BEST LINEAR PREDICTION OF BREEDING VALUES FOR STEM DIAMETER IN A *PINUS RADIATA* IMPROVEMENT PROGRAMME

S. KUMAR, S.D. CARSON, L.D. GEA,
F.C. BURGER, P.A. JEFFERSON

REPORT No 43.   AUGUST 1995

EXECUTIVE SUMMARY

The GF rating of a seedlot can be input into many of the New Zealand growth models in order to obtain predictions of growth for genetically improved seedlots. Since GF rating takes into consideration not only growth but also stem form, a separate genetic rating for growth might improve predictions of increases in growth rate. This report documents the development of a separate rating for diameter for all the parents in the New Zealand breeding population.

BEST LINEAR PREDICTION OF BREEDING VALUES FOR STEM DIAMETER IN A *PINUS RADIATA* IMPROVEMENT PROGRAMME

S. Kumar, S. D. Carson, L. D. Gea, F. C. Burger, and P. A. Jefferson

ABSTRACT

Measurements of diameter from 28 sites on 984 parents belonging to four selection series in the New Zealand radiata pine breeding programme ("268", "850", "875", and "880" series) were used to calculate the BLP (White and Hodge, 1989) of breeding values of these parents. Variance-covariance matrices were constructed over all sites, and a series of linear restrictions (Binet, 1965; James, 1968) were imposed on the solution of index coefficients. Because the data tended to be balanced within but not between series and mean diameters and variances do not appear to differ among series, this provided a more efficient computational method than has been used previously. Breeding values calculated using this method (BLP) and a simpler method, calculation of a 'standard score', were highly correlated (r=0.96). However, 50 percent of the parents selected with a 1 percent selection intensity were different using the two methods. Since the standard score method does not take into account the precision of the parental mean estimates at the different sites (the heritability) or the degree of agreement among sites (genetic and phenotypic correlations), the BLP of breeding values should be more reliable for selecting the top group of parents than the standard score method.

INTRODUCTION

Radiata pine plus trees have been selected in New Zealand since the 1950s. Each group of plus trees, that is, each selection 'series', was selected within a certain time period for a specific set of selection criteria. Progeny of select trees in a series were planted and assessed for important traits on a number of sites as a group, so parents in a series are well tested and ranked against one another. Since there is almost no overlap between series in progeny trials (except for a few control seedlots), parents in different series have not been well tested against each other until the very recent establishment of new trials from which there is no data yet available.

Further, the best parents for use in seed orchards in New Zealand have largely been selected using an index combining their values for different selection traits. The set of selection criteria used and their economic weight reflected breeders' perceptions of the relative importance of the selection traits at the time of selection. With very few exceptions, the existing ranking for

multiple traits represents a compromise in ranking for the various selection criteria.

The advent of control-pollinated orchards has greatly increased flexibility for producing seedlots selected for a wide variety of objectives (Carson *et al.*, 1992). Forest growers now have the opportunity to select a mix of parents to produce seedlots that emphasise the traits they desire. With the increased genetic gains available from increased flexibility, both a better overall ranking of all parents in the breeding programme for individual traits, and sound estimates of comparative breeding values across selection series become essential. The objective of this work was to rank all parents in the New Zealand breeding population for diameter separately from other selection traits.

In order to rank parents, breeders establish progeny tests of various field designs in different years and environments. Parents are ranked based on their performance through measuring the trees in these tests. Various analytical techniques, for example, arithmetic average, least-squares estimates and standard scores, are very commonly used in forestry for obtaining the ranking of parents. Most of these techniques are appropriately used for balanced data sets, and all of these effectively treat the problem of ranking parents as one of estimating fixed effects. However, in forestry experiments the information obtained for different parents is often unbalanced in the sense that

1. only a subset of parents are represented at a given test site,
2. parents are represented in different numbers of test sites, and
3. tests are measured at different ages (Cotterill *et al.*, 1983, Lowe *et al.*, 1983).

For these reasons tests vary dramatically in the level of their precision.

Best linear prediction (BLP), which is an extension of genetic selection index theory developed by Hazel and Lush (1942) and Hazel (1943), is quite well suited to predicting genetic values from a wide variety of sources, ages, qualities and quantities of data (White and Hodge, 1989). This approach, which considers breeding values as random effects to be predicted rather than fixed effects to be estimated, was largely developed by Henderson (1963, 1977, 1984) for dairy cattle breeding programmes. This technique, which in fact is very robust, has been used widely in forest tree improvement programmes (Borralho, 1995; Ericsson, 1994; Gea *et al.*, 1993; Jefferson, 1989; Magnussen and Yanchuk, 1994; White *et al.*, 1986; etc.).

Breeding values for diameter of 984 parents belonging to four different selection series and tested using different mating and field designs in progeny trials at 28 sites were predicted by using a selection index approach separately for each group of parents tested together on the same sites, then

combining breeding values across groups. Performance in multiple environments was treated in an analogous manner to multiple traits (Burdon, 1977). Variance and covariance matrices including all test sites were constructed, and linear restrictions (Binet, 1965; James, 1968) were imposed on the solution of the index coefficients vector for each groups of parents. By imposing Binet restrictions on variance and covariance matrices which included all 28 sites, the genetic gain on all sites was maximised, even when a parent does not appear at that site.

Since previous analysis which compared performance of the different series with control seedlot means suggested that means and variances of the series did not differ (Carson *et al.*, 1993 unpublished), breeding values for the different groups were combined directly into aggregate breeding values. These methods yielded the same results as BLP methods described by White and Hodge (1989). The BLP breeding values obtained using these methods were compared to those developed using a standard score method (Cotterill *et al.*, 1983; Hatcher *et al.*, 1981; Lowe *et al.*, 1983) in order to determine the impact of using BLP compared to a far simpler method.

MATERIAL AND METHODS

Offspring of 984 parents were planted in progeny trials from 1969 to 1981. Selection of parents is reviewed in Shelbourne *et al.* (1987). For most trials seedlings were reared in a research nursery in a replicated design and field planted one year from seed in a sets-in-replicates design. Most trials utilised open-pollinated seed, but some parents were tested using control-pollinated seed crossed in either a NC-II or a diallel design. Parents were represented on a subset of the 28 sites almost exclusively with parents of the same selection series. There were six combinations of breeding series and mating designs (Table 1). Trials were assessed for diameter at breast height (dbh) (as well as other traits) at various ages, and genetic parameters including heritability and genetic variances were calculated and reported (Carson, 1991; Johnson, 1987; Johnson and Burdon, 1990; Shelbourne and Low, 1980; Wilcox *et al.* 1975).

The selection index approach

An overall breeding value for diameter across selection series for dbh was calculated using one assessment per site. The measurement of the oldest age trees from each of the 28 sites was utilised. All programming and calculations described in the following sections were carried out using SAS (SAS Institute, 1988).

The well known selection index formulae for predicting the genetic worth of a candidate genotype (W_j) (Hazel, 1943; Hazel and Lush, 1942) is

$$W_j = a_1 g_{1j} + a_2 g_{2j} + ... + a_p g_{pj} = \sum_{i=1}^{p} a_i g_{ij}$$

where a_i is the economic weight of the ith trait measured; g_{ij} is the unobservable genetic value of the ith trait on the jth candidate genotype; and p is the total number of traits (p=28 in this case). The same equation expressed in matrix notation is

$$W_j = a'g$$

where a is a p x 1 vector of assumed known economic weights corresponding to each trait; and g is a p x 1 vector of unobservable genetic values corresponding to each trait. In this case the target trait is diameter measured at p sites with each site treated as a trait.

If no conditions are imposed and only linear functions of the observed data are considered, than it is well known that the error variance of prediction will be minimum and the correlation between true and predicted genetic worth will be maximum (provided the V and C matrices are estimated without error) only when

$$b = V^{-1}Ca$$

where b is a p x 1 vector of index coefficients to be estimated, V is a p x p matrix of phenotypic variances and covariances among family means, and C is a p x p matrix of covariances between phenotypic means and their genetic values.

Estimation procedures

The vector a

This 28 x 1 vector contains the economic weights associated with different sites. These were calculated as the inverse of the square root of the phenotypic variance of family means at the corresponding site, which implies that a gain expressed as a proportion of the total variance was of equal importance on a site with low phenotypic variance as on a site with a high phenotypic variance. Since low variance sites in New Zealand tend to be slower growing sites (Carson, 1989), this implies that, say, a 5% gain on a slow growth site is of equal value as a 5% gain on a fast growing site.

