

**GENETIC TEST ANALYSIS REPORT FOR REGION E
WHITE SPRUCE TREE IMPROVEMENT
15 YEAR RESULTS**

**Technical Report
ATISC #10-28**

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1.0 INTRODUCTION

The Region E white spruce genetic improvement project was started in 1984 by the Alberta Tree Improvement and Seed Centre. It is fully owned and operated by ATISC. The program is well-developed and operational level seed production in the seed orchard was attained in 2003. Region E represents the northeastern lowlands boreal region dominated by mixed wood forest types. Approved operational elevations for deployment of improved seed within the region are 300 to 650 metres.

Progeny tests (G156 series) with a partial set of open-pollinated (op) half-sib seedlots of the orchard parents were established in 1994 at three sites within Region E. These tests include only 53 Region E half-sib seedlots whereas the production population consists of 97 parents. Progeny testing of the remaining parents will be carried out in future Phase II progeny trials. The primary objectives of the trials are to assess the performance of white spruce families on three sites representative of the environmental diversity in Region E; to assess the magnitude of the genotype \times environment interactions; and to refine the Region E boundary. The applicable controlled parentage program (CPP) is the Region E White Spruce Tree Improvement Program.

2.0 MATERIALS AND METHODS

All progeny trials include op single tree seedlots from the following sources:

- 53 superior tree selections from within breeding Region E,
- 11 superior tree selections from adjacent white spruce breeding Region D1.

Six bulk seedlots representing various Alberta provenances are also established in the trials for comparison purposes and to provide links to other white spruce trials established in the province.

Tests were established in May, 1994 with plug+1 planting stock grown in SB121-70cc styrobloc containers. The stock was seeded in January, 1992 and transplanted into bareroot fields in July, 1992. Stock was lifted and boxed April 25-28, 1994 and placed in cold storage. On May 16, the stock was shipped in a refrigerated van to the planting sites. Test sites are described in Table 1.

The experimental design is randomized complete block (RCB) with seven replications and 5-tree row plots. Tree spacing is 2.5×2.5 metres. A border row was established around each plantation.

Table 1. Location and characteristics of test sites in the G156 trial series.

Site	Latitude	Longitude	Elevation (m)	Climate*	Site Characteristics
G156A – Kinosis Lake	56.30	110.97	495	MAP – 522 GDD – 1300 NDD – 2129	<u>natural subregion</u> : central mixed wood <u>soil classification</u> : orthic grey luvisols <u>soil texture</u> : clay loam to sandy clay loam <u>moisture regime</u> : mesic <u>nutrient regime</u> : permesotrophic
G156B – Wandering River	55.20	112.50	567	MAP – 488 GDD – 1283 NDD – 1875	<u>natural subregion</u> : dry mixed wood <u>soil classification</u> : orthic and gleyed grey luvisols; small area of organic soils <u>soil texture</u> : silty clay <u>moisture regime</u> : subhygric <u>nutrient regime</u> : mesotrophic
G156C – Calling Lake	55.28	113.15	625	MAP – 488 GDD – 1254 NDD – 1901	<u>natural subregion</u> : central mixed wood <u>soil classification</u> : gleyed and orthic grey luvisols <u>soil texture</u> : clay loam <u>moisture regime</u> : subhygric <u>nutrient regime</u> : mesotrophic

*As predicted with the Alberta Climate Model (Alberta Environment 2005)

MAP=mean annual precipitation GDD=growing degree days >5°C NDD=negative degree days i.e. degree days <0°C

3.0 TEST MEASUREMENTS

The first assessment, in the fall of 2002, was at 11 years from seed. Traits measured or assessed were survival, plant damage, height and white pine weevil (wpw) attack. Fifteen year assessments were completed in October 2006; the same traits were measured.

4.0 OBJECTIVES OF THE ANALYSIS

The objective of the analysis is to calculate parental breeding values for 15 year height for the 53 Region E op families represented in the progeny trials. Parental breeding values of the 11 Region D1 families will also be calculated and, based on their rankings relative to Region E parents, the Region D1 parents may be considered for inclusion in the Region E breeding and production populations. The bulk seedlots will also be analyzed; their performance will provide information on the effects of transferring seedlots away from their point of origin and could help redefine the breeding region boundary.

5.0 DATA REVIEW

Data were reviewed for errors and trees classified as dying or trees assigned condition code L, i.e. distinctly atypical for some readily noted reason, were excluded from the height analysis. In total, 27, 8 and 33 trees were excluded from the height analysis for G156A, B, and C, respectively. All living trees were included in the survival analysis.

6.0 DATA ANALYSIS PROCEDURES

6.1 Dataset

Data files used in the 15 year analysis are G156A15.DCF, G156B15.DCF and G156CR.DCF.

6.2 Spatial Analysis

The analysis of 11 year height indicated that the RCB design was not adequately accounting for field variation resulting in high error terms and very low heritabilities particularly at sites B (Wandering River) and C (Calling Lake). In order to improve the estimation of family effects and, thereby, improve the prediction of breeding values, a spatial analysis was used on the 15 year data using the ASReml (Gilmour et al 2006) statistical package.

To assess the nature of the spatial variability at each site, individual site spatial analyses were done in order to generate semivariograms for each site. These graphs are a standard tool for describing spatial variation and are automatically produced by ASReml in a spatial analysis. The semivariance is defined as one-half the variance of the difference between two observations a given distance apart (Littell et al 2006) and the semivariogram is a plot of the semivariance against the distance between observations. A spatial association is indicated if the semivariance increases with distance indicating that values closer together are more similar than those further apart. If the semivariogram plateaus at greater distances, or reaches a sill, then it is stationary; this indicates independence of the errors after some distance apart (Dutkowski and Kerr 2008). If a sill is not reached, the semivariogram is non-stationary and the presence of large scale global variation or extraneous variation is indicated. For example, if an environmental gradient exists across the test site, the variance between two observations will increase linearly with distance and stationarity will not be achieved (Gilmour et al 1997). The semivariograms indicated that both stationary and non-stationary spatial variability occurred at all sites; consequently, the linear models for the individual site analyses varied according to the nature of the non-stationary variability occurring at a given site.

To model the stationary or local variation, a first-order auto-regressive (AR1) process in two dimensions (row and column) was used. In this model, the RCB design features, a spatially dependent error term as described by the AR1 process and a spatially independent or random error term were fitted together (Dutkowski et al. 2002, 2006).

The trees in each trial were designated a row and column number and empty positions were identified as missing values. The two spatial dimensions, row and column, are assumed to be separable AR1 processes described by the following correlation matrix:

$$AR1(\rho) = \begin{bmatrix} 1 & \rho & \rho^2 & \dots & \rho^n \\ \rho & 1 & \rho & \dots & \vdots \\ \rho^2 & \rho & 1 & \dots & \vdots \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho^n & \dots & \dots & \dots & 1 \end{bmatrix} \quad [1]$$

where ρ is the autocorrelation parameter. Under the AR1 model, correlation between adjacent errors is ρ , it is ρ^2 for any pair of errors two rows or two columns apart and it is ρ^n for errors n rows or n columns apart (Littell et al. 2006).

To obtain the most robust estimates of ρ , all trees in the trial were used in the analyses including trees from the Region D1 families and the bulk seedlots; in a typical RCB analysis, these would be excluded. In ASReml, the terms in the spatial analysis model are specified to distinguish between these different entries so that the appropriate variances can be determined.

The non-stationary or global variation is not modeled by the AR1 correlation structure and is accounted for by including linear and non-linear (spline) row and column effects in the model (Table 2).

The data were analyzed using the spatial mixed linear model:

$$Y = Xb + Zu + \xi + \eta \quad [2]$$

where Y is the vector of data; b and u are vectors of fixed and random effects, respectively; X and Z are design matrices relating the observations to the fixed and random effects, respectively; ξ is a spatially dependent random error vector and η is a vector of random residuals. Estimates of the fixed and random effects in [2] (b and u) were obtained by solving the mixed model equations (Henderson 1984):

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix} \quad [3]$$

where R is the variance-covariance matrix of the residuals and G is the direct sum of the variance-covariance matrices of each of the random effects.

In a RCB analysis, R is defined as $\sigma_e^2 I$, where I is an identity matrix; however, in the spatial analysis, with R split into spatially dependent (ξ) and spatially independent errors (η), the R matrix becomes

$$R = \sigma_{\xi}^2 [AR1(\rho_{col}) \otimes AR1(\rho_{row})] + \sigma_{\eta}^2 I \quad [4]$$

where σ_{ξ}^2 is the spatial error variance, σ_{η}^2 is the independent residual variance, I is an identity matrix and $AR1(\rho)$ is as previously defined (Dutkowski et al. 2002).

For all sites, the local, stationary spatial variation was modeled in the R matrix with the $AR1$ structure as described above. Significant linear row effects were also found at each site i.e. height varied linearly with row. At the Calling Lake site (G156C), there was also a linear column effect. These linear effects are modeled in X , or the fixed effects portion of the model. The non-linear row effect at the Wandering River site (G156B) was accounted for by using a cubic smoothing spline; the spline component is random and is included in Z or the random effects portion of the model. The model components used to account for the spatial variability at each site are summarized in Table 2.

Table 2. Individual site spatial variability models for analysis of 15 year height.

Site	Global Variation	Local Variation
Kinosis Lake (G156A)	linear(row)	AR1xAR1
Wandering River (G156B)	linear(row)+spline(row)	AR1xAR1
Calling Lake (G156C)	linear(row)+linear(col)	AR1xAR1

The variance parameters (R and G) were estimated by the method of restricted maximum likelihood (reml); the likelihood of the variance parameters given the data is maximized iteratively and convergence is obtained when variance component estimates change by less than 1% between iterations and the log likelihood (logl) changes less than 0.002 x the current iteration number (Gilmour et al. 2006). The mean, site effects and linear row and column effects were considered fixed; all other effects were considered random. The ASReml command files used in the individual and combined sites analyses are provided in Appendix I.

