A compact trial design with competition analysis to evaluate stand density and genetic effects in teak (*Tectona grandis*)

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Abstract
Careful management of stand density and deployment of advanced genetic material are important tools for manipulating stand growth and structure in teak (*Tectona grandis*) and other plantation species. Classical plot-based spacing trials have a number of shortcomings: in the range of inference provided, the number of sites that are usually represented, assumptions of environmental homogeneity, and sensitivity to mortality. Alternative spacing trial designs feature systematical variation in tree spacing, often in radial configurations. They are more compact and efficient but they may also be sensitive to environmental heterogeneity and mortality. Many teak plantations around the world are now established with clones which may have specific optimum density management schedules so a good spacing trial design should also allow for different genetic entries.

In this paper I present a compact systematic spacing trial design that is compatible with mechanized operations and allows for the inclusion of a genetic factor. The associated analysis to determine stand density and genetic (clone) effects on growth is demonstrated using simulated data. Periodic growth increment of individual trees was regressed on a competition index (CI) that represented distance to, and relative size of neighbours. The analysis successfully estimated the direct effects of age, clone, CI, and environmental blocks on growth increment as well as clone×age and clone×CI interactions. These results were translated into clone-specific growth responses to stocking and thinning over time. The proposed trial design lends itself to sound statistical analysis, is relatively insensitive to mortality, and enables the efficient collection of growth response data. Importantly, it is also compact and operationally convenient so it could be replicated multiple times in each region.

Keywords stand density management, spacing, thinning, competition, clone evaluation, trial design

Introduction

Around the world, managers of teak (*Tectona grandis*) plantations are faced with the task of achieving satisfactory investment returns using relatively short rotations of 20-30 years (Kollert & Cherubini 2012). In most cases this is only possible with careful management of stand density (spacing) and genetic selection to increase the growth rate of individual trees. Field trials of spacing treatments usually form the scientific basis of recommendations for initial stocking and thinning schedules. A common trial design includes rectangular plots to represent treatments of initial stocking or thinning intensity (examples for teak include: Callister 1997; Kanninen et al. 2004; Ola-Adams 1990). Although these trials have provided much information, they have a number of important limitations (Binkley 2008; Stape & Binkley 2010). The investigation is usually of a small number of treatments, which limits the range of inference and the potential for accurate interpolation. These trials are large so results from one or two sites are often applied across regions without adequate representation of site conditions. The large areas needed for each replicate can violate assumptions of site homogeneity and prevent the inclusion of a genetic factor with more than a couple of levels. Plot-based spacing trials are also sensitive to patchy mortality.

An alternative approach to spacing trial design is to systematically vary the tree positions in either radial (Nelder 1962) or rectangular arrangements (Lin & Morse 1975; Marynen 1963). These approaches are more compact so they are more easily replicated and they provide a more continuous representation of tree spacing. Although the radial designs outlined by Nelder (1962) have been the most commonly adopted designs for systematic spacing of forest trees, they also have drawbacks. Within-trial environmental trends are not estimable, and the highest density treatment is only replicated in one position within each trial. Missing trees still have a large influence on the analysis of systematic spacing trials and imputation has been used to replace missing values (Bar-Hen 2002).

Analysis of data from systematic spacing trials is usually based on regression of tree growth against the growing space available to each tree. A powerful alternative is to represent the competitive pressure on each tree using a competition index as the predictor for individual-tree growth. Competition indices can account for mortality and the effects of variations in neighbouring tree size. Competition indices are now well established in growth modeling applications (Chapter 8 of Pretzsch 2009; Chapter 2 of Weiskittel et al. 2011) and have been recommended for use in mixed-species trials (Bristow et al. 2006; Vanclay 2006).

Stand density effects on tree growth often depend on genotype. For example, spacing treatments have caused rank changes in growth amongst clones of eucalypt hybrids (Bouvet et al. 2003; Brouard & John 1999). *E. globulus* (Rodriguez Schafer & Ponce 2007), and poplar hybrids (Panetsos 1980). Spacing was also reported to affect genetic gain in douglas fir deployment (Ye et al. 2010). Although the evaluation and deployment of teak clones is now routine around the world (Goh et al. 2007; Monteuuis & Maitre 2007), the sensitivity of clones to spacing effects has not been reported.

