Greater specialisation of improved seedlots in New Zealand: New developments for efficient selection of parents and evaluation of performance

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Abstract
Profitability for New Zealand radiata pine forestry could be improved by using seedlots selected to target specific sites or specific end products. Trees selected from the tree improvement programme are being ranked for a number of selection criteria to facilitate selection of seed orchard parents for different mixes of characteristics. Research is progressing towards specifying genetic changes in stem form in planning and prediction models so that log quality of specialised seedlots can be predicted, as is already being done for genetic improvement in growth rate. Ratings for the major selection criteria could be incorporated in the New Zealand Seed Certification System, making selection of specialised seedlots easier and allowing prediction of performance of specific seedlots.

Introduction
Gain resulting from genetic improvement of radiata pine in New Zealand over the last 35 years has been high (Figures 1 and 2).

Control-pollinated seed orchards (Figure 3) have allowed increased genetic gain by making it possible to produce genetically-improved planting stock from crossing among small numbers of parents. Resulting seed can be used directly as production seedlots, or vegetatively multiplied (Figure 4) to extend the plantation area on which it can be planted. Control-pollinated seed orchards make it possible to achieve the high selection intensity required for effective production of "designer seedlots", that is, seedlots selected for specific traits (selection criteria) to maximise profitability for specific sites and/or for specific end uses (Carson, M. 1987, Carson, M. et al. 1990, Carson, M. 1991).
Selection criteria relevant to the specific problem and/or end use.

Forest managers will want to predict yield and log and wood quality of designer seedlots. Genetic changes in growth rate are already being modelled by modified stand growth models (Carson and Garcia, unpublished), with constantly improving predictions expected over the next 20 years as additional data from genetic gain trials become available. Research is under way aimed at modifying planning models to take genetic changes in stem form traits into account.

Control-pollinated orchards have greatly increased flexibility for producing designer seedlots. A higher selection intensity is achieved through flexibility in choice of parents and through reduction in the number of parents used to produce a production seedlot (Burdon, Carson, M. 1986 and 1987, Carson, M. et al., 1992, Sweet and Krugman 1977). Also, pollen can be collected in one location and applied to female clones at another location, and parent clones can be held in clonal blocks without the risk of selfing or pollen contamination. Resulting genetic gains can be much larger with this approach.

Selection of parents for designer seedlots
Predictions of relative performance of seed-orchard parents appear to be valid for all parts of the country where radiata pine has been tested. Genotype-by-environment interaction does not appear to be large enough in New Zealand to warrant selection for adaptation to local climate and site conditions. The predicted increase in genetic gain calculated for regionalised vs non-regionalised seed orchard strategies was small (Carson, S. 1991, Johnson and Burdon 1990, Shelbourne and Low 1980) and would require substantial extra cost for progeny testing to capture. It appears instead that designer seedlots produced by varying the mix of selection traits for end-product improvement will increase profitability more than specialisation aimed at increasing adaptation to local climate and site.

The NZ Radiata Pine Breeding Cooperative is developing a separate rating of potential seed-orchard parents for each important selection criterion. These national breeding values predict the average performance in New Zealand plantations. A matrix of national breeding values is being constructed as illustrated in Table 1. Parents in the different series as well as those in the same series are rated relative to one another for each selection trait. These ratings will be more useful for selecting parents for designer seedlots, where choice of selection traits is customised, than were previous rankings of parents based on multiple traits.

Genetic improvements in different selection traits, while often correlated overall, are not closely linked when considering selection of top parents. The very best parents for one trait are not often the very best for other selection criteria. For example, although Dothistroma resistance and growth rate are clearly positively correlated when all parents are considered (Carson, S. 1989, Carson and Garcia, unpublished), some of the best parents for growth traits are quite poor for Dothistroma resistance. The data in Table 1 are hypothetical, but illustrate the nature of typical trade-offs among selection criteria.