6.3 Genotype by Environment Interaction

The magnitude of the genotype \times environment interaction ($G \times E$) was assessed using four different correlation models:

- 1) Uniform correlation, single family variance (CORUV), assumes the genetic correlation between sites is uniform and that family variances are homogenous;
- 2) Uniform correlation, heterogenous family variances (CORUH), assumes a uniform genetic correlation between sites as with model 1), but family variances are considered to be heterogenous;
- 3) General correlation, single family variance (CORGV), assumes non-uniform genetic correlations between sites but homogenous family variances;
- 4) General correlation model, heterogenous family variances (CORGH) assumes genetic correlations between sites are non-uniform and family variances are heterogenous.

The CORUV model assumptions are the same as those made in a standard RCB analysis. With this model the size and significance of the site \times family effect are considered to indicate the

magnitude of the $G \times E$. However, this interpretation is appropriate only if family variances are equal across sites (Dutkowski and Kerr 2008).

All models were evaluated using the Akaike information criterion (AIC):

$$-2 \times \log \text{likelihood} + 2p,$$

where p = number of parameters to be estimated and the model with the smallest AIC is preferred.

To examine the significance of the $G \times E$ interaction within the target environment of breeding Region E, the overall coefficient of genetic correlation was estimated as

$$r_b = \frac{\sigma_F^2}{\sigma_F^2 + \sigma_{SF}^2},$$

where r_b is the genetic correlation and σ_F^2 and σ_{SF}^2 are the family and site \times family variance components, respectively, from the combined sites analysis. $G \times E$ is also assessed with the K value, defined as

$$\frac{\sigma_{SF}^2}{\sigma_F^2}$$

where σ_F^2 and σ_{SF}^2 are as previously defined. According to Xie (2003), if r_b is less than 0.7, stratifying the region into different breeding zones may be considered. On the other hand, Shelbourne (1972) considered a K-value of greater than 0.5 as an indicator of a practically significant $G \times E$, justifying a review and partitioning of the region into separate breeding zones.

K and r_b are both statistics that assume equal family variances across sites. This may or may not be an appropriate assumption for a given trial series; however, if this assumption is kept in mind, these statistics remain useful guidelines in the assessment of $G \times E$. In addition, both r_b and K are ratios of variance components, which are subject to greater estimation errors. Thus, their practical use in deciding the integrity of the breeding region should also consider the quality of the test trials and data, and the model used in the analysis and its inherent assumptions.

6.4 Heritabilities

Heritabilities and their standard errors are calculated by ASReml using a .pin file which specifies the functions of the variance components required in the calculation. The following formulae were used for single site, individual tree (h^2_i) and family (h^2_f) heritabilities for 15 year height:

$$h^2_i = \frac{4\sigma_F^2}{\sigma_e^2 + \sigma_{RF}^2 + \sigma_F^2} \quad h^2_f = \frac{\sigma_F^2}{\frac{\sigma_e^2}{nr} + \frac{\sigma_{RF}^2}{r} + \sigma_F^2}.$$

For the combined sites analysis, the following formulae were used:

$$h^2_i = \frac{4\sigma^2_F}{\sigma_e^2 + \sigma_{RF}^2 + \sigma_{SF}^2 + \sigma_F^2} \quad h^2_f = \frac{\sigma_F^2}{\frac{\sigma_e^2}{nrs} + \frac{\sigma_{RF}^2}{rs} + \frac{\sigma_{SF}^2}{s} + \sigma_F^2}$$

Symbol definitions are as follows: σ^2_F = family variance; σ^2_e = error variance; σ^2_{RF} = replicate x family variance; σ^2_{SF} = site x family variance; n = number of trees per plot; r = number of replicates per site; s = number of sites. For unbalanced data, coefficients n , r and s are generated by ASReml.

6.5 Breeding Values

Best linear unbiased prediction (BLUP) breeding values (bv) for 15 year height were predicted for all families using a numerator relationship matrix (NRM). The NRM indicates the additive relationship between all trees including parents and op offspring and allows simultaneous prediction of breeding values for both. The diagonals of the matrix are 1+F, where F is the inbreeding coefficient, and off diagonals are twice the kinship coefficients (Dutkowski and Kerr 2008). Based on a pedigree file, the NRM is created by ASReml, or, more correctly, its inverse, AINVERSE.BIN, is constructed. The pedigree file must start with individual tree (genotype), mother and father fields. In the case of op half-sib progeny trials, the father field is always 0 since the pollen parent is unknown. The data file used in the analysis can serve as the pedigree file as long as genotype, mother and father fields are first.

6.6 Genetic Gain

The genetic gain expected to accrue from the Region E orchard is based on two components: gain due to family selection and gain due to intensive phenotypic selection of parent trees. To calculate the gain due to family selection, parental bvs are expressed as a percentage of the mean 15 year height across all test sites. The percentage breeding values are then weighted by the cumulative proportional contribution of the parent to all operational orchard seed crops and the projected percentage gain for 15 year height is obtained by summing the weighted breeding values over all parents. This approach provides a realistic genetic gain expectation especially for rolling front seed orchards where new material is being added more or less continuously and younger ramets will not be contributing to seed crops. The procedure for calculating genetic gain follows the method described in Appendix 20 of the Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS 2009). For Region E, seed crops from the years 1999, 2002, 2003, 2005, 2007 and 2009 were used in estimating genetic gain. All had an effective population size greater than 18 and/or consisted of more than 300 g of seed.

As a rule, genetic gain is calculated relative to the mean of unselected or operational lot controls appropriate to the CPP. If such controls are not established in the progeny trials, then the mean of the tested parents is used. When parents have been selected intensively from wild stands and there is documented height over age superiority, a 2% gain in height is added to the parental bv to compensate for the fact that genetic gain will be underestimated using the mean of the tested parents to calculate breeding values. This is because the mean of unselected trees will be lower than the mean of intensively selected, dominant parent trees.

To estimate the height gain expected at rotation age, the phenotypic correlation between rotation age height and assessment age height is calculated as follows:

$$r_a(j,m) = 1.02 + 0.308 \ln(j/m)$$

where $r_a(j,m)$ is the phenotypic correlation between performance at a measurement age (j) and rotation age (m) and $\ln(j/m)$ is the natural logarithm of the age ratio j/m (FGRMS 2009, App 31). In this case, the phenotypic correlation is assumed to provide a better estimate of the corresponding genetic correlation, given that the latter cannot be calculated due to unavailability of height measurements at the rotation age. For Region E, the approved rotation age is 105 years. Gain from family selection at 15 years multiplied by r_a gives the estimated gain in height at rotation age.

Because the E orchard is subject to contamination from non-orchard pollen, the projected gain must be reduced to compensate for the proportion of seed fertilized by foreign pollen. The pollen contamination (PC) estimate used is 25%; this is an average PC weighted for seed production over the years 2002, 2003, 2005, 2006, 2007 and 2009, the years for which data are available. The reduction in gain due to pollen contamination is calculated as follows:

$$G_{adj} = 0.5 \times [(1 - PC) \times G_{unadj} + G_{unadj}]$$

where

G_{adj} = total gain in height adjusted for pollen contamination,

G_{unadj} = total gain in height unadjusted for pollen contamination,

PC = proportion of contaminating pollen.

This computation assumes that contaminant pollen has a breeding value of zero and that all clones contribute equal numbers of male and female gametes.

7.0 RESULTS

7.1 Summary Statistics

7.1.1 Fifteen Year Height and Survival

A summary of 15 year assessment results is provided in Table 3. Overall survival at all sites is good and no substantial mortality has occurred between ages 11 and 15 years (ATISC 2004). The lower survival at Wandering River is due to flooding in the last ten rows of the trial. As at 11 years, height growth is best at Wandering River, but performance at all three sites is similar. Predicted family mean heights for all sites are listed in Appendix II.

Table 3. Summary statistics for 15 year height and survival of 53 OP Region E families in the G156 Progeny Trial Series.

Trait/Site	G156A-Kinosis Lake				G156B-Wandering River				G156C-Calling Lake			
	N*	Mean	Range	C.V. (%)	N*	Mean	Range	C.V. (%)	N*	Mean	Range	C.V. (%)
Survival (%)	370	86.9	71.4-100	8.0	370	78.4	48.6-100	13.9	371	91.7	68.6-100	7.1
Height (cm)	1571	363	286-434	8.1	1436	412	316-501	9.1	1666	379	297-437	8.8

*N=number of plots for survival and number of trees for height

Tables 4 and 5 provide summary statistics for the Region D1 families and the Alberta bulk provenance seedlots represented in the trials. On average, height growth of Region D1 families was poorer than that of Region E families at all sites but the differences are not great. Average survival was similar at each site for the Region E and Region D1 families. Except for the Slave Lake bulk seedlot (0019) at Wandering River (G156B), all bulk seedlots performed below the Region E family average for 15 year height growth. Seedlot 0019 was also the best performing bulk seedlot at the Calling Lake site (G156C) performing slightly below the Region E family average. This Slave Lake seedlot is from essentially the same latitude as Wandering River and Calling Lake and from an elevation within 50 metres of these two test sites indicating that the climate is likely similar at each location. The best performing bulk seedlot at the Kinosis site (G156A) was the Peace River seedlot (0021) performing about 10cm below the Region E family average. Average survival of the bulk seedlots at each site was close to the average survival of Region E families.

Table 4. 15 year height performance of Region D1 Families and Bulk Seedlots in the G156 Progeny Trial Series.

	Kinosis Lake (G156A)			Wandering River (G156B)			Calling Lake (G156C)		
	N	Mean	Range**	N	Mean	Range**	N	Mean	Range**
Region D1	324	347	316-394	286	372	265-441	339	354	317-428
Footner Lake (0002)*	31	297	115-451	22	379	171-535	20	316	140-870
Slave Lake (0015)*	31	345	140-475	28	398	160-579	31	359	170-630
Slave Lake (0019)*	32	346	125-480	19	456	203-656	34	371	105-580
Peace River (0021)*	30	354	228-503	26	352	152-500	31	282	130-580
Edson (0032)*	30	319	135-464	24	341	100-544	34	287	110-500
Cypress Hills (0446)*	18	310	162-396	10	379	262-511	15	296	160-420

*bulk seedlot

**range of family means for Region D1 and range of individual tree heights for bulk seedlots

Table 5. Percentage 15 year survival of Region D1 Families and Bulk Seedlots in the G156 Progeny Trial Series.