This paper describes a compact spacing trial design with systematically variable within-row spacing and evenly spaced rows that could have been prepared for operational planting. The design accommodates the evaluation of genetic entries such as clones across the range of spacings that is trialed. The analysis of simulated data from this trial design is demonstrated using regression of periodic growth increment on a competition index.

Methods

Trial design

The foundational repeating unit of the spacing trial is two rows wide and 54 metres long (Figure 1) and it can be replicated many times in either dimension as necessary. With an inter-row spacing of 3.5 m the design provides between 3.5 m^2 and 42 m^2 of growing space per tree, equivalent to stand density between 2860 and 240 stems per hectare (sph; Table 1).

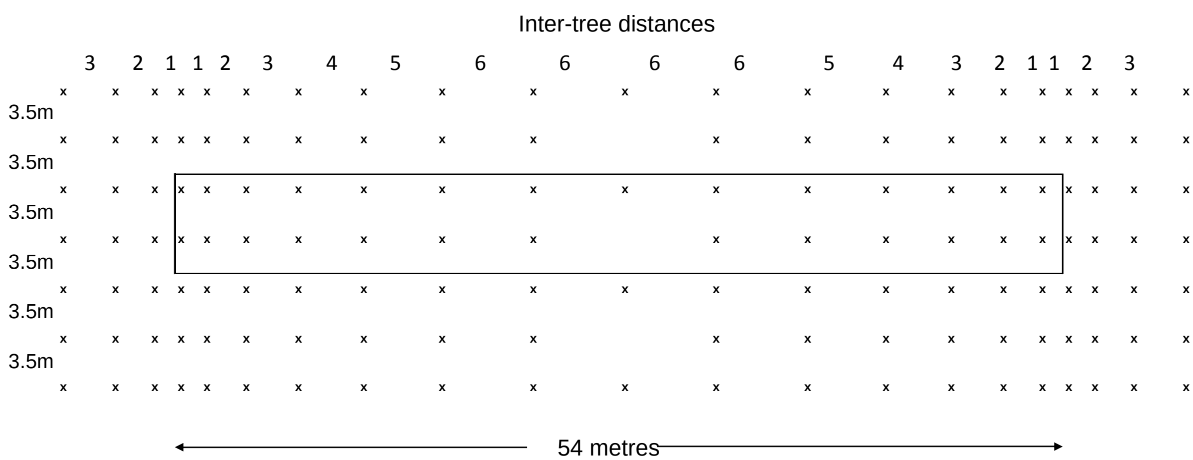

Figure 1. Diagram of the foundational repeating unit of the trial design (within the lines), comprising 29 trees in an area 7 m × 54 m. Rows are regularly spaced at 3.5 m. Tree positions are indicated by crosses.

Table 1. Representation of growing space per tree in the trial design illustrated in Figure 1.

Growing space (m^2)	Stand density (sph)	Rectangularity (length/width)	Representation
3.5	2857	3.5	14%
5.25	1905	2.3	14%
8.75	1143	1.4	14%
12.25	816	1.0	14%
15.75	635	1.3	14%
19.25	519	1.6	14%
26.25	381	1.7	14%
42	238	1.2	3%

The complete trial design used in this exercise was 10 repeating units wide (20 rows) and 8 repeating units long (432 m) and was divided into 16 blocks for environmental control, each 10 rows x 54 m. Five clones (A to E) were represented in the trial. Clones were allocated randomly to two adjacent rows (width of one repeating unit) within each 10-row half of the trial and were represented along the entire length of the trial. Although it would be preferable to allocate clones to repeating units in each of the 16 blocks, the continuation of each clone through the length of the trial was considered as a simpler alternative.

