Growth Model development of radiata pine clones: A gap analysis

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EXECUTIVE SUMMARY

To date, the current Stand Growth Modelling Cooperative (SGMC) growth models have been based on information from seedlings, and have not included clones. However, as clonal forestry becomes more important in New Zealand, SGMC models will need to consider clones. The SGMC therefore formed a sub-committee to discuss the needs for the future and how clones might be incorporated into models. This report comes as a result of that work, and directly addresses the question: Are there current clonal trials or clonal blocks that we could utilise for building clonal models?

This report presents the results of an extensive survey of clonal trials and clonal blocks, including information on the forest location, trial designs and IP owners. Clonal trials are defined as plantings that are planted in a known, replicated trial design, whereas clonal blocks are defined as plantings of clones with no replication.

There were a large number of clonal trials documented from the survey. The majority were below the age of 15, and single-tree-plot (STP) designs. The STP trials available were numerous. They may be utilised in two ways; to validate existing models for clones, or; they may be able to be utilised through the development of distance-dependent models, which would allow us to understand how individual clones grow in mixtures.

The clonal trial series with the greatest potential for modelling, is managed by Ensis Environment (ex. Soils & nutrition) and is planted on a wide range of sites. This trial series should be considered for setting up PSP's, although this would need to be negotiated with the owners. Physiological age would need to be taken into account with these trials.

Only five clonal blocks were documented from survey respondents. Of these, the block of most interest to SGMC would be the PanPac-controlled single-clone block based at Gwavas. The blocks documented, however, may be of limited use as they only represent a limited number of sites, and genetics are not consistent between them.

A number of survey respondents declined to provide information for this report, but did indicate that they may be prepared to consider the establishment of PSP's on an *ad hoc* basis.

Overall though, it was shown there is a very limited amount of clonal information available for PSP's to build individual-tree models - therefore, some creative thinking is required in the future.

There are some fundamental questions that should be addressed in the medium term. These include

- examining the way clones grow when they are grown in mixtures versus monoclonal blocks,
- validating the existing models through clonal trials already available, such as the Ensis Environment series
- and to consider the design and feasibility of developing response-surface trials for future modelling purposes.

Contents

Introduction 1
A survey of clonal resources 1
Results from the survey participants 1
  General results 1
  Clonal trials surveyed 1
  Clonal blocks surveyed 4
Seedlot-based model requirements 5
Current models 7
Key requirements for clonal information in individual-tree models 7
Models for clonal populations 8
  Clonal variance and growth models 8
  Development of a distance-dependent model 9
Gaps 9
  The single-tree-plot resource 9
  Response-surface modelling trials 9
Research areas and project recommendations 10

Appendix 1 13
Appendix 2 14
Appendix 3 15

Growth Model development of radiata pine clones: a gap analysis

Introduction

This project was initiated after a sub-committee review of the needs of the SGMC for the incorporation of clonal data into models and the PSP system (Dungey *et al.* 2004). The current system is based only on seedling material, and there was a consensus that clonal data did need to be accounted for in the near future.

There are a number of options to incorporate clonal material. These include the use of current trials or clonal blocks and/or the planting of areas or trials specifically for clonal PSP measurement and long-term monitoring. In the longer-term, it is likely that some trials will be established, although it is acknowledged that clonal trials are expensive to establish and any series of new trials should be carefully planned to meet the future needs of the SGMC. In the interim, however, it is likely that existing data and trials, or clonal plantings, can be made available for testing and validation studies on clones.

This project therefore aims to provide a first step towards the efficient use of already existing material for incorporating clones into models by the SGMC. Details of clonal trials and clonal plantings from the survey are given and the current uses of the trials will be identified and ownership outlined where possible. The key issues and needs for the use of clonal material in models will be addressed. Possible uses of the trials, in a SGMC context will be suggested and whether the trials are suitable for PSP installation and subsequent measurement. Finally, projects that will be important in building the knowledge base will be recommended.

A survey of clonal resources

A survey was sent out to SGMC members and other industry representatives to determine the extent of clonal resources that would be available for modelling, and included separate surveys for clonal blocks and clonal trials. The content of the survey has been summarised in Appendix 1. A list of participants is given in Appendix 2.

Results from the survey participants

Results from participants in the survey are given in Appendix 3. A summary of the information is given below.

General results

All forest owners would allow PSP's to be set up and subsequent measurements used for model development but in most cases, permission from the germplasm owners (e.g. Horizon2, CellFor, RPBC, Ensis) would be required. Permission for PSP's was a requirement in 5 of the trials surveyed and one of the clonal blocks, and is likely to be a common requirement in the future. Clonal identity would need to be masked or negotiated with germplasm owners in the majority of cases. Use of the trials would also need to be negotiated.

Clonal trials surveyed

The age-range of the trials in the survey is described in Figure 1. The majority of trials were in the range 5-10 years, although there were a number of trials (39) over half-rotation age (>15). This looked promising until the designs were examined further.

The trial designs could be split into 5 groups:

1. Single-tree-plot designs, including STP/row.
2. Large-block (LB) and block designs
3. Row-plots
4. Block/row plots
5. Demonstrations

The majority of trials in the survey were single-tree-plot designs (STP, Figure 2, Appendix 3). However, there were 24 block, block/row or large block designs, which have traditionally been more useful for modelling purposes.

Figure 1. Age-distribution of the trials surveyed by the SGMC (a summary of Appendix 3).