	Kinosis Lake (G156A)			Wandering River (G156B)			Calling Lake (G156C)		
	N**	Mean	Range***	N**	Mean	Range***	N**	Mean	Range***
Region D1	77	86	77-94	77	74	54-86	77	89	77-97
Footner Lake (0002)*	7	89	60-100	7	63	0-100	5	84	40-100
Slave Lake (0015)*	7	91	60-100	7	80	0-100	7	89	40-100
Slave Lake (0019)*	7	94	80-100	6	67	0-100	7	97	80-100
Peace River (0021)*	7	86	80-100	7	74	0-100	7	89	40-100
Edson (0032)*	7	86	60-100	7	69	0-100	7	100	.
Cypress Hills (0446)*	4	90	60-100	3	67	20-100	3	100	.

*bulk seedlot

**N is the number of plots

***range of family means for Region D1 and range of plot means for bulk seedlots

7.1.2 White Pine Weevil Incidence and Plant Damage

White pine weevil incidence was greatest at the Calling Lake site (G156C); the mean incidence including Region E and Region D1 families and the bulk seedlots was $10.1 \pm 1.3\%$. Mean wpw incidence at Kinosis (G156A) and Wandering River (G156B) was $1.0 \pm 0.2\%$ and $0.9 \pm 0.2\%$, respectively. Weevil incidence was also highest at the Calling Lake site at 11 years and the family mean correlation between the two assessment years is 0.61 ($p < 0.0001$). This moderate correlation suggests that most of the resistant or susceptible families were the same at both ages. Family mean percent wpw incidence is tabulated by site in Appendix III.

Table 6 presents the percent incidence of the major plant damage categories on each site. Terminal shoot dieback is usually a result of winter kill in the year immediately prior to the assessment; the ‘terminal bud dead’ category includes trees with noticeable loss of terminal growth in the assessment growing season or 1 - 3 years prior to it. Damage incidence is similar across sites except terminal shoot dieback and forking at base both have noticeably higher incidence at the Calling Lake site.

Table 6. G156 Progeny Trial Series 15 year assessment percentage of damaged trees by site.

Type of Damage	Kinosis (G156A)	Wandering River (G156B)	Calling Lake (G156C)
Chlorosis	1.0	0.5	1.2
Terminal shoot dieback	0.5	1.1	4.2
Forking at base	6.7	8.0	19.3
Terminal bud dead	6.0	5.8	5.7

7.2 Individual Site Analyses

Table 7 presents variance components in absolute values and as percentages of the total variance resulting from the spatial analysis of 15 year height at the individual sites. For comparison, Table 8 provides the corresponding values from the RCB analysis.

With the spatial analysis, estimates of zero are reported for the replicate variance at Wandering River and the replicate \times family variance at Kinosis. A value of zero indicates that a variance component estimate was trending below zero and has been fixed at zero by the ASReml algorithm. Negative variances may arise due to legitimately very low variance components or they may indicate problems in the data. However, since a major decrease in the design effects, i.e., replicate, replicate \times family, is typical with a spatial analysis (Dutkowski et al. 2002) and since data were reviewed prior to analysis, negative (set to zero) estimates of variance components are considered to indicate lack of variation. The design effects were substantially reduced at all sites in comparison to the RCB analysis resulting in significant increases in the percentage of family variance at all sites.

ASReml output files showing the analysis results are provided in Appendix IV.

Table 7. Variance components and percentages of variance components (in parentheses) for 15 year height spatial analysis of Region E Progeny Trial Series G156.

Component	Site		
	Kinosis Lake (G156A)	Wandering River (G156B)	Calling Lake (G156C)
Replicate	68 (1)	0	242 (3)
Family	418 (8)	395 (9)	591 (7)
Replicate. Family	0	44 (1)	195 (2)
Independent error	4771 (91)	4126 (90)	7533 (88)
Spatially dependent error	2756	3128	3694
ρ row	0.88	0.83	0.86
ρ column	0.69	0.93	0.77

Table 8. Variance components and percentages of variance components (in parentheses) for 15 year height RCB analysis of Region E Progeny Trial Series G156.

Component	Site		
	Kinosis Lake	Wandering River	Calling Lake
Replicate	478 (6)	118 (1)	3119 (21)
Family	494 (6)	0	368 (2)
Replicate. Family	989 (12)	9107 (66)	2549 (17)
Error	6162 (76)	4584 (33)	9137 (60)

7.3 Combined Sites Analysis and G \times E

In Table 9, the different correlation models used in the combined sites analysis and their AICs are presented. The model that best explained the data (lowest AIC) was CORGV: the family variances are homogenous across sites but the correlations are not uniform. Although the family variances at Kinosis (G156A) and Wandering River (G156C) differ considerably from the family variance at Calling Lake (G156C) (Table 6) suggesting that the G \times E may be due to scale effects i.e., heterogenous family variances, modeling for heterogeneity (CORGH) did not improve the

correlations between Kinosis and Calling Lake and Wandering River and Calling Lake. The ASReml output file is provided in Appendix V.

Table 9. Comparison of correlation models for analysis of combined sites 15 year height of Region E Progeny Trial Series G156.

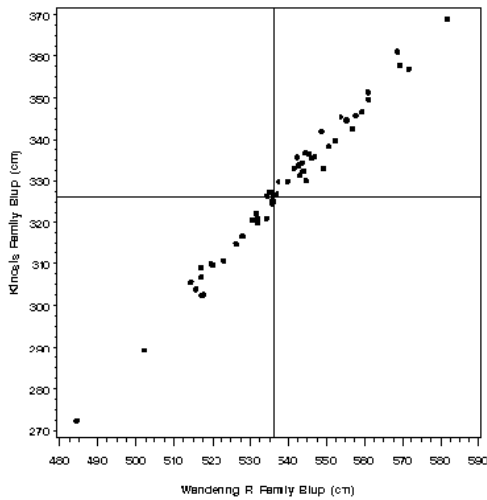
Model	LogL	p	AIC
Uniform correlation; homogenous family variances (CORUV)	-30005.54	17	60045.08
Uniform correlation; heterogenous family variances (CORUH)	-30003.49	21	60048.98
General correlation; homogenous family variances (CORGV)	-30002.97	17	60039.94
General correlation; heterogenous family variances (CORGH)	-30000.65	21	60043.3

Where Logl=log likelihood , p=number of variance parameters being estimated, AIC=Akaike information criterion

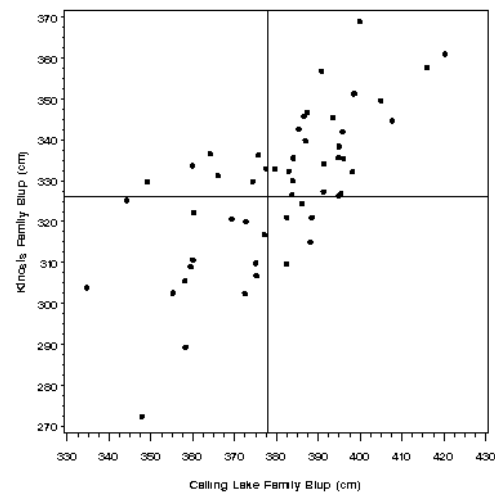
The genetic correlations between sites A and B, A and C and B and C, respectively, are 0.95 ± 0.1 , 0.56 ± 0.2 and 0.55 ± 0.2 . The corresponding Pearson's correlations of predicted family means are 0.99, 0.70, and 0.70, respectively. All correlations were highly significant ($P < 0.0001$) (Fig. 1). The correlations indicate significant $G \times E$ between Kinosis and Calling Lake and between Wandering River and Calling Lake.

When considering the location, climate and other characteristics of each site (Table 1), a lower correlation between Kinosis and the other two sites would be expected since it is about 1° of latitude north of the other two sites, has different climatic attributes and different moisture and nutrient regimes. On the other hand, Wandering River and Calling Lake are essentially the same; they are very close in terms of latitude, longitude and elevation and have similar climates. That the genetic correlation between these sites is quite low (0.55) suggests that it is not explaining the differences in family adaptability between these sites very well. White pine weevil incidence and climatic damage (see Sec 7.1.2) at the Calling Lake site may be a major factor in the low correlation between the two sites.

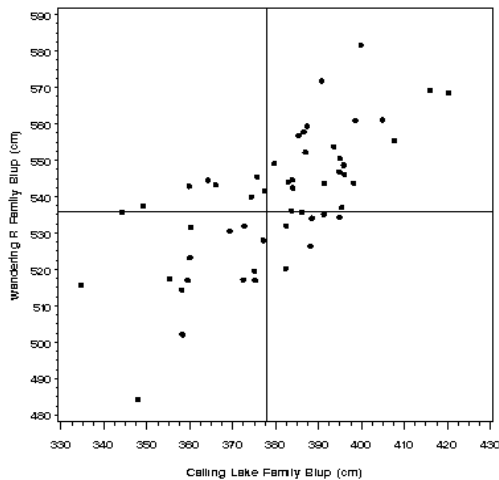
Fig. 1. Family G × E correlations between site pairs in the Region E Progeny Trial series G156*.



1a. Family mean correlation for 15 year height between Kinosis Lake (G156A) and Wandering River (G156B) ($r=0.99$)



1b. Family mean correlation for 15 year height between Kinosis Lake (G156A) and Calling Lake (G156C) ($r= 0.70$)



1c. Family mean correlation for 15 year height between Wandering River (G156B) and Calling Lake (G156C) ($r = 0.70$)

*The vertical and horizontal lines in the scatter graphs indicate the 15 year blup height means for each site.

