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TRIALS DESIGNED TO QUANTIFY GROWTH & YIELD GAINS FROM GENETICALLY IMPROVED RADIATA PINE

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FRI/INDUSTRY RESEARCH COOPERATIVES

EXECUTIVE SUMMARY

This report outlines the history of genetic gain trials in New Zealand, lists the reasons for them, suggests appropriate experimental designs, and documents in detail the trials supported by the Stand Growth Modelling Cooperative.

Recommendations include:

- a multi-disciplinary approach to quantifying genetic gain;
- separate seed certification scales for genetic improvement in growth and improvement in other traits (including form),
- use of seedlot controls of widely different genetic quality along with commercially important seedlots in genetic gain trials
- constant review of the utility of the various experimental designs used for genetic gain trials in New Zealand, and
- support of a long-term research project toward making preliminary growth predictions from single-tree plot progeny trials at the time of plus-tree selection, which would be many years before information from genetic gain trials becomes available.

Appendicies now contained in Report No. 24A, March 1994

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TRIALS DESIGNED TO QUANTIFY GROWTH AND YIELD GAINS FROM GENETICALLY-IMPROVED RADIATA PINE

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INTRODUCTION

Tree improvement is carried out to increase the profitability of growing plantation forests. "Genetic gains" or desired changes in various traits should result from tree improvement effort. These genetic gains bring about predictable changes in the growth and yields of the species concerned, and can have important effects on the forest growing cycle (including effects on cash flows, "allowable cuts", etc.). Unfortunately, most forest planning information and most predictive models are based on data from forest stands that are genetically unimproved, leading to likely underpredictions of volume and value returns from stands planted with improved tree stocks. The Stand Growth Modelling Cooperative requires hard information on the performance of improved seedlots (preferably before they are widely planted) over the full range of sites and management regimes in order to predict growth and yield of improved stands, while tree breeders seek to validate their gain predictions in order to maintain support for tree improvement programmes.

Trials designed to provide information on changes in various traits resulting from tree improvement can be grouped into the broad category identified as genetic gain (GG) trials. Tree breeders and mensurationists are both interested in genetic gain trials but they have somewhat different objectives. Tree breeders have been traditionally interested in trials that yield statistically different rankings of candidate seedlots, while mensurationists wish to accurately measure and predict the magnitude of differences. The difference in approach of the two disciplines to evaluating genetic gain typically results in different choices of experimental design and data collection methods. Tree breeders have traditionally relied on quick and inexpensive assessment methods along with extensive replication on a few sites to obtain the information necessary for selection and breeding, while mensurationists typically use a sampling approach and very accurately measure a few trees at numerous sites. **There is an important challenge to coordinate the efforts of tree breeders and forest mensurationists in order to ensure that information required to meet their genetic gain objectives is obtained in an efficient and productive manner.**

The first objective of this report is to outline the various reasons both the breeders and mensurationists have for establishing genetic gain trials and to suggest experimental designs most appropriate for achieving these goals. The second objective of this report is to document the current status of the substantial series of trials which the Stand Growth Modelling Cooperative is supporting for the purpose of modelling the growth of genetically improved breeds of radiata pine.

DESIGN AND USE OF GENETIC GAIN TRIALS

QUANTIFYING GENETIC GAIN FOR RADIATA PINE IN NEW ZEALAND

Genetic gains in tree improvement are progressive and continuous, that is, small increments of gain become available in improved planting stock through time. Gains come from new information on the performance of selected trees, development of plant or seed propagation methods which allow the use of higher selection intensities, and, of course, from the concentration of good genes that results from the process of turning over breeding generations. This continuous improvement in the genetic quality of planting stock available for afforestation is reflected in the continuous scale of Improvement Ratings (GF - Growth and Form rankings) assigned by the New Zealand Seed Certification Service (Vincent, 1987).