**TABLE 1. Hypothetical national breeding values**

<table>
<thead>
<tr>
<th>Parent</th>
<th>Diameter (mm)</th>
<th>Dothistroma Resistance (%)</th>
<th>Breeding Value</th>
<th>Internode Frequency</th>
<th>Needle Retention</th>
</tr>
</thead>
<tbody>
<tr>
<td>268.A</td>
<td>20</td>
<td>13</td>
<td>6</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>268.B</td>
<td>19</td>
<td>5</td>
<td>3</td>
<td>4</td>
<td>3.5</td>
</tr>
<tr>
<td>875.C</td>
<td>19</td>
<td>12</td>
<td>6</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>850.D</td>
<td>18</td>
<td>0</td>
<td>7</td>
<td>2</td>
<td>2.5</td>
</tr>
<tr>
<td>880.F</td>
<td>18</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>3.5</td>
</tr>
<tr>
<td>880.H</td>
<td>17</td>
<td>14</td>
<td>7</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>268.G</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>1.5</td>
<td></td>
</tr>
<tr>
<td>880.H</td>
<td>0</td>
<td>5</td>
<td>5</td>
<td>2</td>
<td>2.5</td>
</tr>
<tr>
<td>850.I</td>
<td>18</td>
<td>5</td>
<td>6</td>
<td>1.5</td>
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<td>850.J</td>
<td>19</td>
<td>7</td>
<td>4</td>
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<tr>
<td>875.K</td>
<td>19</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>3.5</td>
</tr>
<tr>
<td>268.L</td>
<td>20</td>
<td>12</td>
<td>4</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

1. Subjective scores from 1 to 9, with 9 being very straight or very multi-nodal.
2. Subjective scores from 1 to 6, with 6 representing full retention of three seasons' needles.
National breeding values tend to be distributed in a bell-shaped normal curve as illustrated in Figure 5. They represent the relative amount of gain contributed by each individual parent when compared to the mean of all parents. The relative worth of a parent contributing to a control-pollinated seedlot is estimated as the weighted average of the parental values. Comparisons of genetic change calculated for different combinations of parents represent valid predictions of gain from potential production seedlots, and thus provide quantification of relative trade-offs between different selection criteria.

**Prediction of genetic worth**

<table>
<thead>
<tr>
<th>Worst</th>
<th>Best</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breeding value</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 5. Distribution of national breeding values.**

**Predicting Yield and Quality of “Designer Seedlots”**

**Conversion of changes in selection criteria to differences in selection objectives**

While national breeding values quantify relative genetic worth very well, they do not predict very accurately the absolute economic value of genetic changes. Tree breeders select trees by measuring specific characteristics related to the economic worth of end products. Because of the long rotation of forest crops, selection needs to take place at young ages rather than when the economic worth of final end products can be directly measured. Therefore, translation of genetic changes in selection criteria into economic gain in selection objectives is required; that is, national breeding values require translation into predictions of yield and log quality.

The impact of selecting for diameter at about age eight can be translated into changes in final stand yield through use of genetic gain multipliers in growth models, as is being done by the Stand Growth Modelling Cooperative (Carson, S. and Garcia, unpublished). The rate of change of the height, stocking and basal area functions is increased with genetic improvement, and has been quantified by measuring genetic gain trials grown on different sites and with different silviculture. Currently, the values of the multipliers are indicated by specifying the ‘GF rating’ of a seedlot. This is assigned by the New Zealand Seed Certification Service based on breeding values for growth and stem form combined (Vincent 1987). Growth is given twice the weight as stem form, so the GF rating gives a strong indication of genetic worth for growth. A seedlot’s genetic worth is thus used along with designation of region, site index, and spacing to predict final stand volume.