Since the analysis indicated that family variances were uniform across sites, the K value and overall coefficient of genetic correlation (r_b) may be considered legitimate estimators of the scope of the G × E in breeding Region E as represented by the G156 trial series. The K value was 0.41 and r_b was 0.71. These values suggest that the Calling Lake site could belong to a different breeding region than the Kinosis Lake and Wandering River sites. However, both of these statistics are at or near the borderline values suggested by Xie (2003) and Shelbourne (1972) (see Sec 6.3) and, considering the strong geographic, climatic and edaphic similarities of the test site pairs with only moderate genetic correlations, the G × E should not unduly affect

selection of superior, broadly adapted genotypes for deployment throughout the E CPP region. Consequently, single breeding values were predicted for each parent represented in the trials.

7.4 Heritabilities

Heritabilities for 15 and 11 year heights are given in Tables 10 and 11, respectively. Individual and family heritabilities have increased substantially from age 11 to 15 years. Although this could be partially attributed to periodic fluctuations in genetic and environmental variances, much of the improvement in heritabilities is due to the decrease or elimination of the experimental error variance (family \times replication interaction) resulting from the spatial analysis. Combined sites heritabilities for 15 year height were not calculated because the calculation relies on the assumption of homogenous error variances across sites (see formula in Sec 6.4). However, the model that best fit the combined sites data specified heterogenous error variances i.e., an independent error was estimated for each site. Consequently, a combined sites heritability could not be calculated.

Table 10. G156 progeny trials individual and family heritabilities for 15 year height.

Site	σ^2_{phen}	σ^2_{Fbar}	$h^2_i \pm \text{se}$	$h^2_f \pm \text{se}$
Kinosis Lake (G156A)	5189	581.1	0.32 ± 0.09	0.72 ± 0.06
Wandering River (G156B)	4564	572.1	0.35 ± 0.10	0.69 ± 0.08
Calling Lake (G156C)	8319	857.4	0.28 ± 0.09	0.69 ± 0.08

Where σ^2_{phen} = phenotypic variance (denominator in h^2_i calculations); σ^2_{Fbar} = family mean variance (denominator in h^2_f calculations); h^2_i = individual tree heritability; h^2_f = family heritability; se = standard error

Table 11. G156 progeny trials individual and family heritabilities for 11 year height.

Site	σ^2_{phen}	σ^2_{Fbar}	$h^2_i \pm \text{se}$	$h^2_f \pm \text{se}$
Kinosis Lake (G156A)	2158.3	247.0	0.25 ± 0.07	0.54 ± 0.09
Wandering River (G156B)	3770.0	573.6	0.07 ± 0.05	0.11 ± 0.06
Calling Lake (G156C)	4022.5	281.6	0.03 ± 0.04	0.12 ± 0.05

Where symbols are as defined in Table 11.

7.5 Breeding Values and Genetic Gain

Parental breeding values and gain calculations are provided in Appendix VI and the estimated components of the genetic gain to be accrued from the Region E orchard are summarized in Table 12. The correlation between rotation age height and assessment age height ($r_a(j,m)$) was calculated as 0.42. Of the 97 parents in the E orchard, 75 are eligible for the 2% lift due to intensive phenotypic selection; based on the cumulative contribution of these parents to the orchard seed crops, total gain due to intensive selection is 1.6%. This component of the gain is not adjusted with r_a because the selected trees are mature and at rotation age.

Table 12. Components of genetic gain (%) for G259 Region E White Spruce Clonal Seed Orchard.

	Family Selection	Intensive Phenotypic election	Total Gain	Total Gain adjusted for pollen contamination
Height at 15 years	3.2	1.6	4.8	4.2
Height at rotation (105 years)	1.3	1.6	2.9	2.6

7.6 Implications for Region E Project Development

Based on the 15 year height analysis, a slight increase in gain could be achieved by roguing all parents with negative breeding values. This would entail the removal of 102 trees representing 10 parents based on the orchard composition in 2009. However, roguing should also take into account incidence of wpw. Of seven families identified as highly susceptible to wpw in the 15 year analysis, five remain in the orchard and only two have positive breeding values for height; the latter are in the lower ranks and are represented in the orchard by a total of 13 trees. Removing all 115 trees would result in an estimated gain for 15 year height of 6.1%.

Increased expected gain can also be achieved by increasing the proportion of higher breeding value parents in the orchard; this strategy was implemented after the first orchard roguing in 2005. However, greater gains cannot be expected until the 52 untested parents in the orchard are progeny tested.

Although, on average, the Region D1 families performed below the Region E families in height growth, there are three Region D1 parents that rank in the top 20-30% of tested parents that could be included in the Region E production population (Appendices VII and VIII).

8.0 ASSOCIATED REPORTS

- Revised Delineation of Breeding Region E for Genetic Improvement of White Spruce Project. Genetics and Tree Improvement Section, Alberta Forest Service. March 1991.
- Establishment Report G156A White Spruce OP Progeny Test (Region E), Kinosis Genetics Experimental Area. November, 1994.
- Establishment Report G156B White Spruce OP Progeny Test (Region E), Wandering River Genetics Experimental Area. November, 1994.
- Establishment Report G156C White Spruce OP Progeny Test (Region E), Calling Lake Genetics Experimental Area. November, 1994.
- Genetic Test Analysis Report for Region E White Spruce Tree Improvement. Tech. Rpt. ATISC 04-22 Draft Example. November, 2004.
- Selection of Trees from the Region E White Spruce Progeny Trial (G156B) from Wandering River Experimental Site. Tech. File Rpt. ATISC #05-18. October, 2005.

9.0 LITERATURE CITED

- Alberta Environment. 2005. Alberta Climate Model (ACM) to provide climate estimates (1961-1990) for any location in Alberta from its geographic coordinates. Publ. No. T/749. 33 pp.
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- Shelbourne, C.J.A. 1972. Genotype-environment interaction: its study and its implications in forest tree improvement. *In Proceedings of Joint Symposia for the Advancement of Forest Tree Breeding of the Genetics Subject Group, IUFRO, and Section 5, Forest Trees, SABRAO. Government Forest Experiment Station of Japan, Tokyo.* pp. B-1 I 1-28.
- Xie, C.-Y. 2003. Genotype by environment interaction and its implications for genetic improvement of interior spruce in British Columbia. *Can. J. For. Res.* 33: 1635-1643.

Appendix IA. ASReml Job File (.as) Single Site Analyses

Region E OP Progeny Trial (G156) 15 year Height Analysis

Title: allsite_15yr.

```
seedlot !!
acc !!
dad
rep *
blk *
row *
tree *
s11 *
h11 !!
s15 *
h15
type *
col *
predh15
site *
```

```
allsite_15yr.TXT !SKIP 1 !maxit 50 !dopart 1 !filter site !select 1
```

Fifteen year height (h15) is the variate. The fixed portion of the models includes the mean (μ) and linear row and/or column effects. Random effects, following !r, include replicate (rep), rep x seedlot interaction, seedlot and an independent error term (units). 'Type' refers to seedlot type i.e. Region E op half-sib families (type 1), Region D op half-sib families (type 2) and bulk provenance seedlots (type 3). The type.seedlot and type.units terms generate variances for each seedlot type. Spline effects are also included in the random portion of the model. Missing values (mv) are fitted as a sparse fixed term (!f) (Gilmour et al 2009).

!part 1

This model was the best fit for the Kinosis (G156A) data.

```
h15 ~ mu, lin(row) !r rep rep.seedlot type.seedlot type.units !f mv
```

AR1 spatial analysis of the residuals

The first line is the variance header (Gilmour et al. 2009): there is one error (R) structure which is the direct product of two variance matrices (AR1xAR1) and there are two explicit random term (G) structures. Hence, 1 2 2. In subsequent lines, the initial col and row refer to the number of rows and columns at the site, the following col and row cause an internal sort of the data row within column to ensure that the data match the direct product structure specified (Gilmour et al 2009). AR specifies the autocorrelation matrix and 0.1 is the starting value of the autocorrelation parameter (ρ).

```
1 2 2
col col AR 0.1
row row AR 0.1
```

The two explicit G structures

1) Modelling seedlot variation

The seedlot variance structure is the direct product of two matrices: a diagonal matrix (DIAG) of order 3 (the number of seedlot types) and an identity matrix (IDEN) of order number of seedlots per type. DIAG specifies heterogenous variances so a different seedlot variance is determined for each seedlot type. The 1s are starting values for the variances.

```
type.seedlot 2
type 0 DIAG 1 1 1
seedlot 0 IDEN
```

2) Modelling the independent error (units)

The units variance structure is the direct product of two matrices: a diagonal matrix (DIAG) of order 3 (the number of seedlot types) and an identity matrix (IDEN) of order number of units (trees). DIAG specifies heterogenous variances so a different independent error variance is determined for each seedlot type. The 1s are starting values for the variances.

```
type.units 2  
type 0 DIAG 1 1 1  
units 0 IDEN
```

!part 2

This model was the best fit for the Calling Lake (G156C) data.

```
h15 ~ mu lin(row) lin(col) !r rep rep.seedlot type.seedlot type.units !f mv
```

```
1 2 2  
col col AR 0.1  
row row AR 0.1
```

```
type.seedlot 2  
type 0 DIAG 1 1 1  
seedlot 0 IDEN
```

```
type.units 2  
type 0 DIAG 1 1 1  
units 0 IDEN
```

!part 3

This model was the best fit for the Wandering River (G156B) data.

```
h15 ~ mu lin(row) !r rep rep.seedlot type.seedlot type.units spl(row) !f mv
```

```
1 2 2  
col col AR 0.1  
row row AR 0.1
```

```
type.seedlot 2  
type 0 DIAG 1 1 1  
seedlot 0 IDEN
```

```
type.units 2  
type 0 DIAG 1 1 1  
units 0 IDEN
```

Appendix IB. ASReml Job File (.as) for Combined Sites Analysis

Region E OP Progeny Trial (G156) 15 year Height Analysis

```
Title: allsite_15yr.  
seedlot !!  
acc !!  
dad  
rep *  
blk *  
row *  
tree *  
s11 *  
h11 !!  
s15 *  
h15  
type *  
col *  
predh15  
site *  
typene1 !=type !>1
```

```
allsite_15yr.TXT !SKIP 1 !maxit 50
```

