FUTURE FORESTS RESEARCH

RADIATA MANAGEMENT TECHNICAL NOTE Site Productivity

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Matching Genotypes to Site Resources and Silvicultural Inputs for Optimising Radiata Pine Health, Growth and Wood Quality

Summary

As forest managers move toward site-specific management, an understanding of how genotypes perform at specific sites and with silvicultural treatments is necessary. Matching the most appropriate planting stock to local conditions will help to optimise tree health, growth and wood quality in intensively managed radiata pine forests. This technical note summaries the relative contributions of site, silvicultural inputs and deployment of genetically improved genotypes in improving productivity of radiata pine plantations and their interactions across a range of sites with contrasting climatic and soil characteristics.

We measured tree health, growth and wood quality of radiata pine growing under a range of site conditions. The important results are:

- There were significant site, genotype and silvicultural effects, and interactions of site x genotype and silviculture x genotype for tree growth and health (especially for nutrition-related upper mid-crown yellowing), stem slenderness and wood stiffness.
- Site condition or resource availability is the most important factor in determining tree health, growth and wood quality of radiata pine.
- Within a climatic zone, more growth gain could be obtained through manipulating silvicultural inputs than deployment of genetically improved genotypes, especially at low rainfall sites.
- Tree breeders should consider the interaction of genotype by environment to avoid missing a genotype that performed, on average, poorly but did well when grown at a specific site (or silvicultural regimes) or selecting a genotype that, on average, performed well but did poorly when grown in a particular environment (or silvicultural regime).

In the near future, a robust site/soil classification system also needs to be developed for site specific management to optimise the product output from radiata pine plantations through managing the interaction between site, genetics and silvicultural inputs (e.g. fertilisers, weed control).

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Introduction

Increasing per ha yield and reducing the unit cost of wood production is an important component of sustained global competitiveness for plantation forest products exported from New Zealand. The key to doubling forest production is increased efficiency in the utilisation of resources. That means increased productivity per hectare and per dollar. The genetic improvement of planting stock and maximising growth through silvicultural practice are two strategies for achieving higher yield [1].

As forest managers move toward site-specific management, an understanding of how genotypes respond to site resources (e.g. water and nutrient availability) and silvicultural inputs is necessary. This will help match the most appropriate planting stock to local conditions, and optimise forest health, growth and wood quality in intensively managed radiata pine forests. Most tree improvement programmes have selected families or clones that perform well across a wide range of sites. These ‘‘generalist’’ genotypes have been valuable in deployment programs, but as genetic and silvicultural inputs intensify, the question remains: are these genotypes optimal for every silvicultural system, site type, and end product [2]?

For example, the nutritional needs and responses of radiata pine stands to fertiliser additions vary considerably across New Zealand [3]. Despite improvements in making site-specific management prescriptions, both researchable and practical questions remain regarding the interactions among, and decisions made in, genetic deployment and silvicultural treatment inputs. Undoubtedly, large additional improvements will result in managing the health, productivity, and value of radiata pine stands

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as the nature and magnitude of these interactions are better understood.

As tree breeders learn more about the trade-offs between risk and gain from more genetically homogeneous plantations [4], we expect that fewer and fewer genotypes will be deployed across the landscape. Knowledge about how these limited numbers of genotypes will respond to silvicultural treatments, climatic, edaphic variables, and diseases will be critical for landowners to optimise deployment decisions [1, 2].

The aim of this study is to measure the relative contributions of site, silvicultural inputs and deployment of genetically improved genotypes to increase productivity of radiata pine plantations across a range of sites.

Materials and Methods

Trial Design and Genetic Material

A nationwide clonal trial series was established in 2002-05 at 14 sites covering a range of soils and climates (Figure 1) [5].

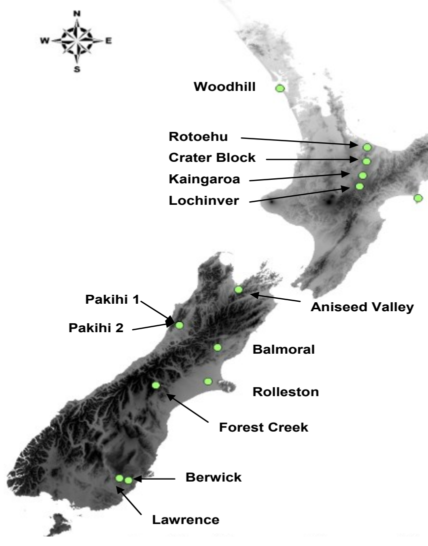

Figure 1. Locations of 14 trials.

For each of 14 trials, there are 4 plots. Three ramets of each of 40 radiata pine clones were randomly planted in each plot.