**Proposal: modify planning models to reflect genetic changes influencing log quality**

Planning models, including STANDPAK (West 1993, Whiteside 1990), typically utilise different modules to predict the final characteristics of a stand (Figure 6). For example, growth models predict stand volume, while a branch model is used to predict knot size. Results from all modules are brought together to construct an overall prediction of the volume and quality of different log types and product mixes. Predictions are used for evaluating different management options, scheduling of pruning and thinning operations, and predicting wood yields by log-quality classes. If the relative genetic worth of a seedlot for quality traits could be specified in the appropriate module of a planning model, predictions of log and wood quality might improve for designer seedlots.

A seedlot’s genetic worth relative to other seedlots can be determined by its average breeding value. However, the absolute performance of seedlots will differ from region to region (Figure 7). For example, trees on average are much straighter when grown on the Auckland sands than in the Central North Island, no matter what their genetic make-up. Also, trees grown on sandy soils tend to have finer branches, and shorter internodes than those grown on most other sites. In fact, the large morphological differences in radiata pine grown in different regions provide one of the bases for using breeds with a varying mix of selection traits (Carson, M. 1991).

**Figure 6. Modules in STANDPAK.**

**Figure 7. Distribution of economic differences for a single selection trait (hypothetical).**

In addition to regional differences in the overall average performance of different seedlots, the magnitude of differences among seedlots will also differ from region to region. This is because genetic variance differs; that is, the magnitude of differences among genetically-improved parents (Figure 7). For
example, the difference between the best and the worst parents 
for straightness will be much greater on Central North Island sites 
than on the Auckland sands. An actual measurement of internode 
length on offspring of the same parents in progeny trials planted on both the Auckland sands and in the Central North 
Island illustrates these points by showing both a strong regional 
difference in mean performance and a large difference in varia-
tance among parents (Carson, M. and Inglis 1989) (Figure 8).

Determining optimal economic weights of selection traits
When it becomes possible to input a seedlot's genetic value for 
specific selection criteria directly into planning models, designer 
stand value can be assessed. Eventually, the appropriate modules in planning models may 
be developed to address different objectives. Objective measures closely related to economic 
worth are being related to national breeding values. In essence, 
straightness as input in order to improve prediction of the qual-
ity and value of a stand.

Future Direction of New Zealand Seed Certification
The New Zealand Seed Certification Service has so far devel-
oped three separate rating scales (three separate improvement rat-
ings) for quantifying a seedlot's genetic worth (Table 2). A seedlot can be rated for any of the breeds, and a seedlot will have different ratings for each of them, because each breed emphasizes a different set of selection criteria (Table 2). In addition to the 
Growth and Form Breed (GF), ratings for two special-purpose 
breeds are available. The Dothistroma-Resistant Breed ranks seedlots to achieve optimum volume growth on high-risk Doth-
istroma sites. The Long-Internode Breed rating provides a rank-
ing for internode frequency. Certification for special-purpose 
breeds also includes the rating for the growth and form breed. A 
wood density breed (emphasising increased density and growth) 
and a pole breed (emphasising multiple branching and straight-
hess) are available from the tree improvement programme but are 
not yet rated by the Seed Certification Service.

The New Zealand Seed Certification Service is progressing 
towards an enhancement of the rating system where, in addition 
to the improvement ratings now available, individual trait ratings 
are provided. Trait ratings could be presented on the certificate 
as “DI 22 ST 7 IF 6 DR 18”, that is, with diameter (DI), straight-
hess (ST), internode frequency (IF), and Dothistroma resistance 
(DR) ratings. The first application of these trait ratings will be the 
use of the diameter rating for the prediction of growth by growth 
models. A more precise prediction of stand volume should be 
achieved by using diameter rating to indicate a seedlot's genetic 
worth instead of GF rating, since the GF rating indicates genetic 
worth for a combination of growth and form traits, rather than just for growth. The Stand Growth Modelling Cooperative is 
implementing this change.