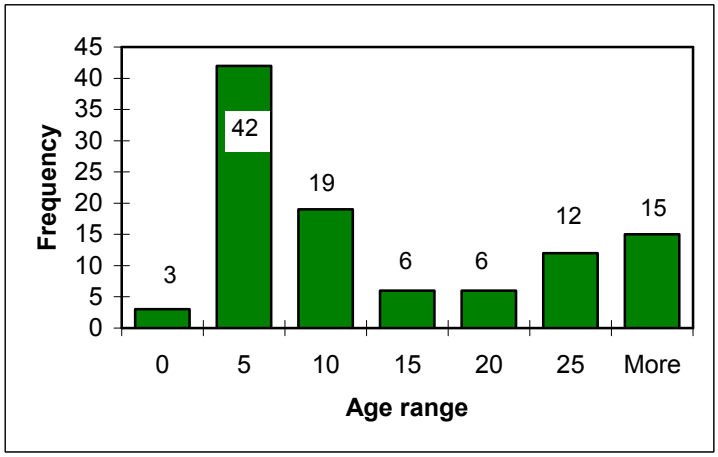
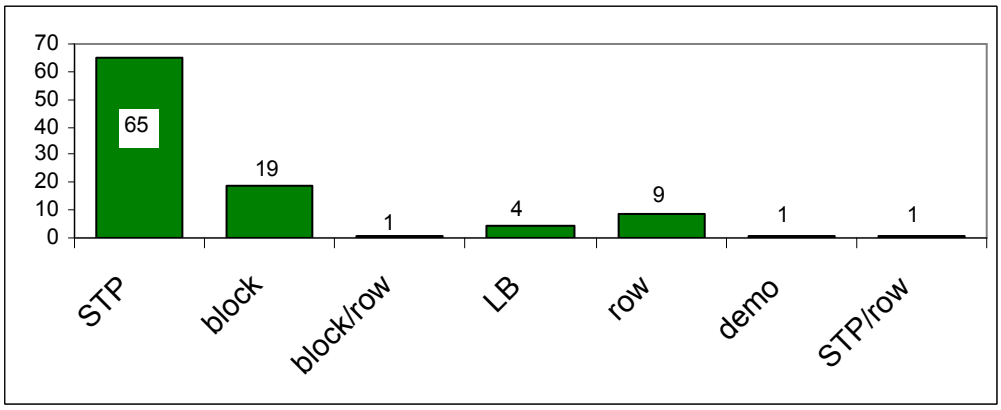


Figure 2. Distribution of the different trial designs from the SGMC survey. Note, these are only for the trials that specified a trial design, all details can be found in Appendix 3.



When the age distributions of trials were examined for each design type (Figure 3), most trials where designs were specified were in the 0-15 years age range (STP and row plots), large blocks (LB) were distributed unevenly with two trials from 0-5 and two trials from 10-15. Trials with blocks were more commonly under 5 years of age, but five were in the range 5-10 years old.

A large proportion of trials did not have the plot type/design specified. The frequency of age distributions of these trials is given in Figure 4. There was quite a large age range for these trials. On closer examination, all the trials 18-years-of-age or over were Ensis Genetics (ex GTI) and/or RPBC trials. The majority of these are STP designs, or row plots. There was one trial series, of 33 years of age that appeared to be large blocks. However, on closer investigation these trials were established for studying seed production, from aged cuttings and thus would not be suitable for PSP establishment.

One of the most promising trials was a 17-year-old Plantation Management Cooperative (PMCoop) trial at Tui Glenn. This trial is designed to look at clonal mixes versus monoclonal blocks, which is important for the SGMC to address. Although this is the only trial in New Zealand (there is a sister trial in Australia in Tumbarumba, NSW), it could be used to determine whether a difference between clonal mixes and monoclonal blocks does exist. If there is a difference we will know that

we have to account for both clonal mixes and monoclonal blocks in models. It would also provide evidence that we should develop a distance-dependent model, at least for research purposes to understand how clones interact with each other. If there is no difference, then it is more likely that current models will extend more readily to clones.

The majority of trials were located in the Bay of Plenty (100), Waikato (WK, 26), Auckland (15) or Hawkes Bay (15) regions (Table 2). However, there were trials across most of New Zealand.

Figure 3. Age frequency distributions for the different plot types in the trials documented by the SGMC survey. STP = single tree plot, LB = large block. Most of the trials with blocks were less than 5 years of age, and always below 15 years of age.

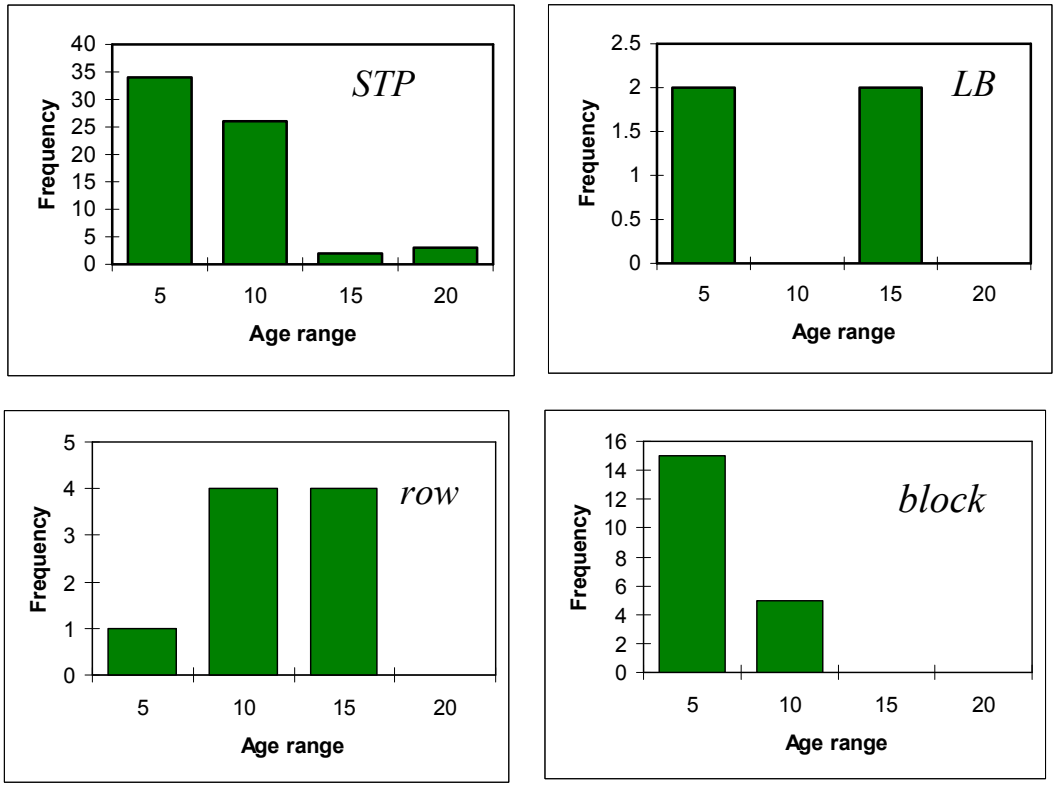


Figure 4. Age frequency distributions for the trials where no plot type was specified. The majority of these were Ensis Genetics/RPBC trials, which were likely to be STP or row-plot designs.

Where the clone type was specified, the majority of clonal trials contained clonal mixes. Only two of the nine single-clone types were planted in large blocks and these were only 2 years old (trials 32 and 33, Forest Genetics). All others were in row plots. Where specified, all trials had controls.

