

**SECOND ESTIMATION OF GENETIC GAIN MULTIPLIERS
USING DATA FROM 1978-1980 LARGE-BLOCK
GENETIC GAIN TRIALS**

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Executive Summary

Genetic gain multipliers have been incorporated in regional growth models in order to predict stand volume at rotation age. These multipliers reduce the time required for stand growth parameters to reach a given size relative to the amount of genetic gain expected. As more and more data from large-block genetic gain trials becomes available, better and better estimates of genetic gain multipliers can be made.

This second estimation of the multipliers used data from the 1978-80 genetic gain trials up to age 15, which represents PSP measurements from seven to nine years of data for GF7 and GF14 seedlots and three years of data for GF2 and GF22 seedlots. Multiplier estimates for GF14 were almost identical to estimates made three years previously (SGMC Report No. 35). Estimates for GF2 and GF22 are somewhat different, but are made from much more data than the previous estimate.

Height growth was 5% faster for both GF14 and GF22, but the change in basal area and stocking was 13% faster for GF14 and 26% faster for GF22. The average predicted volume increase at a rotation age of 30 years for the genetic gain trial sites is 13% for open pollinated (GF14) and 22% for control pollinated seedlots (GF22).

Second estimation of genetic gain multipliers using data from 1978-1980 large-block genetic gain trials

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ABSTRACT. *Pinus radiata* D. Don seedlots of varying genetic quality were compared in ten large-block genetic gain trials representing the range of site types in New Zealand. Permanent sample plots were measured annually for growth from age 6–8 years from planting to mid-rotation (ages 15–17). Seedlots from first generation open-pollinated seed orchards and progeny from control-crossing of the top performing clone in progeny trials were on average 4.5% and 5.3% taller and had 6% and 11% larger mean diameter, 12% and 30% more basal area, and 15% and 34% more stem volume, respectively, than seedlots originating from mild selection in harvested stands (climbing select). Growth increases were quantified as changes in growth rate over that predicted by pre-existing growth models. Seedlots from first generation seed orchards and control crossing the top clone grew 5.1% and 4.5% faster in height and changed 13% and 26.4% faster in basal area and stocking, respectively, than the baseline growth models which were based on climbing select. These estimated rates of change are being used to predict growth of genetically improved seedlots.

ADDITIONAL KEYWORDS. *Pinus radiata*, growth modelling, genetic gain, tree improvement.

The New Zealand forest industry extensively utilises genetically improved *Pinus radiata* D. Don planting stock resulting from an intensive tree improvement program begun in the early 1950's (Carson *et al.* 1990). The genetic quality of planting stock has steadily improved since that time. Before 1950 seed was collected without selection from land race stands, which developed since the 1880's after importation of seed from California. Tree improvement efforts were initiated about 1955 when seed were collected from the best trees just before a stand was felled (Carson *et al.* 1990, Shelbourne 1987). This "climbing select" seed was widely planted until the mid-1980's when enough open-pollinated orchard seed became available to supply all of New Zealand's needs. Open-pollinated orchards of vegetatively propagated plus trees selected from land race stands produced the genetically best seed available from the early 1970's until the mid 1980's, when commercial planting stock from control-crossing parents which performed best in progeny trials began to be produced. About 20% of the reforested area is currently from control-pollinated seed sources. Control crossing is expected to increase gain because of the exclusion of pollen from unselected parents which occurs in open-pollinated seed orchards and because of increased selection intensities (Shelbourne *et al.* 1989).

With the intensive forest management practiced in New Zealand, quantification of genetic gain is important in order to identify the pay-offs from investment in tree improvement, to compare results from different breeding strategies and to accurately assign economic weights to selection criteria (Burdon 1982). More importantly, accurate planning of wood flows from a forest estate greatly enhances profitability of a forest enterprise, both for precise regulation of yield and for planning processing facilities. Predictions of stand growth are also used to analyse the economics of silviculture and to determine optimum time of pruning, thinning, and felling specific stands (Goulding 1994).

Accurate measurement of changes in yield with genetically improved stock requires comparison of improved and unimproved stock planted as large-blocks. Tree breeders have been very effective at selecting parents which produce faster growing trees through efficient progeny testing. Gain from genetic selection can be predicted from progeny tests using quantitative genetic theory (Falconer 1989), but these gains apply only when conditions in the progeny trials exactly mirror the conditions in which the selected populations will be grown. A typical progeny test consists of a large number of genotypes, where both high and low performers are grown inter-mixed. Since the typical improved stand will have only the highest performers, and competition has a profound effect on growth and final tree size, predictions from progeny tests may not represent actual realised gain very well.

Many studies have fitted growth models to provenance trial or progeny test data (some of which was from large-block trials) (Buford 1986, Buford 1989, Buford and Burkhart 1987, Hamilton and Rehfeldt 1994, Knowe and Foster 1989, Nance and Wells 1981a and 1981b, Rehfeldt *et al.* 1991, Schmidting 1988, Schmidting and Froelich 1993, Sprinz *et al.* 1989), but there are few reports for coniferous forest species of large-block trials comparing volume per unit area for seedlots produced by tree improvement programs and unimproved seedlots. Wood volumes of large blocks of improved and unimproved *P. radiata* in New Zealand have been reported in a few cases. In one comparison a pre-extraction thinning inventory showed improved stands to have 20.5% more basal area, and 19.6% more recoverable volume, while extraction thinning yielded 20% more wood tonnage (Gleed 1982). In another comparison there was no difference in average tree size between improved and unimproved stands, but a higher conversion of standing volume to merchantable volume meant that 16% more volume was recovered in an extraction thinning (Cleland 1985). Another stand inventory (Johnson *et al.* 1992) showed 11% more volume per hectare from improved progeny in a

replicated comparison with an unimproved seedlot. These comparisons have given useful “snap shots” in time of specific situations, but generalisation to other stands is tenuous.

This paper reports results to half rotation (a rotation being 30 years) from ten large-block trials comparing seedlots of *P. radiata* with a range of genetic improvement representing successive stages of tree improvement in New Zealand. This is the most extensive information available on realised genetic gain from tree improvement in coniferous plantation forests. Mean differences among seedlots were compared, and relative differences in rates of growth were calculated using growth models in order to account for site and stocking differences which occurred in the trials. The use of these estimates of differences in rates of change in growth models for prediction of growth of genetically improved seedlots is examined.

MATERIALS AND METHODS

GENETIC GAIN TRIALS

Ten genetic gain trials were planted in a randomised complete block design with six replicate blocks of each seedlot. Seven were planted in 1978 (AK1058 in Aupouri Forest in the north of the North Island; RO2103/1 and RO2103/2 in Kaingaroa Forest in the Central North Island; NN530/2 in Golden Downs Forest in the northern South Island; and two trials in the southern South Island: CY421/1 in Waimate Forest and SD564 in Longwood Forest), two were planted in 1979 (RO2103/3 in Kaingaroa Forest; and NN530/1 in Golden Downs Forest) and one in 1980 (SD682 in Dean forest in the south of the South Island) (see Appendix 1). In nine of these trials, blocks were ten by ten trees treated with a direct sawlog regime, that is, planted at 1111 stems per hectare, thinned to 300 stems per hectare in two stages and pruned in three lifts to 6.2m. For one trial (RO2103/2) blocks

were eight by eight trees treated with a pulpwood regime, that is, planted at 711 stems per hectare, with no thinning, and pruning only to 2.2m.

GENETIC WORTH OF SEEDLOTS IN GENETIC GAIN TRIALS

The New Zealand Seed Certification Service rates commercial seedlots based on their genetic worth as determined largely by relative performance of parents and mixed seedlots in progeny trials (Vincent 1987a&b). The GF rating, a rating for the Growth and Form Breed, reflects a seedlot's genetic worth for growth and stem form characteristics combined. Because two-thirds of the weight is on diameter and one third on stem form (mainly straightness and lack of malformation), the GF rating gives a strong indication of genetic worth for growth. Seedlot ratings represent relative genetic worth, that is, they are a ranking not intended to indicate the absolute magnitude of differences between seedlots. Climbing select seedlots are used as benchmarks for seed certification and are arbitrarily assigned ratings of GF7, and open-pollinated seed orchard seed from a specific set of 25 parents are assigned a rating of GF14. Unselected land race stands are arbitrarily assigned a GF2. GF ratings of GF20 and above are from controlled pollinations (with the highest ratings of single-pair crosses of existing plus trees being GF30), while ratings between GF14 and GF20 generally are from mother tree collections in open-pollinated seed orchards. As well as several other seedlots, trials planted in 1978 included seedlots with improvement ratings of GF2, GF7, GF14, and GF22, and 1979 and 1980 trials included GF7 and GF14.

The seedlot rated GF2 in the trials is a bulk collection from a land-race stand at Kaingaroa Forest in the Central North Island and represents the genetic resource before tree improvement efforts began. Several climbing select seedlots (rated GF7), are included in the trials. Six of the genetic gain trials included the same climbing select seedlot collected from Kaingaroa Forest (seedlot RO/C/76/1), and

three included local sources of climbing select seed (seedlot NN/C/75/2 from Golden Downs Forest in trial NN530/2; seedlot CY/C/75/40 from Balmoral Forest in trial CY421/1; seedlot SD/C/75/27 from Rankleburn Forest in trial SD564), which have not been tested in any other trials. The genetic gain trial in Dean Forest (SD682) did not include a climbing select seedlot, so PSP were established in the adjacent stand, which originated from seedlot SD/C/76/2, a climbing select seedlot from Rankleburn Forest. The seedlot (WN/76/2/3) rated GF14 in the trials planted in 1978 was from Gwavas Seed Orchard, which is used as the benchmark for seed certification. In trials planted in 1979 and 1980, the GF14 seedlot (FRI 78/2300) was a mixture of control pollinated crosses of first generation selections made up of plus trees which as a group performed similarly for diameter in progeny trials to the Gwavas Seed Orchard seedlot. The GF22 seedlot is a mixture of control-cross seed resulting from crossing the plus tree which was the best performing parent for diameter across progeny tests of over 1000 plus trees with one of seven to twelve other parents, which showed average performance.

MEASUREMENT OF DIFFERENCES AMONG SEEDLOTS

Circular permanent sample plots (PSP) (Dunlop 1994, Ellis and Dunlop 1997) were established in 1986 in all plots of seedlots rated GF7 and GF14. In 1991 PSP were established in two additional seedlots rated GF2 and GF22 in trials planted in 1978, with three plots of each seedlot per site. PSP were measured annually through 1995 for total height and diameter at 1.4m. Mean top height (mean height of the 100 trees per ha with the largest diameter), basal area per ha, quadratic mean diameter, mean top diameter (quadratic mean diameter of the 100 trees per ha with the largest diameter) and volume per ha were calculated using standard mensurational methods (Dunlop 1994, Ellis and Dunlop 1997).

Percent gain was calculated for the 1995 measurements for mean top height, basal area per hectare, quadratic mean diameter, and volume per hectare

$$P_{K/J} = \frac{[H_K - H_J]}{H_J} \times 100\%$$

where $P_{K/J}$ is percent gain of seedlot K over seedlot J, H_K is mean of seedlot K, and H_J is mean of seedlot J.

QUANTIFICATION OF DIFFERENCES IN GROWTH RATES

Differences in rates of growth among seedlots rated GF2, GF14, and GF22 as compared to seedlots rated GF7 were calculated using the New Zealand growth models. Existing growth models (Goulding 1993) were built for each of seven regions from survey data collected mainly from measurements of climbing select stock. The growth models, therefore, provide predictions for a baseline of performance for GF7 seedlots. The regional models for eight of the ten trial sites predict growth using sets of three differential equations, which model the rates of change in three state variables as functions of the current values of these variables. The models include as state variables the mean top height (H), basal area (B), and number of stems per hectare (N):

$$\begin{aligned} \frac{dH}{dt} &= f_1(H) \\ \frac{dB}{dt} &= f_2(H, B, N) \\ \frac{dN}{dt} &= f_3(H, B, N) \end{aligned} \tag{1}$$

The differential equations are a multivariate extension of the Bertalanffy-Richards model (García 1979, 1984, 1988, 1994). Growth models for two of the trial sites

(AK1058 and WN777) were more complicated and, therefore, were not used in this analysis.