Extension to Clonal Forestry
True clonal forestry, that is, the use of tested clones, would allow 
even greater flexibility in the choice of designer plantations. 
When ranking information is available, a similar system for rat-
ing and predicting the performance of tested clones using plan-
ning models could be developed in the same way as that proposed 
here for family forestry. Prediction of performance of a single 
clonal block may not be as accurate as for control-pollinated seedlots 
(for the same reasons that improvement rating for a single con-
trol-pollinated family is not as reliable as for a mix of several par-
ents), but may be acceptable for a mix of clones or a group of 
single clone blocks. Just as with the system being developed for 
predicting performance of control-pollinated seedlots, a predic-
tion system for clones would require development and testing 
before its utility can be ascertained.

Conclusions
The increasing use of control-pollinated seed and vegetatively-

![Figure 8. Distribution of average internode length in two contrast-
regions.](image-url)
multiplied cuttings for radiata pine production forests provides a vehicle for forest owners not only to increase gain from tree breeding, but also to customise the emphasis placed on selection criteria, such as growth rate, straightness, internode frequency and disease resistance. This could maximise profitability on sites with particular characteristics (for example, high risk for disease or sand dune sites) or in forest stands destined for specific end uses (for example, poles or pulp).

National breeding values are being developed for each commonly used selection trait. This will facilitate selection of designer seedlots, that is, seedlots intended to maximise genetic gain on specific sites or for specific end uses (see Table 3). National breeding values for internode frequency and straightness are being related to log quality so that genetic changes can be taken into account in planning models. This will allow changes in selection criteria to be translated into changes in selection objectives, which are often specific to site and silviculture. Predicted performance of specific seedlots could be obtained by specifying Seed Certification ratings for separate selection traits and using these to adjust the appropriate modules of planning models to reflect the effects of genetic change.

**TABLE 3. Steps being carried out for selection and evaluation of designer seedlots**

<table>
<thead>
<tr>
<th>Development</th>
<th>Pay-off</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Calculate breeding values for commonly-used selection criteria so that all parents in the New Zealand breeding population can be compared for each trait separately.</td>
<td>Efficient selection of designer seedlots.</td>
</tr>
<tr>
<td>2. Relate national breeding values to regional differences in mean performance and magnitude of differences among parents by measuring progeny trials and genetic gain trials in different regions.</td>
<td>Clearer nomination of the optimum mix of selection criteria for designer seedlots.</td>
</tr>
<tr>
<td>3. Modify modelling systems to allow input of seedlot ratings for other traits in addition to growth rate.</td>
<td>More accurate prediction of performance of designer seedlots.</td>
</tr>
</tbody>
</table>

Complete implementation will require several years of research and, as such, represents a long-term goal. However, we now have a framework for focusing the incorporation of genetic changes into prediction models. Implementation would enable more efficient selection and better prediction of performance of designer seedlots. The New Zealand Seed Certification Service, and planning models (including STANDPAK) would be the vehicles for technology transfer of this information.

**Glossary**

- **breed**: a specified set of selection criteria and economic weights aimed at achieving breeding goals appropriate for a particular site type or end use.
- **breeding objective**: the characteristic with a direct effect on profitability which changes as a result of genetic selection. For example, increased volume at rotation age is the breeding objective achieved through selection on diameter measured at age eight years (see selection criteria).
- **breeding population**: the set of tree genotypes (called clones or parents) which is considered to represent the best performers intended for crossing and re-selection for the next generation.
- **breeding value**: a number that represents a parent’s relative genetic worth compared to other parents. May represent genetic worth for a single trait or for a mix of traits, each with a specific economic weight.
- **clonal forestry**: planting of tested clones in production forests.
- **designer seedlots**: offspring of parents selected for their genetic potential to perform optimally on specific sites or for the production of specific end products.
- **economic weight**: the relative weight given to a unit of variation in a selection criterion reflecting its economic importance compared to the other selection traits.
- **genetic gain**: a change in performance of a stand of trees as a result of genetic selection and breeding.
- **GP rating**: a rating assigned by the New Zealand Seed Certification Service for the Growth and Form Breed, which reflects a seedlot’s relative genetic worth for growth and stem form, with growth given twice as much weight as stem form.
- **improvement rating**: a number assigned by the New Zealand Seed Certification Service reflecting a particular seedlot’s relative genetic worth for a particular breed, that is, for a specified set of selection criteria, each with a specific economic weight.
- **production population**: the set of tree genotypes (called clones or parents) which is considered to represent the very best performers intended for current seed orchard production.
- **ramset**: a vegetatively-propagated genetic copy of a tree.
- **selection criterion**: the attribute or variable upon which genetic selection is performed, for example, diameter at age eight years (see breeding objective).
- **trait rating**: a number assigned by the New Zealand Seed Certification Service which reflects a particular seedlot’s relative genetic worth for one specific selection criterion.