The diagonal elements of matrix V

The diagonal elements of the 28 x 28 matrix V, that is, the phenotypic variances of family means, were obtained from previous calculations (Carson, 1991; Johnson, 1987; Johnson and Burdon, 1990; Shelbourne and Low, 1980;

Wilcox *et al.* 1975) where analysis of variance was used to calculate these variances. Because this study involved data from trials which used different mating designs, the models used for obtaining these diagonal elements differed by mating design.

For full-sib family trials

$$Y_{jklm} = \mu + B_j + f_k + h_l + fh_{kl} + p_{jkl} + e_{jklm}$$

where μ is the overall mean; B_j is the fixed effect of the jth replicate block with $j=1,2,...,b$; f_k is the random effect of the kth female with $E(f_k)=0$ and $Var(f_k)$ $=\sigma_f^2$; h_l is the random effect of the lth male with $E(h_l)=0$ and $Var(h_l)=\sigma_h^2$; fh_{kl} is the specific combining ability effect of the klth full-sib family with $E(fh_{kl})=0$ and $Var(fh_{kl})=\sigma_d^2$; p_{jkl} is the random plot error of the klth family in the jth block with $E(p_{jkl})=0$ and $Var(p_{jkl})=\sigma_p^2 + \sigma_e^2/n$; and e_{jklm} is the random error of the mth tree in the jklth plot with $m=1,2,...n$, $E(e_{jklm})=0$, and $Var(e_{jklm})=\sigma_e^2$. Parental breeding values were calculated, and the phenotypic variances of half-sib family means ($\sigma_{P_{hs}}^2$) were estimated for each site where mating design was a diallel as

$$\sigma_{P_{hs}}^2 = \frac{\sigma_f^2 + \sigma_h^2}{2} + \frac{\sigma_d^2}{3} + \frac{\sigma_p^2}{b} + \frac{\sigma_e^2}{bn}.$$

In addition, the repeatability of parental breeding values, h_{hs}^2, was calculated as

$$h_{hs}^2 = \frac{\left(\sigma_f^2 + \sigma_m^2\right)/2}{\dfrac{\sigma_f^2 + \sigma_m^2}{2} + \dfrac{\sigma_d^2}{3} + \dfrac{\sigma_p^2}{b} + \dfrac{\sigma_e^2}{bn}}.$$

The phenotypic variance of half-sib family means for NCII trials were estimated. There was no significant difference between the phenotypic variances of half-sib family means for tester and clones and therefore, the common phenotypic variance (Burdon *et al.*, 1983) of half-sib family means was calculated as

$$\sigma_{P_{hs}}^2 = \frac{K\sigma_f^2 + L\sigma_h^2}{K+L} + \frac{\sigma_d^2}{4} + \frac{\sigma_p^2}{b} + \frac{\sigma_e^2}{bn}.$$

where K and L are number of females (testers) and male parents, respectively. The repeatability of half-sib family means, h^2_{hs}, was calculated as

$$h^2_{hs} = \frac{\left(K\sigma^2_f + L\sigma^2_h\right)/(K+L)}{\dfrac{K\sigma^2_f + L\sigma^2_h}{K+L} + \dfrac{\sigma^2_d}{4} + \dfrac{\sigma^2_p}{b} + \dfrac{\sigma^2_e}{bn}}$$

For half-sib family trials

$$Y_{jkl} = \mu + B_j + f_k + p_{jk} + e_{jkl}$$

where μ is the overall mean; B_j is the fixed effect of the jth block with $j=1,2,...b$; f_k is the random effect of the kth family with $E(f_k)=0$ and $Var(f_k)=\sigma^2_f$; p_{jk} is the random plot error of the kth family in the jth block with $E(p_{jk})=0$ and $Var(p_{jk})=\sigma^2_p + \sigma^2_e/n$; and e_{jkl} is the random error of the lth tree in the jkth plot with $l=1, 2, ...n$, $E(e_{jkl})=0$ and $Var(e_{jkl})=\sigma^2_e$. Therefore, the phenotypic variance of half-sib family means becomes

$$\sigma^2_{P_{hs}} = \sigma^2_f + \frac{\sigma^2_p}{b} + \frac{\sigma^2_e}{bn} .$$

In addition, the repeatability of half-sib family means, h^2_{hs}, was calculated as

$$h^2_{hs} = \frac{\sigma^2_f}{\sigma^2_f + \dfrac{\sigma^2_p}{b} + \dfrac{\sigma^2_e}{bn}} .$$

The number of families, blocks and trees per plot were not consistent across different sites. The data within a series and mating design combination tended to be nearly balanced with respect to parental representation and number of offspring per parent on each site but not balanced between such combinations.

The off-diagonal elements of matrix **V**

Since parents are expected to perform similarly on different sites, all the off-diagonal elements of this matrix were expected to be non-zero. Since a large number of parents are represented at the same set of sites, the off-diagonal

elements could be estimated from the data. The covariances between family means at different sites were calculated on the basis of Type B family mean correlations or, in the case of full-sib trials, parental breeding value correlations (Burdon, 1977). The estimates of these correlations were calculated for all site pairs within the six balanced subsets (series and mating design combinations, see Table 1).

Correlations used in the V matrix were the average correlation for site pairs in a subset. Using the individual site pair correlations for constructing the matrices resulted in many elements in the vector of index coefficients, $\mathbf{b}$, being negetive, which is cointer- intuitive because parents are expected to perform similarily on all sites. Using the average correlations within subsets resulted in all positive elements in the vector of index coefficients. For covariances between pairs of sites belonging to different series and mating designs, the overall average correlation was used.

The analytical procedure for calculating covariances between parental breeding values or family means at sites i and i' was

$$Cov(\overline{Y}_{i.k.}, \overline{Y}_{i'.k.}) = r_f \left[\left(\sigma^2_{P_{hs_i}} \right) \left(\sigma^2_{P_{hs_{i'}}} \right) \right]^{1/2}$$

where $\overline{Y}_{i.k.}$ and $\overline{Y}_{i'.k.}$ are family means or parental breeding values from the ith and the i'th site; r_f is the average Type B phenotypic correlation of family or breeding value means for the appropriate subset, and $\sigma^2_{P_{hs_i}}$ and $\sigma^2_{P_{hs_{i'}}}$ are the variances of family means or breeding values for the ith and the i'th site. After formulating the complete matrix, its eigen values were calculated. All the eigen values were positive, making the V matrix positive definite.

The matrix C

The elements of this 28 x 28 matrix are genetic covariances between the observed family means for the ith site and the corresponding breeding value. The variances of family means at different sites are quite heterogeneous (Table 2) and, therefore, the elements of the C matrix were obtained using the following methods (White and Hodge, 1989). Off diagonal elements were defined as

$$2r_f \left[\left(\sigma^2_{P_{hs_i}} \right) \left(\sigma^2_{P_{hs_{i'}}} \right) \right]^{1/2}.$$

and diagonal elements are defined as

$$2r_f \sigma^2_{P_{hs_i}}.$$

Average phenotypic correlations (r_f) were used in the same manner as for the off-diagonal elements of matrix V.

The matrix C, which is calculated using this formula and is symmetric in this case, must be positive definite (Hayes and Hill, 1981). However, some of its characteristic roots were found to be negative. The negative roots were, therefore, set to zero without altering the characteristic vectors, and a matrix C^*, the amended matrix of genetic variances and covariances, was defined as

$$C^* = UAU^{-1}$$

U is the matrix of characteristic vectors of C, and A is the diagonal matrix with characteristic roots of C as its elements, but with negative roots replaced by zero.

The vector b

The vector of index coefficients was calculated as

$$b = V^{-1}C^*a .$$

Linear restrictions imposed on vector b

Since the data was unbalanced in that not all the parents were deployed at all the sites but tests involving parents within a particular breeding series tended to be balanced, all of the 984 parents could be uniquely assigned to one of 24 groups which shared common sites (Table 3). The zeros and ones corresponding to all the 28 sites in Table 3 indicate the presence and absence, respectively, of the group of parents at those sites.

A vector corresponding to each of the 24 groups was calculated by imposing a linear restriction on the earlier solution of the vector of coefficients b (James, 1968) as

$$b^*_j = \left[I - V^{-1}K_j{}' (K_j V^{-1}K_j{}')^{-1} K_j \right] b$$

where b^*_j is the $p \times 1$ vector of coefficients for the jth group of parents with $j = 1,2,...,24$; I is the identity matrix of the order p; K_j is the $p \times 1$ vector with elements of zeros and ones for the jth group (see Table 3); and $K_j{}'$ is the transpose of vector K_j. The purpose of imposing these restrictions was to maximise the correlation between true and predicted breeding values and also to reduce the error variance of predictions by maximising gain on all sites, even those sites where a particular group of parents was not

represented. This is equivalent to using a Binet restriction (Binet, 1965). A separate set of coefficients (the $b^{*}{}_{j}$) was obtained for each of the 24 groups of parents.