Very little information was given on the number and age of current measurements. Most of the trials with measurements specified were either very young (<5) or measurement details were inadequate for determining the usefulness of the trials for models. Trial 188, a Weyerhaeuser-controlled trial, was planted in clonal blocks in 1996. This trial looks useful, but appears to be only on one site, in Golden Downs.

There were no trials with clonal blocks planted across multiple sites (>3) that were even approaching half-rotation age. Perhaps the trial series with the most potential is that of Ensis – Environment (ex-Sustainable Forest Management, SFM) represented by the FR442-series (trials 138-151). These trials are still young (<3 years-of-age), but are planted in blocks of mixed clones across a wide range of sites. Setting up PSP's within them may be able to be negotiated. The trials at Puruki (Ensis-Environment /122-126 FR443-series) are also related to the FR442-series and were planted specifically to address key clones versus seedling comparisons.

There is some concern about the degree of maturation in this series of Ensis Environment trials. Some of the clones appear to have a particularly advanced physiological age (Mike Dibley, pers. comm.). Please note: maturation is defined as the process of change from juvenile to mature state (due to ontogenetic processes). Physiological age is defined as the apparent maturation state of a tree, which is the result of ontogenetic processes that are largely irreversible, plus the more easily reversible loss of vigour associated with increasing age (Aimers-Halliday *et al.* 2003).

With deployment clonal material in general, it is important to consider the effects of maturation. Maturation of clonally propagated material has been the main barrier to successful clonal forestry with radiata pine, and this barrier has not yet been fully overcome (Aimers-Halliday *et al.* 2003). The main trends in field performance, which are associated with increasing physiological age, are reduced early diameter and volume growth, but improved tree form (Menzies *et al.* 1991, Aimers-Halliday *et al.* 2003). Physiological age should, therefore, be taken into account in evaluation of clonal trial material, and it is important that it is considered in any clonal growth model. A particular physiological age of a clonal propagule can be assessed, based on the presence of phase-specific characters (Menzies *et al* 2000).

Clonal blocks surveyed

Three Cooperative members gave information on clonal blocks (Table 2). However, Horizon2 has previously indicated that clonal block plantings existed on their estate, but provided no details, and that they would consider PSP's being established within these blocks. Applications for use and measurement within clonal block plantings would be considered on an *ad hoc* basis.

Two of the five clonal blocks in the age range of 5-10 years, were demo blocks, and most of the clonal plantings had low numbers of clones.

The large single-clone stand owned by PanPac (block 1, Table 3), was recently planted (2004) and may provide an opportunity to impose some silviculture, once more details on the clone type and plot size can be determined.

All members would allow PSP's and allow the data to be used in the development of models, although PanPac (clonal block No. 1) required the agreement of Horizon2. Only the Ensis Genetics

Clonal trial at Tokoiti, planted in 2000, had heights measured at Age 1. All other clonal blocks had not been measured to date. Clonal identity was required to be masked in 3 of the 5 blocks (blocks 1, 4, 5). All clonal blocks recorded were young, with the oldest, controlled by City Forests, planted in 1998, now 7-years-of-age.

SGMC will therefore need to partner with individual company members for particular PSP/experimental establishment in the future.

Clonal blocks were located in the Bay of Plenty (2), Otago (2) and one in Hawkes Bay (Table 2).

Seedlot-based model requirements

Any individual-tree model requires data on the same trees from a large age range, from early ages after planting, to rotation age, up until around age 30 years. Although silviculture is important, and would need to be represented through a number of different regimes, it has little effect on the relative amount of genetic improvement in growth (Carson *et al.* 1999). A robust model would therefore need to represent a broad range of genetic material that is, in itself, as representative as possible of the planted forests where the models will be applied.

Minimum data requirements would include at least three measurements more than one-year apart, commencing from age five. Data would need to cover from just after planting to rotation. At least three trees per plot would need to be measured for competition and survival models. At least 15 trees per plot with a minimum plot size of 0.04ha would be needed for individual tree models. Plots would need to be measured regularly, across three different age ranges (Mina van der Colff pers. comm.).

A PSP of clonal trees would ideally be an average of around 0.04 ha, or around 25 trees, similar to that of seedlings. Smaller plots may be acceptable if clonal variation is found to be lower than seedlot variation.

Table 2. The number of trials and clonal blocks located in each region across New Zealand.

Region	Clonal trials	Clonal blocks
AK	15	
BP	100	2
CY	5	
GS	8	
HB	15	1
MB	3	
NN	9	
NT	11	
OT	7	2
SD	8	
WC	4	
WK	26	
WM	8	
WN	1	

Table 3. Clonal block information obtained from the SGMC survey.

Clonal block number	Name/ID	Controller	Location	Year Planted	No of clones in block	Plot size	Treatments	Clone Type	Controls
1	stand 97.05	PanPac	Gwavas	2004	3000 trees - 1 clone	none	non specified	not sure	N
2	Ensis Genetics Clonal Trial (T17)	City Forests	Tokoiti CPT 35/01	2000	42	24m×24m	Nil	check workplan	Y
3	Fletcher Challenge Forests Clonal Trial (T18)	City Forests	Tokoiti CPT 38/01	1998	6	30m×30m	100% Access Prune ,To 2m Ht		N
4	demo block	CHHF	Bongo Rd, Kinleith	1999	2	-	thin & prune	somatic embryogenesis	Y
5	demo block	CHHF	Kakariki Rd, Kinleith	2002	12	0.4 - 3.0 ha	PL 500 s/ha	somatic embryogenesis	N

Current models

Table 4 lists the growth and quality models that have been developed for industry use. These models cover the key growth and quality parameters that may also be applied to clonal forestry.

All models will need to be validated for clonal material before they are used for clones. Some models may not be appropriate and/or may have to be re-parametised or adjusted prior to being applied to clones.

Table 4. Growth and stand quality models currently available, and whether they are/aren't in the public domain. For more detail, see also Farm and Forest Plantation Management Cooperative Report No. 55, page 3.