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**Preferences for scenarios of land-use change in the Mackenzie/Waitaki Basin**

John R. Fairweather* and Simon R. Swaffield†

**ABSTRACT**

Earlier research on the effects of land-use change on a range of landforms in the Mackenzie/Waitaki Basin identified three dominant preference themes: for plantations, for a combination of grazing and trees, and for conservation (Fairweather and Swaffield, 1995). These themes were used to generate five scenarios of land-use change for the area, for each of which the detailed visual, economic, and social effects were modelled (Evison and Swaffield, 1994). This article reports on preferences for these scenarios.

The results suggest that preferences for the effects of land-use change are relatively stable, that detailed information on effects had only minor influence upon the ordering of preferences for scenarios, and that levels of acceptability for the preferred scenarios were high. Overall, there was support for a significant increase in plantations, shelterbelts and improved pasture, but wilding management was considered essential. The diversity of preferences suggests that a widening range of land uses can be expected to occur in the future.

**INTRODUCTION**

The Forest Research Institute's Planning for Rural Environments research programme has brought a number of research perspectives to bear on rural planning, with the overall aim of developing improved methods for managing land-use change. In particular, the programme has focused on potential land-use changes in the Mackenzie/Waitaki Basin study area, employing a suite of techniques useful for predicting and evaluating the visual, economic and social effects of particular combinations of agriculture and forestry (Evison and Swaffield, 1994). These techniques include GIS research and computer visualisation (Hock et al., 1995; Bennison and Swaffield, 1994), attitude surveys (Fairweather and Swaffield, 1995), socio-economic analysis of forestry/agriculture options, and property-level economic analysis of land-use change. Findings on the effects of land-use change in the study area can be used by farmers and others involved in high-country management, whilst the improved planning procedures contribute generally to the development of decision support systems for rural planners throughout New Zealand.

An essential part of the FRI study has been the presentation of data on predicted effects of land-use change involving forestry to a range of interested parties, in order to assess the acceptability of the options available. The procedure adopted in the early stages of the research in 1993-94 was to disaggregate and simplify the complex of variables potentially involved, in order to present relevant information in a cost-effective and meaningful way. Landform and rainfall were selected as key biophysical variables determining the viability of land-use options. A Geographic Information System (GIS) database was developed for the study area, from which four landform categories were defined and for which the effects of different land-use options were estimated. The landforms were: hills slopes between 16° and 35°, lower slopes between 8° and 16°, and flats less than 8° (all three with less than 800 mm annual rainfall), and flats less than 8° with less than 800 mm annual rainfall. The analysis highlighted a number of operational issues involved in applying GIS to an extensive study area with complex landforms. As a result, some expert interpretation of anomalies in the data set was needed (for example, to distinguish 'lower' slopes, which were taken to be slopes and debris flows adjacent to the basin floor, from small areas of modest slope angle located at higher elevations). Similarly, given the goal of broad-scale categorisation, small areas of distinct landform with an area of less than 10 ha (for example, small moraines, or flatter hill tops) were aggregated with the adjacent landform type. Detailed explanation of the derivation of these categories is given in Hock et al. (1995).

For each landform a set of information cards had been pre-

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