Differences in growth rates with genetic improvement for both height and basal area were calculated separately since the physiological mechanisms of growth are different for height and diameter (that is, meristematic growth versus cambium growth). Several assumptions were required in order to do this. Because the form of the models means that the basal area and stocking equations are difficult to separate, the change in growth rate estimated for the basal area equation was assumed to be the same as that for the tree stocking equation.

Rate of change in height

The rate of growth in height with genetic improvement was calculated to be m times higher than the growth represented by the first growth model equation in (1) for the model appropriate for each genetic gain trial site:

$$\frac{dH}{dt} = m f_1(H)$$

The multiplier (m) may also be seen as a time-scaling factor:

$$\frac{dH}{d(mt)} = f_1(H)$$

so that on integration the height-age curve takes the form

$$H = F(mt)$$

with $m = 1$ for the existing model and $m > 1$ for increased height growth.

Therefore, the effect of genetic improvement with this approach is a compression

of the time axis, decreasing by a factor of m the time needed to reach a given height. Note that the asymptote, the ultimate height achievable, is assumed to remain constant.

For a pair of consecutive measurements H_1 and H_2 at ages t_1 and t_2 , if the model were exact we would have

$$m = \frac{F^{-1}(H_2) - F^{-1}(H_1)}{t_2 - t_1} \quad (2)$$

This expression provides the basis for estimating m from field measurements, as explained later.

Rate of change in basal area and stocking

Multipliers could be similarly added to the last two equations in (1) by assuming a common multiplier for basal area and stems per hectare. A model incorporating genetic effects could be constructed by multiplying each of the growth rate equations of an existing model (1) by a genetic gain multiplier (m_i), with the same multiplier for the last two equations. The multipliers represent the relative growth improvement for the various state variables. Note, however, that the interpretation as a compression of the time axis, valid when looking only at top height, breaks down when adding the other variables.

An alternative and slightly different formulation was used because it was easier to implement, taking advantage of the nature of the multivariate Richards model. Instead of applying multipliers to the last two equations in (1), these were first transformed into equations of the form $dz_i/dt = g_i(z_i)$. Here the z_i are two transformations of the state variables that “uncouple” the equations, so that now not only the height growth equation, but also the other two, are independent and

self-contained. The difference between the two approaches is unlikely to be important in practice.

In detail, the multivariate Richard's model may be written as

$$\frac{dz_i}{dt} = \lambda_i z_i, \quad i = 1, 2, 3, \quad (3)$$

where

$$z_i = \sum p_{ij} (H^{c_{j1}} B^{c_{j2}} N^{c_{j3}} - a_j),$$

and the λ_i , p_{ij} , c_{ij} , and a_i are model parameters. The parameters $p_{12} = p_{13} = c_{12} = c_{13} = 0$, so that the first equation in (3) is equivalent to the usual univariate Richards model for height growth (García 1979, 1994).

Each right-hand side of (3) is multiplied by a genetic gain multiplier m_i where m_i is the multiplier for the height growth equation, m_2 is for the basal area equation, m_3 is for the tree stocking equation, and $m_2 = m_3$. These equations are easily integrated:

$$z_i(t) = e^{m_i \lambda_i (t-t_0)} z_i(t_0)$$

The equivalent of (2) is then

$$m_i = \frac{\ln z_i(t_2) - \ln z_i(t_1)}{\lambda_i (t_2 - t_1)} \quad (4)$$

The multipliers (m_i) were calculated using equation (4) for all annual measurement pairs of data from each PSP. For estimation of the height growth

rate multiplier for a particular GF rating, an average m_1 was calculated by first averaging over replicate PSP at a given age and site, then over age at that site, and then over sites. The multiplier for height for a seedlot with a specific improvement rating K (M_{1K}) was calculated as

$$M_{1K} = m_{1K} - m_{1J} + 1$$

where K is from seedlots with a rating of GF2, GF14, or GF22 and J is from seedlots with a rating of GF7. Similarly, for basal area and tree stocking, multipliers were obtained for annual measurement pairs of individual PSP by calculating m_2 and m_3 separately, then averaging them to obtain an overall estimate. (Silviculture used in estimation of multipliers from each of the genetic gain trials is listed in Appendix 8.)

Analysis of variance of multiplier estimates for annual measurement pairs of each plot were used to test for significance of differences in the height multiplier (m_i) among sites, ages, and seedlots. Similarly, a second analysis of variance of multiplier estimates was performed, this time for differences in pooled estimates of m_2 and m_3 . Errors from annual measurement pairs from the same plots may be correlated, but no bias was detected in an inspection of mean annual increments and estimates of multipliers for each site.

The potential for using the multiplier estimates with the existing growth models for predicting growth of improved seedlots was examined. The multiplier estimates were inserted into the regional models appropriate for predicting growth on each of the eight trial sites used to calculate the growth rate multipliers. The rates of change in growth rate were assumed to be constant over the life of a stand, silvicultural regimes, sites, and regions. Growth was predicted to the age of the last measurement using starting values of mean top height, basal area, and

stocking from the first measurement of the GF7, GF14 and GF22 seedlots. Growth was predicted using the unmodified model as well as the multiplier estimates for GF14 and GF22 and the predictions of mean top height, basal area and volume were compared.

In order to obtain an estimate of realised gain at rotation age, the average percent gain in mean top height, diameter, basal area and volume was predicted for ages 15-40 using the growth models with the growth model multipliers. The models were run without starting values and using the silvicultural regimes applied to the trial sites. Percent gain was calculated for each age at each site as before, then averaged over sites.

RESULTS

DIFFERENCES IN PERFORMANCE AMONG SEEDLOTS

Genetically improved seedlots were larger at mid-rotation, generally increasing with improvement rating (Table 1). Mean top height of GF14 seedlots ranged from -1 to 10 percent greater than GF7 with a mean over all sites of 4.5 percent, and for the GF22 seedlot ranged from 2 to 13 percent with a mean of 5.3 percent. Percent gain over GF7 in diameter was slightly higher, ranging from 2 to 12 percent for GF14 (with a mean of 5.6 percent) and 5 to 14 percent for GF22 (with a mean of 11.4 percent) (Table 2). Differences among seedlots for basal area per ha were substantially higher, with percent gain for GF14 ranging from 1 to 26 percent (with a mean of 11.9 percent) and for GF22 ranging from 13 to 49 percent (with a mean of 30.4) (Table 3).

Volume per ha differences among seedlots were substantial with percent gain of GF14 compared to a GF7 ranging from -8 to 33 percent (with a mean of 15.0 percent), and of GF22 ranging from 16 to 50 percent (with a mean of 33.6 percent)

(Table 4). Volume differences reflected the GF rating in every case except three. For two of the cases the GF22 at Kaingaroa and the GF14 at Longwood, the seedlots had substantially lower stocking than the other seedlots at the same site (Table 5). The third case, the GF7 at Waimate, was a locally collected seedlot which has not been tested in any other trials and may not perform as well as other climbing select (GF7) seedlots.

DIFFERENCES IN GROWTH RATE

Large-block genetic gain trial data suggests that both the open-pollinated (GF14) and control-pollinated seedlots grew 5% faster in height than climbing select (GF7) (Table 6), although growth rate multipliers of seedlots with differing genetic quality were not significantly different for height. The relative rate of basal area growth increased substantially with genetic improvement with open-pollinated (GF14) changing 13% faster than climbing select (GF7) and control pollinated (GF22) changing 26% faster. Differences in growth rate multipliers for basal area were highly significant among seedlots, but not significantly different among ages or sites (Table 7). The average growth rate multipliers reflected the genetic improvement rating of the seedlots (Figure 1). (Site by year multipliers are presented in Appendices 2-5, and plotted in Appendix 6.)

Estimates of growth rate multipliers for GF14 calculated in 1993 (Carson *et al.* 1994) were virtually identical to estimates calculated in 1995 (Appendix 7), implying that the relative rate of growth was the same from 1993 - 1995 as in previous years. The growth rate multipliers for GF22 calculated in 1995 were lower for height but higher for basal area/stocking than those calculated in 1993. The 1995 estimates are based on much more data and more sound methodology than the 1993 estimates.

Growth rate multipliers for two additional seedlots were calculated, a long-internode seedlot (FR78/2301) rated a GF8 planted at three sites and measured from ages 4-17, and a seedlot from the now defunct open-pollinated seed orchard made up of plus trees selected from Canterbury which is also rated a GF8 and was measured at one site from ages 4-15. For the long-internode seedlot, the height multiplier was estimated at 1.058, which is higher than it's rating would suggest, and the basal area/stocking multiplier was estimated at 0.943, which is lower than it's rating would suggest. For the Canterbury Seed Orchard seedlot, the height and basal area/stocking multipliers (0.979 and 1.087, respectively) were just slightly lower than would be expected for its GF rating.

Predictions of mean top height were not effected when the growth rate multipliers were added to the growth model equations. However, predictions of basal area and volume were improved. All errors in prediction with the multipliers were below 2% while without the multipliers some errors were over 5% (Table 8). (Appendix 9 shows predicted and actual, with and without the multipliers for all sites including Aupouri and Mohaka, which are not included in Table 8.)

The average predicted volume increase at a rotation age of 30 years for the genetic gain trial sites is 13% for open pollinated (GF14) and 22% for the control pollinated seedlot (GF22) (Figure 2). Predictions of average percent gain decrease from age 15 to age 40, even though the differences between seedlots with different genetic qualities constantly increased during that time. The decrease in percent gain with an increase in the absolute gain arises from an increased denominator in the percent gain equation as the trees grow larger.

DISCUSSION

THE MAGNITUDE OF GENETIC GAIN IN NEW ZEALAND *P. RADIATA*

These results clearly show that increased growth resulted from using improved *P. radiata* in New Zealand. Genetic gains reported here are from actual measurements at mid-rotation of ten trials which represent a range of site types and silvicultural regimes in New Zealand. Height growth appeared to increase with plus tree selection (as represented by the GF14 seedlots), but did not increase further with additional improvement. Performance for diameter, basal area and volume largely reflected a seedlot's genetic improvement rating and the successive stages in domestication of radiata pine in New Zealand. The few exceptions appeared to be related to tree stocking differences among seedlots or where seedlot rating was determined not by progeny trial results but by assumption.

The collection of climbing select seed (GF7) did not affect height, but on average improved basal area at mid-rotation by 3%, and volume by 2% over the land race seedlot. This gain is not substantial, but was obtained with very little investment of resources. Open-pollinated orchard seed from an unrouged seed orchard before progeny test information was taken into account (GF14) showed at mid-rotation a 4% increase in height, 17% increase in basal area and 21% increase in volume per ha over the land race seedlot. These increases are substantial and justify plus-tree selection and orchard establishment. Seed from control-pollination of the best performing parent as a female (the GF22 seedlot included in these trials) did not perform better than open-pollinated orchard seedlot for height, but at mid-rotation showed a 29% increase in basal area and a 34% increase in volume over climbing select, which is substantially higher than open-pollinated orchard seed. These increases justify progeny testing and production of commercial seed through control-pollination.

Improvements in performance reported previously from large-block comparisons of *P. radiata* (Cleland 1985, Eldrige 1982, Gleed 1982, and Johnson *et al.* 1992) are

similar to performance of the open-pollinated seedlots (GF14) seedlots reported here. In addition, estimates of percent gain increase given by Vincent (1987 and 1990) appear to be reasonable in view of the data reported here.

Several authors (Franklin 1979, Hamilton and Rehfeldt 1994, Nance and Bey 1979, Rehfeldt *et al.* 1991) have suggested or implied that growth rate increase from genetic selection might decrease or disappear through the rotation, specifically as crown closure occurs and competition becomes important. Data from this study suggest that increased rate of growth will not decline but will continue after crown closure. Even in the pulpwood regime, where crown closure occurred about the time that first measurements began (age 8) and mortality due to competition was occurring well before mid-rotation, multiplier estimates for annual increments did not appear to decrease as the stand aged, or to be very different than those for the direct sawlog regime where crown closure was delayed (but occurred before mid-rotation). There is little reason to believe that rates of growth of the improved seedlots will decrease in the second half of the rotation, although this assumption should be tested.

NATURE OF GENETIC GAIN

Genetic selection of *P. radiata* in New Zealand increased the rate of height growth only very slightly, but effected the rate of change in basal area substantially. Height growth over climbing select (GF7) was on average 5% faster from first generation open-pollinated seed orchard (or their equivalent) (GF14) as well as from control pollination of the best performer as the female parent (GF22). In contrast, basal area changed about 13% faster in stands from open pollinated seed orchard seedlots (GF14) and about 26% faster in stands from control pollination of the best female (GF22). The rates of increase in basal area did not appear to differ over the sites, years and silvicultures tested. Similar increased rates of change in

basal area with genetic improvement were calculated from both fast and slow growing sites, and in both high and slow growth years.

