient selection and evaluation of "designer trees." **Forest and Farm Plantation Management Cooperative Report No 15**. New Zealand Forest Research Institute, Rotorua.
- Eggleston, N. 1992. Comparing the range of regional tree volume and taper tables. **Stand Management Cooperative Report No. 26**. New Zealand Forest Research Institute, Rotorua.
- Falconer, D.S. 1989. **Introduction to Quantitative Genetics. Third Edition**. Longman Scientific & Technical, Longman Group UK Ltd, England.
- Grace, J.C. and M.J. Carson. 1992. Prediction of internode length in *Pinus radiata* stands. **Stand Management Cooperative Report No. 27**. Forest Research Institute, Rotorua.
- Grallelis, S.A. and B.K. Klomp. 1982. Systems for assessing malformation and quality in *P. radiata* stands. **FRI Project Record No. 989**. (unpub).

- Knowles, R.L. and M. Kimberley. 1992. The effect of site stocking and genetics on second-log branching in *Pinus radiata*. **Stand Management Cooperative Report No. 33**. Forest Research Institute, Rotorua.
- Tombleson, J.D., J.C. Grace and C.S. Inglis. 1990. Response of radiata pine branch characteristics to site and stocking. In R.N. James & G.L. Tarlton (Eds.), **New Approaches to Spacing and Thinning in Plantation Forestry**. Proceedings of a IUFRO symposium held at the Forest Research Institute. Rotorua. New Zealand, 10 - 14 April, 1989. pp. 229-231.
- Turner, J.A. 1994. **Quantification of Genetic Gains in the Growth of *Pinus radiata* from "850" Seed Orchards, Central North Island, New Zealand**. Dissertation submitted in partial fulfilment of the requirements for the degree of Bachelor of Forestry Science.
- Turner, J.A. 1995. Comparison of techniques to measure tree internode length. **Project Record No. 4682**
- Vincent, T.G. and J.S. Dunstan. 1989. **Register of Commercial Seedlots Issued by the New Zealand Forest Service**. Ministry of Forestry, Forest Research Institute, FRI Bulletin No. 144, pp. 155.
- West, G.G. and M.O. Kimberley. 1991. Sampling DOS and sweep at the time of pruning. **Stand Management Cooperative Report No. 14**. Forest Research Institute, Rotorua.
- Woods, N.G. 1988. **A Method of Predicting Mean Internode Index on the Improved Breeds of *Pinus radiata* For Use in STANPAC v. 2**. Dissertation submitted in partial fulfilment of the requirements for the degree of Bachelor of Forestry Science.
- Woods, N.G. and M.J. Carson. 1988. Internode length estimates for improved breeds of *Pinus radiata*. **Stand Management Cooperative Report No. 7**. Forest Research Institute Ltd., Rotorua.

APPENDIX I: A GLOSSARY OF MALFORMATION TYPES AND DEFECTS IN *PINUS RADIATA*

The malformation definitions given below are based on those by Grallelis and Klomp (1982).

Double leader: Where a single stem forks into two separate leaders, either diameter to be at least half the diameter of the main stem.

Multiple leader: Where a stem has more than two leaders.

Ramicorn: A large, steeply angled branch with a diameter of less than half the stem diameter.

Diameter reduction: An abrupt decrease in stem diameter at a single point, eg., resulting from the loss of a leader, ramicorn branches in a tight cluster or other damage.

Kink: An abrupt deviation from straightness of the stem affecting a maximum of 1 m of stem length. There may be more than one kink per stem.

Wobble: A multiple or complex sweep involving several directions in one or more planes.