Deviations of parental means from test environment means, expressed as a vector D_j and having the same number of rows as parents in group j, were calculated for each group as

$$D_j = Y_j - \alpha$$

where Y_j is a matrix of phenotypic parent means or breeding values for each site which has p columns and the same number of rows as parents in group j; and α is a p x 1 vector containing the fixed effects of the p test environments. The average of all parents at a site was used as an estimate of the fixed effects, as is assumed in BLP (White and Hodge, 1989).

Breeding values of parents in the jth group were predicted as

$$G_j = b^{*}{}_{j}{}' D_j$$

where G_j is the vector of predicted breeding values for the parents in the jth group of parents; and $b^{*}{}_{j}{}'$ is the vector of coefficients which corresponds to the sites where the jth group of parents is represented.

Standard errors of the indices for the different groups of parents were calculated as

$$\left(b^{*}{}_{j}{}' V^{-1} b^{*}{}_{j}\right)^{1/2}$$

A comparison of the performance of control seedlots and the offspring of parents for diameter in the 28 trials (Carson *et al.*, 1993 unpublished) suggested that the mean and the variance of parental breeding values do not differ among series, and, therefore, among groups. Therefore, breeding values from all groups were aggregated, without adjustment, to give the best linear prediction of breeding values.

Comparison of BLP breeding values to standard scores

A standard score (similar to Hatcher *et al.*, 1981) was calculated for each parent at each site as

$$z = \frac{x - \bar{x}}{s}$$

where x is the parental mean at a particular site; $\bar{x}$ is the mean of all parents at that site; and s is the standard deviation of parental means at that site. In order to obtain on overall standard score for each parent, the standard scores for each parent were averaged over sites for each site in which it was represented. The similarity of the rankings obtained from the two methods were compared by calculating a correlation coefficient and examining the commonality of parents selected at different selection intensities.

RESULTS

The data available for diameter (dbh) for the parents in the New Zealand breeding population represents a wide range of assessment ages, sites, and mating designs. The age of measurement varied from 4 to 13 years and the average diameter from 90.6 to 270.7 cm (Table 1).

The phenotypic variance of family means (the diagonal elements of the V matrix) varied greatly among the 28 test environments (Table 2). Variances differed by as much as ten fold. The repeatability of half-sib family means also varied greatly among sites, and ranged from 0.31 to 0.82 with the exception of one site which was extremely low (h^2_{hs}=0.01).

Estimates of the correlation of parental means or breeding values between sites ranged from -0.22 to 0.74 (Table 4) with an overall average correlation of 0.41. The average correlations over sites within a series and mating design combination (see Table 1) were 0.67 for the "850" series NC-II, 0.30 for the "850" series polycross, 0.41 for the "850" diallel, 0.36 for the "268" open-pollinated trials, 0.56 for the "875" diallel, and 0.15 for the "880" open-pollinated trials.

The V and C matrices used to calculate parental breeding values are presented in Appendices 1 and 2, respectively. For interest, Appendix 3 presents the V matrix calculated using the actual family mean or breeding value correlation for each site pair, rather than the average correlation for a site pair. Appendix 4 presents the coefficient vectors (the b^*_j) for each of the 24 groups of parents, and Appendix 5 lists parents in each of the 24 groups.

The predicted genetic worth for dbh aggregated for the 984 parents ranged from -10.49 to 8.90 cm , and were distributed in a bell-shaped curve with long tails (Figure 1). The standard error of the indices for the different groups of parents ranged from 3.05 to 3.36 cm with a pooled standard error of 3.31. Of the 50 top ranked parents, 7, 4, 9, and 5 percent came from the "850", "268", "875", and "880" selection series, respectively.

There was very good correspondence between BLP breeding values and standard scores (r=0.96). In the top 25 percent of parents determined using both methods, 91 percent were in common. As the selection intensity

increased, however, the commonality decreased until in the top one percent determined using both methods, only 50 percent were in common.

DISCUSSION

The approach we have taken to calculating BLP of breeding values appears to be a efficient and valid method for obtaining rankings for diameter of the 984 parents which have been tested in the New Zealand radiata pine breeding programme. We found the use of Binet restrictions to calculate BLP was computationally more efficient, given the balance of parental representation in our programme, than that described by White and Hodge (1989). Parents in a selection series being tested together on several sites, but largely not with parents in other series, meant that a relatively small number of groups could be handled as a selection index calculated with a Binet restriction. We also found this approach to be more intuitive than an overall BLP calculation as described by White and Hodge (1989).

The breeding value estimates obtained appear to be valid estimates. The standard errors of the indices for the 24 groups of parents were very similar, suggesting that the predictions of genetic worth of the different groups of parents were equally precise. The selection series did not appear to be disproportionately represented in the top group of parents, supporting previous analyses that suggested that the average performances of the series are not different.

The use of family mean correlations averaged within series and mating design combinations may not be the optimal approach. High and low correlations among sites are buffered by using average correlations. While use of individual site pair correlations would be desirable for obtaining the best breeding values (given that the test sites are representative of the target sites), use of individual site pair correlations in this case would lead to greater problems with matrices with negative roots.

The overall rankings of parents obtained from BLP and from standard scores were very similar. The comparison shows that in our case, where there was a large amount of balance in parental representation across several sites, a very simple procedure yields a very similar answer to a very complex one. The specific set of parents selected using high selection intensities, however, was not exactly the same, although there was a substantial amount of overlap. The great extent of heterogeneity of the genetic parameters suggests the need for a robust technique like BLP for predicting the genetic value of the parents involved. The standard score method does not take into account the precision of the parental mean estimates at the different sites (the heritability), nor does it take into account the degree of agreement among sites. The BLP of breeding values, therefore, should be more reliable for selecting the top group of parents than the standard score method.

REFERENCES

Binet; F.E. 1965: On the construction of an index for individual selection. Biometrics 21: 291-299.

Borralho, N.M.G. 1995: The impact of individual tree mixed models (BLUP) in tree breeding strategies. In 'Eucalypt Plantations: Improving Fibre Yield and Quality'. (Eds. B.M. Potts, N.M.G. Borralho, J.B. Reid, R.M. Cromer, W.N. Tibbits and C.A. Raymonds). pp. 141-145. Proc. CRC-IUFRO Conf., Hobart, 19-24 Feb. (CRC for Temperate Hardwood Forestry : Hobart). 488p.

Burdon, R.D. 1977: Genetic correlation as a concept of studying genotype-environment interaction in forest tree breeding. Silvae Genetica 26: 168-175.

Burdon, R. D., C. B. Low and A. Firth 1983. Results to 10 years from NC-II cross among 850 series radiata pine clones. Production Forestry Division, NZ Forest Research Institute, Project Record No. 242-243.

Carson, M. J., T. G. Vincent, and A. Firth. 1992. Control-pollinated and meadow seed orchards of radiata pine. Pp. 100-109. *In* Mass Production of Genetically-Improved Trees: Proceedings IUFRO Conference. Bordeaux, France, Sept. 1992.

Carson, S.D. 1991: Genotype by environment interaction and optimal number of progeny test sites for improving *Pinus radiata* in New Zealand. NZ J. For. Sci. 21: 32-49.

Carson, S. D., M. J. Carson, G. G. West, J. Grace, T. G. Vincent, P. Jefferson, and B. Manley. 1995. A strategy for efficient selection and evaluation of designer "breeds". NZ FRI Project Record No. 4858.

Cotterill, P.P.; Correll, R.L.; Boardman, R. 1983: Methods of estimating the average performance of families across incomplete open pollinated progeny tests. Silvae Genetica 32: 28-32.

Ericsson, T. 1994: Lodgepole pine (*Pinus contorta* var. *latifolia*) breeding in Sweden. PhD Thesis, Swedish University of Agricultural Sciences. 100 p.

Gea, L.D.; Carson, S.D.; Jefferson, P.A. 1993: Prediction of parental values for Dothistroma resistance over sites and series. FRI Project Record No. 3807.

Hatcher, A.V.; Bridgwater, F.E.; Weir, R.J. 1981: Performance level standardised score for progeny test performance. Silvae Genetica 30: 184-187.