Changes in growth rates with genetic improvement were calculated assuming no change in asymptotes or carrying capacity of the site. Evidence suggests that the asymptote for growth can be increased by genetic selection (Buford 1989, Danjon 1995, Knowe and Foster 1989, Nance and Wells 1981b, Schmidting 1988, Schmidting and Froelich 1993), although one study concluded that the asymptote did not vary among seedlots (Sprinz *et al.* 1989) and another concluded that differences were of little practical importance (Golden *et al.* 1981). The assumption of a common asymptote would not have a large effect on the estimates of relative growth rates from the data reported here, because all data was collected well before an asymptote was reached. In practice, it would be exceedingly difficult to distinguish the effect of the different hypothesis, that is, genetic improvement from an increase in growth rate vs. an increase in carrying capacity.

Many studies (Buford 1989, Knowe and Foster 1989, Nance and Wells 1981b, Schmidting 1988, Schmidting and Froelich 1993, Froelich 1993, Spring *et al.* 1989) have shown different height-age curves for seedlots of different genetic origin, implying that site index will be different for improved and unimproved trees which is supported by data reported here. After examining height-diameter curves, Buford (1986) and Buford and Burkhart (1987) suggested that an increase in site index be used to account for increased growth with genetic improvement. For radiata pine in New Zealand use of a change in site index alone would substantially under-predict volume increase from genetically improved seedlots. The change in the rate of increase of basal area was five times greater than the change in rate of increase in mean top height for the best seedlot tested in this study, making increases in growth much greater than would be predicted from increasing site index alone. Additional growth in basal area over and above the

corresponding increase in height growth must, therefore, be taken into account when predicting volume per hectare of genetically improved *P. radiata* stock in New Zealand.

USE OF GROWTH RATE MULTIPLIERS FOR PREDICTING YIELD

The use of pre-existing growth models to quantify relative differences in growth rates among experimental treatments is another approach to avoiding the problematic assumption of a constant percentage increase in growth which is outlined by South (1995). The method outlined here assumes that growth curves are the same for all genetic treatments and are correctly specified by the New Zealand growth models with differences among the treatments quantified as differences in the rate of change. The growth models in effect are used to “adjust” estimates of relative growth rates of experimental treatments for tree size.

Data from different genetic treatments in progeny trials have been fitted to growth model equations a number of times (including Buford 1986 and 1989, Buford and Burkhart 1987, Danjon 1995, Knowe and Foster 1989, Sprinz 1989). This approach, however, has two major problems for prediction of genetic gain in yield of production forests of improved planting stock. First, the non-contiguous nature of progeny trial design (that is, row plots or single-tree plots) introduces a bias because trees surrounding the genetic treatments are of different genetic quality and tree-to-tree competition has a large effect of final tree size. While competition effects are small on height growth, they are large on diameter growth, and our data suggests at least for radiata pine that increases in diameter and basal area with genetic selection are much greater than increases in height. Second, progeny trials are likely to be limited in representation of a forest’s site and silviculture compared to data typically collected for growth modelling purposes.

Pre-existing growth models have been used previously to remove differences in growing conditions which were confounded with genetic experimental treatments (Nance and Wells 1981a, Wells 1983). For ponderosa pine Rehfeldt *et al.* (1991) and Hamilton and Rehfeldt (1994), used early row-plot data (up to 1/4 and 1/5 rotation, respectively) to estimate the annual change in growth with genetically improved stock. In order to predict genetic gain, they incorporated these estimates into a single-tree growth model which had been developed using data from unimproved trees.

The estimates of increased growth rates with genetic improvement from this study are being used in the New Zealand regional growth models to predict gain of genetically improved seedlots, with straight line extrapolations used to estimate multipliers among the improvement ratings represented in the genetic gain trials. The modified growth models allow forest managers to predict yield of the average stand for all site types and qualities in their forest estate and for a range of silvicultural options, with GF rating specified to predict growth of improved seedlots. The genetic gain multipliers improved the predictive ability of the growth models for the trials used to estimate the multipliers, but further validation with data from different sites is required. Additional genetic gain trials are required to validate model predictions and to test assumptions required for implementation.

Use of the genetic gain multipliers for prediction of growth of genetically improved seedlots growing in situations not represented by the genetic gain trials requires the assumption that growth rate increases resultant from genetic selection are constant over regions and site qualities. While not near enough data is available to adequately test this assumption, existing data does not appear to strongly refute it. The assumption that genetic gain multipliers are constant over different tree stockings is also required. Previous studies comparing genetically

different seedlots of forest tree species planted at different spacings (Campbell and Wilson 1973, Campbell et al. 1986, Nance et al. 1983, Panetsos 1980, Stonecypher and McCullough 1981) yielded conflicting results. All of these studies involved relatively few trees measured at young ages and involved either seedlings planted at extremely close spacing or trees in a Nelder design, both of which are quite atypical for planted forest stands. Inferences extended to mature forest stands planted at typical spacing were, therefore, difficult to make. In our study the assumption that growth rates do not change with tree stocking is supported by the multiplier estimated for the one stand that did have a substantially different stocking and silvicultural treatment (the pulpwood regime) being not substantially different from the other sites.

Use of the genetic gain multipliers for prediction of growth of a wide range of genetically improved seedlots also requires the assumption that seedlots in the trials reported here represent the improvement rating that they have been assigned, and that the GF rating (a combined rating for growth and form) accurately reflects their genetic worth for growth. Only a small number of seedlots are included in the genetic gain trials reported here, so testing of additional seedlots in large-block trials is essential to insure generalisation of results.

Growth models are used to quantify the effects of silviculture, region, and site quality, and embody the best understanding of how these influence final stand volume. The expression of genetic gain as a change in growth rate quantified using mensurational methodology is intuitively appealing. Modification of growth models to reflect genetic improvement as a change in the rate of growth results in predictions of genetic gain which take into account tree size and all the important factors that influence it. An increased rate of growth can be implemented in existing models without the need to re-estimate growth model parameters from a limited amount of genetic gain trial data. Instead, the better

estimated parameters from large amounts of data from unimproved trees are utilised and built upon.

Use of the concept of a multiplier allows prediction for circumstances, that is, regions, site qualities, and silvicultural regimes for which no genetic gain data is available. Per-hectare gains can be estimated for ages, sites, and silvicultural options not represented by the genetic gain data. Predictions of this type, which will be outside the range of data from which a model was built, must always be used with caution, yet these predictions may be more accurate than applying a fixed percent gain to stands which have different site qualities and silvicultural histories. Additional genetic gain trials are required to validate model predictions and to test assumptions required for implementation.

Incorporation of the results of genetic selection into growth models has allowed generalisation of genetic gain data from a small set of sites and silviculture to the full range used in forest operations. These generalisations will be tested and refined as further data are collected through to the end of the rotation, including data from additional large-block trials planted at one site in 1984 and at 28 sites across New Zealand from 1987 to 1991. Seedlots in these trials provide a wide representation of genetically improved seedlots and have blocks planted at or thinned to widely differing tree stockings.

The ultimate success of a tree improvement programme is achieved with the planting of forests which produce more wood of a higher quality as a result of genetic selection. All of New Zealand's *P. radiata* forests are being established with improved seed, with the genetic quality constantly increasing. Genetic quality is quantified for forest managers by the New Zealand Seed Certification Service's improvement rating (GF rating), and the expected increase in standing wood volume for the improvement ratings planted on most of New Zealand's

forest plantations can now be predicted by growth models. These achievements represent a major step in the integration of tree improvement efforts with forest management practices.

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Table 1. Mean top height of four seedlots in large-block genetic gain trials.

Planting year	Site	1995 Mean top height (m)			% gain over GF2			% gain over GF7		% gain over GF14		% gain over GF22	
		GF2 ^a	GF7 ^b	GF14 ^c	GF22 ^d	GF7	GF14	GF22	GF7	GF14	GF22	GF7	GF14
1978	Aupouri ^e	f	22.1	23.3	22.5	-	-	-	-	5	-	2	5
	Kaingaroa	30.7	31.3	32.5	32.1	2	6	5	2	4	5	3	4
	Kaingaroa ^g	31.4	30.9	31.3	32.0	-2	0	2	-2	1	2	4	1
	Mohaka ^e	29.8	29.7	31.9	30.9	0	7	4	0	7	4	4	7
	Golden Downs	24.8	24.1	25.6	27.2	-3	3	10	-3	6	10	13	6
	Waimate	22.1	22.2	23.3	24.3	0	5	10	0	5	10	9	5
1979	Longwood	22.1	23.0	22.8	23.5	4	3	6	4	3	6	2	-1
	Kaingaroa	-	28.5	29.1	-	-	-	-	-	2	-	-	2
1980	Golden Downs	-	24.4	26.9	-	-	-	-	-	10	-	-	10
	Dean	-	20.5	21.8	-	-	-	-	-	6	-	-	6
Average						0	4	6	0	4	6	5	5

^a Unselected collection from land race in Kaingaroa Forest.^b Climbing select seedlots, that is, seedlots resulting seed collection from the best trees in harvested stand.^c First generation open-pollinated seed orchard or equivalent.^d Control cross of the best performer for diameter used as a female parent.^e Sites not used for multiplier estimation.^f No data available.^g Pulpwood regime, all other sites sawlog regime.

TABLE 2. Mean top diameter of four seedlots in large-block genetic gain trials.

Planting year	Site	1995 Mean top diameter (cm)			% gain over GF2			% gain over GF7		
		GF2 ^a	GF7 ^b	GF14 ^c	GF22 ^d	GF7	GF14	GF22	GF14	GF22
1978	Aupouri ^e	—	35.6	37.1	39.6	—	—	—	4	11
	Kaingarua	44.4	44.4	48.6	50.4	0	9	14	9	14
	Kaingarua ^g	40.4	40.1	41.8	42.3	-1	3	5	4	5
	Mohaka ^e	45.8	48.4	54.0	55.2	6	18	21	12	14
	Golden Downs	36.7	37.8	38.8	41.9	3	6	14	3	11
	Waimate	41.8	40.8	44.0	45.8	-2	5	10	10	12
1979	Longwood	43.4	44.3	46.0	50.2	2	6	16	4	13
	Kaingarua	—	42.2	43.8	—	—	—	—	4	—
	Golden Downs	—	39.9	40.8	—	—	—	—	2	—
1980	Dean	—	39.5	41.2	—	—	—	—	4	—
	Average					1	8	13	6	11

^a Unselected collection from land race in Kaingarua Forest.^b Climbing select seedlots, that is, seedlots resulting seed collection from the best trees in harvested stand.^c First generation open-pollinated seed orchard or equivalent.^d Control cross of the best performer for diameter used as a female parent.^e Sites not used for multiplier estimation.^f No data available.^g Pulpwood regime, all other sites sawlog regime.

Table 3. Basal area of four seedlots in large-block genetic gain trials.

Planting year	Site	1995 Basal area (m ² /ha)				% gain over GF2			% gain over GF7	
		GF2 ^a	GF7 ^b	GF14 ^c	GF22 ^d	GF7	GF14	GF22	GF14	GF22
1978	Aupouri ^e	f	21.3	23.6	31.8	-	-	-	11	49
	Kaingaroa	32.9	34.2	41.5	40.7	4	26	24	21	19
	Kaingaroa ^g	45.7	46.3	50.1	52.5	1	10	15	8	13
	Mohaka ^e	39.8	42.2	51.7	61.0	6	30	53	23	46
	Golden Downs	25.7	26.5	29.0	34.2	3	13	33	9	29
1979	Waimate	48.1	45.7	57.5	57.3	5	20	19	26	25
	Longwood	37.3	37.1	38.4	49.1	-1	3	32	4	32
	Kaingaroa	-	33.0	36.6	-	-	-	-	11	-
1980	Golden Downs	-	31.4	31.6	-	-	-	-	1	-
	Dean	-	32.6	34.3	-	-	-	-	5	-
	Average	-	-	-	-	3	17	29	12	30

^a Unselected collection from land race in Kaingaroa Forest.^b Climbing select seedlots, that is, seedlots resulting seed collection from the best trees in harvested stand.^c First generation open-pollinated seed orchard or equivalent.^d Control cross of the best performer for diameter used as a female parent.^e Sites not used for multiplier estimation.^f No data available.^g Pulpwood regime, all other sites sawlog regime.