The New Zealand Seed Certification Service certifies the genetic worth of radiata pine seedlots based on the performance of the seedlot parents in progeny tests and genetic gain trials. Improvement ratings are given to a seedlot for one of several "breeds". Each breed represents the use of a different set of selection criteria in obtaining a particular breeding goal. The main breed is the Growth and Form Breed (GF), in which improved growth and form (particularly straightness) is the goal, and growth is weighted twice as much as form. Another breed, the Long-Internode Breed (LI), has the occurrence of very long internodes between branches as the breeding goal. A rating for the LI breed includes a long-internode rating as well as the GF rating the seedlot would have obtained as part of the GF breed.

Improvement ratings (GF levels) were developed to rank seedlots for their genetic quality, that is, to indicate their relative genetic worth. They are not intended to quantify the absolute differences among seedlots. For example, shift from GF13 to GF14 need not necessarily imply the same increase in volume and/or form gain as a shift from GF25 to GF 26. However, a seedlot rated GF14 can be expected to be slightly better in genetic quality than one rated GF13, and so forth. The GF ratings of unimproved seedlots have been arbitrarily set at GF1–GF3 for bulk collections and GF7 for climbing select, since these seedlots have not usually been compared in replicated progeny trials (Vincent, 1987). GF ratings can be used as a rough guide to the improvement for growth rate of seedlots from the New Zealand radiata pine tree improvement programme.

OBJECTIVES OF GENETIC GAIN TRIALS

Genetic Gain trials can fulfil four major objectives:

1. To provide tree breeders with data for evaluating breeding and plant production strategies.

2. To provide demonstrations of the benefits of investing in tree breeding to research managers and representatives of industry and other funding agencies.

3. To assist forest managers in choosing the most appropriate breed for their sites and end uses and in designing optimal silvicultural regimes for improved tree stocks.

4. To provide forest planners with accurate growth and yield data for use in yield prediction and forest estate planning.

The choice of both the appropriate experimental design and number of trials to establish will depend on the priority given to these objectives. Objectives 1 and 2 have traditionally been those of the tree breeder, while objectives 3 and 4 have become much more important to forest managers and planners as genetically improved planting stock has become available in large quantitites. Efforts to obtain data specially for the latter objectives should be made by a team of people which includes both tree breeders and forest mensurationists.

DESIGN OF GENETIC GAIN TRIALS

Genetic gain trials by definition compare planting stock representing different levels of genetic worth. Ideally, the amount of genetic variability within genetic groups would be similar, but this is not always possible. The design of all genetic gain trials should include:

- Seedlots that are representative of the full range of potential commercial breeds and the various levels of improvement within breeds. This may require creating synthetic seedlots from experimental quantities of control-crossed seed.

- The genetically best seedlot that can be constructed (even if this is the open-pollinated progeny of only a single parent or control-pollinated progeny of a two-parent cross) in order to reveal the potential for future improvement. This seedlot is likely to be of higher quality than the best commercially available, will be available only in small quantities, and will usually represent selection using the most recently available information.

- Suitable standard seedlots to subsequently provide "benchmarks" for realised gains. At least one of these should represent a generally-available unimproved seed source, while others should represent the genetic base from which a given plus-tree selection series was derived, for example, an open-pollinated seedlot collected from the original select parents. Standard seedlots should be reproducable so that they can be used for many years of experiments.

- Plant types that are highly likely to be used in future forest planting (e.g. tissue culture plants, cuttings).

Gain Estimation in Support of Tree Breeding Programmes

Tree breeders need to know both the ranking of alternative commercial seedlots and something about the absolute levels of gains they produce in order to confirm their tree improvement strategies. For this purpose design of GG trials should include:

- Sufficient trial coverage of forest regions and/or seed zones to allow regions to be well-delineated for subsequent use of commercial seed-lots (i.e., analogous to the use of provenance trials to delineate seed zones for unimproved seedlots of native forest species).

- Both row-plot and large-plot designs. Row-plots allow cost-efficient and precise discrimination among seedlots, but are less valuable for determining per hectare volume gains owing to row-to-row competition effects. Row plots may be suitable for quantification of seedlot differences in traits not affected by competition, for example, straightness and wood density. Large-plots provide long-term performance data under valid forest stand conditions (and particularly, a neutral tree-to-tree competition environment among trees of similar genetic quality), but are less precise for comparisons among seedlots, and more expensive to establish and measure.

