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Matching Genotypes to Current and Future Production Environments to Maximise Radiata Pine Productivity and Profitability

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Matching Genotypes to Current and Future Production Environments to Maximise Radiata Pine Productivity and Profitability

Prepared for

Forest & Wood Products Australia

by

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Executive Summary

The main aims of this project were to *i*) determine the underlying geo-climatic drivers of genotype by environment interaction (G×E) for radiata pine across planting environments in Australia and New Zealand and *ii*) define site types that maximise genetic gain in productivity by matching genotypes with production environments. The outcomes of this project will facilitate optimal deployment of genetic stock to particular environments and development of software tools for the deployment by the Southern Tree Breeding Association (STBA) in Australia and the Radiata Pine Breeding Company (RPBC) in New Zealand. Future impacts of climate change were also considered.

G×E in STBA trials

As a result of this project, current breeding and deployment regions will be redefined in Australia. It is expected that the number of breeding regions in Australia will be reduced and this could significantly simplify management of the national breeding programme. This should result in additional genetic gains in the breeding and deployment programs, which will come from accounting for G×E variance. This project has provided necessary information including site-site (i.e. inter-trial) genetic correlations for use in breeding value estimation by TREEPLAN®. The project has also provided necessary relationships between site means and variances of different traits for use in customised deployment tools such as SEEDPLAN®. The combination of optimal breeding and deployment of genetic stock to particular environments is likely to significantly improve radiata pine plantation productivity.

New site types were defined by grouping trial sites into clusters using a new analytical methodology (‘rgModel’). The first two most pronounced site clusters were based on minimum temperature, representing Warm and Cool site types. The next cluster split to Cool-Wet and Cool-Dry site types was based on rainfall variables, and it further improved the model fit. This analytical methodology forms a framework for future analyses of a suite of traits, including composite traits, as more and better estimates of site-site genetic correlations are obtained from STBA trials. For industry to fully benefit from this framework, it is important that future trials are genetically well connected both to each other and to past trials already in STBA DATAPLAN®. For all well-connected trials with genetic correlation estimates, more site-specific environmental data are also needed.

G×E in RPBC trials

For RPBC trials in New Zealand and NSW, Australia, previous analyses demonstrated existence of substantial additive G×E for stem diameter measured at breast height (Dbh). Here, on a subset of 24 parents tested across 48 RPBC trials, Multiple Regression Tree (MRT) analyses identified mean annual precipitation and minimum temperature coldest month as the most likely key drivers of G×E in New Zealand. The analyses identified wet sites where certain genotypes performed exceptionally well and cold sites where the same genotypes performed below their overall average performance, but where others performed well.

As more data from genetically well-connected trials and more precise information on environmental variables (silviculture and in particular soils) becomes available it will enable RPBC to make better-informed decisions about development of new site-types for breeding. The information presented in this report will inform how genotypes may be allocated to specific sites, for deployment in the optimal environments to achieve stands of high productivity. For deployment purposes, using a technique such as MRT, it will be possible to create maps to select test sites representative of the target planting zone for progeny trials as well as match genotypes to target environments.

Effects of climate change

The future climate of radiata pine plantation areas will change relative to the climate during the time periods of existing trials. The climate change according to HadGEM2–ES (IPCC 2013) model for the year 2050 will be significant both in Australia and New Zealand: an increase in mean annual temperature of 1.90 and 1.95 deg. C, and a decrease mean annual precipitation of 2% and 8%, respectively. Since the current range of climates at field test sites will often not be representative of the likely future climates in their plantation areas, newly-established field trials will need to target the future climates. In this report we show how to determine where to establish new trials that will be representative of future climates.

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General Introduction

Genotype by environment interaction (G×E) often represents a significant proportion of the overall phenotypic variation between plants (Yan and Kang 2003). Importance of G×E in forest trees has been reviewed by White *et al.* (2007). When G×E is present, the performance of genotypes across a range of environments is considered ‘unstable’. This necessitates defining groups of environments with relatively stable performance (Matheson and Raymond 1986). In other words, breeding and deployment regions are defined so that within these regions G×E is minimised.

Dealing with the issue of G×E requires an estimation of its magnitude as well as identification of its causes. The magnitude of G×E could be quantified by the cross-environment genetic correlation, r_{GE}, in which the same trait measured in two different environments is considered to be two different traits (Falconer and McKay 2006). The magnitude of G×E declines as r_{GE} approaches unity and increases as r_{GE} approaches and transgresses zero. The main approach to identification of causes of G×E has been to characterise test environments in terms of environmental variables (i.e. climate and soil) and identify the main environmental factors driving G×E. However, G×E is often not simply related to a single environmental variable, but rather a number of climatic or other site characteristics (e.g. Matheson and Cotterill 1990).