Table 4. Volume of four seedlots in large-block genetic gain trials.

Planting year	Site	1995 Volume (m ³ /ha)				% gain over GF2			% gain over GF7	
		GF2 ^a	GF7 ^b	GF14 ^c	GF22 ^d	GF7	GF14	GF22	GF14	GF22
1978	Aupouri ^e	<i>f</i>	179	209	268	-	-	-	17	50
	Kaingaroa	339	356	439	423	5	29	25	23	19
	Kaingaroa ^g	483	494	533	575	2	10	19	8	16
	Mohaka ^e	410	424	551	632	3	34	54	30	49
	Golden Downs	214	217	249	308	1	16	44	15	42
	Waimate	370	346	460	473	-6	24	28	33	37
1979	Longwood	319	348	320	424	9	0	33	-8	22
	Kaingaroa	-	319	354	-	-	-	-	11	-
	Golden Downs	-	262	286	-	-	-	-	9	-
1980	Dean	-	234	261	-	-	-	-	12	-
	Average					2	21	34	15	34

^a Unselected collection from land race in Kaingaroa Forest.^b Climbing select seedlots, that is, seedlots resulting seed collection from the best trees in harvested stand.^c First generation open-pollinated seed orchard or equivalent.^d Control cross of the best performer for diameter used as a female parent.^e Sites not used for multiplier estimation.^f No data available.^g Pulpwood regime, all other sites sawlog regime.

Table 5. Stocking of four seedlots in large-block genetic gain trials.

Planting year	Site	1995 Stocking (stems/ha)			
		GF2 ^a	GF7 ^b	GF14 ^c	GF22 ^d
1978	Aupouri ^e	^f	267	267	321
	Kaingaroa	288	283	300	264
	Kaingaroa ^g	622	590	560	615
	Mohaka ^e	311	297	303	316
	Golden	294	290	310	300
	Downs				
	Waimate	502	497	539	454
	Longwood	401	424	328	371
1979	Kaingaroa	–	290	300	–
	Golden	–	307	300	–
	Downs				
1980	Dean	–	313	300	–

^a Unselected collection from land race in Kaingaroa Forest.

^b Climbing select seedlots, that is, seedlots resulting seed collection from the best trees in harvested stand.

^c First generation open-pollinated seed orchard or equivalent.

^d Control cross of the best performer for diameter used as a female parent.

^e Sites not used for multiplier estimation.

^f No data available.

^g Pulpwood regime, all other sites sawlog regime.

Table 6. Relative growth rates of four seedlots in large-block genetic gain trials.

GF	No. trials	Annual increments from age	Height	Basal area/Stocking
2	5	14-17	0.998	0.997
7	–	6-17	1.000	1.000
14	8	6-17	1.051	1.130
22	5	14-17	1.045	1.264

Table 7. Analysis of variance of relative growth rates of four seedlots
in large-block genetic gain trials.

Source	df	Height		Basal area/Stocking	
		MS	F	MS	F
site	8	0.2569	2.82*	0.1384	0.94
rep(site)	37	0.0921	1.11	0.1540	1.94**
year	8	0.1773	2.13*	0.0947	1.19
site x year	41	0.2847	3.42**	0.0648	0.82
rep x year(site)	203	0.1626	1.95	0.0435	0.55
genetic improvement rating	2	0.0392	0.47	1.3740	17.30**
error	412	0.0833		0.0794	

* $P \leq 0.0000$. ** $P \leq 0.01$.

Table 8. Error in predictions with and without growth rate multipliers.

Genetic improvement rating	Stand parameter	Error in prediction ^a (%)	
		without multiplier	with multiplier
GF14	height	0.0	0.0
	basal area	-2.2	0.9
	volume	-2.5	0.4
GF22	height	-1.6	-1.6
	basal area	-5.5	1.4
	volume	-7.7	-0.9

^a Average over eight trials; expressed as a percent of actual stand parameter

Figure 1. Relationship of genetic gain multipliers to GF rating.

Relationship of genetic gain multipliers to GF rating

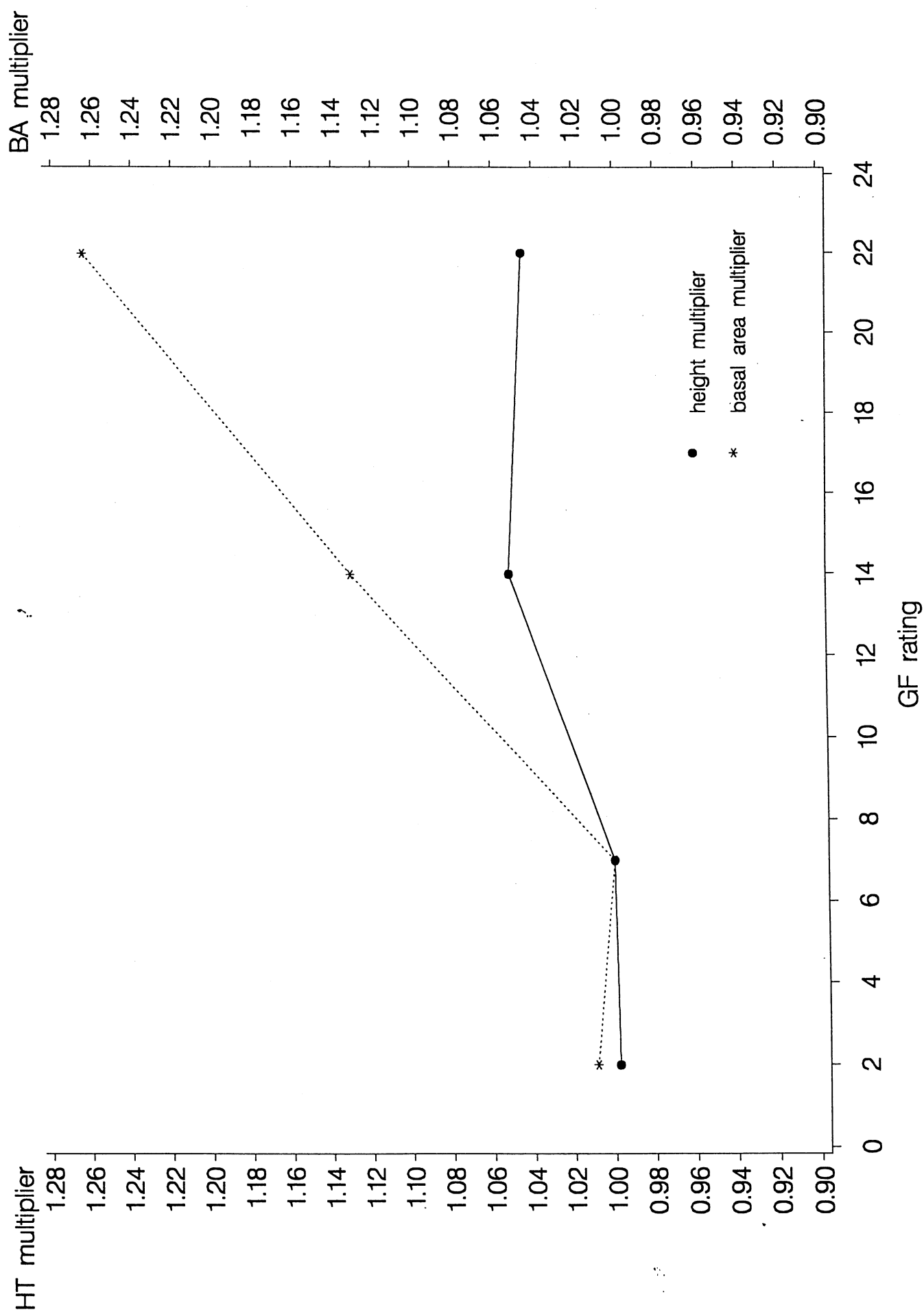


Figure 1

Figure 2. Average predicted percent gain of open-pollinated orchard seed (GF14) and control-pollinated seed (GF22) over climbing select (GF7).

GF14

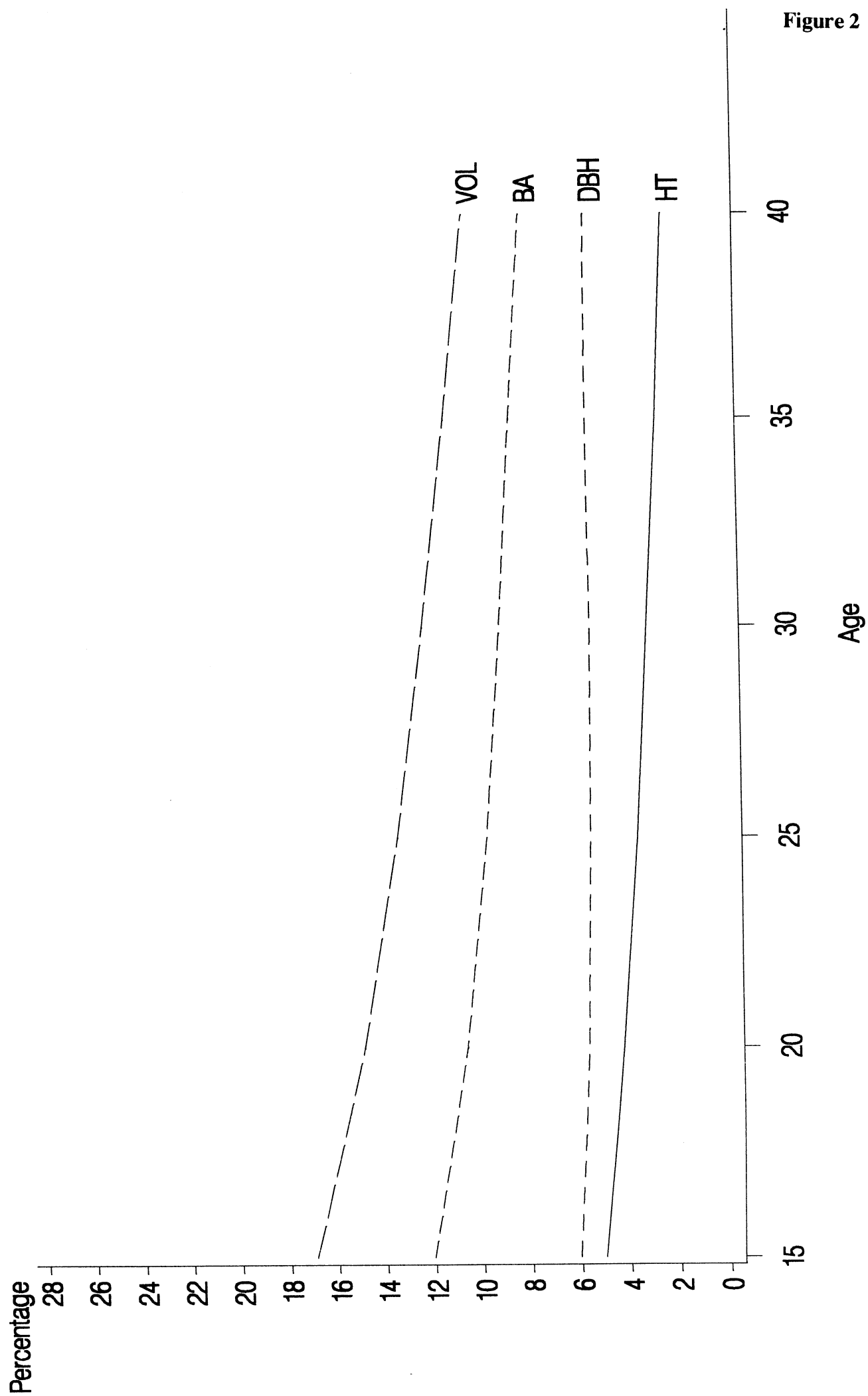
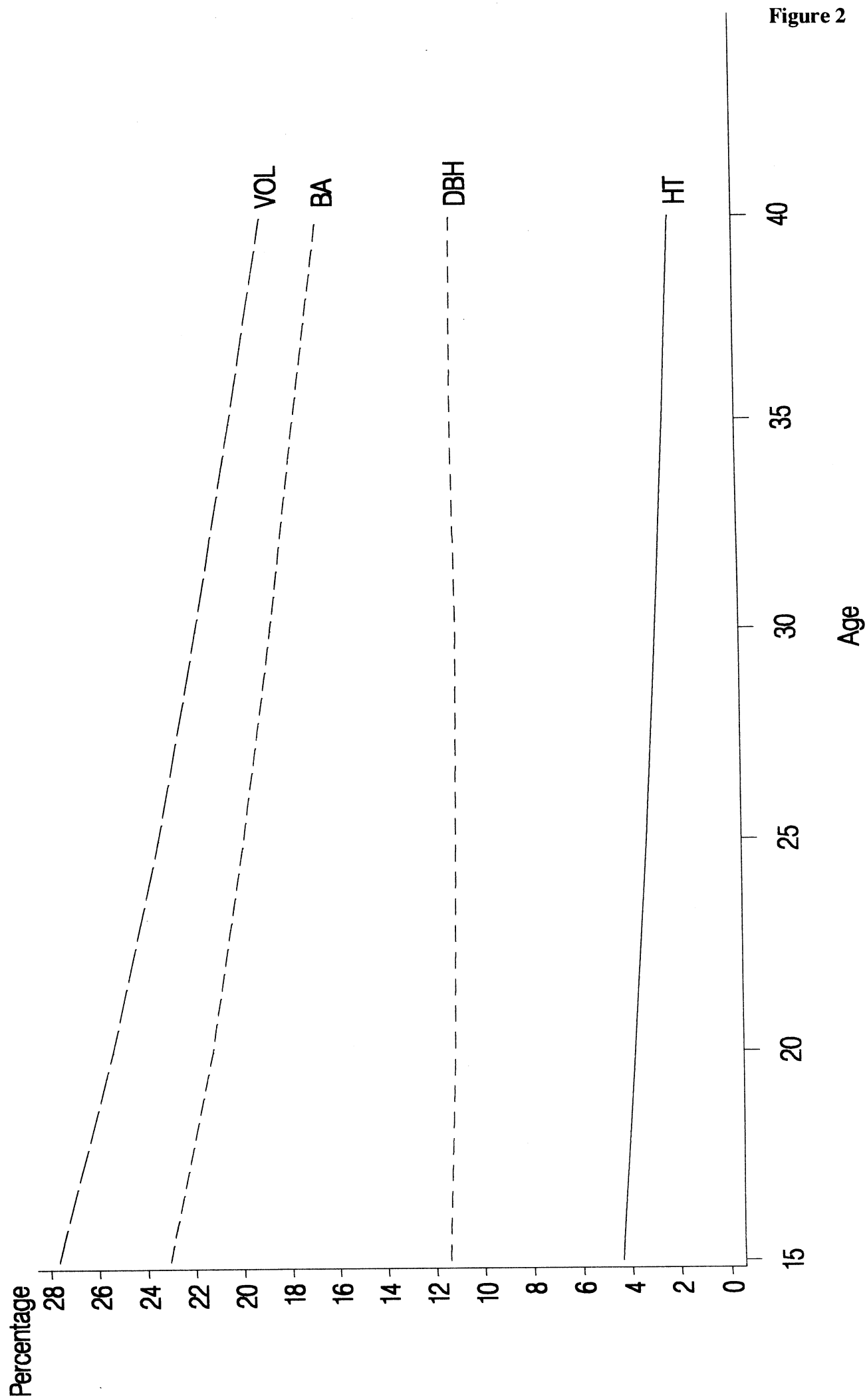