Fifteen year height (h15) is the variate. The fixed portion of the model includes the mean (μ), linear row effects at all sites and linear column effects at site 3 (Calling Lake). Random effects (following !r) are the site x seedlot, site x rep, site x rep x seedlot interaction terms, an independent error term (units) and the spline row effect at site 2 (Wandering River). Missing values (mv) are fitted as a sparse fixed term (!f) (Gilmour et al. 2009). The term 'type' refers to seedlot type i.e. Region E op half-sib families (type 1), Region D op half-sib families (type 2) and bulk provenance seedlots (type 3). The analysis treats types 2 and 3 together i.e. typene1.

```
h15 ~ mu site site.lin(row) at(site,3).lin(col) !r at(type,1).site.seedlot at(typene1,1).site.seedlot,  
site.rep site.rep.seedlot type.site.units at(site,2).spl(row) !f mv
```

AR1 spatial analysis of the residuals

The first line is the variance header (Gilmour et al 2009): there are three error (R) structures, i.e. one for each site, which are the direct products of 2 variance models (AR1xAR1) and there are three explicit random term (G) structures. Hence, site 2 3 or, the equivalent, 3 2 3. In subsequent lines, the leading numbers are the number of rows and columns at each site, e.g. there are 70 rows and 35 columns at the Kinosis site (site 1), the numbers following AR are starting values for the row or column autocorrelation parameters (ρ) and values for !S2 are starting values for the spatially correlated residuals at each site. Starting values are determined from the individual site analyses.

```
site 2 3  
70 row AR 0.88 !S2=3088  
35 col AR 0.72  
43 row AR 0.90 !S2=5666  
60 col AR 0.96  
130 row AR 0.91 !S2=5359  
25 col AR 0.83
```

The three explicit G structures

1) Modelling correlation between sites for Region E op half-sib families (type 1)

The at(type,1).site.seedlot structure is the direct product of two matrices: a correlation structure, CORGV, which assumes non-uniform genetic correlations between sites but homogenous family variances; and an identity matrix (IDEN) of order number of type 1 seedlots, i.e. Region E op half-sib families. The 0.9s are starting values for the between site correlations and 400 is the starting value for the family variance.

```
at(type,1).site.seedlot 2
site 0 CORGV
0.9
0.9 0.9
400
seedlot 0 IDEN
```

2) Modelling correlation between sites for Region D of half-sib families (type 2) and provenance seedlots (type 3)

```
at(type1,1).site.seedlot 2
site 0 CORGV
0.9
0.9 0.9
400
seedlot 0 IDEN
```

3) Modelling the independent error (units)

The units variance structure is the direct product of two matrices: a diagonal matrix (DIAG) of order 9 (3 sites x 3 seedlot types) and an identity matrix (IDEN) of order number of units (trees). DIAG specifies heterogeneous variances so a different independent error variance is determined for each seedlot type at each site. The 1s following DIAG are starting values for the type.site independent variances and !G9P is restraining the values to be above zero.

```
type.site.units 2
9 0 DIAG 1 1 1 1 1 1 1 1 1 !G9P
units 0 ID
```


Appendix IC. ASReml Job File (.as) for Breeding Value Calculation

Region E OP Progeny Trial (G156) 15 year Height Analysis

```
Title: allsite_15yr.  
genotype !P  
mum !!  
dad  
seedlot !!  
acc !!  
rep *  
blk *  
row *  
tree *  
s11 *  
h11 !!  
s15 *  
h15  
type *  
col *  
predh15  
site *  
typene1 !=type !>1
```

```
allsite_15yr_mum.TXT !SKIP 1 !MAKE The pedigree file  
allsite_15yr_gen.TXT !SKIP 1 !MVINCLUDE !maxit 50 The data file
```

The fixed portion of the model remains the same as for the gxe analysis (App IB). In the random portion of the model, the seedlot term is replaced by genotype; this is the term with the associated pedigree. The pedigree of each tree in the data set is specified: for op half-sib family trees, the maternal parent is identified by the accession number and the paternal parent is designated as 0 for unknown; for provenance seedlots, both maternal and paternal parents are 0. In order to generate only one breeding value per parent, interaction terms have been dropped from the model; this approach was considered appropriate for this particular trial series (see Section 7.3). Also, since the family variances were homogenous across sites, transformation of the data to account for family variance heterogeneity was not necessary (Dutkowski and Kerr 2008).

```
h15 ~ mu site site.lin(row) at(site,3).lin(col) !r site.rep genotype site.units at(site,2).spl(row) !f mv
```

```
site 2 3  
70 row AR 0.88 !S2=3088  
35 col AR 0.72  
43 row AR 0.90 !S2=5666  
60 col AR 0.96  
130 row AR 0.91 !S2=5359  
25 col AR 0.83
```

The inverse of the numerator relationship matrix (AINV) is required to determine genotype effects (breeding values)

```
genotype 1  
genotype 0 AINV 400  
  
site.units 2  
3 0 DIAG 1 1 1 !G3P  
units 0 ID
```

Appendix II. Family Blups for 15 Year Height for Region E OP Half-sib Families G156

In order of descending blup

Kinosisk Lake (G156A)

acc	clone	blup
2842	X314	43.2
2809	X362	35.2
2999	X451	31.9
2805	X468	31.1
3020	X574	25.5
2807	X470	23.8
2848	X579	20.9
3004	X561	20.0
3021	X577	19.7
2799	X467	18.9
2843	X578	16.9
2798	X377	16.3
3017	X453	14.0
3006	X569	12.6
3001	X456	10.8
3355	X241	10.5
3363	X582	9.9
2686	X405	9.8
3002	X457	9.7
3014	X372	8.5
2685	X378	7.9
3356	X304	7.2
2841	X446	7.1
2691	X403	6.5
3012	X309	6.4
2806	X447	5.5
3010	X580	4.3
2681	X245	4.1
3009	X575	4.0
3025	X594	1.6
3359	X442	1.1
2682	X246	0.8
3360	X444	0.6
3013	X370	-0.5
3357	X310	-1.3
2687	X406	-3.5
2840	X239	-4.7
3018	X464	-4.7
2688	X407	-5.2
3016	X445	-5.7
3015	X443	-9.0
3008	X571	-10.8
2808	X408	-15.0
3005	X562	-15.9
3007	X570	-16.0
3000	X455	-16.8
3024	X587	-19.0
2797	X301	-20.2
2683	X243	-21.9
3003	X458	-23.2
3011	X591	-23.4
2810	X315	-36.4
3019	X465	-53.3

Wandering River (G156B)

acc	clone	blup
2842	X314	45.2
2805	X468	35.3
2999	X451	32.7
2809	X362	32.1
2807	X470	24.7
3020	X574	24.5
2848	X579	22.9
3004	X561	21.4
2843	X578	20.5
2799	X467	19.0
3021	X577	17.4
3017	X453	15.8
3006	X569	14.1
2841	X446	12.7
2798	X377	12.2
3363	X582	10.4
3002	X457	9.7
3355	X241	9.1
3010	X580	8.2
3001	X456	8.1
2691	X403	7.7
3012	X309	7.3
3014	X372	7.2
2806	X447	6.7
2685	X378	6.4
2686	X405	6.0
3356	X304	5.2
2681	X245	3.5
3009	X575	1.0
3359	X442	0.6
2682	X246	-0.3
3013	X370	-0.6
3357	X310	-0.7
3025	X594	-1.4
3360	X444	-2.1
2840	X239	-2.3
3018	X464	-4.4
3016	X445	-4.6
2687	X406	-4.9
2688	X407	-5.9
3015	X443	-8.5
3008	X571	-10.1
2808	X408	-13.3
3007	X570	-16.2
3005	X562	-16.8
3003	X458	-18.9
3011	X591	-19.3
3024	X587	-19.4
3000	X455	-19.5
2683	X243	-20.7
2797	X301	-22.1
2810	X315	-34.4
3019	X465	-52.1

Calling Lake (G156C)

acc	clone	blup
2809	X362	41.9
2999	X451	37.6
2799	X467	29.4
2807	X470	26.6
2842	X314	21.5
3020	X574	20.2
3012	X309	19.9
3002	X457	17.7
2798	X377	17.5
3359	X442	17.1
3006	X569	16.6
3360	X444	16.5
3363	X582	16.5
3021	X577	15.2
3014	X372	13.0
3025	X594	12.9
2805	X468	12.4
2840	X239	10.1
3008	X571	9.7
2848	X579	9.0
3017	X453	8.5
3004	X561	8.2
3357	X310	7.8
2843	X578	7.0
2686	X405	5.7
3010	X580	5.5
2682	X246	5.3
2691	X403	4.6
3018	X464	4.1
3007	X570	4.0
2841	X446	1.3
3356	X304	-0.9
3015	X443	-1.2
3355	X241	-2.6
3024	X587	-3.2
3005	X562	-3.2
2681	X245	-4.0
3016	X445	-5.7
3011	X591	-5.9
2688	X407	-9.1
2806	X447	-12.4
3001	X456	-14.2
2687	X406	-18.2
2808	X408	-18.3
2685	X378	-18.5
3000	X455	-18.9
2810	X315	-20.1
2797	X301	-20.2
3003	X458	-23.1
3009	X575	-29.3
3019	X465	-30.5
3013	X370	-34.1
2683	X243	-43.7

negative blup at all sites

Positive blup at all sites

In order of accession number

Kinosio Lake (G156A)

acc	clone	blup
2681	X245	4.1
2682	X246	0.8
2683	X243	-21.9
2685	X378	7.9
2686	X405	9.8
2687	X406	-3.5
2688	X407	-5.2
2691	X403	6.5
2797	X301	-20.2
2798	X377	16.3
2799	X467	18.9
2805	X468	31.1
2806	X447	5.5
2807	X470	23.8
2808	X408	-15.0
2809	X362	35.2
2810	X315	-36.4
2840	X239	-4.7
2841	X446	7.1
2842	X314	43.2
2843	X578	16.9
2848	X579	20.9
2999	X451	31.9
3000	X455	-16.8
3001	X456	10.8
3002	X457	9.7
3003	X458	-23.2
3004	X561	20.0
3005	X562	-15.9
3006	X569	12.6
3007	X570	-16.0
3008	X571	-10.8
3009	X575	4.0
3010	X580	4.3
3011	X591	-23.4
3012	X309	6.4
3013	X370	-0.5
3014	X372	8.5
3015	X443	-9.0
3016	X445	-5.7
3017	X453	14.0
3018	X464	-4.7
3019	X465	-53.3
3020	X574	25.5
3021	X577	19.7
3024	X587	-19.0
3025	X594	1.6
3355	X241	10.5
3356	X304	7.2
3357	X310	-1.3
3359	X442	1.1
3360	X444	0.6
3363	X582	9.9