GROWTH & QUALITY MODELS	
MODEL	**AUTHOR(S), YEAR PRODUCED**
Individual Tree GM[2] (silviculture and post-silviculture)	Shula, 2000
TreeBLOSSIM[2]	Grace (Version 3 -SGMC Report 125, 2005)
Branch Model[1]	Kimberley & Knowles 1997
Stand level models	
300-Index GM[1]	Kimberley *et al.*, 2005
NAPIRAD[3]	Garcia and Lawrence 1983, (see Garcia, 1988)
SANDS[3]	Dunningham 1984 (see Garcia, 1988)
CLAYSF[2]	Shula 1987
PPM88[2]	Garcia, Dunningham and Lawrence 1988 (see Garcia 1988).
CANTY[2]	Lawrence 1988
SGM3[2]	Law 1988
NM90[2]	Law 1990
3-D Taper[1]	Gordon and Budiyanto (1999), confidential to PMCoop.
Mature Sweep from Juv. Sweep[1]	Turner & Tombleson, 1999

[1] Proprietary to the Plantation Management Coop

[2] Proprietary to the Stand Growth Modeling Coop

[3] Public domain

Key requirements for clonal information in individual-tree models

For clonal models, the concept of following a tree through from planting to rotation age becomes more complex as it is the characteristic of each clone that largely determines individual trajectories. Clones may also have different growth trajectories when they are planted in clonal mixes or as monoclonal blocks. Different silvicultural regimes will also place another level of complexity that must be captured. To ensure results are representative, it would be ideal to include a broad range of genetic material, which in turn requires a large number of clones to be tested. Clones that are planted commercially change over time. Hence, clonal tests and clonal data may have to be updated regularly in order for the planting stock to be adequately represented. However, if you choose current commercial clones and put them in PSPs, by the end of the rotation they are unlikely to be current clones. Therefore, the idea of following clones for a rotation also has inherent problems. Whatever the approach, testing requirements are likely to be large.

Some creative ideas to address these limitations for clones are addressed in a following section.

Models for clonal populations

There is a very limited amount of clonal information available for PSP's to build individual-tree models with a succession of measurements, differential silviculture which are close to rotation age. Therefore, some creative thinking is required.

Instead of building individual-tree models from those already built from seedlot-based information, there may be more suitable models that can be applied to existing stands. Perhaps one of the most important issues that we face is that in the older trials, most clones are planted in single-tree-plot designs. The advantage of these designs is that the performance of the clones can be measured against other clones in the trial across a number of replications. For models, however, single-tree-plot designs only mimic clonal mixes in commercial plantings. Regardless, single-tree-plot designs also have issues with relative competition, particularly if thinning is not done commercially. However, the best resource for modelling clones that we currently have near rotation-age is in the older single-tree-plot designs. Time-series data could be obtained from these trials from felling and obtaining discs and cores at various sites within individual trees.

Crown architecture is a major factor in determining the physiological age of cuttings when young, so modelling growth from crown structure could be a particularly relevant approach for clones. The physiological age of clones at planting has a large effect on their growth trajectory. Clones that have a physiological age over 6 at planting will have a significantly lower growth rate compared with seedlings or clones with lower physiological ages at planting (Menzies *et al.* 1991). Crown architecture could be used to model a clonal growth trajectory and may, to some extent, take physiological-age differences in clones into account.

Individual tree growth models can be developed by either ignoring individual tree location (distance – independent model) or by including tree location (distance-dependent model). This latter approach allows competition between individual trees to be considered. It is considered that the development of an individual–tree distance dependent model that incorporates crown structure would be an ideal approach to analyse single-tree-plot data. Such a model could then be used to simulate the growing of individual clones in blocks.

When applied to single-tree-plot trials, the crown architecture models will have the advantage of being able to adjust to competition effects between trees. This will mean that the older single-tree-plot trials suddenly become a useful resource.

However, the development of such a model for New Zealand will need an extensive amount of research. There are still a number of issues that will need to be specifically addressed. A few of these are outlined below.

Clonal variance and growth models

Clonal variation needs to be compared with seedlot and/or family variation in order to determine how models might be adjusted for clones. Clonal variation when planted in mono-clonal blocks and in mixes or single-tree-plots needs to be examined. Early results from one site indicates that for growth traits (DBH), clonal variation in mixes is greater than in mono-clonal blocks, but for wood properties, the difference is not significant (Mark Kimberley pers. comm.). However, this work must be further analysed to confirm these early findings. Other sources of such clonal variation patterns also need to be documented. For example, in a recent analysis by Kumar

(2005), the coefficient of variation for DBH of clones at Age 7 was 11% and 17% at Manawahe and Kaingaroa respectively, while the coefficient of variation for open-pollinated progeny taken from 75 of the clones was found to be 16 and 17% at Age 7.

Development of a distance-dependent model

Research required for a distance-dependent model for clones will need to be extensive; but be a logical extension of TreeBLOSSIM development. A PhD-scholarship approach would be ideal in terms of the large amount of science involved and the relative low cost. However, IP would have to be considered, as all PhD students must have the right to publish. If SGMC members require full ownership of such a model, a student will not be suitable.

Gaps

The gaps are large. There are no large-block clonal trials on a number of sites that would be ideal for growth modelling purposes (as documented, Horizon2's resource is currently unknown). There are a number of STP trials, but they are planted on a relatively small number of sites. Clonal blocks appear to be not as common as hoped, and those that are present generally represent only one site. The best option from this material is the nutrition/soils series of trials established through Ensis Environment. This trial series is planted on a large range of sites, and clones are planted in blocks. Although this trial series is all younger than three-years-of-age, it represents the best opportunity for modelling. However, the physiological age of this material must be taken into account. Maturation in some of the clones is likely to affect diameter growth and crown architecture.

The single-tree-plot resource

The STP trials available are numerous, and they may be able to be utilised through the development of distance-dependent models. However, trial series are not often planted on a large range of sites, as is the usual requirement for the development of models that will be useful to growers throughout New Zealand. Therefore, using these trials for model development would be useful only for knowledge on how clones operate at a relatively small scale.

Response-surface modelling trials

Response-surface-type trials, a concept developed by Chris Goulding, is a particular type of trial design that might be useful if we needed to plant more trials. A closer examination should be made of this concept in terms of its applicability to planting clonal trials for model development.

Summary and Recommendations

There are no known trials or clonal blocks that are currently ideal for modelling purposes that are approaching rotation, or even half-rotation age. The most useful trial series represents a clonal series established by Ensis Environment. This young set of trials represents a unique opportunity to SGMC, and the group should seriously consider requesting the setting up of PSP's. There are some clonal blocks which may be suitable for establishing PSP's on an *ad hoc* basis, but the site coverage is not likely to be ideal. Nevertheless, the SGMC should consider partnering with private owners to enable PSP establishment.

There are a number of STP-design trials of suitable age, and although not ideal for PSP establishment are a resource that could be utilised for the development of new distance-dependent models or for validation studies. Although there are fundamental questions on how clones behave planted in mixtures (roughly comparable to STP designs) compared with monoclonal blocks, validation studies would be relatively easy, based on historical data and would move towards understanding how clones may behave relative to seedlings over time.