Figure 2

GF22



Appendix 1. Seedlots used to estimate genetic gain growth rate multipliers.

Site	Planting Year	Unimproved seedlot		Improved seedlot				Regional Growth Model
		GF2	climbing select (assumed GF7)	Canterbury Seed Orchard (GF8)	GF14	GF22	LI19 (GF8)	
1978 Genetic Gain Trial:								
RO2103/1	1978	Kaingaroo Bulk	Kaingaroo RO/76/1	–	Gwavas SO WN/76/2/3	850.55x850.96	–	PPM88
RO2103/2	1978	Kaingaroo Bulk	Kaingaroo RO/76/1	–	Gwavas SO WN/76/2/3	850.55x850.96	–	PPM88
NN530/2	1978	Kaingaroo Bulk	Golden Downs NN/C/75/2	–	Gwavas SO WN/76/2/3	850.55x850.96	–	NM90
AK1058	1978	Kaingaroo Bulk	Kaingaroo RO/76/1	–	Gwavas SO WN/76/2/3	850.55x850.96	–	Sands
CY421/1	1978	Kaingaroo Bulk	Balmoral CY/C/75/40	–	Gwavas SO WN/76/2/3	850.55x850.96	–	Canterbury
SD564/1&2	1978	Kaingaroo Bulk	Rankleburn SD/C/75/27	–	Gwavas SO WN/76/2/3	850.55x850.96	–	Southland
1979 Genetic Gain Trial:								
RO2103/3	1979	–	Kaingaroo RO/76/1	–	FRI78/2300 ¹	–	FRI78/2301	PPM88
NN530/1	1979	–	Kaingaroo RO/76/1	–	FRI78/2300 ¹	–	FRI78/2301	NM90
SD682	1980	–	Rankleburn ¹ SD/C/76/2	CY/C/75/51	FRI78/2300 ¹	–	FRI78/2301	Southland

¹ . Seedlot not part of trial. PSP's established in surrounding stand.

Appendix 2. GF2 genetic gain growth rate multipliers for each site and year.

Year	Age	1978 Genetic Gain Trials					Mean
		RO2103/1	RO2103/2	NN530/2	SD564	CY421/1	
<u>Growth Rate Multiplier for MTH (mean top height)</u>							
1993	15	1.072	0.786	1.519	0.709	0.736	0.964
1994	16	0.859	1.273	0.862	0.935	0.448	0.875
1995	17	0.898	1.059	1.305	1.181	1.326	1.154
Mean		0.943	1.039	1.229	0.942	0.837	0.998
<u>Growth Rate Multiplier for BA (basal area)/Stocking</u>							
1993	15	0.970	1.018	0.934	1.137	0.869	0.986
1994	16	0.935	1.035	1.025	1.156	0.944	1.019
1995	17	1.026	0.985	1.020	0.833	1.063	1.021
Mean		0.977	1.013	0.993	1.042	0.959	0.997

Appendix 3. GF14 genetic gain growth rate multipliers for each site and year.

Year	Age	1978 Genetic Gain Trials				1979 Genetic Gain Trials				Mean		
		RO2103/1	RO2103/2	NN530/2	SD564	CY421/1	Age	RO2103/3	NN530/1		Age	SD682
Growth Rate Multiplier for MTH (mean top height)												
1987	9	1.007	0.984	1.184			8	0.912	1.120	7	1.198	1.068
1988	10		1.071				9			8	1.131	1.101
1989	11	1.209	0.942	1.210			10	1.240	1.115	9		1.143
1990	12	0.813	0.948	0.983			11	1.156	1.174	10	1.341	1.069
1991	13	1.220	0.921	1.077			12	0.825	1.165	11	0.884	1.015
1992	14	0.936	1.036	1.101			13	1.031	0.941	12	0.871	0.986
1993	15	1.094	1.054	1.316	0.825	1.188	14	1.115	1.091	13	1.284	1.121
1994	16	1.025	1.160	1.023	1.127	0.296	15	0.669	1.259	14	0.977	0.942
1995	17	1.082	0.940	1.333	1.059	1.555	16	0.861	1.090	15	0.998	1.115
Mean		1.048	1.006	1.153	1.004	1.013		0.976	1.119		1.086	1.051
Growth Rate Multiplier for BA (basal area)/Stocking												
1987	9	1.096	1.131	1.007			8	1.092	1.168	7	0.694	1.031
1988	10		1.120				9			8	1.100	1.110
1989	11	1.174	1.079	1.050			10	1.123	1.114	9		1.108
1990	12	1.141	1.111	1.097			11	0.993	0.994	10	0.940	1.046
1991	13	1.212	1.362	1.151			12	1.150	1.010	11	1.327	1.202
1992	14	1.179	1.197	0.972			13	1.075	1.064	12	1.217	1.117
1993	15	1.174	1.040	1.107	1.238	1.270	14	1.033	1.122	13	1.068	1.132
1994	16	1.176	1.063	1.096	1.212	1.162	15	1.109	0.980	14	1.160	1.120
1995	17	1.193	1.189	1.114	1.122	1.279	16	1.044	1.041	15	1.161	1.143
Mean		1.168	1.144	1.074	1.191	1.237		1.077	1.062		1.083	1.130

Appendix 4. GF22 genetic gain growth rate multipliers for each site and year.

Year	Age	1978 Genetic Gain Trials					Mean
		RO2103/1	RO2103/2	NN530/2	SD564	CY421/1	
<u>Growth Rate Multiplier for MTH (mean top height)</u>							
1993	15	1.048	0.850	1.128	0.982	1.319	1.065
1994	16	0.980	1.171	0.921	1.139	0.344	0.911
1995	17	0.945	1.076	1.673	0.960	1.136	1.158
Mean		0.991	1.032	1.241	1.027	0.933	1.045
<u>Growth Rate Multiplier for BA (basal area)/Stocking</u>							
1993	15	1.303	1.175	1.307	1.368	1.403	1.311
1994	16	1.292	1.227	1.165	1.276	1.161	1.224
1995	17	1.334	1.337	1.402	1.184	1.026	1.257
Mean		1.310	1.246	1.291	1.276	1.197	1.264

Appendix 5. GF8 and long internode genetic gain growth rate multipliers.

GF8 seedlot

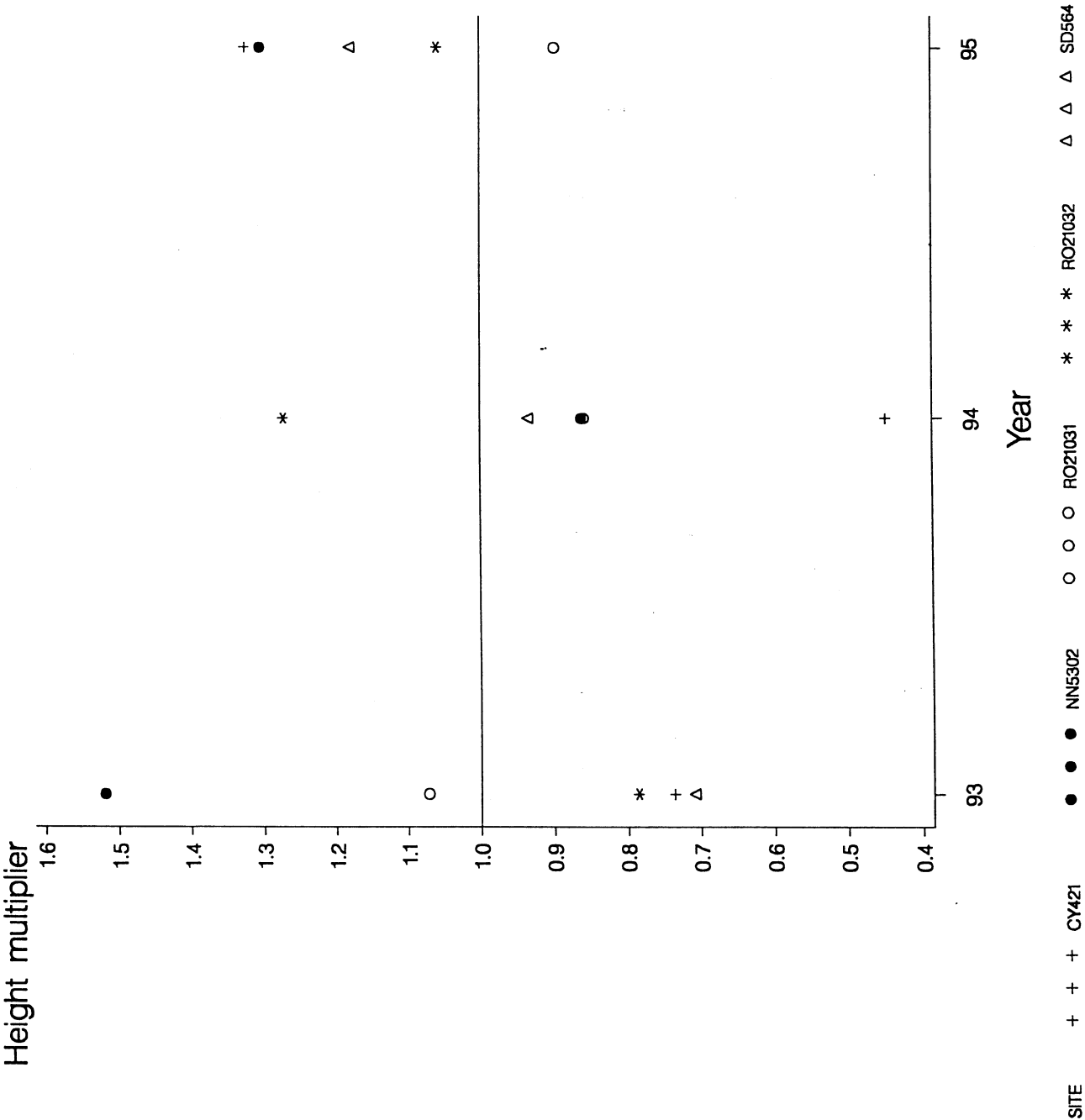
Year	Age	SD682	
		MTH	BA/Stocking
1990	10	0.881	1.160
1991	11	1.200	0.944
1992	12	0.783	1.184
1993	13	1.004	1.086
1994	14	1.025	0.996
1995	15	0.983	1.153
Mean		0.979	1.087