Negative blup at all sites

Wandering River (G156B)

acc	clone	blup
2681	X245	3.5
2682	X246	-0.3
2683	X243	-20.7
2685	X378	6.4
2686	X405	6.0
2687	X406	-4.9
2688	X407	-5.9
2691	X403	7.7
2797	X301	-22.1
2798	X377	12.2
2799	X467	19.0
2805	X468	35.3
2806	X447	6.7
2807	X470	24.7
2808	X408	-13.3
2809	X362	32.1
2810	X315	-34.4
2840	X239	-2.3
2841	X446	12.7
2842	X314	45.2
2843	X578	20.5
2848	X579	22.9
2999	X451	32.7
3000	X455	-19.5
3001	X456	8.1
3002	X457	9.7
3003	X458	-18.9
3004	X561	21.4
3005	X562	-16.8
3006	X569	14.1
3007	X570	-16.2
3008	X571	-10.1
3009	X575	1.0
3010	X580	8.2
3011	X591	-19.3
3012	X309	7.3
3013	X370	-0.6
3014	X372	7.2
3015	X443	-8.5
3016	X445	-4.6
3017	X453	15.8
3018	X464	-4.4
3019	X465	-52.1
3020	X574	24.5
3021	X577	17.4
3024	X587	-19.4
3025	X594	-1.4
3355	X241	9.1
3356	X304	5.2
3357	X310	-0.7
3359	X442	0.6
3360	X444	-2.1
3363	X582	10.4

Calling Lake (G156C)

acc	clone	blup
2681	X245	-4.0
2682	X246	5.3
2683	X243	-43.7
2685	X378	-18.5
2686	X405	5.7
2687	X406	-18.2
2688	X407	-9.1
2691	X403	4.6
2797	X301	-20.2
2798	X377	17.5
2799	X467	29.4
2805	X468	12.4
2806	X447	-12.4
2807	X470	26.6
2808	X408	-18.3
2809	X362	41.9
2810	X315	-20.1
2840	X239	10.1
2841	X446	1.3
2842	X314	21.5
2843	X578	7.0
2848	X579	9.0
2999	X451	37.6
3000	X455	-18.9
3001	X456	-14.2
3002	X457	17.7
3003	X458	-23.1
3004	X561	8.2
3005	X562	-3.2
3006	X569	16.6
3007	X570	4.0
3008	X571	9.7
3009	X575	-29.3
3010	X580	5.5
3011	X591	-5.9
3012	X309	19.9
3013	X370	-34.1
3014	X372	13.0
3015	X443	-1.2
3016	X445	-5.7
3017	X453	8.5
3018	X464	4.1
3019	X465	-30.5
3020	X574	20.2
3021	X577	15.2
3024	X587	-3.2
3025	X594	12.9
3355	X241	-2.6
3356	X304	-0.9
3357	X310	7.8
3359	X442	17.1
3360	X444	16.5
3363	X582	16.5

Positive blup at all sites

Appendix III. Family Mean Percent White Pine Weevil Incidence

G156A

Type	Family/Sdlot	Mean
Region E	2681	7.41
Region D1	3367	7.14
Region E	2840	6.90
Region E	2682	4.17
Region E	2683	3.70
Region E	2842	3.57
Region E	3013	3.57
Region D1	3383	3.57
Region E	2687	3.45
Region E	3020	3.23
Region E	2797	3.23
Region E	3356	3.23
Region E	2798	3.13
Region E	2999	3.13
Bulk	15	3.13
Region D1	3369	3.03
Region D1	3387	3.03
Region E	2686	2.94
Region E	2685	0.00
Region E	2688	0.00
Region E	2691	0.00
Region E	2799	0.00
Region E	2805	0.00
Region E	2806	0.00
Region E	2807	0.00
Region E	2808	0.00
Region E	2809	0.00
Region E	2810	0.00
Region E	2841	0.00
Region E	2843	0.00
Region E	2848	0.00
Region E	3000	0.00
Region E	3001	0.00
Region E	3002	0.00
Region E	3003	0.00
Region E	3004	0.00
Region E	3005	0.00
Region E	3006	0.00
Region E	3007	0.00
Region E	3008	0.00
Region E	3009	0.00
Region E	3010	0.00
Region E	3011	0.00
Region E	3012	0.00
Region E	3014	0.00
Region E	3015	0.00
Region E	3016	0.00
Region E	3017	0.00
Region E	3018	0.00
Region E	3019	0.00

G156B

Type	Family/Sdlot	Mean
Region D1	3370	9.09
Region D1	3371	5.00
Region E	3006	4.76
Region D1	3351	4.55
Region E	3018	4.00
Region E	3019	3.70
Region E	3010	3.70
Region E	3013	3.57
Bulk	15	3.57
Region E	2681	3.45
Region E	3363	3.45
Region D1	3387	3.45
Region E	2798	3.33
Region E	2841	3.23
Region E	2999	2.94
Region E	2682	0.00
Region E	2683	0.00
Region E	2685	0.00
Region E	2686	0.00
Region E	2687	0.00
Region E	2688	0.00
Region E	2691	0.00
Region E	2797	0.00
Region E	2799	0.00
Region E	2805	0.00
Region E	2806	0.00
Region E	2807	0.00
Region E	2808	0.00
Region E	2809	0.00
Region E	2810	0.00
Region E	2840	0.00
Region E	2842	0.00
Region E	2843	0.00
Region E	2848	0.00
Region E	3000	0.00
Region E	3001	0.00
Region E	3002	0.00
Region E	3003	0.00
Region E	3004	0.00
Region E	3005	0.00
Region E	3007	0.00
Region E	3008	0.00
Region E	3009	0.00
Region E	3011	0.00
Region E	3012	0.00
Region E	3014	0.00
Region E	3015	0.00
Region E	3016	0.00
Region E	3017	0.00
Region E	3020	0.00

G156C

Type	Family/Sdlot	Mean
Region E	2683	36.36
Region E	3015	24.24
Bulk	2	23.81
Bulk	15	22.58
Region E	3009	21.88
Region E	3016	20.59
Bulk	32	20.00
Bulk	446	20.00
Region E	2806	18.75
Region E	2681	18.52
Region E	2687	17.65
Region D1	3383	16.13
Bulk	21	16.13
Region E	3359	15.38
Region E	3017	15.15
Region D1	3387	15.15
Region E	3010	14.71
Bulk	19	14.71
Region E	2691	14.29
Region E	3011	14.29
Region E	2842	13.33
Region E	3000	13.33
Region E	3356	13.33
Region E	3357	12.50
Region D1	3367	12.50
Region E	2798	12.12
Region E	2809	12.12
Region E	2682	11.11
Region E	2805	10.00
Region E	3004	10.00
Region E	3005	9.38
Region E	3355	9.38
Region E	2686	9.09
Region E	2688	9.09
Region E	2843	9.09
Region E	3019	9.09
Region D1	3368	9.09
Region E	2810	8.82
Region E	3003	8.82
Region E	3014	8.82
Region E	3018	8.82
Region E	2999	8.57
Region D1	3369	7.41
Region E	2848	6.67
Region D1	3350	6.67
Region E	2841	6.45
Region E	3006	6.45
Region E	3013	6.45
Region E	3007	6.06
Region E	2808	5.88

Type	Family/Sdlot	Mean
Region E	3021	0.00
Region E	3024	0.00
Region E	3025	0.00
Region E	3355	0.00
Region E	3357	0.00
Region E	3359	0.00
Region E	3360	0.00
Region E	3363	0.00
Region D1	3350	0.00
Region D1	3351	0.00
Region D1	3364	0.00
Region D1	3365	0.00
Region D1	3368	0.00
Region D1	3370	0.00
Region D1	3371	0.00
Bulk	2	0.00
Bulk	19	0.00
Bulk	21	0.00
Bulk	32	0.00
Bulk	446	0.00
Mean		1.02

Type	Family/Sdlot	Mean
Region E	3021	0.00
Region E	3024	0.00
Region E	3025	0.00
Region E	3355	0.00
Region E	3356	0.00
Region E	3357	0.00
Region E	3359	0.00
Region E	3360	0.00
Region D1	3350	0.00
Region D1	3364	0.00
Region D1	3365	0.00
Region D1	3367	0.00
Region D1	3368	0.00
Region D1	3369	0.00
Region D1	3383	0.00
Bulk	2	0.00
Bulk	19	0.00
Bulk	21	0.00
Bulk	32	0.00
Bulk	446	0.00
Mean		0.88

Type	Family/Sdlot	Mean
Region D1	3364	5.88
Region E	3001	5.71
Region E	3002	5.71
Region E	3008	3.57
Region D1	3365	3.45
Region E	3012	3.23
Region D1	3351	3.23
Region E	2685	3.12
Region E	3020	3.12
Region E	2807	3.03
Region E	3025	3.03
Region E	2840	2.94
Region E	2797	0.00
Region E	2799	0.00
Region E	3021	0.00
Region E	3024	0.00
Region E	3360	0.00
Region E	3363	0.00
Region D1	3370	0.00
Region D1	3371	0.00
Mean		10.10

Appendix IV. ASReml Individual Site 15 Year Height Spatial Analysis Results

Kinosis (G156A)