- Sufficient replication to ensure that statistically-significant differences can be shown. It may not be necessary or desirable that statistically-significant differences be shown on each site in large-plot designs. Large plot trials are probably better designed so that data can be combined over sites.

- Assessment of relevant growth, form, disease resistance, and log and wood quality traits to provide an indication of end-of-rotation gains for various end-products.

- Site selection, establishment, and management methods that mirror "normal (good) management practice".

Demonstration of Genetic Gains

Genetic gain trials have proved to be very useful in convincing forest managers and funding agencies of the value of tree breeding. For demonstration purposes, experimental design of genetic gain trials additionally should include:

- Replication of trials over time to ensure that good visual comparisons are always available (i.e. some phases of stand development do not yield good observable differences, even though real differences may be present).

- Use of row-plots to allow visual comparisons to be more easily made – best situated on flat land, close to the access road.

Forest Management Information

Forest managers will have the opportunity to choose the breed which is the most appropriate for their sites and end uses and to treat their stands of improved trees with the optimum silviculture. Provision of information to aid forest managers in making these decisions should consider:

- Inclusion of a range of different sites and silvicultural treatments in large plot trials in order to determine whether genetic gains vary with site and silviculture, and to indicate optimal seedlot/silvicultural/site treatment combinations.

- Representation of an extreme range of forest site and silvicultural treatments - both to allow for future swings in management practice, and to provide data for response-surface information involving several "independent" variables (e.g. site quality, stocking density, genetic quality, etc.) which can be very useful in obtaining the maximum amount of information with limited resources.

- Comparisons of varying initial stocking levels in planted trials in order to demonstrate that improved seedlots can yield savings in establishment costs as well as end-of-rotation gains.

Forest Planning Information

Forest planners require accurate predictions of growth and yield of forests. Forest mensurationists seek to build models for growth and yield predictions. Trials designed for this objective will probably involve:

- Periodic assessments (annual until silvicultural treatments are completed) of standard growth, yield and mortality traits in order to provide data for growth modelling use (although mortality may be best estimated in purpose-planted, stand-size blocks rather than only in GG trials).

- Assessment of log and wood quality traits in units useful for yield inventory and for use in developing predictive models (e.g. stem straightness in mm/m of log sweep, and/or wood density in kg/m^3 of wood product).

- Stratifying trials so that they represent the entire managed estate in order to provide data for forest estate level planning.

- Extending trial coverage to pre-empt future change (e.g. climate change, or movement of plantations onto non-traditional sites).

EVOLUTION OF EXPERIMENTAL DESIGN IN NEW ZEALAND

The choice of experimental design for any series of Genetic Gain trials will depend on the mix of objectives chosen (from those above), and their priority. In New Zealand, there has been a clear evolution of objectives, with demonstration of gains as an early priority, and the provision of data for growth models receiving more recent recognition. The Stand Growth Modelling Cooperative focuses on objectives three and four, that is, obtaining forest management and forest planning information.

The large plot designs used for planted GG trials (that is, for the purpose of comparing seedlots of varying genetic quality) in New Zealand are described in Table 1. The first trial was an initial stocking trial which incorporated stock of the highest genetic quality of the day as well as an unimproved control. Large plot genetic gain trials were first planted by tree breeders in 1978. These trials have had permanent sample plots installed in a subset of seedlots and replications and are proving to be vital for prediction of growth and yield.

All of the designs listed in Table 1 are expected to yield useful information for growth modelling, while the last (split-split-block with one replication per site) appears to be a useful compromise in efficiently demonstrating genetic gain and providing growth and yield data over a large number of forest sites. This split-split-block design allows reduced trial size while maintaining numbers of treatments compared. Planted trials of this and similar designs (Silviculture/Breed trials, Table 1) have allowed wide representation of regions and sites, as well as valid statistical comparisons among seedlots and silvicultural treatments. The Silviculture/Breed trials have been planted to represent a matrix of site qualities, regions, breeds, and silvicultural treatments (Table 2) and will eventually provide a strong "backbone" of performance data for use in developing future predictive models for growth and log quality.