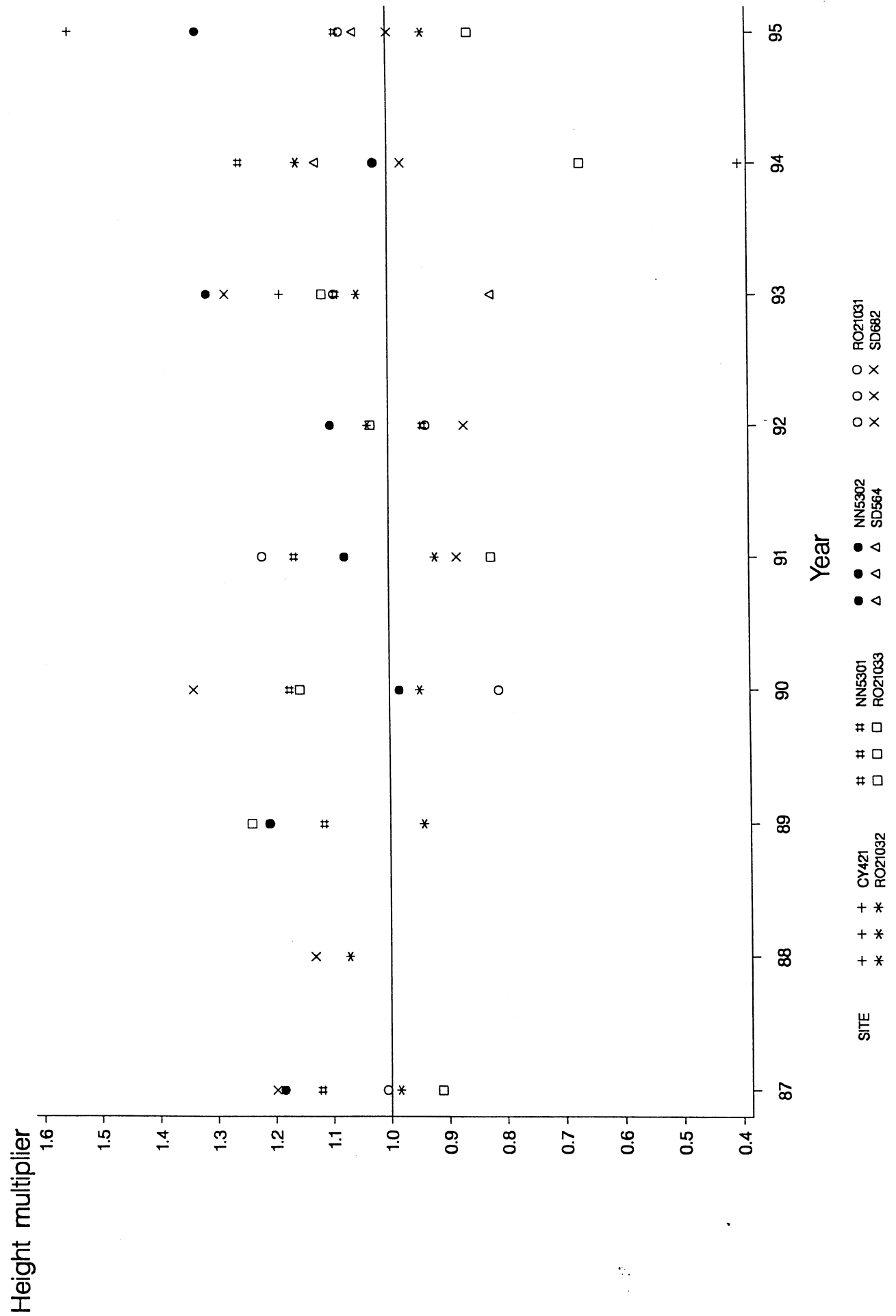
Long Internode seedlot LI19(GF8)

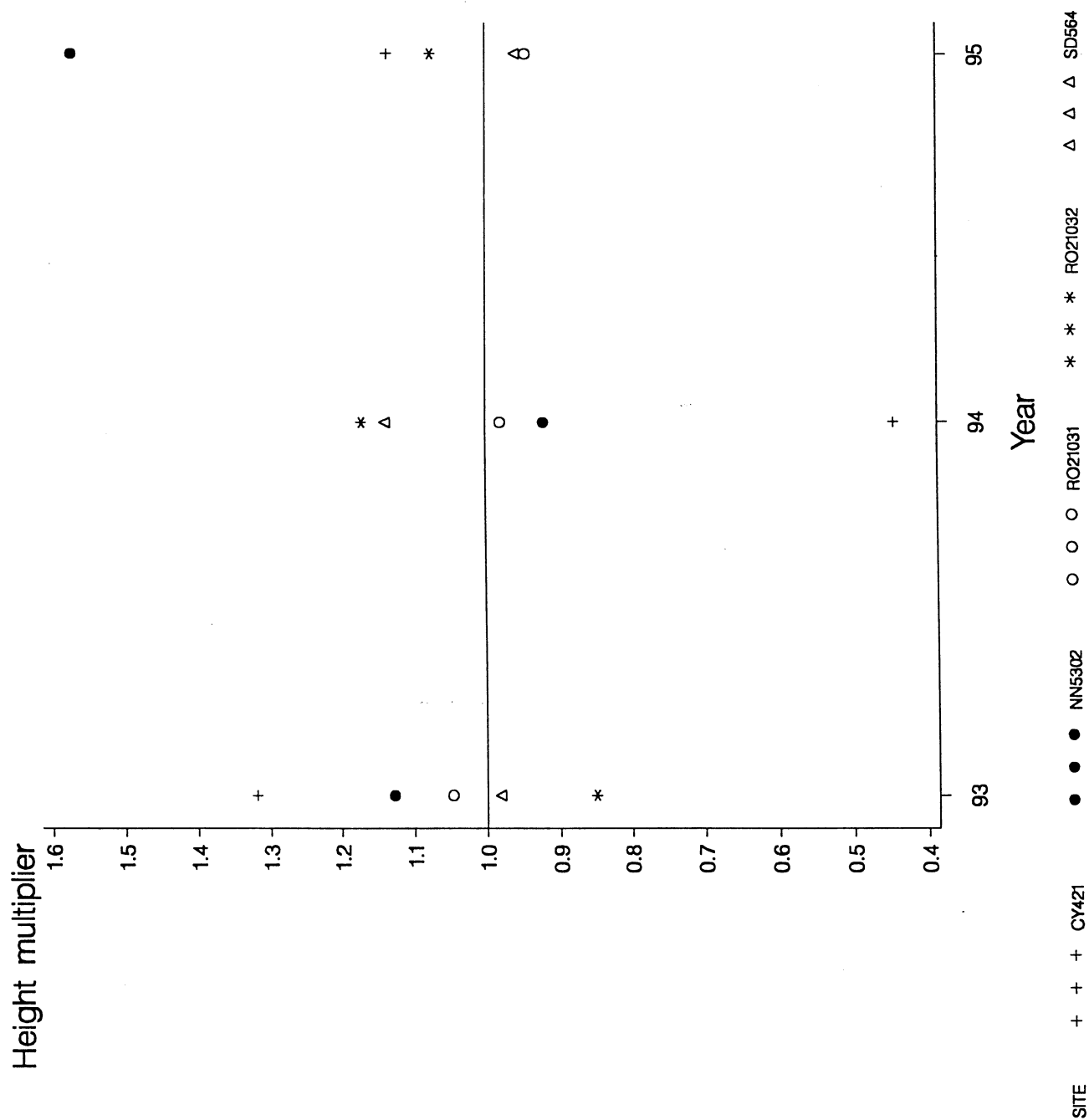
Year	Age	RO2103/3	NN530/1	Age	SD682
<u>Growth Rate Multiplier for MTH</u>					
1987	8	1.053	1.107	7	1.176
1989	10	1.261	1.143	8	1.110
1990	11	1.077	1.059	10	0.921
1991	12	0.872	1.101	11	1.081
1992	13	0.978	1.029	12	1.006
1993	14	1.040	1.167	13	1.029
1994	15	1.030	1.042	14	1.136
1995	16	0.922	0.981	15	1.076
Mean		1.029	1.079		1.067
<u>Growth Rate Multiplier for BA/Stocking</u>					
1987	8	0.782	0.973	7	0.771
1989	10	0.831	0.964	8	0.845
1990	11	0.871	0.898	10	1.010
1991	12	0.939	0.932	11	0.943
1992	13	0.943	1.017	12	1.087
1993	14	0.873	1.018	13	1.056
1994	15	0.846	0.919	14	1.073
1995	16	0.906	0.985	15	1.153
Mean		0.874	0.963		0.992
					1.058
					0.943

Appendix 6. Estimates of multipliers by site and year.

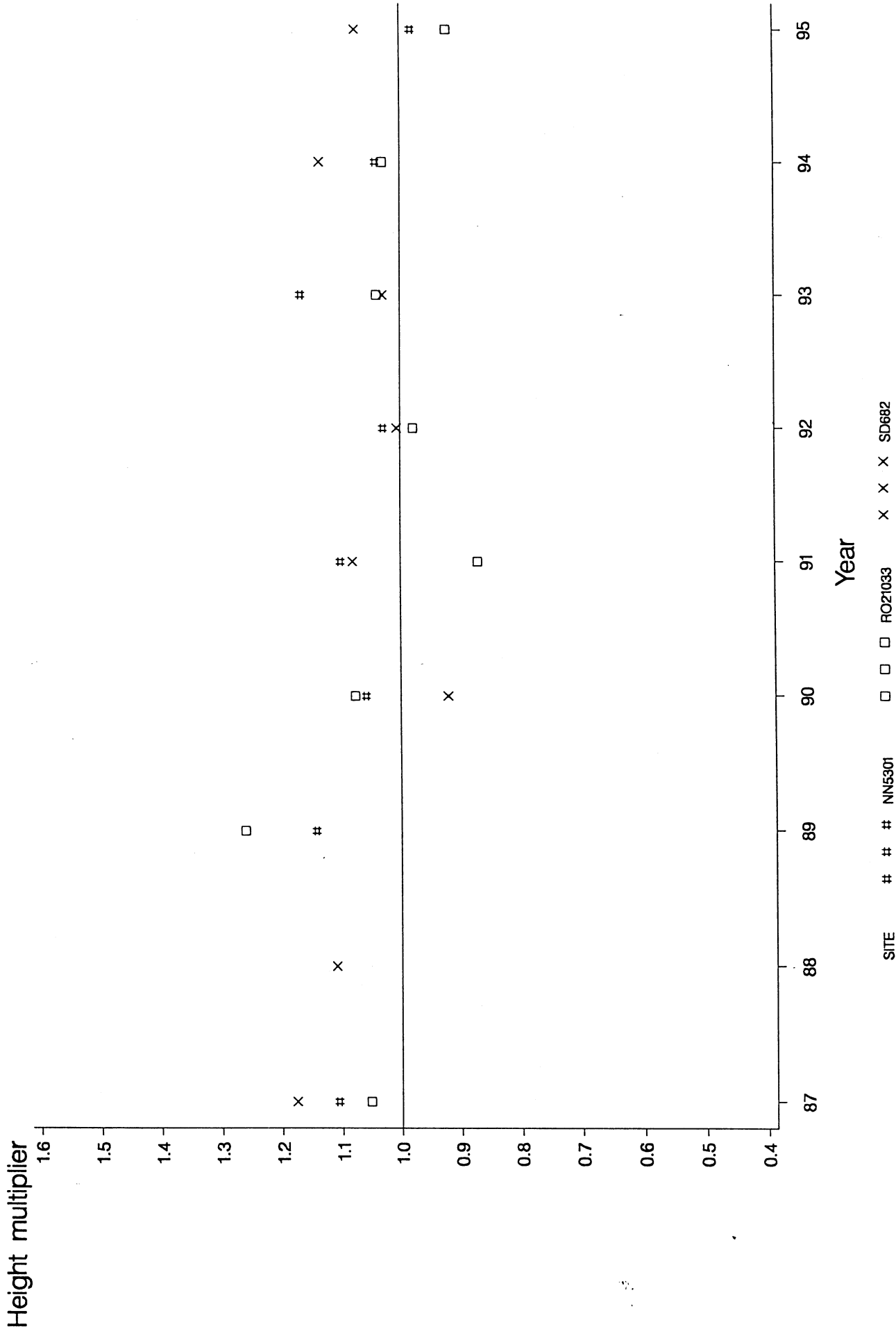
GF2 Genetic Gain Multipliers
Height growth by Site and Year