Generation of simulated data

Diameter at breast height (DBH) data were simulated at 3-yearly intervals from age 3 to 18 years. DBH at 3 years (D3) was first generated:

[1] $D3 = \mu + block + clone + error,$

where μ = 8 cm is the overall mean, *block* is the block effect (Table 2), *clone* is the clone effect (Table 2) and *error* is a random value from a normal distribution with mean 0 and standard deviation 0.30. *D3* ranged from 4.6 to 11.1 cm. Data were generated for border trees on the outsides of the trial area using μ *, block* and *error.*

Table 2. Coefficients used in Equations 1 and 3 to generate simulated data

		D_3	D_{inc} 3-6	D_{inc} 6-9	D_{inc} 9-12	D_{inc} 12-15	D_{inc} 15-18	*Comment*
mu		**8**	**6**	**5**	**5**	**4**	**3**	slowly declining
Block effects	1	-0.5	-0.25	-0.25	-0.2	-0.15	-0.1	
	2	-0.9	-0.45	-0.45	-0.36	-0.27	-0.18	
	3	-0.9	-0.45	-0.45	-0.36	-0.27	-0.18	
	4	-1	-0.5	-0.5	-0.4	-0.3	-0.2	
	5	-0.8	-0.4	-0.4	-0.32	-0.24	-0.16	
	6	-0.6	-0.3	-0.3	-0.24	-0.18	-0.12	
	7	0	0	0	0	0	0	
	8	0	0	0	0	0	0	
	9	0	0	0	0	0	0	
	10	0.5	0.25	0.25	0.2	0.15	0.1	
	11	0.5	0.25	0.25	0.2	0.15	0.1	
	12	0.8	0.4	0.4	0.32	0.24	0.16	
	13	0.2	0.1	0.1	0.08	0.06	0.04	
	14	0	0	0	0	0	0	
	15	-0.5	-0.25	-0.25	-0.2	-0.15	-0.1	
	16	0	0	0	0	0	0	
Direct clone effects	A	-1.5	-1	-0.5	0	0.5	1	Improves (relatively)
	B	-0.5	-0.25	-0.25	-0.2	-0.15	-0.1	Deteriorates slowly
	C	0	0	0.5	0.5	0.5	0.5	Improves (relatively)
	D	0.8	0	-0.5	-0.5	-0.5	-0.5	Deteriorates quickly
	E	2	1	1	1	1	1	Stable and good
CI coefficients for clones	A		-0.3	-0.3	-0.3	-0.3	-0.3	Moderate
	B		-0.3	-0.3	-0.3	-0.3	-0.3	Moderate
	C		-0.1	-0.1	-0.1	-0.1	-0.1	Weak
	D		-0.3	-0.3	-0.3	-0.3	-0.3	Moderate
	E		-0.5	-0.5	-0.5	-0.5	-0.5	Strong

The competition index (*CI*) was calculated using Simile version 5.94 (Simulistics, USA) with a 4 m horizon for each tree at 3 years after Hegyi (1974):

[2] $CI = \sum_j D_j / (D_i . dist_{ij})$,

where D_j is the DBH of a neighbouring tree *j* within the competition horizon, D_i is the DBH of the subject tree, and $dist_{ij}$ is the distance between trees *i* and *j*. *CI* ranged from 0.00 to 5.57. The periodic DBH increment (D_{inc}) in each subsequent period to 18 years was then calculated as follows:

[3] $D_{inc} = \mu + block + clone + CI.clone + error$,

where μ is the mean, *block* is the block effect, *clone* is the direct clone effect, *CI.clone* is the clone-specific response to *CI* at the start of the period, and *error* was a random value from a normal distribution with mean 0 and standard deviation that decreased from 0.33 for D_{inc} *3-6 years* to 0.17 for D_{inc} *9-12 years* and later. Block effects were propagated through time but with changing scale (Table 2). The time trends for direct clone effects were clone-specific to simulate a scenario in which different clones have different growth curves (Table 2). Clone-specific coefficients of *CI* did not change through time, although the competition horizon increased to 6 m at age 6 years, 7 m at age 9 years, and 8 m at ages 12 and 15 years, and the scale of the covariate increased commensurately with the horizon distance. Error effects were correlated at the tree level from age 6 onwards, with correlation coefficients between 0.51 and 0.57 for 3-6 – 6-9, 6-9 – 9-12, and 9-12 – 12-15 and correlation coefficient 0.85 between the periods 12-15 – 15-18.