In the longer-term there are two options. Firstly, clonal trials that suit the development of models need to be established. These trials should be designed to maximise site coverage and represent clones planted in the current forest estate. Collaboration with the Radiata Pine Breeding Consortium or other Cooperatives could be considered to reduce the costs, particularly if a multi-purpose design can be built to suit multiple parties. Secondly, the SGMC could simply wait until inventory data is taken on clonal plantings and use this for model validation and/or development.

Even if no research is undertaken until inventory age, there are a number of fundamental science questions about clones that should be addressed over the next few years. These are outlined below as a number of project proposals.

Research areas and project recommendations

Based on this survey, and the discussion that it stimulated, below are a number of research proposals that SGMC may consider.

1. Mixtures vs MonoClonal blocks
   - Rationale: What are the clonal growth patterns when they are planted in mixtures versus in monoclonal plantings and what is the difference in variance between these and seedlots? If clones grown in mixes or monoclonal stands don't differ significantly, then they should be able to be accounted for in current models.
   - Tui Glen trial at Kawerau recommended for this purpose.
   - Perceived priority: high.
   - Would probably have to be done in collaboration with PMCoop.

2. Validate existing models for clones
   - Rationale: if clonal data can be found that will adequately test the current growth models, then this exercise will help determine if separate models for clones really need to be developed.
   - Process: Good clonal data needs to be used over more than one site.
   - Perceived priority: medium.

3. Next generation of modelling trials
   - Rationale: Develop a resource for future modelling. This would be an investigation on the trial design based on the 'Goulding response surface design'.
   - Process: Trial design and proposal to RPBC/other Cooperatives for collaboration.
   - Perceived priority: medium-low.

4. Distance-dependent model development
   - Rationale: Utilise the STP- design trials that are closer to rotation age to examine the behaviour of clones
   - Process: Intensive research for new distance-dependent model development (possibly PhD student).
   - Perceived priority: medium.

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Appendix 1. Clonal survey questions.

A: Clonal trials

Trial name
Controller
Trial location
Region
Year Planted
No of clones in trial
Plot size
Treatments
Clone Type
Plot Type
No. Reps
Controls
Would you allow PSPs to be set up in trial?
If yes - would you allow the PSP data to be used in model development?
Current Measurements
Available modelling?
Would you require the clonal identity masked?
Design
Current use/Purpose of the trial

B: Clonal blocks

Name/ID
Controller
Location
Year Planted
No of clones in block
Plot size
Treatments
Clone Type
Controls
Would you allow PSPs to be set up in the block?
IF Yes - would you allow the PSP data to be used in model development?
Current Measurements
Would these current measurements be available to SGMC for modelling purposes?
Would you require the clonal identity masked?
Describe the current use of the block

Appendix 2. Participants in the clonal survey.

NAME	COMPANY	REPLY RECEIVED
Hugh Goodacre	Carter Holt Harvey Forests	►
Peter Oliver	City Forests Ltd	►
Steve Dowman	Ernslaw One Ltd	-
Ross Wade	Hikurangi Forest Farms Ltd	► (no clones)
Brian Garnett	Pan Pac Forest Products Ltd	►
Jeff Schnell	P.F. Olsen & Co Ltd	-
Doug Long	Rayonier NZ Ltd	► (via Cellfor)
Hugh Stevenson	Selwyn Plantation Board	-
Ross Jackson	Timberlands West Coast Ltd	-
Simon Papps	Kaingaroa Timberlands	► (no information)
James McEwan	Wenita Forest Products Ltd	►
Marion Hughes	Weyerhaeuser NZ Inc	►
Dave Lowry	Horizon2	► (would not fill in survey)
Ian Jenkin	Hancock Forest Management	► (via J. Snook)
Mike Carson	Carson Asscociates/Forest Genetics	►
Paul Jefferson	Radiata Pine Breeding Consortium	-
Ensis Internal		
Toby Stovold	Ensis Genetics	► (from original survey)
Mark Dean	Plantation Management Coop.	► (from original survey)
Peter Beets	Health + Site productivity	► (from original survey)

Appendix 3. Clonal trial details for all the survey respondents. Note, not all information was available for all trials.
(STP = single-tree plot, SIR = sets-in-replicates, LB = large blocks, RB = Randomised block, RCB = randomised complete block, RIB = randomised incomplete block. Blank boxes indicate that no data was supplied, although it still may be available.

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
1	Part stand 42.06	PanPac	Esk	HB	1999	168	32mx24.4m	no thin, 100% prune to 6.5m	Mixed	STP	5	Yes	annual
2		PM Coop[1]	Walwa	NSW	1989	20		Nelder	Single		2	Yes	
3	3525 TH23	CHHF	Omataroa	BP	2000	1	0.06 in 0.16	Plant & leave (333,555,833,1111 s/ha), Thin early & thin late (833 -> 333)		Blocks	4		only pre-thin
4	AK 840/1	Ensis Genetics/RPBC	POUT	NT	1984		2.6						
5	AK 840/2	Ensis Genetics/RPBC	HOSK	NT	1984								
6	AK 842/0	Ensis Genetics/RPBC	TIRU	WK	1979		0.4						
7	AK973/1	Ensis Genetics/RPBC	TIRU	WK	1983		0.125						
8	AK973/2	Ensis Genetics/RPBC	POUT	NT	1983		8.1						
9	CHH Clonal trial 1 - WI003	Weyerhaeuser	Golden Downs	NN	2001	287	24mx27m	Single Tree Plots	Refer to Horizon2	STP	9	GF17	No
10	CHH Clonal trial 2 - WI006	Weyerhaeuser	Golden Downs	NN	2003	251	24mx27m	Single Tree Plots	Refer to Horizon2	STP	9	GF17	No
11	CNZ_1999a_1	Forest Genetics[2]		GS	1999	170		Na	Mixed	STP	5	Y	
12	CNZ_1999a_2	Forest Genetics		HB	1999	170		Na	Mixed	STP	5	Y	
13	CNZ_1999a_3	Forest Genetics		WM	1999	170		Na	Mixed	STP	5	Y	
14	CNZ_1999a_4	Forest Genetics		SD	1999	130		Na	Mixed	STP	5	Y	
15	CNZ_2000a_1	Forest Genetics		WM	2000	300		Na	Mixed	STP	5	Y	
16	CNZ_2000a_2	Forest Genetics		WM	2000	125		Na	Mixed	STP	5	Y	
17	CNZ_2000a_3	Forest Genetics		GS	2000	250		na	Mixed	STP	5	Y	
18	CNZ_2000a_4	Forest Genetics		HB	2000	170		na	Mixed	STP	5	Y	