However, a strategy of using only planted trials means that the most useful, end-of-rotation results are not known for many years. For interim indications of the magnitude of the effects of silviculture on increases in growth and yield with genetic improvement, advantage has also been taken of existing trials of suitable origin (particularly single-tree-plot progeny trials) by imposing area-based plots and/or thinning treatments some years after planting. Of the trials of this type, that is, with no seedlot comparison, are the balanced final crop stocking trials (AK1056, RO2098, NN529/1 and CY597 and FR60), a silviculture comparison (FR58), and a silviculture and site comparison (FR59).

It is important to recognise that no single design will meet all objectives, and that combinations of complementary designs may yield the most information in the most cost-effective manner.

GENETIC GAIN TRIALS SUPPORTED BY THE STAND GROWTH MODELLING COOPERATIVE

The designs employed in the series of trials supported by the Stand Growth Modelling Cooperative fall into two categories: those which consist of plots superimposed on existing trials (Tables 3a, 3b, and 3 c) and those which were designed and planted specifically for provision of genetic gain data for growth models (Tables 4a and 4b). The plots superimposed on existing trials are from 7 to 21 years old, while the oldest of those designed and planted specifically to obtain data for growth modelling are only four years old. A sizable (and increasing) growth and yield data-set is available from the first set of trials, while only early height measurements (age 2) have so far been made in the second set. A summary of the GF ratings of seedlots in all of the trials by region and site type (Table 5) shows that seedlots representing a wide range of GF ratings are being tested on several sites in each region.

PSP's Superimposed on Existing Trials

Plots have been superimposed on existing trials which were originally designed to meet a number of different objectives, including comparisons of:

- seedlots with different levels of genetic gain,
- initial or final stocking levels,
- silvicultural or site variables.

Several sets of plots were superimposed on single-tree-plot progeny tests containing stock with a wide range of genetic quality. A key feature of these trials is the assumption that the seedlot(s) used in the original trial are relevant to future growth and yield objectives. If plots are of the non-contiguous or single-tree type, then their aggregation into larger "area" plots requires the additional assumption that the resulting mixture of genotypes adequately represents a future seedlot of economic interest. GF rankings of gentoypes in these types of aggregate plots have been estimated (G. Vincent, pers. comm.), but these are at best approximate because of the imprecise nature of the aggregations. While the information from the planted trials will be more precise, the PSP's in existing trials will yield indicative information long (something like 10 years) before data from the planted trials are available.

The **Initial Stocking/Breeds (RO972)** trial (Tables 3a and 3b) utilised the **EFM Initial Crop Stocking Trial** established in 1970 in a completely randomised design **(Appendix 1)**. The trial compares initial stocking levels with a fixed final crop stocking. The trial contains primarily GF13 planting stock with a GF4 seedlot planted at one stocking level. A major complication in the trial is that treatment allocation was confounded with within-site variation in growth rate. However, the genetic gain comparison has been particularly useful because it is the only large-plot trial with a genetic gain comparison (at age 21) for trees older than 13 years. Two plots in the trial contain a third planting stock type consisting of cuttings which are of unknown origin and were produced before nursery cutting technology was well developed (Wilcox, unpublished). The two plots of cuttings do not need to be measured further.

The **Final Crop Stocking Trial (AK1056, RO2098, NN529, CY597)** (Tables 3a and 3b) was superimposed on the **GTI "850" Polycross Trial** planted in 1975 in a randomised complete block design with sets of seedlots **(Appendix 2)**. The trial was designed as a progeny test of about 100 "850" selections from both the North and South Islands. With progeny planted in single-tree-plots and a consistent initial crop stocking, differential thinning of various replications and sets yields a replicated final crop stocking trial in four regions for a seedlot rated approximately GF13.