- Of the 40 clones, 20 clones (referred to as GTI clones) were created through fascicle cuttings from the control-pollinated families selected for high volume growth rate and improved stem form (GF24-31) but unknown nutritional characteristics.
- The remaining 20 clones (referred to as Puruki clones) were created through fascicle cuttings from the seedlings of open-pollinated families (GF7) selected for different nutrition-related upper mid-crown yellowing (UMCY) symptom scores and diameter growth.

Measurements and Data Analyses

Height and DBH were measured for individual trees in each trial at age 5. Tree stem volume was calculated from both DBH and height.

UMCY symptom was scored at a scale of 1-5 for young trees before canopy closure for five of 14 sites more susceptible to Mg deficiency (Lochinver, Kaingaroa, Crater Block, Berwick and Lawrence) [6]. Wood stiffness, measured as the modulus of elasticity (MOE), was determined by using IML electronic hammer on standing trees in the Rolleston and Kaingaroa trials only [5]. Foliar $\delta^{13}C$, an indicator for water use efficiency (WUE) [7], was analysed for the Aniseed Valley, Balmoral and Mahia trials.

Data Analysis

Two-way analyses of variance were conducted to test the main effects and interaction of clone and site, or fertiliser or weed control (WC) on growth, UMCY, WUE ($\delta^{13}C$), stem slenderness and MOE. Duncan's multiple range test was used for multiple comparisons.

Results and Discussion

There were significant effects of site and clone on tree volume, stem slenderness, MOE, UMCY score and WUE (Table 1). The site-by-clone interactions were significant for all measured parameters except WUE (Table 1). For all measured parameters except MOE, site had stronger effect than clone, while the interactions of site-by-clone were relatively smaller (Table 1). The best and worst 5 clones for each measured trait are in Appendix 1.

Table 1. F-values and *p* values for the site, clone and interaction effects on the measured parameters.

	Tree Volume (cm^3)	Stem slender-ness (m/m)	Stem MOE (GPa)	UMCY score	WUE ($\delta^{13}C$, ‰)
Site	138	1088	21.8	83.2	1472
	p<0.001	p<0.001	p<0.001	p<0.001	p<0.001
Clone	6.92	2.90	23.5	17.1	5.31
	p<0.001	p<0.001	p<0.001	p<0.001	p<0.001
S x C	5.09	2.50	3.80	2.99	1.15
	p<0.001	p<0.001	p<0.001	p<0.001	n.s.

Some site-by-clone interactions could be driven by soil factors (Figure 1) or both climatic and edaphic factors (Figure 2). Some site-by-clone interactions could be mainly driven by rainfall (e.g. Aniseed Valley vs Balmoral sites), or temperature (e.g. Mahia vs Berwick sites) differences (data not shown).

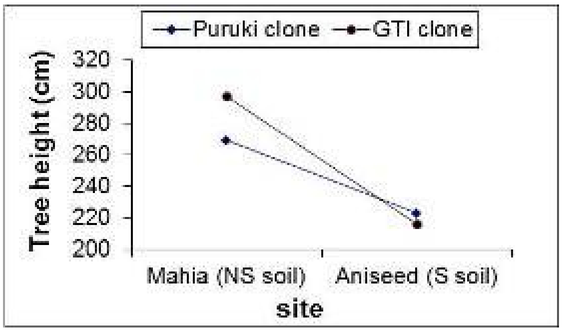

Figure 1. Tree height responses of clones to site heterogeneity in resource availability

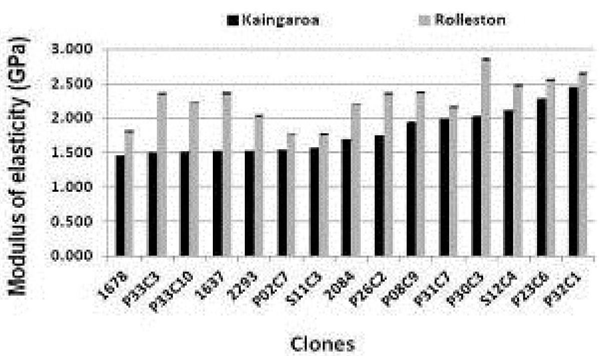

Figure 2. Tree modulus of elasticity (MOE) responses of clones to site heterogeneity in resource availability

Tree health, growth, WUE and wood quality varied with site conditions. The significant clonal effects indicate the average gains (e.g. 31 mm increment in DBH) in tree health and growth and wood quality could be generally achieved through deployment of the overall better clones (generalist genotypes). However, the significant interactions of site-by-clone indicate that the additional gain (e.g. 21 mm increment in DBH) could be obtained by matching specific clones (specialist genotypes) to site conditions.

Similarly, there were significant effects of the silvicultural inputs (i.e. WC or N fertilisation), clone and silvicultural input-by-clone interactions on tree volume, stem slenderness and MOE (Table 2). Silvicultural inputs had stronger effect (than clone) on tree growth and stem slenderness, while clone had stronger effect on stem MOE. The interactions of silvicultural input-by-clone were relatively smaller (Table 2). The overall best and worst 5 clones for each measured trait are in Appendix 1.