[1] PM Coop = Plantation Management Cooperative
[2] CellFor trading through Forest Genetics

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
19	CNZ_2000a_5	Forest Genetics		SD	2000	170		na	Mixed	STP	5	Y	
20	CNZ_2000a_6	Forest Genetics[3]		NN	2000	280		na	Mixed	STP + row	5	Y	
21	CNZ_2000a_7	Forest Genetics		SD	2000	250		na	Mixed	STP	5	Y	
22	CNZ_2001a_1	Forest Genetics		BP	2001	250		na	Mixed	STP	7	Y	
23	CNZ_2001a_2	Forest Genetics		BP	2001	250		na	Mixed	STP	7	Y	
24	CNZ_2001a_3	Forest Genetics		HB	2001	250		na	Mixed	STP	7	Y	
25	CNZ_2001a_4	Forest Genetics		SD	2001	210		na	Mixed	STP	7	Y	
26	CNZ_2001a_5	Forest Genetics		SD	2001	210		na	Mixed	STP	7	Y	
27	CNZ_2001a_6	Forest Genetics		GS	2001	210		na	Mixed	STP	7	Y	
28	CNZ_2001a_7	Forest Genetics		WM	2001	170		na	Mixed	STP	7	Y	
29	CNZ_2001a_8	Forest Genetics		SD	2001	170		na	Mixed	STP	7	Y	
30	CNZ_2003a_1	Forest Genetics		SD	2003	22		na	Single	LB	2	Y	
31	CNZ_2003a_2	Forest Genetics		BP	2003	22		na	Single	LB	2	Y	
32	CNZ_2003b_1	Forest Genetics		BP	2003	440		na	Mixed	STP	10	Y	
33	FR 129/1	Ensis Genetics/RPBC	KINL	WK	1990								
34	FR 129/2	Ensis Genetics/RPBC	GWAV	HB	1990		1.9						
35	FR 131/0	Ensis Genetics/RPBC	KINL	WK	1990		0.48						
36	FR 173/1	Ensis Genetics/RPBC	KINL	WK	1992		1.6						
37	FR 173/2	Ensis Genetics/RPBC	ROEU	BP	1992		2.4						
38	FR 174/1	Ensis Genetics/RPBC	KINL	WK	1992		0.1						
39	FR 174/2	Ensis Genetics/RPBC	KANG	BP	1992		0.1						
40	FR 205/1	PM Coop	WOOD	AK	1993	20	11.34						
41	FR 205/2	PM Coop	TAWE	BP	1993	20	11.34						
42	FR 218/0	Ensis Genetics/RPBC	ROEU	BP	1992	30	0.22		Single	Row pl	2		
43	FR 219/1	Ensis Genetics/RPBC	ROEU	BP	1993	36	1.57		Mixed	STP	5		
44	FR 219/2	Ensis Genetics/RPBC	TAWE	BP	1993		0.8		Single	Row	6		
45	FR 230/0	Ensis Genetics/RPBC	ROEU	BP	1993	6	0.8		Single	Row	4		
46	FR 231/0	Ensis Genetics/RPBC	KANG	BP	1994		3.52						
47	FR 232/1	Ensis Genetics/RPBC	HKGI	NT	1994								
48	FR 232/10	Ensis Genetics/RPBC	GLEL	OT	1994		2						

[3] CellFor trading through Forest Genetics

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
49	FR 232/11	Ensis Genetics/RPBC	LONG	SD	1994		0.7						
50	FR 232/2	Ensis Genetics/RPBC	TIRU	WK	1994								
51	FR 232/3	Ensis Genetics/RPBC	KINL	WK	1994		1.2						
52	FR 232/4	Ensis Genetics/RPBC	WIND	GS	1994		0.9						
53	FR 232/5	Ensis Genetics/RPBC	RUKU	HB	1994		1.05						
54	FR 232/6	Ensis Genetics/RPBC	HOWV	NN	1994		0.58						
55	FR 232/7	Ensis Genetics/RPBC	BALM	CY	1994		0.63						
56	FR 232/8	Ensis Genetics/RPBC	ALLA	OT	1994		0.6						
57	FR 232/9	Ensis Genetics/RPBC	GLEL	OT	1994		0.9						
58	FR 233/0	Ensis Genetics/RPBC	RUKU	HB	1994		2.15						
59	FR 233/0	Ensis Genetics/RPBC	RUKU	HB	1994		2.15						
60	FR 234/1	Ensis Genetics/RPBC	CWMV	BP	1994		0.31						
61	FR 234/2	Ensis Genetics/RPBC	MAMA	BP	1994		0.31						
62	FR 235/1	Ensis Genetics/RPBC	TIRU	WK	1994		0.05						
63	FR 235/2	Ensis Genetics/RPBC	KINL	WK	1994		0.2						
64	FR 235/3	Ensis Genetics/RPBC	FRIG	BP	1994		0.01						
65	FR 236/0	Ensis Genetics/RPBC	CWMV	BP	1994		6.25						
66	FR 264/0	Ensis Genetics/RPBC	KINL	BP	1995	16	1.8		Mixed	STP	20		
67	FR 265/0	Ensis Genetics/RPBC	WOOD	AK	1995		1.7		Single	Row	4		
68	FR 266/0	Ensis Genetics/RPBC	RUAT	GS	1995	48	1.2		Mixed	STP	15		
69	FR 267/0	Ensis Genetics/RPBC	ROEU	BP	1995	48	2.14		Mixed	STP	10		
70	FR 268/0	Ensis Genetics/RPBC	MAMA	BP	1995		1.7						
71	FR 270/0	Ensis Genetics/RPBC	MAMA	BP	1995		0.3						
72	FR 271/0	Ensis Genetics/RPBC	MAMA	BP	1995		0.15						
73	FR 283/0	Ensis Genetics/RPBC	ROEU	BP	1996		2						
74	FR 284/0	Ensis Genetics/RPBC	KANG	BP	1996		2						
75	FR 285/0	Ensis Genetics/RPBC	BRAN	BP	1996		1.7						
76	FR 286/1	Ensis Genetics/RPBC	BRAN	BP	1996	20	0.32		Mixed	STP	10		
77	FR 286/2	Ensis Genetics/RPBC	WAPU	NT	1996	20	0.32		Mixed	STP	10		
78	FR 290/0	Ensis Genetics/RPBC	WAPU	NT	1996								
79	FR 291/0	Ensis Genetics/RPBC	KINL	BP	1996	42	3.03		Mixed	STP	5		
80	FR 293/0	Ensis Genetics/RPBC	KINL	BP	1996		1.5			Demo			