The **1978 Genetic Gain Trials (AK1058, RO2103/1, WN377, NN530/2, CY421/1, SD564/1)** (Tables 3a and 3b) were planted by GTI in 1978 in a randomised complete block design **(Appendix 3)**. These trials have been grown under a direct sawlog regime. Two additional sites of the **1978 Genetic Gain Trial (RO2103/2, SD564/2)**, which are situated in the same compartment as RO2103/1 and SD564/1, respectively (Tables 3a and 3b), used the same design and seedlots but were grown under a pulpwood regime **(Appendix 4)**. Very good genetic gain comparisons among a wide range of improvement levels (GF2 to GF22) are available from these trials. One of these seedlots (the climbing select seedlot) differs in origin from site to site. This would probably not be a serious problem with two seedlots with the same improvement rating, but most climbing select seedlots have not been tested against known genetic benchmarks, and climbing select seedlots cannot be reproduced, nor can their origin be accurately identified. Climbing select seedlots have, therefore, been arbitrarily assigned a GF rating of 7, even though it is clear that some climbing select lots are genetically superior to others. Using a variable climbing select lot as a comparison with seedlots with a higher GF rating makes for imprecise comparisons of performance across sites but represents a seedlot which is perhaps typical of those upon which the local growth model was based.

In 1986 permanent sample plots (PSP's) were superimposed on two of the seven seedlots (GF7 and GF14) on fives sites of the **1978 Genetic Gain Trials** for the purpose of obtaining data for growth modelling. In 1991 and 1992 PSP's will be established on the three remaining sites and in an additional two seedlots (see Appendices 3 and 4).

The **1979 Genetic Gain Trials (RO2103/3, NN530, SD682)** (Tables 3a and 3b) were planted by GTI in either 1979 or 1980, again in a randomised complete block design **(Appendix 5)**. The silviculture regime used was a direct sawlog regime. The range of improvement ratings of the seedlots in this trial (GF7 to GF18) is not as great as in the 1978 Genetic Gain Trials, but good comparisons of the different GF levels can be made. Also in 1986, permanent sample plots (PSP's) were superimposed on four of the five seedlots in the trial for the purpose of obtaining data for growth modelling. Again, one of these seedlots (the climbing select seedlot) varies from site to site, which makes for somewhat imprecise comparisons of the performance across sites.

In 1987 a survey of Stand Growth Modelling Cooperative members' PSP's was undertaken to determine whether PSP's were monitoring genetically improved stock (Wilcox and Carson, 1990). The survey revealed that there were very few plots in improved stands, but especially few in the Auckland Clays region (Wilcox, 1988, PR 2013). Therefore, plots were established in three stands with improved stock in this region (Tables 3a and 3b). First, plots which embodied a **Silvicultural Comparison** were established in the **G. Will Best Practices Trial (FR58) (Appendix 6)**. The trial was intended to illustrate to forest managers the potential benefits of optimum establishment techniques. Seedling stock rated GF14 was used, with two unreplicated stocking and thinning regimes.

Second, another **Silvicultural/Site Comparison (FR59)** was superimposed on the **GTI "880" Progeny Test** planted in 1981 in a randomised complete block design with sets of seedlots grouped within replications **(Appendix 7)**. The trial was designed as a single-tree-plot progeny test of about 170 "880" series selections. Seedlots were open-pollinated mother tree collections from ortets in the GTI "268" series progeny trial planted at Kaingaroa, Cpt. 1350. Replications were divided between two blocks about 1 kilometre apart. Growth on the two blocks proved to be very different, probably due to soil type. Final crop stocking and pruning treatments received by the two blocks were, therefore, different. In 1988 PSP's were established in each of the blocks for a silviculture/site comparison for a seedlot with an improvement rating of approximately GF16.

Third, a **Final Crop Stocking Comparison (FR60)** was superimposed on the GTI "268"x"875" paircross progeny trial planted in 1982 again in a randomised complete block design with sets of seedlots grouped within replications **(Appendix 8)**. The planted trial was designed as a single-tree-plot progeny test of 128 full-sib families. With progeny planted in single-tree-plots and a consistent initial crop stocking, differential thinning of various replications and sets yields a replicated final crop stocking trial in the Auckland Clay region (with volcanic soil on top of clay soil) for a seedlot with approximately a GF16 rating.