Source	Model	terms	Gamma	Component	Comp/SE	%	C
rep	7	7	2.47E-02	68.0211	0.44	0	P
rep.seedlot	490	490	3.28E-08	9.03E-05	0	0	B
Variance ¹	2450	2065	1	2756.32	7.19	0	P
Residual ²	AR=AutoR	35	0.689661	0.689661	13.87	0	U
Residual ³	AR=AutoR	70	0.87779	0.87779	36.89	0	U
type.seedlot ⁴	DIAGonal	1	0.151619	417.911	3.27	0	U
type.seedlot	DIAGonal	2	0.128201	353.363	1.45	0	U
type.seedlot	DIAGonal	3	0.257195	708.91	1.4	0	U
type.units ⁵	DIAGonal	1	1.73105	4771.32	21.81	0	U
type.units	DIAGonal	2	1.49692	4125.97	10.16	0	U
type.units	DIAGonal	3	0.892391	2459.71	6.79	0	U

Wandering River (G156B)

Source	Model	terms	Gamma	Component	Comp/SE	%	C
rep	7	7	2.18E-07	6.83E-04	0	0	B
spl(row)	41	41	0.177415	554.954	0.72	0	P
rep.seedlot	490	490	1.39E-02	43.5857	0.34	0	P
Variance ¹	2580	1849	1	3128.01	4.52	0	P
Residual ²	AR=AutoR	60	0.932267	0.932267	47	0	U
Residual ³	AR=AutoR	43	0.833513	0.833513	20.05	0	U
type.seedlot ⁴	DIAGonal	1	0.126223	394.827	3.08	0	U
type.seedlot	DIAGonal	2	0.3922	1226.8	1.75	0	U
type.seedlot	DIAGonal	3	0.491641	1537.86	1.37	0	U
type.units ⁵	DIAGonal	1	1.31893	4125.63	22	0	U
type.units	DIAGonal	2	2.06868	6470.85	10.59	0	U
type.units	DIAGonal	3	1.54657	4837.69	7.07	0	U

Calling Lake (G156C)

Source	Model	terms	Gamma	Component	Comp/SE	%	C
rep	7	7	6.56E-02	242.155	0.88	0	P
rep.seedlot	490	490	5.27E-02	194.584	0.94	0	P
Variance ¹	3250	2167	1	3693.54	6.39	0	P
Residual ²	AR=AutoR	25	0.772847	0.772847	16.37	0	U
Residual ³	AR=AutoR	130	0.859803	0.859803	27.04	0	U
type.seedlot ⁴	DIAGonal	1	0.160063	591.198	3.06	0	U
type.seedlot	DIAGonal	2	0.158898	586.895	1.32	0	U
type.seedlot	DIAGonal	3	0.287137	1060.55	1.13	0	U
type.units ⁵	DIAGonal	1	2.03958	7533.26	21.76	0	U
type.units	DIAGonal	2	2.58469	9546.64	11.12	0	U
type.units	DIAGonal	3	2.59823	9596.67	7.78	0	U

¹ spatially dependent error

² autocorrelation parameter (ρ) for rows

³ autocorrelation parameter (ρ) for columns

⁴ family variance for Region E op half-sib families

⁵ independent error for Region E op half-sib families

Appendix V. ASReml Combined Sites 15 Year Height Spatial Analysis Results

Source	Model	terms	Gamma	Component	Comp/SE	%	C
Residual	8280	6081					
site.rep	21	21	84.827	84.827	0.92	0	P
at(site,2).spl(row)	48	48	102.09	102.09	0.75	0	P
site.rep.seedlot	1470	1470	29.9264	29.9264	0.39	0	P
Variance[1] ¹	2450	0	2655.94	2655.94	7.24	0	P
Residual ²	AR=AutoR	70	0.877473	0.877473	36.7	0	U
Residual ³	AR=AutoR	35	0.677285	0.677285	12.97	0	U
Variance[2] ¹	2580	0	3036.5	3036.5	4.5	0	P
Residual ²	AR=AutoR	43	0.837476	0.837476	20.85	0	U
Residual ³	AR=AutoR	60	0.929311	0.929311	45.63	0	U
Variance[3] ¹	3250	0	3786.48	3786.48	6.73	0	P
Residual ²	AR=AutoR	130	0.856364	0.856364	28.15	0	U
Residual ³	AR=AutoR	25	0.772494	0.772494	16.9	0	U
at(type,1).site.seed ⁴	CORRelat	3	0.945306	0.945306	8.6	0	U
at(type,1).site.seed ⁵	CORRelat	3	0.557601	0.557601	3.03	0	U
at(type,1).site.seed ⁶	CORRelat	3	0.554016	0.554016	2.96	0	U
at(type,1).site.seed ⁷	CORRelat	3	472.422	472.422	4.61	0	U
at(typene1,1).site.s ⁸	CORRelat	3	0.750795	0.750795	3.94	0	U
at(typene1,1).site.s ⁹	CORRelat	3	0.823406	0.823406	4.18	0	U
at(typene1,1).site.s ¹⁰	CORRelat	3	0.778637	0.778637	3.6	0	U
at(typene1,1).site.s ¹¹	CORRelat	3	853.343	853.343	2.74	0	U
type.site.units ¹²	DIAGonal	1	4761.36	4761.36	21.53	0	P
type.site.units ¹²	DIAGonal	2	4123.84	4123.84	22.27	0	P
type.site.units ¹²	DIAGonal	3	7615.53	7615.53	22.06	0	P
type.site.units ¹³	DIAGonal	4	4093.27	4093.27	10.15	0	P
type.site.units ¹³	DIAGonal	5	6612.68	6612.68	10.62	0	P
type.site.units ¹³	DIAGonal	6	9655.68	9655.68	11.24	0	P
type.site.units ¹⁴	DIAGonal	7	2463.48	2463.48	6.76	0	P
type.site.units ¹⁴	DIAGonal	8	4858.86	4858.86	7.1	0	P
type.site.units ¹⁴	DIAGonal	9	9723.36	9723.36	7.84	0	P

Legend

- ¹ spatially dependent error at G156A [1], G156B [2] and G156C [3], respectively
- ² autocorrelation parameter (ρ) for columns at G156A, B and C, respectively
- ³ autocorrelation parameter (ρ) for rows at G156A, B and C, respectively
- ⁴ genetic correlation between sites G156A and G156B for Region E op half-sib families
- ⁵ genetic correlation between sites G156A and G156C for Region E op half-sib families
- ⁶ genetic correlation between sites G156B and G156C for Region E op half-sib families
- ⁷ variance component for Region E op half-sib family
- ⁸ genetic correlation between sites G156A and G156B for Region D op half-sib families and bulk seedlots
- ⁹ genetic correlation between sites G156A and G156C for Region D op half-sib families and bulk seedlots
- ¹⁰ genetic correlation between sites G156B and G156C for Region D op half-sib families and bulk seedlots
- ¹¹ variance component for Region D op half-sib family and bulk seedlot
- ¹² independent error for Region E op half-sib families at G156A, B and C, respectively
- ¹³ independent error for Region D op half-sib families at G156A, B and C, respectively
- ¹⁴ independent error for bulk seedlots at G156A, B and C, respectively

Appendix VI. G156 Half-sib Progeny Trials 15 Year Height Parental Breeding Values and Calculation of Genetic Gain for the Region E Clonal Seed Orchard (G259)

acc no.	clone no.	bv ¹	bv% ¹	%lift	pc ²	weighted bv%	scaled by r _m ³	weighted %lift	remarks
2681	245	9.874	2.6	2	0.0052	0.0135	0.0057	0.0104	
2682	246	12.5	3.3	0	0.0000	0.0000	0.0000	0.0000	
2683	243	-47.81	-12.6	2	0.0000	0.0000	0.0000	0.0000	
2685	378	9.743	2.6	2	0.0063	0.0162	0.0068	0.0126	
2686	405	28.89	7.6	2	0.0020	0.0149	0.0063	0.0039	
2687	406	-8.94	-2.3	2	0.0000	0.0000	0.0000	0.0000	
2688	407	-4.346	-1.1	2	0.0331	-0.0377	-0.0159	0.0661	
2691	403	23.32	6.1	2	0.0077	0.0473	0.0199	0.0155	
2797	301	-28.31	-7.4	2	0.0000	0.0000	0.0000	0.0000	
2798	377	41.13	10.8	2	0.0639	0.6905	0.2905	0.1278	
2799	467	56.63	14.9	2	0.0025	0.0372	0.0157	0.0050	
2805	468	66.17	17.4	2	0.0299	0.5203	0.2189	0.0598	
2806	447	10.65	2.8	2	0.0262	0.0734	0.0309	0.0525	
2807	470	57.83	15.2	2	0.0150	0.2284	0.0961	0.0301	
2808	408	-20.59	-5.4	2	0.0030	-0.0163	-0.0068	0.0060	
2809	362	86.02	22.6	2	0.0458	1.0360	0.4358	0.0917	
2810	315	-48.35	-12.7	2	0.0000	0.0000	0.0000	0.0000	
2840	239	8.821	2.3	0	0.0008	0.0018	0.0007	0.0000	
2841	446	27.75	7.3	2	0.0000	0.0000	0.0000	0.0000	
2842	314	82.24	21.6	2	0.0007	0.0141	0.0059	0.0013	
2843	578	42.11	11.1	2	0.0000	0.0000	0.0000	0.0000	
2848	579	44.61	11.7	2	0.0251	0.2940	0.1237	0.0502	
2999	451	77.14	20.3	2	0.0006	0.0120	0.0050	0.0012	
3000	455	-22.01	-5.8	2	0.0003	-0.0019	-0.0008	0.0007	
3001	456	16.86	4.4	2	0.0017	0.0077	0.0033	0.0035	
3002	457	34.14	9.0	2	0.0022	0.0201	0.0085	0.0045	
3003	458	-33.54	-8.8	2	0.0179	-0.1575	-0.0663	0.0358	
3004	561	47.62	12.5	2	0.0043	0.0537	0.0226	0.0086	
3005	562	-13.23	-3.5	2	0.0000	-0.0001	0.0000	0.0001	
3006	569	40.53	10.6	2	0.0016	0.0171	0.0072	0.0032	
3007	570	-11.49	-3.0	2	0.0058	-0.0175	-0.0074	0.0116	
3008	571	1.502	0.4	0	0.0000	0.0000	0.0000	0.0000	
3009	575	-1.458	-0.4	2	0.0016	-0.0006	-0.0003	0.0032	
3010	580	20.05	5.3	2	0.0022	0.0114	0.0048	0.0043	
3011	591	-22.33	-5.9	2	0.0569	-0.3338	-0.1404	0.1138	
3012	309	31.8	8.4	2	0.0000	0.0000	0.0000	0.0000	
3013	370	-7.1	-1.9	2	0.0000	0.0000	0.0000	0.0000	
3014	372	27.82	7.3	2	0.0148	0.1082	0.0455	0.0296	
3015	443	-5.319	-1.4	2	0.0283	-0.0395	-0.0166	0.0566	
3016	445	-1.581	-0.4	2	0.0059	-0.0025	-0.0010	0.0119	
3017	453	37.7	9.9	2	0.0156	0.1550	0.0652	0.0313	
3018	464	7.534	2.0	2	0.0023	0.0046	0.0019	0.0046	
3019	465	-83.63	-22.0	0	0.0002	-0.0038	-0.0016	0.0000	
3020	574	57.6	15.1	2	0.0038	0.0574	0.0242	0.0076	
3021	577	50.84	13.4	2	0.0000	0.0000	0.0000	0.0000	