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
81	FR 3/2	Ensis Genetics/RPBC	WAIP	BP	1987		2.92						
82	FR 305/3	Ensis Genetics/RPBC	PURU	WK	1997		0.1						
83	FR 308	PM Coop	TAWE	BP	1995	16	0.1225		Mixed		3		3
84	FR 311/0	Ensis Genetics/RPBC	WOOD	AK	1997		1.7		Single	Row	6		
85	FR 311/0	Ensis Genetics/RPBC	WOOD	AK	1997		1.7						
86	FR 313/0	Ensis Genetics/RPBC	MANT	GS	1997		1.3			Row	5		
87	FR 313/0	Ensis Genetics/RPBC	MANT	GS	1997		1.3						
88	FR 340/1	Ensis Genetics/RPBC	LMIL	BP	1997		0.32						
89	FR 340/2	Ensis Genetics/RPBC	CHAS	BP	1997		0.22						
90	FR 366/0	Ensis Genetics/RPBC	WATR	WM	1999		1.25						
91	FR 377/0	Ensis Genetics/RPBC	WATR	WM	1999	24	0.35		Mixed	STP	10		
92	FR 382/0	Ensis Genetics/RPBC	COXI	NT	2000		1						
93	FR 398/0	Ensis Genetics/RPBC	GWAV	HB	2000		0.8		Single	Row	5		
94	FR 421/1	Ensis Genetics/RPBC	OLIP	BP	2001	250	2.8		Mixed	STP	6		
95	FR 421/2	Ensis Genetics/RPBC	SLAB	WK	2001	250	2.8		Mixed	STP	6		
96	FR 422/0	Ensis Genetics/RPBC	ONUK	BP	2001	30	2.02		Mixed	STP	8		
97	FR 423/ 6 CLONAL	Weyerhaeuser	Golden Downs 132/11	NN	2001	287?	18mx24m		Refer to Ensis	Single Tree	3		Yes
98	FR 423/ 7 CLONAL	Weyerhaeuser	Wairau Nth 1/6	MB	2001	287?	18mx24m		Refer to Ensis	Single Tree	3		Yes
99	FR 423/1	Ensis Genetics/RPBC	OLIP	BP	2001	220	1.04		Mixed	STP block	3		
100	FR 423/2	Ensis Genetics/RPBC	SLAB	WK	2001	220	1.04		Mixed	STP block	3		
101	FR 423/3	Ensis Genetics/RPBC	WAPI	OT	2001	220	1.04		Mixed	STP block	3		
102	FR 423/4	Ensis Genetics/RPBC	KELP	NT	2001	220	1.04		Mixed	STP block	3		
103	FR 423/5	Ensis Genetics/RPBC	WOOK	AK	2001	220	1.04		Mixed	STP block	3		
104	FR 423/6	Ensis Genetics/RPBC	GDNE	NN	2001	220	1.04		Mixed	STP block	3		Yes
105	FR 423/7	Ensis Genetics/RPBC	WIRU	MB	2001	220	1.04		Mixed	STP block	3		
106	FR 423/8	Ensis Genetics/RPBC	WMWD	WC	2001	220	1.04		Mixed	STP block	3		
107	FR 423/9	Ensis Genetics/RPBC	FLAP	CY	2001	220	1.04		Mixed	STP block	3		
108	FR 442 / 01	Ensis Environment	ANIS	NN	2002	40	1.5		Mixed	block	4	1 mxd plot 10 diff seedlings	

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
109	FR 442 / 02	Ensis Environment	MAHI	HB	2002	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
110	FR 442 / 03	Ensis Environment	BALM	CY	2002	40	1.3		Mixed	block	4	1 mxd plot 10 diff seedlings	
111	FR 442 / 04	Ensis Environment	LVER	WK	2002	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
112	FR 442 / 05	Ensis Environment	FOCR	CY	2003	40	1.23		Mixed	block	4	1 mxd plot 10 diff seedlings	
113	FR 442 / 06	Ensis Environment	BERK	OT	2003	40	0.8		Mixed	Block	4	1 mxd plot 10 diff seedlings	
114	FR 442 / 07	Ensis Environment	LAWF	OT	2003	40	1.4		Mixed	block	4	1 mxd plot 10 diff seedlings	
115	FR 442 / 08	Ensis Environment		BP	2005	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
116	FR 442 / 09	Ensis Environment		BP	2004	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
117	FR 442 / 10	Ensis Environment		BP	2005	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
118	FR 442 / 11	Ensis Environment		WC	2004	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
119	FR 442 / 12	Ensis Environment		WC	2004	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
120	FR 442 / 14	Ensis Environment		AK	2005	40			Mixed	block	4	1 mxd plot 10 diff seedlings	
121	FR 442 / 15	Ensis Environment		AK	2004	40			Mixed	Block	4	1 mxd plot 10 diff seedlings	
122	FR 443/1	Ensis Environment	PURU	WK	1997	400	1.5		Mixed	Block	6		
123	FR 443/2	Ensis Environment	PURU	WK	1997	80	2.5		Mixed	Block	10	GF30 and Puruki conrols, GF7 KS	
124	FR 443/4	Ensis Environment	PURU	WK	1997	80	1.1		Mixed	Block	81	surrounded by Jeff's clones	
125	FR 443/5	Ensis Environment	PURU	WK	1997		1.8		Seedlots	Block/row		rows of control seedlots	