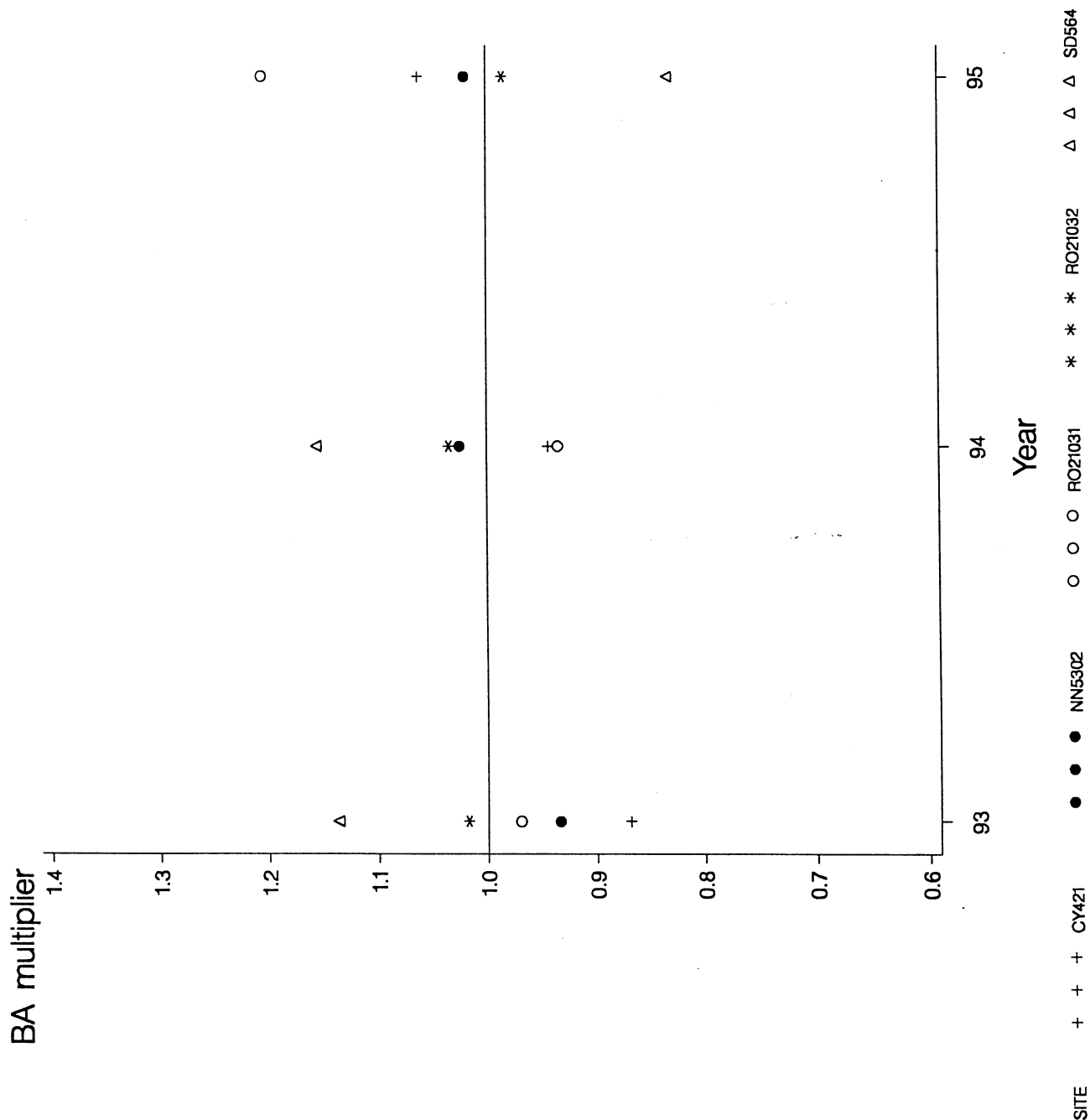




L119(GF8) Genetic Gain Multipliers
Height growth by Site and Year

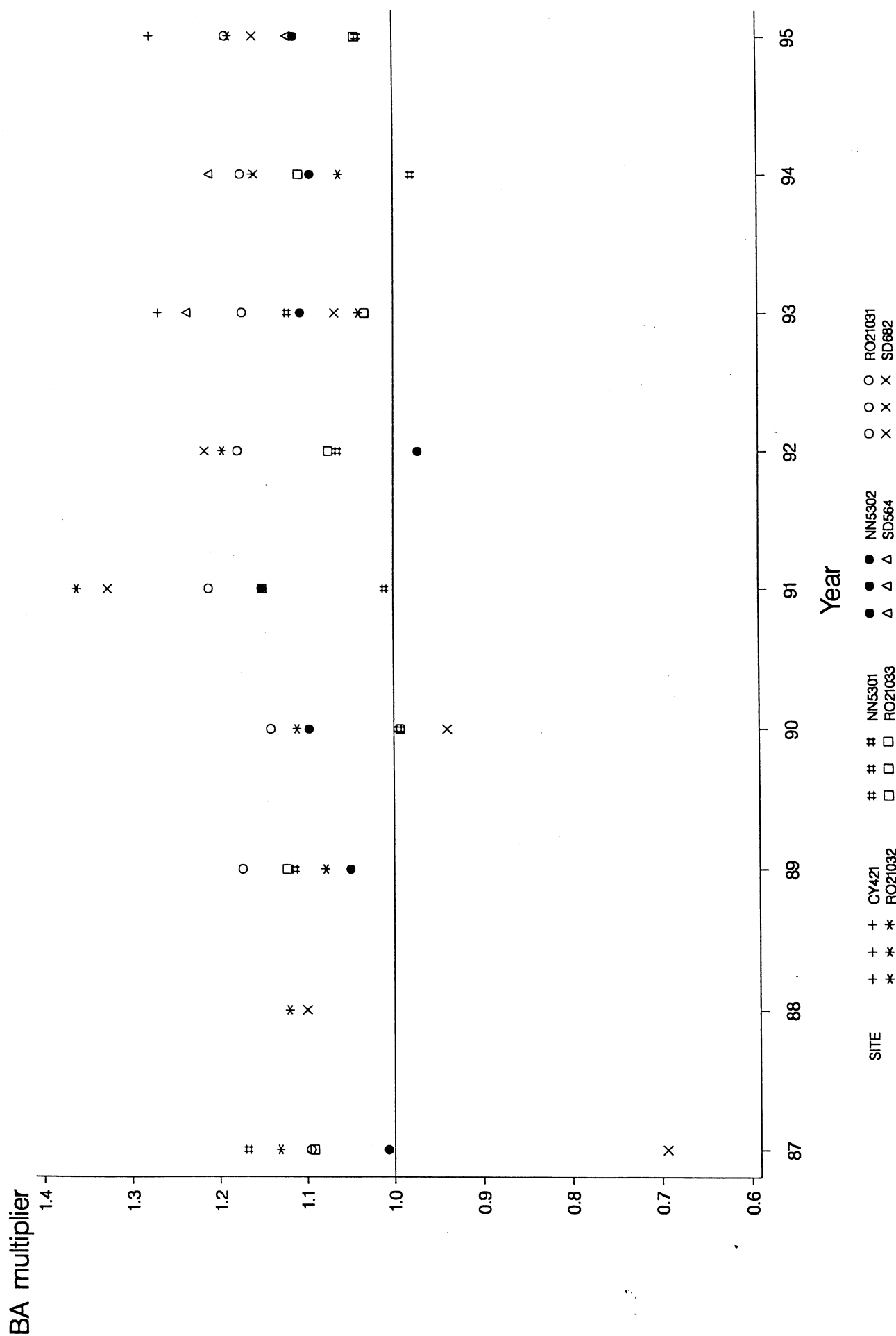


GF2 Genetic Gain Multipliers Basal Area growth by Site and Year

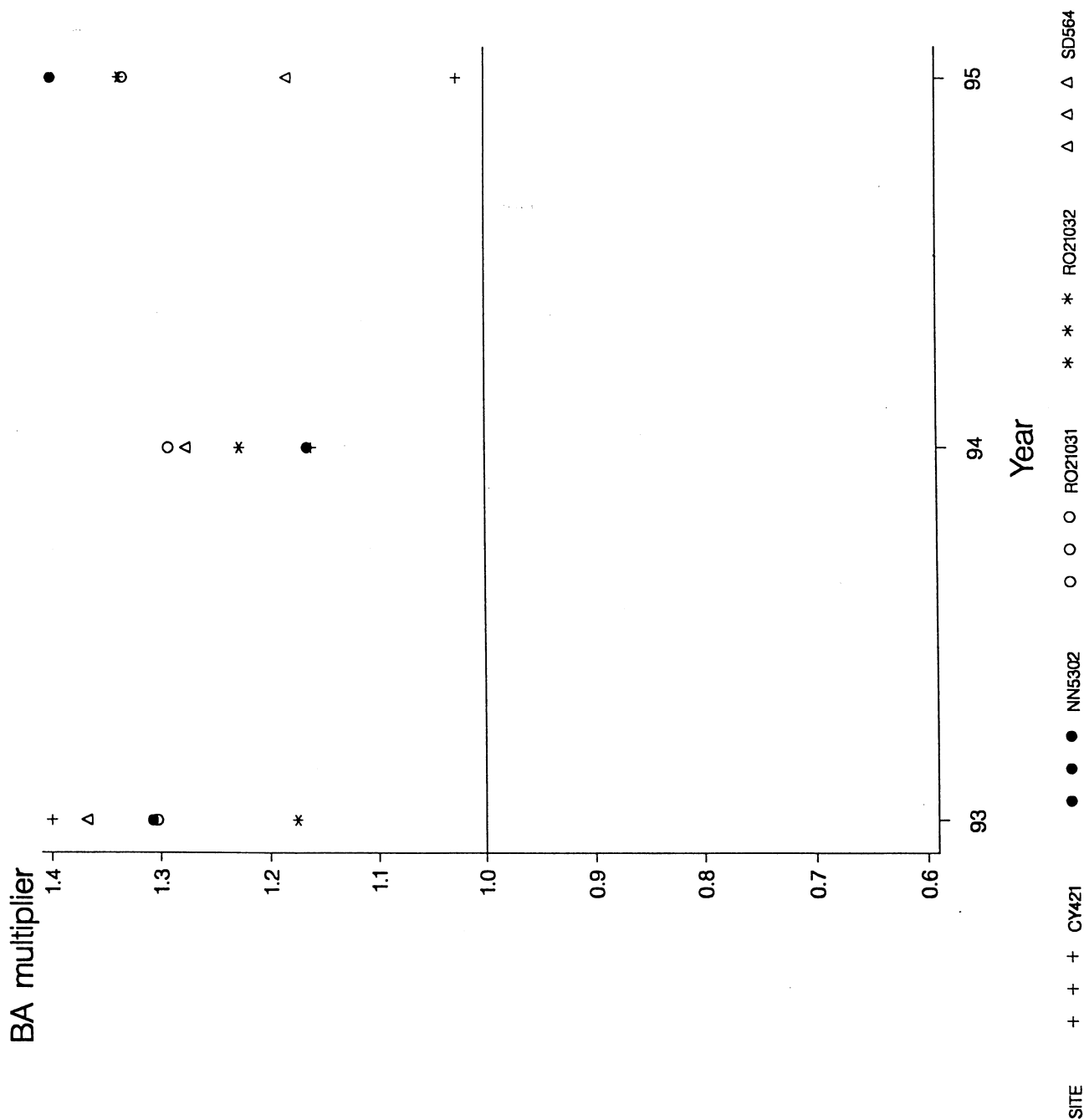


GF14 Genetic Gain Multipliers

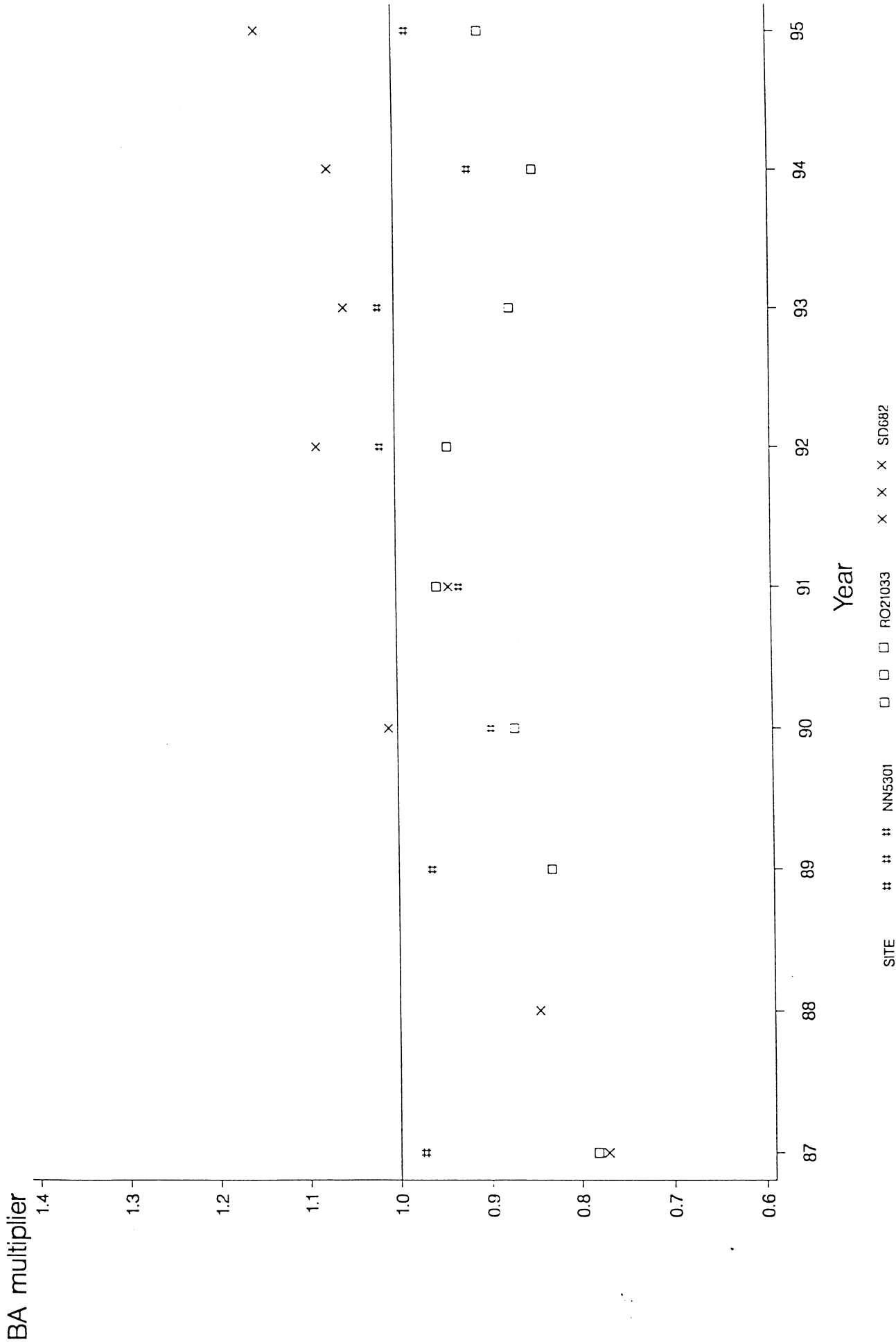
Basal Area growth by Site and Year



GF22 Genetic Gain Multipliers Basal Area growth by Site and Year



LI19(GF8) Genetic Gain Multipliers
Basal Area growth by Site and Year



Appendix 7. Genetic gain multipliers estimated in 1993 and 1995.

Seedlot		Growth Rate Multiplier			
		MTH		BA/Stocking	
		1995	1993	1995	1993
GF2	Kaingaroa Bulk	0.998	0.960	0.997	0.890
GF7	Kaingaroa Bulk	1.000		1.000	
GF14	Gwavas Seed Orchard	1.051	1.048	1.130	1.134
GF22	55x96 cross	1.045	1.078	1.264	1.220
GF8	Canterbury Seed Orchard	0.979		1.087	
LI19(GF8)	Long Internode Breed	1.058	1.069	0.943	0.892

Appendix 8. Site indices and silvicultural regimes for genetic gain trials.

Trial	Age at Last Meas	No. Plots	Site Index	Seedlots GF	Regime Used
RO2103/1	17	24	34.2	2,7,14,22	Initial stocking 1111 s/ha Prune to 2.2m at age 5 Thin to 600 s/ha at age 5.5 Prune to 4.2m at age 6 Prune to 6m at age 10 Thin to 300 s/ha at age 10
RO2103/2	17	24	34.1	2,7,14,22	Initial stocking 711 s/ha Prune to 2.2m at age 5
RO2103/3	16	12	33.4	7,14,LI	Initial stocking 1111 s/ha Prune to 2.2m at age 4.9 Thin to 600 s/ha at age 5.8 Prune to 4.2m at age 6.6 Thin to 300 s/ha at age 8.9
CY421/1	17	12	25.9	2,7,14,22	Initial stocking 1111 s/ha Thin to 600 s/ha at age 6 Prune to 2m at age 5 Thin to 400 s/ha at age 8 Prune to 4m at age 8
NN530/1	16	19	29.4	7,14,LI	Initial stocking 1111 s/ha Thin to 600 s/ha at age 6 Thin to 300 s/ha at age 9
NN530/2	17	18	29.0	2,7,14,22	Initial stocking 884 s/ha Thin to 600 s/ha at age 8 Thin to 300 s/ha at age 10
SD564/1	17	12	27.0	2,7,14,22	Initial stocking 1111 s/ha Thin to 555 s/ha at age 8 Prune to 2m at age 6 Prune to 4m at age 8 Thin to 300 s/ha at age 10
SD564/2	17	11	27.9	2,7,14,22	Initial stocking 692 s/ha Prune to 2m at age 6 Prune to 4m at age 8
SD682	15	19	28.7	7,8,14,LI	Initial stocking 600 s/ha Thin to 300 s/ha at age 8

Appendix 9. Predictions with and without genetic gain multipliers.*

Plantin g year	Site	Increment (years from planting)	Height				Basal area				Volume			
			Predicted		Residual/actual x 100%		Predicted		Residual/actual x 100%		Predicted		Residual/actual x 100%	
			without		with		without		with		without		with	
			mult.	mult.	mult.	mult.	mult.	mult.	mult.	mult.	mult.	mult.	mult.	mult.