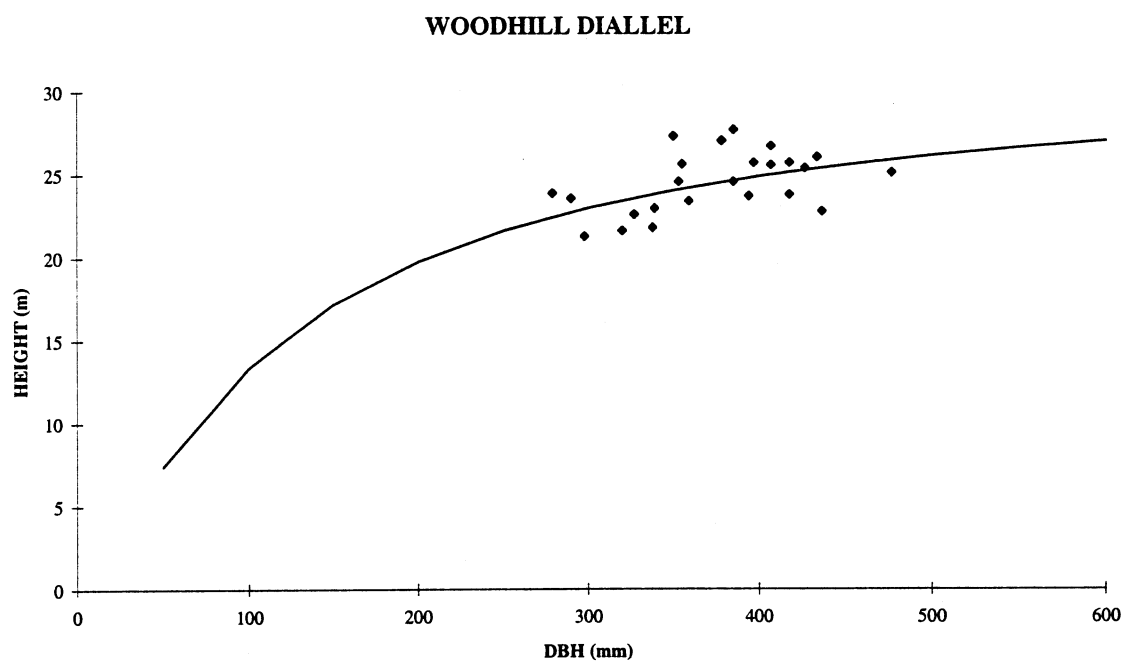
APPENDIX II: PETTERSON CURVES FOR KAINGAROA AND WOODHILL

Fig I. Pettersson curve for the Woodhill disconnected diallel.

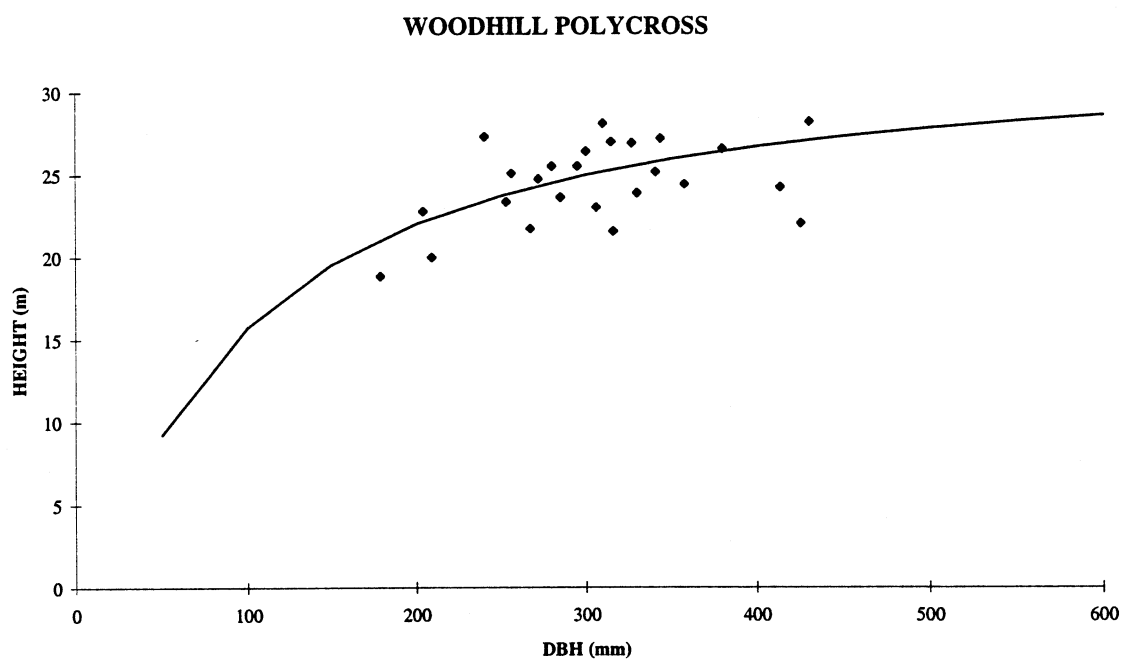


Fig II. Pettersson curve for the Woodhill polycross.