Hayes, J.F. and W. G. Hill. 1981. Modification of estimates in the construction of genetic selection indices ('bending'). Biometrics, 37 : 483-493.

Hazel, L. N. and J. L. Lush. 1942. The efficiency of three methods of selection. J. Heredity. 33:393-399.

Hazel, L. N. 1943. The genetic basis for constructing selection indexes. Genetics 28:476-490.

Henderson, C.R. 1963: Selection index and expected genetic advance. Pp 141-163 *In* Hanson WD, Robinson HF (eds) Statistical genetics and plant breeding. NAS-NRC Publ No. 982, Washington/DC.

Henderson, C.R. 1977: Prediction of future records. Pp 615-638 *In* Pollack E, Kempthorne O, Bailey T (eds) Proc Int Conf Quan Genet. Iowa State University Press, Ames/IA.

Henderson, C.R. 1984: Application of linear models in animal breeding. University of Guelph, Ontario, Canada, 462 pp.

James, J.W. 1968: Note on index selection with restrictions. Biometrics 24: 1015-18.

Jefferson, P.A. 1989: Discriminant functions in tree breeding. PhD Thesis, University of Alberta. 271pp.

Johnson, G.R. 1987: Comparison of rankings in four clonal series of the growth and form breed. NZ Radiata Pine Breeding Cooperative Report No 5.

Johnson, G.R. and Burdon, R.D. 1990: Family-site interaction in *Pinus radiata*: Implications for progeny testing strategy and regionalised breeding in New Zealand. Silvae Genetica 39: 55-62.

Lowe, W.J.; Stonecypher, R.; Hatcher, A.V. 1983: Progeny test data handling and analysis. Pp 51-68 *In* Progeny testing of forest trees. South Coop Ser Bull No. 275. Texas A and M University, College Station/ TX.

Magnusen, S. and Yanchuk, A.D. 1994: Time trends of predicted breeding values in selected crosses of coastal Douglas-fir in British Columbia: A methodological study. Forest Sci, 40: 663-685.

SAS Institute 1988: SAS/STAT/IML User's Guide. Release 6.03 Edition. SAS Institute Inc., Cary, North Carolina, 357 p.

Shelbourne, C.J.A. and Low, C.B. 1980: Multi-trait index selection and associated genetic gains of *Pinus radiata* progenies at five sites. NZ J. For. Sci., 10: 307-324.

Shelbourne, C. J. A., R. D. Burdon, S. D. Carson, A. Firth, And G. Vincent, 1987. Development plan for radiata pine breeding. Forest Research Institute, Rotorua, New Zealand. 142p.

Wilcox, M.D.; Firth, A.; Low, C.B.; McConchie, D.L. 1975: First assessment of the *Pinus radiata* open pollinated progeny test of the '268' series parents. FRI Project Record No 78.

White, T.L.; Hodge, G.R.; Delorenzo, M.A. 1986: Best linear prediction of breeding values in forest tree improvement. Pp 99-122 *In* Proc Genet Breed Southern Pines, June 25-26, Gainesville, FL.

White, T.L. and Hodge, G.R. 1988: Bets linear prediction of breeding values in a forest tree improvement program. Theor Appl Genet, 76: 719-727.

White, T.L. and Hodge, G.R. 1989: Predicting breeding values with application in forest tree improvement. Kluwer Academic Publishers. 368 p.

Table 1: Diameter (dbh) data used to rank parents in the breeding population.

Site No.	Forest/ Site	Mating design	Selection Series	Assessment Age (yrs)	Average Diameter (mm)
1	Kaingaroa	NC II	850	10	244.56
2	Wiamihia	NC II	850	10	248.41
3	Maramarua	Polycross	850	8	150.17
4	Woodhill	Polycross	850	8	192.60
5	Kaingaroa 327	Polycross	850	8	158.08
6	Golden Down	Polycross	850	8	144.98
7	Eyrwell	Polycross	850	8	122.55
8	Woodhill	Diallel	850	9	212.99
9	Maramarua	Diallel	850	9	168.63
10	Kaingaroa 327	Diallel	850	9	254.23
11	Awahonu	Diallel	850	9	234.51
12	Ruatoria	Diallel	850	9	204.45
13	Golden Down	Diallel	850	9	152.68
14	Mawhera	Diallel	850	9	190.96
15	Eyrwell	Diallel	850	9	125.90
16	Kaingaroa 905	Diallel	850	9	234.66
17	Berwick	Diallel	850	9	98.20
18	Taringatora	Diallel	850	9	165.97
19	Kaingaroa	Open pollinated	268	10	240.15
20	Waimihia	Open pollinated	268	10	238.06
21	Gwavas	Open pollinated	268	10	228.85
22	Woodhill	Open pollinated	268	13	221.64
23	Otago	Open pollinated	268	13	247.60
24	Onepu	Diallel	875	7	232.31
25	Kaingaroa 327	Diallel	875	7	181.18
26	Moerewa	Open pollinated	880	7	169.80
27	Taupo	Open pollinated	880	4	90.64
28	Rotoehu	Open pollinated	880	11	270.74

Table 2: Variance components and family- mean heritability at different sites.

Sites	Variance components		
	$\sigma^2_{P_{hs}}$ [a]	h^2_{hs} [b]	Economic weights [c]
1	84.70	0.64	0.109
2	45.06	0.77	0.149
3	66.59	0.34	0.123
4	100.39	0.59	0.099
5	113.14	0.80	0.094
6	40.29	0.55	0.158
7	32.19	0.74	0.176
8	158.00	0.79	0.079
9	42.00	0.31	0.154
10	109.00	0.82	0.096
11	122.00	0.81	0.091
12	67.00	0.46	0.122
13	35.00	0.43	0.169
14	65.00	0.50	0.124
15	30.00	0.25	0.183
16	77.00	0.64	0.114
17	34.00	0.01	0.171
18	47.00	0.56	0.146
19	149.73	0.60	0.082
20	116.37	0.58	0.093
21	113.90	0.40	0.094
22	40.38	0.52	0.157
23	49.64	0.58	0.142
24	43.75	0.79	0.151
25	19.68	0.74	0.225
26	133.43	0.46	0.087
27	13.18	0.62	0.275
28	160.87	0.55	0.079

a = phenotypic variance of family mean and genotypic variances respectively.
b = genetic repeatibility of a half-sib family mean.
C = the reciprocal of the standard deviation of family means.

Table 3: Groups showing presence or absence of parents at different sites.

Sites	\ Groups	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1		0	0	1	0	0	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
2		0	0	1	0	0	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
3		0	0	0	0	0	1	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0
4		0	0	0	1	1	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5		0	0	0	0	1	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6		0	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
7		0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
8		0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14		0	0	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16		0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1
17		0	0	1	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	1	1
18		0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0	0	1	1	1	1	1
19		0	0	1	1	0	0	0	1	1	1	1	0	0	0	0	0	0	1	0	1	1	1	1	1
20		0	1	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	1	1	1	1	1
21		0	1	1	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1
22		1	1	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	1	1	1	0	0	1	1
23		1	1	0	1	1	1	0	0	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1
24		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25		1	1	0	1	1	1	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1
26		1	1	0	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1
27		1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1
28		1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1
No. of parents in the group		3	1	2	2	3	16	7	2	87	1	2	20	5	2	2	16	2	33	17	2	171	96	5	1

0 and 1 indicate the presence or absence respectively, of the group of clones on the corresponding site.

Table 4: Phenotypic correlation(above diagonal) and genetic correlation(below diagonal) of family means between sites.