Table 2. F-values and p values for the WC, N fertilisation, clone and interaction effects on the measured parameters.

	Tree Volume (cm^3)	Stem slenderness (m/m)	Stem MOE (GPa)	Tree Volume (cm^3)
WC	675	51.6	11.7	42.1
(or N)	p<0.001	p<0.001	p<0.001	p<0.001
Clone (C)	7.26	12.9	52.4	7.17
(Clone)	p<0.001	p<0.001	p<0.001	p<0.001
WC x C	1.59	2.06	5.45	1.45
(or N x C)	p<0.01	p<0.05	p<0.01	p<0.05

WC: weed control; N: N fertilisation. The N, clone and NxC effects are presented in the highlighted column.

The site-by-clone interactions could be mainly driven by soil moisture (Figure 3) or soil N fertility (Figure 4).

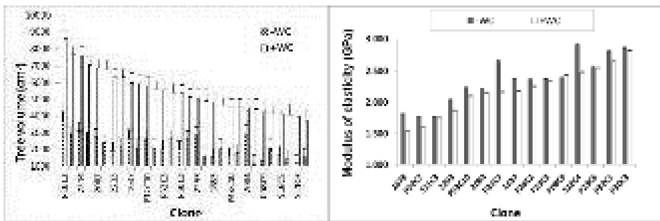

Figure 3. The tree volume (left) and MOE (right) responses of clones to different level of Weed Control (WC).

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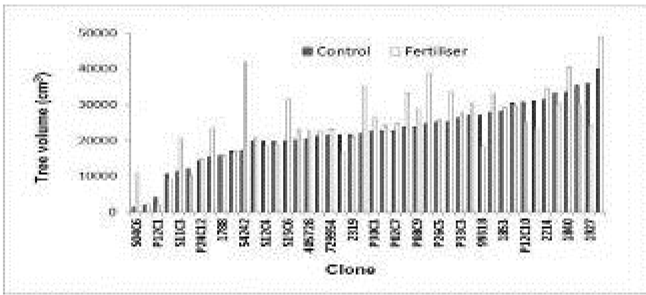

Figure 4. The tree volume responses of clones to N fertiliser treatments

These results highlight manipulating silvicultural inputs and genotype deployment could considerably change tree growth and wood quality. Again the significant interactions of silvicultural input-by-clone indicate that the additional gain in tree growth (e.g. 0.04 m^3 volume increment) and wood quality (e.g. 0.9 GPa MOE increment) could be obtained by matching specific clones (specialist genotypes) to local silvicultural regimes.

Conclusions

- Site condition (mainly resource availability) is the most important factor in determining tree health, growth and wood quality of radiata pine.
- Within the same climatic zone, more growth gain could be obtained through manipulating silvicultural inputs (e.g. fertiliser and weed control) than deployment of genetically improved genotypes, especially in low rainfall sites.
- Tree breeders should consider the genotype by environment interaction (GEI) to avoid missing a genotype that performed, on average, poorly but did well when grown in specific environments (or silvicultural regimes) or selecting a genotype that, on average, performed well but did poorly when grown in a particular environment (or silvicultural regime).
- Tree breeders can identify genotypes with specific adaptation as well as those with broad adaptation. Broad adaptation provides stability against the variability inherent in an ecosystem, but specific adaptations may provide a significant growth advantage in particular environments.
- Large GEI presents many challenges for breeders and has significant implications in tree breeding programmes. The breeder may be faced with developing separate populations for marginal sites where genotypic rankings drastically change and/or be faced with selecting genotypes that generally perform well across many sites.
- It is also important to develop robust site/soil classification systems in the future for site specific management to optimise or maximise the product output from radiata pine plantations through managing the interaction between site, genotypes and silvicultural inputs (e.g. fertilisers).

Acknowledgements

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Appendix 1. Identified clones with contrasting characteristics

	Growth	WUE ($\delta^{13}C$)	N response type	MOE	Slender-ness	Weed responsive -ness	UMCY status
Top 5 clones							
1	P26C2	1966	1537	P32C1	P30C3	P26C2	1840
2	1840	1927	1840	P30C3	P23C6	2214	2468
3	2319	2293	2214	P23C6	S15C6	1840	2583
4	P08C9	2002	P33C10	S12C4	P33C3	1678	1678
5	1788	P26C2	1927	P26C2	P26C2	2002	S12C4
Bottom 5 clones							
1	S15C6	S16C5	P12C1	1678	P24C12	S11C3	S07C8
2	2168	P32C1	2168	P02C7	2233	P23C6	2084
3	P24C12	2110	1788	S11C3	1853	P31C7	P08C9
4	P31C7	P33C3	2084	2293	2168	P24C12	P07C10
5	1608	2469	S15C6	2084	1608	P02C7	S02C1

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