Analysis of simulated data

Competition indices with a 6m horizon were calculated using Equation 2 and DBH at each measurement. Although the data simulation process used varying horizons to mimic the increasing influence of more distant trees as the stand grows, a constant horizon was used in the analysis for ease of converting *CI* values into stand density values. The relationship between stand density (*SD*; sph) and average *CI* with 6 m horizon was determined:

[4] $CI=0.0036SD-0.9351$, or $SD=274CI+262$.

Periodic DBH increment data for individual trees were analysed using general linear regression in Genstat version 13 (VSN International, UK):

[5] $D_{inc} = \mu + age + block + clone + CI + age.clone + CI.clone + residual$.

Results

The regression model accounted for 93.4 % of variation and the accumulated analysis of variance table indicated that every model term was highly significant (Table 3). The effects of age and competition (which is represented as equivalent stand density values) on predicted DBH increment are presented in Figure 2 for three selected clones. The greater sensitivity of Clone E to growing space is apparent by the greater spread between lines, whereas the DBH increment of Clone C is incredibly insensitive to competition (Figure 2). The rate of decline in DBH increment with age is apparent from the slopes of the lines in Figure 2.

Table 3. Accumulated analysis of variance table

Change	d.f.	s.s.	m.s.	v.r.	F pr.
+ age	1	12663	12663	91968	<.001
+ block	15	491	33	238	<.001
+ Clone	4	2757	689	5006	<.001
+ CI	1	3350	3350	24330	<.001
+ age.clone	4	1090	272	1978	<.001
+ CI.clone	4	580	145	1054	<.001
Residual	10770	1483	0.14		
Total	10799	22413	2.08		

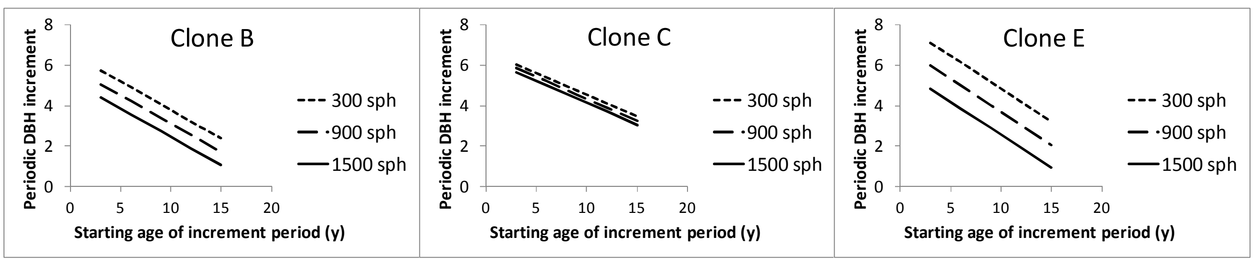

Figure 2. Relationships between predicted DBH increment and age in block 1 for three selected clones at three values of *CI* that correspond to stand density of 300 sph, 900 sph, and 1500 sph

The coefficients for *age*, *clone*, *CI*, *age.clone*, and *CI.clone* were combined with μ and the coefficient for block 1 to form a matrix of predicted DBH increment for each clone across a range of *CI* in the five periods. These predicted increments were added to the clone predictions for *D3* in block 1 to generate a matrix of predicted DBH that is presented graphically in Figure 3.

Clone values for DBH at 3 years are insensitive to competition (which is expressed as equivalent stand density on the x-axis), although from 6 to 18 years the clone-specific effects of competition tolerance are evident (Figure 3). Clone C maintains the least relationship with competition and over time it rises in rank from third to first (for stand density > 800 sph) or second (for stand density < 800 sph) (Figure 3). The strong sensitivity of Clone E to competition is also clearly shown by its stronger relationship with stand density (Figure 3). The predicted DBH for Clones A, B, and D merge over time due to different relationships with age, until they are virtually equal at age 18 years (Figure 3).