Site Number

Site	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1																												
2	0.95																											
3		0.67		0.09	0.28	0.31	0.03																					
4			0.20		0.36	0.34	0.50																					
5			0.54	0.52		0.48	0.24																					
6			0.71	0.59	0.72		0.38																					
7			0.05	0.76	0.31	0.60																						
8									0.27	0.54	0.55	0.47	0.58	0.47	0.45	0.51	0.24	0.22										
9								0.55		0.20	0.15	-0.06	0.16	0.31	0.03	0.13	-0.22	0.20										
10								0.67	0.39		0.74	0.57	0.68	0.53	0.32	0.60	0.48	0.62										
11								0.69	0.31	0.74		0.59	0.70	0.45	0.48	0.67	0.52	0.62										
12								0.79	-0.16	0.93	0.97		0.51	0.40	0.48	0.56	0.46	0.44										
13								1.00	0.45	1.14	1.17	0.51		0.28	0.46	0.50	0.43	0.53										
14								0.74	0.80	0.82	0.70	0.82	0.59		0.33	0.69	-0.02	0.17										
15								1.02	0.10	0.71	1.08	1.42	1.39	0.93		0.38	0.37	0.39										
16								0.71	0.29	0.83	0.93	1.04	0.94	1.22	0.96		0.34	0.31										
17								2.41	-3.46	4.69	5.04	5.89	5.69	-0.22	6.48	3.68		0.53										
18								0.33	0.48	0.93	0.93	0.88	1.09	0.33	1.04	0.52	6.28											
19																				0.43	0.32	0.29	0.39					
20																			0.73		0.33	0.20	0.27					
21																			0.66	0.69								
22																			0.56	0.43			0.27					
23																			0.79	0.61		0.47						
24																									0.56			
25																								0.73				
26																											0.17	-0.04
27																										0.86		0.99
28																										-0.19	0.33	

Table 5: Comparison of parental selection based on standard scores compared to BLP.

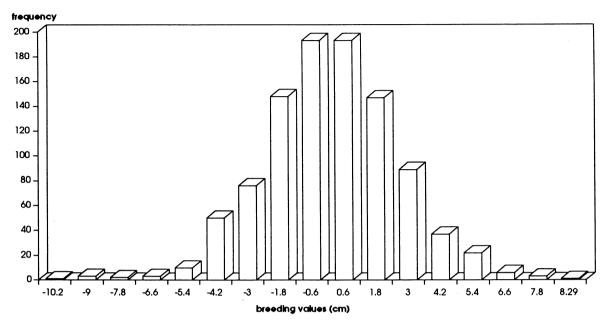| Sampling Intensity (%)	Mean aggregate breeding value (cm)		Common parents selected (%)
	BLP	Standard score	
1	6.95	5.67	50.00
5	5.32	4.89	72.00
10	4.43	4.17	78.00
15	3.86	3.65	78.66
20	3.45	3.37	90.00
25	3.10	3.05	91.00

Figure 1.: Distribution of breeding values for stem diameter.

Appendix1. The V matrix (phenotypic var-covariance) based on average correlations.

Site Number

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	84.70	41.39	30.79	37.81	40.13	23.95	21.40	47.43	24.45	39.39	41.68	30.89	22.32	30.42	20.67	33.11	22.00	25.87	46.17	40.70	40.27	23.98	26.58	24.96	16.74	43.58	13.70	47.86
2	41.39	45.06	22.46	27.58	29.27	17.47	15.61	34.59	17.84	28.73	30.40	22.53	16.28	22.19	15.07	24.15	16.05	18.87	33.67	29.69	29.37	17.49	19.39	18.20	12.21	31.79	9.99	34.91
3	30.79	22.46	66.59	24.54	26.05	15.54	13.89	39.26	20.24	32.61	34.50	25.57	18.48	25.18	17.11	27.41	18.21	21.41	38.24	33.72	33.34	19.86	22.02	20.67	13.86	36.10	11.35	39.64
4	37.81	27.58	24.54	100.40	31.98	19.09	17.06	48.20	24.85	40.04	42.36	31.39	22.69	30.92	21.00	33.65	22.36	26.29	46.96	41.40	40.95	24.39	27.04	25.38	17.02	44.34	13.93	48.67
5	40.13	29.27	26.05	31.98	113.10	20.26	18.11	51.17	26.38	42.50	44.97	33.32	24.09	32.82	22.30	35.72	23.74	27.91	49.85	43.95	43.48	25.89	28.70	26.95	18.07	47.06	14.79	51.67
6	23.95	17.47	15.54	19.09	20.26	40.29	10.81	30.54	15.74	25.36	26.83	19.89	14.37	19.59	13.31	21.32	14.17	16.66	29.75	26.23	25.95	15.48	17.13	16.08	10.78	28.08	8.83	30.83
7	21.40	15.61	13.89	17.06	18.11	10.81	32.19	27.30	14.07	22.67	23.99	17.77	12.85	17.50	11.89	19.05	12.66	14.89	26.59	23.44	23.19	13.81	15.31	14.37	9.64	25.10	7.89	27.56
8	47.43	34.59	39.26	48.20	51.17	30.54	27.30	158.00	32.99	53.16	56.24	41.68	30.12	41.05	27.89	44.68	29.69	34.91	58.91	51.93	51.38	30.59	33.92	31.84	21.36	55.60	17.48	61.00
9	24.45	17.84	20.24	24.85	26.38	15.74	14.07	32.99	42.00	27.41	29.00	21.49	15.53	21.16	14.38	23.04	15.31	18.00	30.37	26.78	26.49	15.77	17.49	16.42	11.01	28.67	9.01	31.48
10	39.39	28.73	32.61	40.04	42.50	25.36	22.67	53.16	27.41	109.00	46.71	34.62	25.02	34.10	23.16	37.11	24.66	28.99	48.93	43.14	42.68	25.41	28.17	26.45	17.74	46.19	14.52	50.72
11	41.68	30.40	34.50	42.36	44.97	26.83	23.99	56.24	29.00	46.71	122.00	36.62	26.47	36.07	24.51	39.26	26.09	30.67	51.76	45.65	45.15	26.88	29.81	27.98	18.77	48.87	15.36	53.66
12	30.89	22.53	25.57	31.39	33.32	19.89	17.77	41.68	21.49	34.62	36.62	67.00	19.62	26.73	18.16	29.10	19.33	22.73	38.36	33.82	33.46	19.92	22.09	20.74	13.91	36.21	11.38	39.76
13	22.32	16.28	18.48	22.69	24.09	14.37	12.85	30.12	15.53	25.02	26.47	19.62	35.00	19.32	13.13	21.03	13.97	16.43	27.73	24.44	24.18	14.40	15.96	14.99	10.05	26.17	8.23	28.74
14	30.42	22.19	25.18	30.92	32.82	19.59	17.50	41.05	21.16	34.10	36.07	26.73	19.32	65.00	17.89	28.66	19.04	22.39	37.78	33.31	32.95	19.62	21.76	20.42	13.70	35.67	11.21	39.16
15	20.67	15.07	17.11	21.00	22.30	13.31	11.89	27.89	14.38	23.16	24.51	18.16	13.13	17.89	30.00	19.47	12.94	15.21	25.67	22.63	22.39	13.33	14.78	13.88	9.31	24.23	7.62	26.61
16	33.11	24.15	27.41	33.65	35.72	21.32	19.05	44.68	23.04	37.11	39.26	29.10	21.03	28.66	19.47	77.00	20.73	24.37	41.12	36.25	35.87	21.36	23.68	22.23	14.91	38.82	12.20	42.63
17	22.00	16.05	18.21	22.36	23.74	14.17	12.66	29.69	15.31	24.66	26.09	19.33	13.97	19.04	12.94	20.73	34.00	16.19	27.33	24.09	23.83	14.19	15.73	14.77	9.91	25.80	8.10	28.33
18	25.87	18.87	21.41	26.29	27.91	16.66	14.89	34.91	18.00	28.99	30.67	22.73	16.43	22.39	15.21	24.37	16.19	47.00	32.13	28.32	28.02	16.69	18.50	17.37	11.65	30.33	9.53	33.30
19	46.17	33.67	38.24	46.96	49.85	29.75	26.59	58.91	30.37	48.93	51.76	38.36	27.73	37.78	25.67	41.12	27.33	32.13	149.70	47.78	47.27	29.76	33.00	31.00	20.79	54.14	17.01	59.44
20	40.70	29.69	33.72	41.40	43.95	26.23	23.44	51.93	26.78	43.14	45.65	33.82	24.44	33.31	22.63	36.25	24.09	28.32	47.78	116.37	41.68	26.24	29.09	27.33	18.33	47.73	15.00	52.40
21	40.27	29.37	33.34	40.95	43.48	25.95	23.19	51.38	26.49	42.68	45.15	33.46	24.18	32.95	22.39	35.87	23.83	28.02	47.27	41.68	113.90	25.96	28.78	27.04	18.13	47.22	14.84	51.84
22	23.98	17.49	19.86	24.39	25.89	15.48	13.81	30.59	15.77	25.41	26.88	19.92	14.40	19.62	13.33	21.36	14.19	16.69	29.76	26.24	25.96	40.38	12.09	16.10	10.80	28.11	8.84	30.87
23	26.58	19.39	22.02	27.04	28.70	17.13	15.31	33.92	17.50	28.17	29.81	22.09	15.96	21.76	14.78	23.68	15.73	18.50	33.00	29.09	28.78	12.09	49.64	17.85	11.97	31.17	9.80	34.23
24	24.96	18.20	20.67	25.38	26.95	16.08	14.37	31.84	16.42	26.45	27.98	20.74	14.99	20.42	13.88	22.23	14.77	17.37	31.00	27.33	27.04	16.10	17.85	43.75	16.46	29.26	9.20	32.13
25	16.74	12.21	13.86	17.02	18.07	10.78	9.64	21.36	11.01	17.74	18.77	13.91	10.05	13.70	9.31	14.91	9.91	11.65	20.79	18.33	18.13	10.80	11.97	16.46	19.68	19.63	6.17	21.55
26	43.58	31.79	36.10	44.34	47.06	28.08	25.10	55.60	28.67	46.19	48.87	36.21	26.17	35.67	24.23	38.82	25.80	30.33	54.14	47.73	47.22	28.11	31.17	29.26	19.63	133.40	6.46	22.56
27	13.70	9.99	11.35	13.93	14.79	8.83	7.89	17.48	9.01	14.52	15.36	11.38	8.23	11.21	7.62	12.20	8.10	9.53	17.01	15.00	14.84	8.84	9.80	9.20	6.17	6.46	13.18	7.09
28	47.86	34.91	39.64	48.67	51.67	30.83	27.56	61.00	31.48	50.72	53.66	39.76	28.74	39.16	26.61	42.63	28.33	33.30	59.44	52.40	51.84	30.87	34.23	32.13	21.55	22.56	7.09	160.90