acc no.	clone no.	bv ¹	bv% ¹	%lift	pc ²	weighted bv%	scaled by r _{jm} ³	weighted %lift	remarks
3024	587	-18.29	-4.8	0	0.0016	-0.0077	-0.0033	0.0000	
3025	594	17.31	4.5	2	0.0186	0.0848	0.0357	0.0373	
3355	241	24.21	6.4	2	0.0010	0.0060	0.0025	0.0019	
3356	304	21.56	5.7	0	0.0083	0.0468	0.0197	0.0000	
3357	310	13.72	3.6	2	0.0025	0.0089	0.0037	0.0049	
3359	442	19.84	5.2	2	0.0061	0.0317	0.0133	0.0122	
3360	444	20.19	5.3	2	0.0125	0.0666	0.0280	0.0251	
3363	582	33.03	8.7	2	0.0124	0.1073	0.0451	0.0247	
na	1834	57.37	15.1	0	0.0000	0.0000	0.0000	0.0000	fwd sel X3094
na	1835	19.09	5.0	0	0.0000	0.0000	0.0000	0.0000	fwd sel X4064
na	1836	37.2	9.8	0	0.0000	0.0000	0.0000	0.0000	fwd sel X4464
na	1837	41.43	10.9	0	0.0000	0.0000	0.0000	0.0000	fwd sel X5774
na	1838	51.84	13.6	0	0.0000	0.0000	0.0000	0.0000	fwd sel X5784
3354	240			0	0.0110	0.0000	0.0000	0.0000	
3472	585			2	0.0172	0.0000	0.0000	0.0344	
3473	586			2	0.0004	0.0000	0.0000	0.0007	
3474	595			2	0.0059	0.0000	0.0000	0.0118	
3475	901			2	0.0000	0.0000	0.0000	0.0001	
3491	908			0	0.0010	0.0000	0.0000	0.0000	
3492	909			0	0.0008	0.0000	0.0000	0.0000	
3493	910			0	0.0027	0.0000	0.0000	0.0000	
3494	907			2	0.0032	0.0000	0.0000	0.0063	
3495	242			2	0.0035	0.0000	0.0000	0.0070	
3496	303			2	0.0015	0.0000	0.0000	0.0031	
3497	306			0	0.0039	0.0000	0.0000	0.0000	
3499	364			2	0.0012	0.0000	0.0000	0.0025	
3500	366			2	0.0006	0.0000	0.0000	0.0011	
3501	450			0	0.0139	0.0000	0.0000	0.0000	
3503	466			2	0.0145	0.0000	0.0000	0.0289	
3506	581			2	0.0121	0.0000	0.0000	0.0241	
3507	583			2	0.0098	0.0000	0.0000	0.0196	
3508	584			2	0.0000	0.0000	0.0000	0.0000	
3509	596			2	0.0231	0.0000	0.0000	0.0462	
3510	597			2	0.0069	0.0000	0.0000	0.0137	
3518	452			2	0.0043	0.0000	0.0000	0.0085	
3519	598			2	0.0142	0.0000	0.0000	0.0284	
3520	463			0	0.0475	0.0000	0.0000	0.0000	
3523	462			2	0.0138	0.0000	0.0000	0.0276	
3524	568			2	0.0078	0.0000	0.0000	0.0156	
3988	906			2	0.0006	0.0000	0.0000	0.0012	
4435	368			2	0.0238	0.0000	0.0000	0.0475	
4436	375			2	0.0150	0.0000	0.0000	0.0299	
5504	305			2	0.0062	0.0000	0.0000	0.0124	
5505	307			0	0.0020	0.0000	0.0000	0.0000	
5507	374			2	0.0201	0.0000	0.0000	0.0403	
5510	402			0	0.0941	0.0000	0.0000	0.0000	
5512	441			2	0.0036	0.0000	0.0000	0.0071	

acc no.	clone no.	bv ¹	bv% ¹	%lift	pc ²	weighted bv%	scaled by r _{jm} ³	weighted %lift	remarks
5514	449			0	0.0003	0.0000	0.0000	0.0000	
5515	459			2	0.0051	0.0000	0.0000	0.0103	
5516	460			2	0.0007	0.0000	0.0000	0.0013	
5518	523			2	0.0569	0.0000	0.0000	0.1137	
5519	567			2	0.0139	0.0000	0.0000	0.0279	
5521	576			2	0.0105	0.0000	0.0000	0.0210	
5522	588			2	0.0066	0.0000	0.0000	0.0132	
5523	589			2	0.0049	0.0000	0.0000	0.0099	
5524	593			2	0.0057	0.0000	0.0000	0.0113	
5525	902			2	0.0017	0.0000	0.0000	0.0034	
5715	461			2	0.0000	0.0000	0.0000	0.0000	
5719	592			2	0.0001	0.0000	0.0000	0.0002	
5720	885			0	0.0036	0.0000	0.0000	0.0000	
5721	914			0	0.0029	0.0000	0.0000	0.0000	
5722	916			0	0.0030	0.0000	0.0000	0.0000	
	308			2	0.0005	0.0000	0.0000	0.0010	
	469			2	0.0002	0.0000	0.0000	0.0005	
	883			0	0.0012	0.0000	0.0000	0.0000	
SUM					1.0000	3.1679	1.3326	1.6027	
						4.8	2.9		

¹If this field is blank, the parent is not in test

²the cumulative proportional contribution of the parent to orchard seedlots

³r_{jm} = juvenile/mature correlation = 0.42 (assuming 105 year rotation)

⁴ fwd sel = forward selection based on 11-year height analysis; no surviving grafts from parental clone

	% height gain due to family selection at 15 years
	% height gain due to family selection at rotation (105 years)
	% height gain due to intensive parent tree selection
	total % height gain at 15 years (unadjusted for pollen contamination)
	total % height gain at rotation (unadjusted for pollen contamination)

adjustment for estimated pollen contamination of 25%

0.5 x ((1-0.25) x 0.048 + 0.048) =	4.2	%height gain at 15 years adjusted for pollen contamination
0.5 x ((1-0.25) x 0.029 + 0.029) =	2.6	% height gain at rotation adjusted for pollen contamination

Appendix VII. Family Blups for 15 Year Height for Region D1 OP Half-sib Families in the G156 Progeny Trials

In order of descending blup

Kinosis Lake (G156A)


acc	clone	blup
3369	685	25.01
3383	713	14.78
3364	688	10.55
3365	687	6.252
3367	681	-6.243
3350	686	-12.2
3351	682	-12.7
3387	941	-22.92
3368	684	-24.05
3371	746	-30.72
3370	692	-40.62

Wandering River (G156B)

acc	clone	blup
3369	685	13.39
3365	687	10.66
3364	688	5.468
3383	713	-8.775
3367	681	-9.856
3351	682	-9.92
3387	941	-18.89
3371	746	-20.49
3350	686	-21.55
3368	684	-22.66
3370	692	-70.97

Calling Lake (G156C)

acc	clone	blup
3365	687	22.03
3369	685	20.94
3364	688	13.21
3383	713	8.35
3351	682	-5.417
3350	686	-10.56
3367	681	-17.69
3368	684	-22.95
3387	941	-30.51
3371	746	-32.42
3370	692	-38.62

 positive blup at all sites

In order of accession number

Kinosis Lake (G156A)


acc	clone	blup
3350	686	-12.2
3351	682	-12.7
3364	688	10.55
3365	687	6.252
3367	681	-6.243
3368	684	-24.05
3369	685	25.01
3370	692	-40.62
3371	746	-30.72
3383	713	14.78
3387	941	-22.92

Wandering River (G156B)

acc	clone	blup
3350	686	-21.55
3351	682	-9.92
3364	688	5.468
3365	687	10.66
3367	681	-9.856
3368	684	-22.66
3369	685	13.39
3370	692	-70.97
3371	746	-20.49
3383	713	-8.775
3387	941	-18.89

Calling Lake (G156C)

acc	clone	blup
3350	686	-10.56
3351	682	-5.417
3364	688	13.21
3365	687	22.03
3367	681	-17.69
3368	684	-22.95
3369	685	20.94
3370	692	-38.62
3371	746	-32.42
3383	713	8.35
3387	941	-30.51

 positive blup at all sites

Appendix VIII. Parental Breeding Values for 15 Year Height for Region D1 Parents Represented in the G156 Progeny Trials

In order of descending blup

acc	clone	blup
3369	685	47.77
3364	688	33.94
3365	687	33.64
3383	713	16.36
3351	682	-5.961
3367	681	-11.38
3350	686	-16.19
3387	941	-32.46
3368	684	-32.97
3371	746	-38.12
3370	692	-85.79

In order of accession number

acc	clone	blup
3350	686	-16.19
3351	682	-5.961
3364	688	33.94
3365	687	33.64
3367	681	-11.38
3368	684	-32.97
3369	685	47.77
3370	692	-85.79
3371	746	-38.12
3383	713	16.36
3387	941	-32.46