The model [5] parameters were used to construct a simple decision support tool in Microsoft Excel for predicting average DBH of the five clones to age 18 years on this hypothetical site. The stand density was an input for each of the six ages. Results from two contrasting management scenarios are presented in Figure 4. Predicted DBH at age 18 years with a dense stand management scenario (1500 sph to age 6, 1200 sph to age 12, 600 sph to age 18 years) is greatest for Clones C (30.6 cm) and E (29.0 cm) (Figure 4A). However, Clone E was clearly superior under the sparse stand management scenario (900 sph to age 6, 300 sph to age 18 years) with a predicted DBH of 34.7 cm at age 18 years (Figure 4B). The change in clone rankings over time is consistent with the results presented in Figure 3.

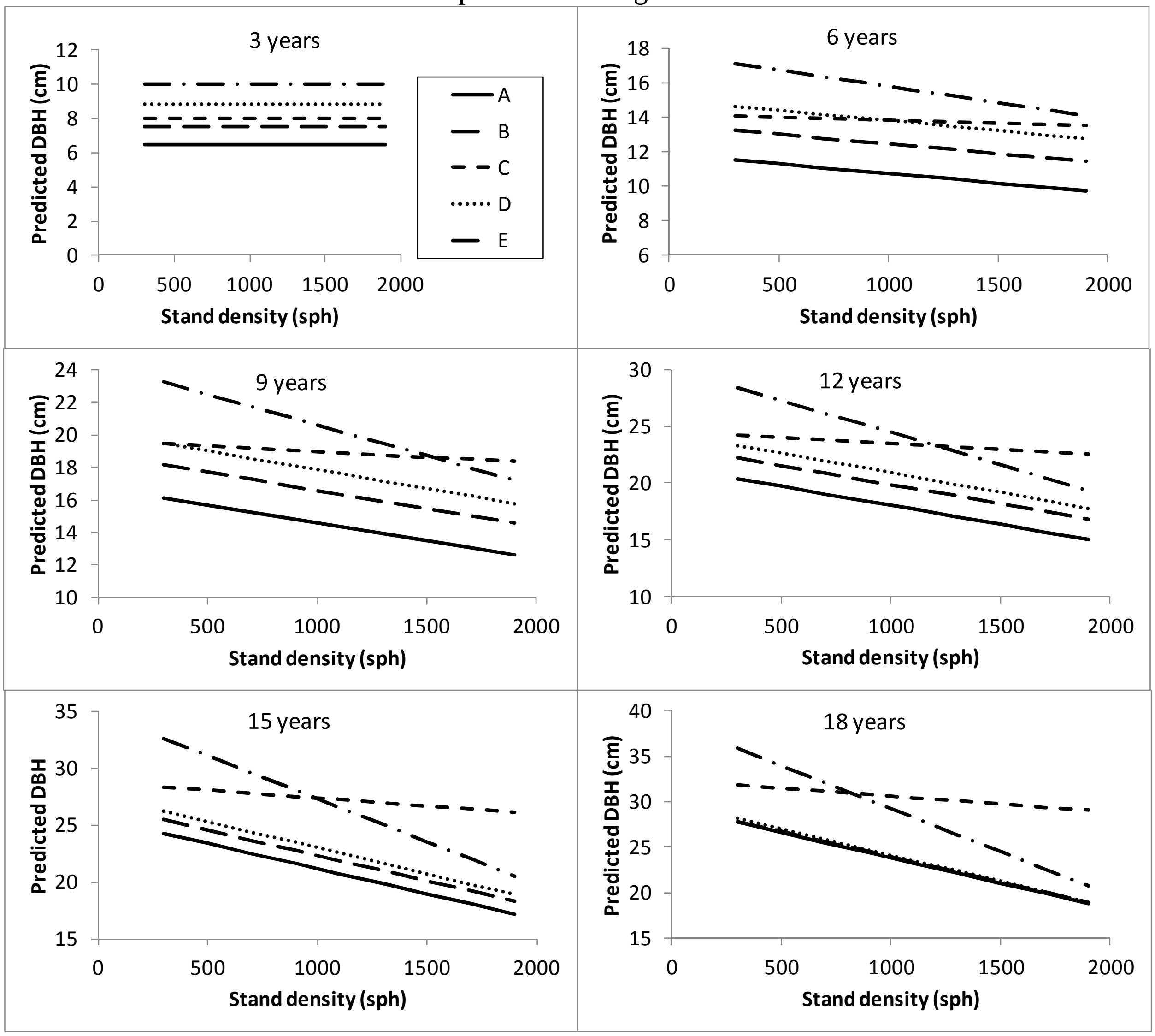

Figure 3. Relationships between predicted DBH and stand density for five clones (A-E) at six ages in block 1