Appendix 2. The C matrix : Genetic variances and covariances between phenotypic means and their breeding values.

Site Number

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
113.50	82.78	61.58	75.62	80.26	47.90	42.80	94.86	48.90	78.78	83.36	61.78	44.64	60.48	41.34	66.22	44.00	51.74	92.34	81.40	80.54	47.96	53.16	49.92	33.48	87.16	27.40	95.72
82.78	60.38	44.92	55.16	58.54	34.94	31.22	69.18	35.68	57.46	60.80	45.06	32.56	44.38	30.14	48.30	32.10	37.74	67.34	59.38	58.74	34.98	38.78	36.40	24.42	63.58	19.98	69.82
61.58	44.92	39.47	49.08	52.10	31.08	27.78	78.52	40.48	65.22	69.00	51.14	36.96	50.36	34.22	54.82	36.42	42.82	76.48	67.44	66.68	39.72	44.04	41.34	27.72	72.20	22.70	79.28
75.62	55.16	49.08	60.25	63.96	38.18	34.12	96.40	49.70	80.08	84.72	62.78	45.38	61.84	42.00	67.30	44.72	52.58	93.92	82.80	81.90	48.78	54.08	50.68	34.04	88.66	27.86	97.34
80.26	58.54	52.10	63.96	67.91	40.52	36.22	102.30	52.76	85.00	89.94	66.64	48.18	65.64	44.60	71.52	47.48	55.82	99.70	87.90	86.96	51.78	57.40	53.90	36.14	94.12	29.58	103.30
47.90	34.94	31.08	38.18	40.52	24.18	21.62	61.08	31.48	50.72	53.66	39.78	28.74	39.18	26.62	42.64	28.34	33.32	59.50	52.46	51.90	30.96	34.62	32.16	21.56	56.16	17.86	61.66
42.80	31.22	27.78	34.12	36.22	21.62	19.32	54.30	28.14	45.34	47.98	35.53	25.70	35.00	24.30	38.10	25.32	29.78	53.18	46.88	46.38	27.62	31.00	28.74	19.28	50.20	15.78	55.12
94.86	69.18	78.52	96.40	102.30	61.08	54.30	127.98	65.98	106.32	112.48	83.36	60.24	82.10	55.78	89.36	59.38	69.82	117.80	103.90	102.80	61.18	67.84	63.68	42.72	111.20	34.96	122.00
48.90	35.68	40.48	49.70	52.76	31.48	28.14	65.98	34.02	54.82	58.00	42.98	31.06	42.32	28.76	46.08	30.62	36.00	60.74	53.56	52.98	31.54	35.00	32.84	22.02	57.34	18.02	62.96
78.78	57.46	65.22	80.08	85.00	50.72	45.34	106.32	54.82	88.29	93.42	69.24	50.04	68.20	46.32	74.22	49.32	57.98	97.86	86.28	85.36	50.82	56.34	52.90	35.48	92.38	29.04	101.40
83.36	60.80	69.00	84.72	89.94	53.66	47.98	112.48	58.00	93.42	98.82	73.24	52.94	72.14	49.02	78.52	52.18	61.34	103.50	91.28	90.30	53.76	59.62	55.96	37.54	97.74	30.72	107.30
61.78	45.06	51.14	62.78	66.64	39.78	35.53	83.36	42.98	69.24	73.24	54.27	39.24	53.46	36.32	58.20	38.66	45.46	76.72	67.64	66.92	39.84	44.18	41.48	27.82	62.42	22.76	79.52
44.64	32.56	36.96	45.38	48.18	28.74	25.70	60.24	31.06	50.04	52.94	39.24	28.35	38.64	26.26	42.06	27.94	32.86	55.46	48.88	48.36	28.80	31.92	29.98	20.10	52.34	16.46	57.48
60.48	44.38	50.36	61.84	65.64	39.18	35.00	82.10	42.32	68.20	72.14	53.46	38.64	52.65	35.78	57.32	38.08	44.78	75.56	66.62	65.90	39.24	43.52	40.84	27.40	71.34	22.42	78.32
41.34	30.14	34.22	42.00	44.60	26.62	24.30	55.78	28.76	46.32	49.02	36.32	26.26	35.78	24.30	38.94	25.88	30.42	51.34	45.26	44.78	26.66	29.56	27.76	18.62	48.46	15.24	53.22
66.22	48.30	54.82	67.30	71.52	42.64	38.10	89.36	46.08	74.22	78.52	58.20	42.06	57.32	38.94	62.37	41.46	48.74	82.24	72.50	71.74	42.72	47.36	44.46	29.82	77.64	24.40	85.26
44.00	32.10	36.42	44.72	47.48	28.34	25.32	59.38	30.62	49.32	52.18	38.66	27.94	38.08	25.88	41.46	27.54	32.38	54.66	48.18	47.66	28.38	31.46	29.54	19.82	51.60	16.20	56.66
51.74	37.74	42.82	52.58	55.82	33.32	29.78	69.82	36.00	57.98	61.34	45.46	32.86	44.78	30.42	48.74	32.38	38.07	64.26	56.64	56.04	33.38	37.00	34.74	23.30	60.66	19.06	66.60
92.34	67.34	76.48	93.92	99.70	59.50	53.18	117.80	60.74	97.86	103.50	76.72	55.46	75.56	51.34	82.24	54.66	64.26	108.40	95.56	94.54	59.52	66.00	62.00	41.58	108.30	34.02	118.90
81.40	59.38	67.44	82.80	87.90	52.46	46.88	103.90	53.56	86.28	91.28	67.64	48.88	66.62	45.26	72.50	48.18	56.64	95.56	84.25	83.36	52.48	58.18	54.66	36.66	95.46	30.00	104.80
80.54	58.74	66.68	81.90	86.96	51.90	46.38	102.80	52.98	85.36	90.30	66.92	48.36	65.90	44.78	71.74	47.66	56.04	94.54	83.36	82.46	51.92	57.56	54.08	36.26	94.44	29.68	103.70
47.96	34.98	39.72	48.78	51.78	30.96	27.62	61.18	31.54	50.82	53.76	39.84	28.80	39.24	26.66	42.72	28.38	33.38	59.52	52.48	51.92	21.64	24.18	32.10	21.60	56.22	17.68	61.74
53.16	38.78	44.04	54.08	57.40	34.62	31.00	67.84	35.00	56.34	59.62	44.18	31.92	43.52	29.56	47.36	31.46	37.00	66.00	58.18	57.56	24.18	26.60	35.70	23.94	62.34	19.60	68.46
49.92	36.40	41.34	50.68	53.90	32.16	28.74	63.68	32.84	52.90	55.96	41.48	29.98	40.84	27.76	44.46	29.54	34.74	62.00	54.66	54.08	32.10	35.70	49.09	32.92	58.52	18.40	64.26
33.48	24.42	27.72	34.04	36.14	21.56	19.28	42.72	22.02	35.48	37.54	27.82	20.10	27.40	18.62	29.82	19.82	23.30	41.58	36.66	36.26	21.60	23.94	32.92	22.08	39.26	12.34	43.10
87.16	63.58	72.20	88.66	94.12	56.16	50.20	111.20	57.34	92.38	97.74	62.42	52.34	71.34	48.46	77.64	51.60	60.66	108.30	95.46	94.44	56.22	62.34	58.52	39.26	41.10	12.92	45.12
27.40	19.98	22.70	27.86	29.58	17.86	15.78	34.96	18.02	29.04	30.72	22.76	16.46	22.42	15.24	24.40	16.20	19.06	34.02	30.00	29.68	17.68	19.60	18.40	12.34	12.92	4.46	14.18
95.72	69.82	79.28	97.34	103.30	61.66	55.12	122.00	62.96	101.40	107.30	79.52	57.48	78.32	53.22	85.26	56.66	66.60	118.90	104.80	103.70	61.74	68.46	64.26	43.10	45.12	14.18	49.55