The **1984 Genetic Gain Trial (RO1897)** (Tables 3a and 3b) was planted by GTI in 1984 in a randomised complete block design **(Appendix 9)**. This trial has been so far treated as for a direct sawlog regime. Very good genetic gain comparisons among a range of improvement levels (GF7 to GF17) are available from this trial. PSP's were superimposed in six of the eleven stock types (GF7 to GF17) in 1990 and in one additional seedlot in 1991 for the purpose of obtaining data for growth modelling. With ten replications there is scope to impose a replicated final crop stocking trial across this wide range of seedlots.

Silviculture/Breed Trials

The planted **Silviculture/Breed Trials** established since 1987 (Table 4) have been designed so that when combined they represent NZ's eight major forest growing regions, with up to four levels of site quality tested within each region (Table 2). Site quality categories are high basal area (ex-pasture sites) and high, medium, and low site indices and are classified within regions. Seedlots in most trials represent a wide range of improvement ratings. At least one long internode seedlot is often included. Cuttings with high improvement ratings are included at some locations. In many of these trials silvicultural treatments have been designed with a constant ratio of initial to final crop stocking. An unpruned, unthinned control is also usually included. Some of the trials include plots comparing thinning regimes for unpruned trees. Many trials include treatments which represent local seedlots and/or locally favoured silvicultural regimes. Seedling height is being measured in all trials at age 2. PSP's will be established at the time of first silviculture.

Silviculture/Breed Trials established in **1987 (FR7, FR8, FR9, FR10, FR11, FR12)** are in an incomplete block design with seedlings of GF7 to GF21 **(Appendix 10)**. Initial/final crop stocking ratios are held constant and there is an unthinned/unpruned control. Three of the six sites include local seedlots and local silvicultural regimes.

Silviculture/Breed Trials established in **1988 (FR54, FR55, FR56, FR57)** are in various designs with seedlings and cuttings from seedlots with high GF ratings **(Appendices 11, 12, and 13)**. No climbing select control was included in the 1988 plantings. Initial/final crop stocking ratios are held constant and there is usually an unthinned/unpruned control. Local seedlots and/or silvicultural regimes are included.

Silviculture/Breed Trials established in **1989 (FR77, FR78, FR84, FR85, FR86)** are (with one exception) in a split block design with silvicultural treatments assigned to major plot effects, and stock types to minor plot effects. The Kawerau site (FR84) was planted in a completely randomised design, but has the potential to be made into a split-block experiment with two replications. Stock types represent a wide range of improvement ratings (usually GF5 to GF25) **(Appendices 14, 15, 16, 17)**. Cuttings are included at four of the five sites. Planting stock used at each site was from at least two nurseries, so nursery effects will be confounded with stock type. Initial/final crop stocking ratios are held constant within each trial and there is an unthinned/unpruned control. Only two or three silvicultural regimes were included in the 1989 plantings.

Silviculture/Breed Trials established in **1990 (FR121/1, FR121/2, FR121/3, FR121/4, FR121/5, FR121/6, FR121/7)** are in an unbalanced split-split block design with final stocking allocated to major plot treatments, pruning allocated to secondary treatments, and seedlots allocated to minor plot treatments. Seedlings of GF7 to GF25 are included **(Appendices 18, 19, 20, 21, and 22)**. Initial/final crop stocking ratios are usually held constant and there are several thinning treatments which are to remain unpruned. There is an unthinned/unpruned control. Local silvicultural regimes are sometimes included. A long internode seedlot is included on appropriate sites, but cuttings are not represented.

Silviculture/Breed Trials established in **1991** (FR121/8, FR121/9, FR121/10, FR121/11, FR121/12, FR121/13) used the same unbalanced split-split block design used in the 1990 plantings with similar seedlots **(Appendix 18)**. Silvicultural treatments are the same as in 1990. Local silvicultural regimes will be included if desired by the plantation owner. A long internode seedlot will be included on appropriate sites, but cuttings will not be represented.

Analysis of Data from Silviculture/Breed Trials

A large volume of data will be generated from the silviculture/breed trials in the coming years. Data collection will span something like 15-20 years or longer. Possible analysis of variance tables for analysis of plot means for the Silviculture/Breed trials are presented in Appendices 23-29. Analysis of individual tree data would include a within-plot error term at the bottom of the table. It is assumed that the silviculture and seedlot factors are fixed effects.