Discussion

An important strength of the proposed trial design is that it facilitates the estimation of environmental effects within the trial area. This strength could be further improved for sites with patchy microsite effects by fitting an autocorrelated spatial structure to residuals and analysing the data with a mixed model.

The fixed inter-row spacing could be considered a weakness of the design because it results in a large amount of rectangularity for trees that are closest together (Table 1). A consequence may be the confounding of rectangularity and spacing effects on sensitive traits such as those related to canopy form. On the other hand, the regular row spacing is likely to reduce the costs of trial establishment and maintenance and the rectangularity will be less pronounced in operations with closer rows. Competition-induced mortality is likely to present a complication that will be addressed in future analyses of real data.

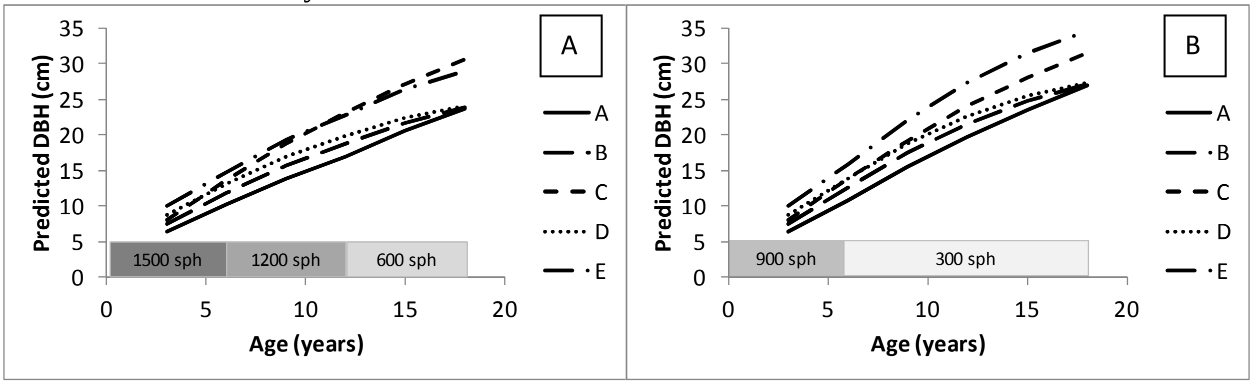

Figure 4. Relationships between predicted DBH and age for five clones (A to E) being managed on two hypothetical stand density regimes; (A) dense – 1500 sph to age 6, 1200 sph to age 12, and 600 sph to age 18, and (B) sparse – 900 sph to age 6, and 300 sph to age 18. It was assumed that the environment was equivalent to that of block 1.

The estimation of model effects that were deliberately embedded in the simulated data was a simple tool to demonstrate one form of analysis and interpretation that could be applied to real data. Competition indices have been presented in literally hundreds of forms (Pretzsch 2009) and other CIs may have greater explanatory power than the Hegyi (1974) index that I used. However, the use of a more complex CI such as one with a competition horizon that varies with the size of neighbouring trees should be considered carefully because the relationship between CI and stand density will not be as simple. Other refinements to the analysis could include more interactions between main effects, and non-linear relationships with competition and age. Although the simulated data that I used did not contain any effects of mortality, the loss of trial trees has been proven be well accommodated by the competition index analysis approach (Bristow et al. 2006).

Conclusions

I have described a systematic spacing design that lends itself to sound statistical analysis, is relatively insensitive to mortality, and enables the efficient collection of growth response data. Importantly, it is also operationally convenient so it could be replicated on many sites in a region. The design allows for the evaluation of genetic effects and genetic interactions with time and competition, making it attractive for simultaneously evaluating teak clones and spacing effects.

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