Appendix 3. The V matrix based on actual rather than correlations averaged over sites within a series

Site number

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
84.70	41.39	30.79	37.81	40.13	23.95	21.40	47.43	24.45	39.39	41.68	30.89	22.32	30.42	20.67	33.11	22.00	25.87	46.17	40.70	40.27	23.98	26.58	24.96	16.74	43.58	13.70	47.86
41.39	45.06	22.46	27.58	29.27	17.47	15.61	34.59	17.84	28.73	30.40	22.53	16.28	22.19	15.07	24.15	16.05	18.87	33.67	29.69	29.37	17.49	19.39	18.20	12.21	31.79	9.99	34.91
30.79	22.46	66.59	7.36	24.39	15.85	1.16	39.26	20.24	32.61	34.50	25.57	18.48	25.18	17.11	27.41	18.21	21.41	38.24	33.72	33.34	19.86	22.02	20.67	13.86	36.10	11.35	39.64
37.81	27.58	7.36	100.39	38.37	21.43	28.54	48.20	24.85	40.04	42.36	31.39	22.69	30.92	21.00	33.65	22.36	26.29	46.96	41.40	40.95	24.39	27.04	25.38	17.02	44.34	13.93	48.67
40.13	29.27	24.39	38.37	113.14	32.14	14.42	51.17	26.38	42.50	44.97	33.32	24.09	32.82	22.30	35.72	23.74	27.91	49.85	43.95	43.48	25.89	28.70	26.95	18.07	47.06	14.79	51.67
23.95	17.47	15.85	21.43	32.14	40.29	13.70	30.54	15.74	25.36	26.83	19.89	13.31	21.32	14.17	16.66	19.59	26.23	29.75	26.23	25.95	15.48	17.13	16.08	10.78	28.08	8.83	30.83
21.40	15.61	1.16	28.54	14.42	13.70	32.19	27.30	13.70	22.67	23.99	17.77	12.85	26.40	14.91	19.05	12.66	17.59	26.59	23.44	23.19	13.81	15.31	14.37	9.64	25.10	7.89	27.56
47.73	34.59	39.26	48.20	51.17	30.54	27.30	158.00	21.99	70.87	76.36	48.36	43.13	47.63	18.96	56.25	17.59	18.96	58.91	51.93	51.38	30.59	33.92	31.84	21.36	55.60	17.48	61.00
24.45	17.84	20.24	24.85	26.38	15.74	13.70	21.99	42.00	13.53	10.74	-3.18	6.13	16.20	1.06	7.39	-8.31	8.89	30.37	26.78	26.49	15.77	17.49	16.42	11.01	28.67	9.01	31.48
39.39	28.73	32.61	40.04	42.50	25.36	22.67	70.87	13.53	109.00	85.33	48.71	42.00	44.61	18.30	54.97	29.22	44.38	48.93	43.14	42.68	25.41	28.17	26.45	17.74	46.19	14.52	50.72
41.68	30.40	34.50	42.36	44.97	26.83	23.99	76.36	10.74	85.33	122.00	53.34	45.74	40.07	29.04	64.94	33.49	46.95	51.76	45.65	45.15	26.88	29.81	27.98	18.77	48.87	15.36	53.66
30.89	22.53	25.57	31.39	33.32	19.89	17.77	48.36	-3.18	48.71	53.34	67.00	24.70	26.40	21.52	40.22	21.96	24.69	38.36	33.82	33.46	19.92	22.09	20.74	13.91	36.21	11.38	39.76
22.32	16.28	18.48	22.69	24.09	13.31	12.85	43.13	6.13	42.00	45.74	24.70	35.00	13.36	14.91	18.26	11.82	14.64	27.73	24.44	24.18	14.40	15.96	14.99	10.05	26.17	8.23	28.74
30.42	22.19	25.18	30.92	32.82	21.32	26.40	47.63	16.20	44.61	40.07	26.40	13.36	65.00	14.57	40.22	14.83	9.40	37.78	33.31	32.95	19.62	21.76	20.42	13.70	35.67	11.21	39.16
20.67	15.07	17.11	21.00	22.30	14.17	14.91	18.96	1.06	18.30	29.04	21.52	14.91	14.57	30.00	29.04	14.91	14.64	25.67	22.63	22.39	13.33	14.78	13.88	9.31	24.23	7.62	26.61
33.11	24.15	27.41	33.65	35.72	16.66	19.05	56.25	7.39	54.97	64.94	40.22	18.26	40.22	29.04	77.00	17.40	18.65	41.12	36.25	35.87	21.36	23.68	22.23	14.91	38.82	12.20	42.63
22.00	16.05	18.21	22.36	23.74	19.59	12.66	17.59	-8.31	29.22	33.49	21.96	11.82	14.83	14.91	17.40	34.00	18.65	27.33	24.09	23.83	14.19	15.73	14.77	9.91	25.80	8.10	28.33
25.87	18.87	21.41	26.29	27.91	26.23	17.59	18.96	8.89	44.38	46.95	24.69	21.50	9.40	14.64	18.65	18.65	47.00	32.13	28.32	28.02	16.69	18.50	17.37	11.65	30.33	9.53	33.30
46.17	33.67	38.24	46.96	49.85	29.75	26.59	58.91	30.37	48.93	51.76	38.36	27.73	37.78	25.67	41.12	27.33	32.13	149.73	56.63	42.31	22.55	33.62	31.00	20.79	54.14	17.01	59.44
40.70	29.69	33.72	41.40	43.95	26.23	23.44	51.93	26.78	43.14	45.65	33.82	24.44	33.31	22.63	36.25	24.09	28.32	56.63	116.37	38.22	13.71	20.52	27.33	18.33	47.73	15.00	52.40
40.27	29.37	33.34	40.95	43.48	25.95	23.19	51.38	26.49	42.68	45.15	33.46	24.18	32.95	22.39	35.87	23.83	28.02	42.31	38.22	113.90	25.96	28.78	27.04	18.13	47.22	14.84	51.84
23.98	17.49	19.86	24.39	25.89	15.48	13.81	30.59	15.77	25.41	26.88	19.92	14.40	19.62	13.33	21.36	14.19	16.69	22.55	13.71	25.96	40.38	12.09	16.10	10.80	28.11	8.84	30.87
26.58	19.39	22.02	27.04	28.70	17.13	15.31	33.92	17.49	28.17	29.81	22.09	15.96	21.76	14.78	23.68	15.73	18.50	33.62	20.52	28.78	12.09	49.64	17.85	11.97	31.17	9.80	34.23
24.96	18.20	20.67	25.38	26.95	16.08	14.37	31.84	16.42	26.45	27.98	20.74	14.99	20.42	13.88	22.23	14.77	17.37	31.00	27.33	27.04	16.10	17.85	43.75	16.46	29.26	9.20	32.13
16.74	12.21	13.86	17.02	18.07	10.78	9.64	21.36	11.01	17.74	18.77	13.91	10.05	13.70	9.31	14.91	9.91	11.65	20.79	18.33	18.13	10.80	11.97	16.46	19.68	19.63	6.17	21.55
43.58	31.79	36.10	44.34	47.06	28.08	25.10	55.60	28.67	46.19	48.87	36.21	26.17	35.67	24.23	38.82	25.80	30.33	54.14	47.73	47.22	28.11	31.17	29.26	19.63	133.43	7.13	-5.86
13.70	9.99	11.35	13.93	14.79	8.83	7.89	17.48	9.01	14.52	15.36	11.38	8.23	11.21	7.62	12.20	8.10	9.53	17.01	15.00	14.84	8.84	9.80	9.20	6.17	7.13	13.18	15.20
47.86	34.91	39.64	48.67	51.67	30.83	27.56	61.00	31.48	50.72	53.66	39.76	28.74	39.16	26.61	42.63	28.33	33.30	59.44	52.40	51.84	30.87	34.23	32.13	21.55	-5.86	15.20	160.87

Appendix 4: The coefficient vectors for each group of parents.