In many of the trials, the silviculture treatments can be divided into several basic prune/thin prescriptions, each of which is applied to one or more stocking. It is appropriate to separately test for differences between the prune/thin treatments and for stocking effects. Stocking effects can further be divided into polynomial contrasts. The linear contrast tests for a general trend in response to stocking, the quadratic contrast for a curvilinear response, and the remaining degrees of freedom test the lack of fit of this response (see Appendicies 23-29). A transformation of stocking (e.g. log) could be appropriate before this analysis is performed.

A variety of analyses of variance can be applied to the silviculture/breed trials, depending, for example, on which contrasts are of most interest, or whether trials at several locations are combined. The tables in the appendices should therefore be regarded as guidelines only. However, it is probably desirable that the same form of analysis of variance be used through the years in order to aid comparison across years. Analysis of variance of data from the silviculture/breed trials would make a good starting point, but data from these trials will probably be analysed in many ways. They are probably more suited to analysis by a modelling rather than an ANOVA approach.

RECOMMENDATIONS FOR DESIGNING GENETIC GAIN TRIALS

Incorporation of the effects of genetic gain into growth models requires the quantification of absolute differences at all improvement levels available for planting in New Zealand's forests now and in the future. Improvement ratings (GF levels) are based on the combined consideration of genetic merit for both growth and form. Incorporation of the effects of genetic gain into growth models requires separation of the different traits so that relative increases in growth can be identified separately from relative improvement in form traits. In a modelling system used for prediction of outputs from forest stands, genetic merit for growth would be an input into growth models (which predict volume), while genetic improvement in form would suggest inputs into other modules of the modelling system dealing with estimation of sweep, branch size and frequency, malformation, etc. **The Seed Certification System should evolve toward providing separate scales for (1) improvement in growth and (2) improvement in form traits.** Until this is done, interpretation of trial results for growth using current GF ratings should be done with care, as genetic worth for growth rate is confounded with genetic worth for form traits.

Experience with designing and using data from genetic gain trials in New Zealand has highlighted the importance of a multi-disciplinary approach. The different approaches of both tree breeders and mensurationists are necessary for the quantification of genetic gain. Experts from both disciplines should be part of a team that designs, collects, analyses, and interprets genetic gain data. Tree breeders bring an understanding of the nature of genetic gain, while mensurationists have the knowledge necessary for quantifying and predicting growth and yield.

If a wide range of genetic worth is covered by the set of seedlots in a genetic gain trial, the resulting data becomes much more useful for quantification and especially prediction of genetic gain. The genetically best seedlot in a trial would ideally represent a commercial seedlot which would be commonly planted over several years. Further, a number of standard controls which can be used for many years and reproduced should be identified and used in every GG trial. One standard control might be an unimproved lot collected in a large quantity and used for as many as ten years. Another might be a seedlot representing the base population from which selections were made. Standard control seedlots will provide the benchmarks against which all genetic gain can be measured. Also, seedlots and stock types representing all those which are currently and which will in the future be commercially available for operational afforestation should be included.

Experimental designs should be constantly under review. When data from the New Zealand GG trials becomes available, it may be found that one design is better at young ages and another at older ages. The utility of the split-split block designs used for GG trials should be compared against the randomised complete block designs as data becomes available. Further, results from row plot trials should be compared with those from large plot trials to see if they could be used for predicting growth and yield. Also, extensive replication of large plots on one site may give some types of information that could not be gained by only one replication on a site.

In the long term, development of methodology for predicting growth and yield from single-tree plot progeny trials should be investigated. If this could be done, predictions of the performance of different mixes of parents could be carried out at the time of their selection. Genetic gain trials can be designed and planted at the time of selection of seed orchard parents, but data from them will not be available until the trials reach suitable age for measurement of growth and yield and satisfactory prediction of final rotation gains. Although predictions from progeny trials at best can be only provisional (and should be confirmed by GG trials) they nonetheless could give valuable indications of gains from tree improvement many years before GG trial results would be available.

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