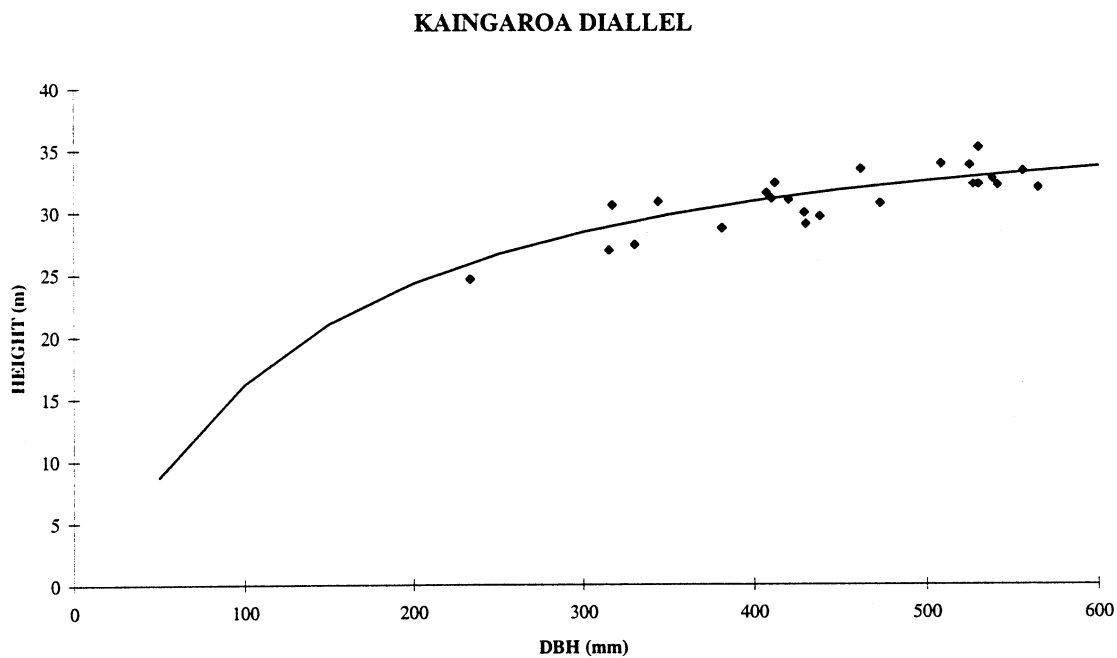


Fig III. Peterson curve for the Kaingaroa disconnected diallel.

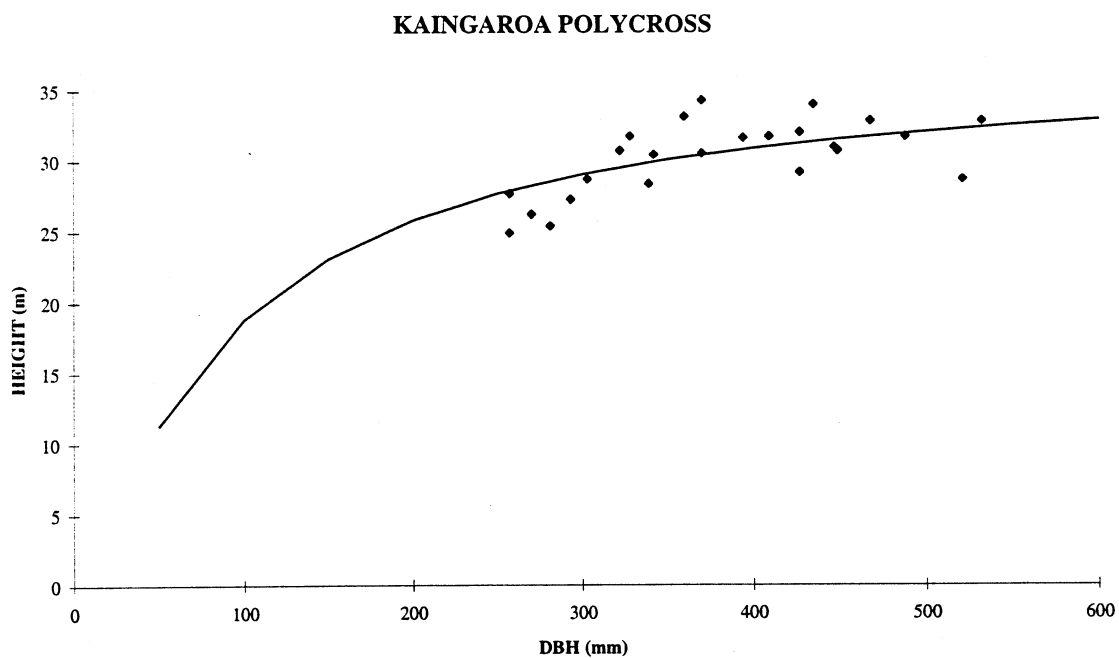


Fig IV. Peterson curve for the Kaingaroa polycross.