Group	\#1	\#2	\#3	\#4	\#5	\#6	\#7	\#8	\#9	\#10	\#11	\#12	\#13	\#14
									Sites					
1	0.351	0.481	0.299	0.245	0.231	0.390	0.433	0.191	0.371	0.230	0.218	0.272	0.407	0.298
2	0.369	0.507	0.353	0.289	0.272	0.460	0.511	0.203	0.394	0.245	0.231	0.290	0.432	0.317
3	-	-	0.358	0.293	0.276	0.467	0.518	0.217	0.422	0.262	0.248	0.312	0.462	-
4	0.369	0.506	0.327	-	0.252	0.426	0.474	0.205	0.399	0.248	0.234	0.294	0.438	0.321
5	0.415	0.569	-	-	-	-	-	0.232	0.451	0.280	0.265	0.335	0.495	0.363
6	0.463	0.634	-	-	-	-	-	0.263	0.511	0.317	0.300	0.383	0.560	0.411
7	-	-	0.755	0.615	0.580	0.976	1.088	-	-	-	-	-	-	-
8	-	-	0.580	0.473	0.446	0.752	0.837	-	-	-	-	-	-	-
9	-	-	0.906	0.738	0.696	1.171	1.306	-	-	-	-	-	-	-
10	-	-	1.103	0.899	-	-	1.589	-	-	-	-	-	-	-
11	-	-	-	0.994	-	-	1.758	-	-	-	-	-	-	-
12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
13	-	-	-	-	-	-	-	-	-	-	-	-	-	-
14	-	-	-	-	-	-	-	-	-	-	-	-	-	-
15	0.954	1.308	-	-	-	-	-	-	-	-	-	-	-	-
16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	-	-	-	-	-	-	-	-	-	-	-	-	-	-
18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	-	-	-	-	-	-	-	-	-	-	-	-	-	-
20	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	-	-	-	-	-	-	-	-	-	-	-	-	-	-
23	-	-	1.101	-	0.846	1.422	-	-	-	-	-	-	-	-
24	-	-	1.202	-	0.924	-	-	-	-	-	-	-	-	-

| | | | | | | | Sites | | | | | | |
Group	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	0.439	0.274	0.412	0.351	0.199	0.226	0.228	-	-	-	-	-	-	-
2	0.467	0.291	0.438	0.373	-	-	-	-	-	-	-	-	-	-
3	0.499	0.312	-	0.399	-	-	-	-	-	0.451	0.674	0.136	0.479	0.133
4	-	0.295	0.444	0.377	0.216	0.245	0.248	-	-	-	-	-	-	-
5	0.535	0.334	0.501	0.427	0.261	0.296	0.299	-	-	-	-	-	-	-
6	0.605	0.378	0.568	0.483	-	-	-	-	-	-	-	-	-	-
7	-	-	-	-	-	-	-	0.666	0.605	-	-	-	-	-
8	-	-	-	-	-	-	-	-	-	0.550	0.822	0.420	1.382	0.392
9	-	-	-	-	-	-	-	-	-	-	-	-	-	-
10	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
12	-	-	-	-	0.533	0.605	0.611	1.070	0.969	-	-	-	-	-
13	-	-	-	-	0.580	0.657	-	1.196	1.082	-	-	-	-	-
14	-	-	-	-	0.616	0.699	0.706	1.071	-	-	-	-	-	-
15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	-	-	-	-	0.619	0.702	0.709	-	0.957	-	-	-	-	-
17	-	-	-	-	0.685	0.777	-	-	1.087	-	-	-	-	-
18	-	-	-	-	0.700	0.794	0.803	-	-	-	-	-	-	-
19	-	-	-	-	0.790	0.896	-	-	-	-	-	-	-	-
20	-	-	-	-	-	-	-	-	-	0.718	1.071	0.901	2.914	0.830
21	-	-	-	-	-	-	-	-	-	-	1.888	1.086	3.501	0.998
22	-	-	-	-	-	-	-	-	-	1.265	-	-	-	-
23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
24	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Appendix 5: List of parents falling in different groups.

Group	Selection Series	Clone Number
1	850	87 96 191
2	850	89
3	999	1
4	850	81 120
5	850	37 55 119
6	850	7 19 80 82 88 90 91 93 97 98 99 100 108 110 117 121
7	850	231 235 273 317 371 372 377
8	999	8
9	850	32 34 36 38 41 83 86 92 101 109 112 113 114 116 171 172 181 221 222 224 225 226 227 228 230 232 233 234 236 237 238 239 240 245 246 248 250 272 274 276 281 283 314 315 316 318 319 320 363 370 373 376 392 393 395 402 407 422 473 477 530 534 536 540
10	850	275
11	850	400 478
12	268	6 9 12 18 20 21 22 23 26 27 31 32 33 37 38 39 42 46 48 49 54 58 68 72 76 77 81 82 83 87 89 97 98 101 102 103 105 106 112 113 115 117 121 122 123 126 132 133 135 136 137 139 140 142 143 145 147 149 159 162 169 173 176 182 183 188 189 194 197 198 199 210 213 214 215 218 219 221 223 226 228 229 232 234 244 247 250 258 262 269 270 277 279 280 287 288 289 291 293 297 298 305 310 318 319 320 323 326 327 329 331 333 335 338 349 352 354 356 359 360 362 363 366 367 369 376 377 380 389 392 393 400 401 402 405 407 408 411 412 421 423 424 427 429 431 432 437 444 450 451 452 480 484 485 486 493 495 498 499 500 506 507 512 514 517 518 524 527 530 531 533 538 546 550 551 552 559 565 566 569 570 573 574 576 577 578 580 587 588 608 999 9
13	268	65 172 328 526 532
14	268	290 534
15	850	104 111
16	268	1 14 15 66 160 233 254 261 272 285 299 537 562 563 564 590

Appendix 5: continued

Group	Selection Series	Clone Number
17	268	8 180
18	268	2 3 4 5 7 10 11 16 17 19 24 25 28 29 30 34 35 36 40 47 41 50 51 52 55 56 57 59 64 67 69 70 71 73 74 75 78 79 80 84 85 86 88 90 96 99 100 104 107 108 110 111 114 116 118 119 120 124 127 131 134 138 141 144 146 148 150 152 158 161 163 166 168 170 171 174 175 177 178 179 181 184 185 186 190 192 193 195 200 209 211 212 216 217 220 222 224 225 227 230 231 235 243 245 246 248 249 251 253 255 256 259 260 263 268 273 276 278 281 284 286 292 294 296 300 304 306 309 311 312 314 317 322 324 325 330 332 336 337 340 348 350 353 355 361 364 365 368 370 371 372 375 378 379 382 388 390 391 394 398 403 406 409 410 413 420 425 426 428 433 435 438 443 445 448 454 455 457 459 462 464 465 467- 469 471- 479 481 487- 491 494 496 502 503 505 508 509 510 513 515 519 523 525 528 529 535 536 537 548 553 554 556- 558 560 561 567 568 571 572 575 579 581 586 589 591 594 601 607 609 619 622 632
19	268	13 53 109 125 151 313 321 334 357 358 463 492 497 504 516 549 624
20	999	2 3
21	880	27 83 97 601 650 652 677 679 693 695 716 721 727 748 751 753 764 766 768 770 772 774 776 788
	999	4
22	875	6 7 9 12 15 18 20 21 30 31 33 35 40 41 43 44 46 48 50 51 54 58 62 63 65 69 71 72 74 80 88 90 93 95 96 99 202 207 210 213 215 216 218 220 222 223 225 229 230 235 239 244 247 250 251 253 257 261 262 265 268 270 274 276 280 284 288 289 292 296
	999	5 6 7
23	850	115 394 427 537 538
24	850	542

Note : Selection series '999' represents the control seedlots represented by clone numbers 1 - 9 and their particular identity is as follows:

1. Kaingaroa bulk; 2. Kaingaroa climbing select; 3. Bulk of 268 CP crosses; 4. Bulk of 875 OP and CP crosses; 5. Año Nuevo; 6. Moneterey; 7. Cambria; 8. 850 seed orchard; 9. Kaingaroa seed orchard