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
126	FR 443/6	Ensis Environment	PURU	WK	1997	20	1.25		Families/ clones	Row	?6	rows of control seedlots	
127	FR 450/0	PM Coop	KA23 (Tui Glen)	BP	1988	4	0.1225				2		2(PSP)
128	FR 450/1	PM Coop	TUMB	AUS	1989	4	0.1				2		1(PSP)
129	FR 125/1	Ensis Genetics/RPBC	TAHO	BP	1990	225	3.78	Prune, no thin	Mixed	STP	10:8	Y	
130	FR 125/2	Ensis Genetics/RPBC	TAHO	BP	1990	35	1.72	Prune, no thin	Single	Row	2:0	Y	
131	FR 205/1	Ensis Genetics/RPBC	WOOD	AK	1993	23	11.34	Prune, 2 thin regimes	Mixed	LB	2:?		
132	FR 205/2	Ensis Genetics/RPBC	TAWE	BP	1993	23	11.34	Prune, 2 thin regimes	Mixed	LB	2:?		
133	FR 221/0	Ensis Genetics/RPBC	KANG	BP	1994		1.53						
134	FR 261/1	Ensis Genetics/RPBC	KANG	BP	1995	200	1.9		Mixed	STP	2:7	Y	
135	FR 305/1	Ensis Genetics/RPBC	TAWE	BP	1997	500	2		Mixed	STP	6		
136	FR 305/1	Ensis Genetics/RPBC	TAWE	BP	1997	190	2		Mixed	STP	6:5	Y	
137	FR 305/1	Ensis Genetics/RPBC		BP	1997	330			Mixed	STP	6:10	Y	
138	FR 305/2	Ensis Genetics/RPBC	WOOD	AK	1997	500	2		Mixed	STP	6		
139	FR 305/2	Ensis Genetics/RPBC	WOOD	AK	1997	190	2		Mixed	STP	6:5	Y	
140	FR 305/2	Ensis Genetics/RPBC		AK	1997	330			Mixed	STP	6:10	Y	
141	FR 353/1	Ensis Genetics/RPBC	TAWE	BOP	1999	500	4.32		Mixed	STP	6		
142	FR 353/1	Ensis Genetics/RPBC	TAWE	BP	1999	530	4.32		Mixed	STP	6:9	Y	
143	FR 353/2	Ensis Genetics/RPBC	KINL	BP	1999	500	4.32		Mixed	STP	6		
144	FR 353/2	Ensis Genetics/RPBC	KINL	WK	1999	530	4.32		Mixed	STP	6:9	Y	
145	FR 353/3	Ensis Genetics/RPBC	WOOD	AK	1999	500	4.32		Mixed	STP	6		
146	FR 353/3	Ensis Genetics/RPBC	WOOD	AK	1999	530	4.32		Mixed	STP	6:9	Y	
147	FR6	Ensis Genetics/RPBC	KANG	BP	1987	430	3.7		Mixed	STP	6:8	Y	
148	Part stand 42.06	PanPac	Esk	HB	2000	168	30.4x22.8m	no thin, 100% prune to 6.5m	Mixed	Single tree	5	Yes	annual
149	Part stand 79.01	PanPac	Esk	HB	2001	252	30.4x22.8m	no thin, 100% prune to 6.5m	Mixed	Single tree	7	Yes	annual
150	RO 157	FR G&Q[4]		BP	1972		0.15						
151	RO 161	FR G&Q		BP	1972		0.15						
152	RO 158	FR G&Q		BP	1972		0.15						

[4] current ownership not identified

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
153	RO 162	FR G&Q		BP	1972		0.15						
154	FR425	PM Coop	HORT	UK	1992	168	0.1		Mixed	STP	6		3 (PSP)
155	RO 1887/1	Ensis Genetics/RPBC	KANG	BP	1983		2						
156	RO 1887/2	Ensis Genetics/RPBC	LTAU	WK	1983		2						
157	RO 1887/3	Ensis Genetics/RPBC	TIKI	BP	1983								
158	RO 1887/4	Ensis Genetics/RPBC	TAWE	BP	1983								
159	RO 1954/0	Ensis Genetics/RPBC	KANG	BP	1978		6						
160	RO 1972/2	Ensis Genetics/RPBC	KANG	BP	1979		0.38						
161	RO 1973/0	Ensis Genetics/RPBC	KANG	BP	1979								
162	RO 1990/1	Ensis Genetics/RPBC	ROEU	BP	1979		0.4						
163	RO 2004/1	Ensis Genetics/RPBC	TIKI	BP	1984		2.6						
164	RO 2004/2	Ensis Genetics/RPBC	TAWE	BP	1984		2.6						
165	RO 2004/3	Ensis Genetics/RPBC	MILA	BP	1984		2.6						
166	RO 2004/4	Ensis Genetics/RPBC	TAHO	WK	1984		2.6						
167	RO 2004/5	Ensis Genetics/RPBC	LTAU	WK	1984		2.6						
168	RO 2005/1	Ensis Genetics/RPBC	MTNG	BP	1984								
169	RO 2058/1	Ensis Genetics/RPBC	KANG	BP	1985		0.6						
170	RO 2058/2	Ensis Genetics/RPBC	KANG	BP	1985		1.1						
171	RO 368/0	Ensis Genetics/RPBC	HORO	BP									
172	RO 585/0	Ensis Genetics/RPBC	HORO	BP									
173	RO 586/0	Ensis Genetics/RPBC	HORO	BP	1970		0.4						
174	RO 599/0	Ensis Genetics/RPBC	KANG	BP	1974								
175	RO 961/1	Ensis Genetics/RPBC	HORO	BP	1965								
176	RO 961/10	Ensis Genetics/RPBC	HORO	BP									
177	RO 961/4	Ensis Genetics/RPBC	HORO	BP	1965								
178	RO 961/5	Ensis Genetics/RPBC	HORO	BP									
179	RO 961/6	Ensis Genetics/RPBC	HORO	BP									
180	RO 961/8	Ensis Genetics/RPBC	HORO	BP									
181	RO 961/9	Ensis Genetics/RPBC	HORO	BP									
182	RO 962/2	Ensis Genetics/RPBC	MAMA	BP	1969		2						
183	RO 964/0	Ensis Genetics/RPBC	MAMO	BP									
184	RO 965/1	Ensis Genetics/RPBC	MAMO	BP									

Trial No.	Trial name	Controller	Trial location	Region	Year	No of clones in trial	Plot size	Treatments	Clone Type	Plot Type	No. Reps	Controls	Current Measmts
185	RO2097/1	Ensis Genetics	MANW	BP	1986	190	1.77	Thin after age 10	Mixed	STP	5:5	Y	
186	RO2097/2	Ensis Genetics	KANG	BP	1986	190	1.82	Thin after age 10	Mixed	STP	5:5	Y	
187	Stand 140.06	PanPac	Mohaka	HB	2004	264	24x27m	no thin - prune all @ age5 to 2m	Mixed	STP	9	Y	
188	Tree and Tech (H2) Clonal Trial 5082	Weyerhaeuser	Golden Downs 60/7	NN	1996	35	30x18m	Blocks	Refer to Horizon2	Clonal Blocks		Y (GF19)	Yes
189	WN 287/1	Ensis Genetics/RPBC	WILG	HB	1984								
190	WN 287/2	Ensis Genetics/RPBC	GATJ	WN	1984								