1978	Kaingaroa (sawlog) (RO 2103/1)	14-17 2 8-17 7 8-17 14 14-17 22	29.7 30.3 31.5 31.4	29.7 30.3 31.5 31.4	-3.3 -3.2 -3.1 -1.9	-3.3 -3.2 -3.1 -1.9	35.9 36.4 38.8 36.8	35.9 36.4 38.8 36.8	9.1 6.4 -6.5 -9.6	9.1 6.4 -6.5 -9.6	350 363 401 378	350 363 401 378	3.3 2.1 -8.7 -10.6	3.3 2.1 -8.7 -10.6
1978	Kaingaroa (pulpwood) (RO 2103/2)	14-17 2 8-17 7 8-17 14 14-17 22	30.9 30.5 30.3 31.7	30.9 30.5 30.3 31.7	-1.6 -1.3 -3.2 -0.9	-1.6 -1.3 -3.2 -0.9	55.1 53.7 53.3 56.6	55.1 53.7 53.3 56.6	20.6 16.0 6.4 7.8	20.6 16.0 6.4 7.8	560 539 532 589	560 539 532 589	15.9 9.1 -0.2 2.4	15.9 9.1 -0.2 2.4
1979	Kaingaroa (RO 2103/3)	7-16 7 7-16 14	27.8 29.3	27.8 29.3	-2.5 0.7	-2.5 0.7	34.3 36.6	34.3 36.6	3.9 0.0	3.9 0.0	314 353	314 353	-1.3 -0.3	-1.3 -0.3
1978	Waimate (CY 421)	14-17 2 14-17 7 14-17 14 14-17 22	22.0 21.7 22.8 24.0	22.0 21.7 22.8 24.0	-0.5 -2.3 -2.1 -1.2	-0.5 -2.3 -2.1 -1.2	46.7 43.7 53.0 54.9	46.7 43.7 53.0 54.9	-2.9 -4.4 -7.8 -7.3	-2.9 -4.4 -7.8 -7.3	348 323 407 441	348 323 407 441	-5.9 -6.6 -11.5 -9.7	-5.9 -6.6 -11.5 -9.7
1978	Longwood (SD 564)	14-17 2 14-17 7 14-17 14 14-17 22	22.6 23.4 23.3 23.8	22.6 23.4 23.3 23.8	1.8 1.7 4.0 1.3	1.8 1.7 4.0 1.3	42.0 43.9 39.9 48.7	42.0 43.9 39.9 48.7	-1.2 -0.5 -1.7 -8.1	-1.2 -0.5 -1.7 -8.1	334 358 329 404	334 358 329 404	4.7 2.9 3.5 -6.5	4.7 2.9 3.5 -6.5
1978	Golden Downs (NN 530/2)	14-17 2 8-17 7 8-17 14 14-17 22	23.0 25.6 25.6 25.8	23.0 25.6 25.6 25.8	-7.3 6.2 0.0 -5.1	-7.3 6.2 0.0 -5.1	24.9 26.5 26.4 30.6	24.9 26.5 26.4 30.6	-3.1 0.0 -9.0 -10.5	-3.1 0.0 -9.0 -10.5	196 228 239 265	196 228 239 265	-8.4 5.1 -9.2 -14.0	-8.4 5.1 -9.2 -14.0
1980	Dean (SD 682)	7-15 7 7-15 14	22.1 23.7	22.1 23.7	7.8 8.7	7.8 8.7	38.4 38.1	38.4 38.1	17.8 11.1	17.8 11.1	300 316	300 316	28.2 21.1	28.2 21.1
1979	Golden Downs (NN 530/1)	7-16 7 7-16 14	23.4 25.6	23.4 25.6	-4.1 -4.8	-4.1 -4.8	25.5 28.4	25.5 28.4	-18.8 -10.1	-18.8 -10.1	203 244	203 244	-22.5 -14.7	-22.5 -14.7
1978	Mohaka (WN 377)	14-16 2 8-16 7 8-16 14 14-16 22	27.9 29.1 30.6 29.5	27.9 29.1 30.6 29.5	2.6 5.1 3.4 1.4	2.6 5.1 3.4 1.4	37.6 45.7 48.0 52.1	37.6 45.7 48.0 52.1	3.0 18.1 0.2 -7.3	3.0 18.1 0.2 -7.3	350 442 486 510	350 442 486 510	2.0 22.4 2.5 -7.1	2.0 22.4 2.5 -7.1
1978	Aupori (AK 1058)	8-16 7 8-16 14 14-16 22	23.2 25.7 23	23.2 25.7 23	8.9 15.8 4.5	8.9 15.8 4.5	22.8 24.4 28.6	22.8 24.4 28.6	16.3 13.0 -2.4	16.3 13.0 -2.4	199 234 248	199 234 248	25.2 27.2 2.5	25.2 27.2 2.5

*Predictions are from GROPAK using actual starting values for tree size & stocking for specific seedlots