Because of these complexities many tree improvement programmes are not generally able to completely resolve the issue of G×E beyond the level of identification of best provenances for larger geographic areas. However, benefits of genetic improvement can be fully realised only if both best provenances and improved genotypes are well matched to environments. Radiata pine (*Pinus radiata* D. Don), breeding populations in Australia and New Zealand are based on land races derived mainly from two native provenances (i.e. Monterey and Año Nuevo, respectively), and are now in advanced (i.e. fourth) breeding generation. Therefore provenance effects are probably not as important as for species with less advanced breeding programs. At the same time, radiata pine advanced generation breeding and deployment zones are not based on biological patterns of G×E, but rather on plantation inventory boundaries, which may be strongly defined by cadastral considerations. While adaptation of forests depends on the response of genotypes to future climate conditions, current breeding and deployment zones cannot be adapted (i.e., modified) to changing climate conditions (e.g. Schreiber *et al.* 2011).

Previous research

Provenance trials provide information about a species’ climatic adaptation that can be used to predict the productivity in new (i.e. exotic) environments. Burdon *et al.* (1997) investigated the relative performance of three mainland provenances of radiata pine (Año Nuevo, Monterey and Cambria) and three regional land-race stocks, 'Kaingaroa', 'Nelson' and 'Southland', on different site categories. The land-race stocks were included to provide New Zealand controls, these being predominantly from select-tree seed collections within unimproved stands and three NZ non-select controls (Kaingaroa, Nelson and Southland). Strong differences among provenances in their relative performance on different site categories were reported, suggesting provenance-by-site interactions. Sites were grouped into five categories, representing infertile clays, coastal dunes, volcanic plateau, central and southern south island (Burdon *et al.* 1997). Susceptibility to *Dothistroma* needle blight may have had a negative effect on performance of some provenances, as it has previously been shown for the ‘Cambria’ provenance (Gapare *et al.* 2011).

Significant G×E among radiata pine families has been observed in several experiments in Australia. For example, G×E for growth and stem characteristics of radiata pine assessed at age 9 years across ten sites in southern Australia was reported by Wu and Matheson (2005). They showed that two high elevation sites in New South Wales contributed disproportionately to G×E variance compared with the other sites. In the same set of trials assessed at age 20 years, G×E was found for diameter growth, but not for wood density (Gapare *et al.* 2010). In another set of eight trials in Australia (two trials were located in South Australia, two in Victoria, one in Western Australia, and three in Tasmania) there was also evidence of G×E for tree diameter and branching (Baltunis *et al.* 2010). Although these studies reported evidence of G×E, the authors never attempted to formally identify the causes of the observed G×E, because of the limited number of sites did not warrant such analysis.

Raymond (2011) reported significant G×E at family level for diameter growth, with elevational differences between sites being a key driver of G×E in New South Wales. A recent study by Gapare *et al.* (2012) confirmed those results and divided New South Wales sites into high-elevation high-rainfall and low-elevation low-rainfall groups. Ivković *et al.* (2014) used 20 genetically well-connected trials across southern Australia to obtain estimates of genetic correlations between performances at different trial sites and concluded that interaction at transcontinental scale can be correlated with the climatic variables, primarily rainfall and temperature, but may also be related to smaller scale environmental variation (i.e. soil and terrain variation).

In New Zealand, significant family by environment interactions were observed in radiata pine between pumice and clay soil sites (Johnson and Burdon, 1990). In a progeny test of 25 parents mated in a series of five, five-parent, disconnected diallels established on 11 sites chosen to represent all major site types for growing radiata pine in New Zealand, Carson (1991) found G×E to be significant for stem diameter (Dbh). However, minimal genetic gains were found with regionalisation. McDonald (2009) reported moderate to negative site-site genetic correlations (<0.60) for Dbh, indicating the presence of G×E, driven by extreme maximum temperatures and altitude (these two climatic variables proxies for moisture availability). Apiolaza (2011) reported moderate to high (0.46–0.96) genetic correlation estimates (many not significantly different from 1.0) indicating that there was little interaction for basic density.

Most tree improvement programmes have not resolved the issue of G×E because of the lack of sufficiently genetically-connected trials and difficulty of interpreting G×E with respect to mappable geo-climatic variations. Radiata pine tree improvement programmes in Australia and New Zealand are among the most advanced in the world. Significant improvement has been made in growth, form and wood quality traits (Wu *et al.* 2007). However, current radiata pine breeding value prediction and deployment in Australia is based largely on the National Plantation Inventory (NPI) regions (Gavran and Parsons 2011), rather than on environmental drivers of G×E. In practice the large number of regions means that general performance breeding selections are made (except for *Dothistroma* susceptible sites), while deployment can use these regions more fully. Similarly, in New Zealand no regionalisation based on environmental drivers of G×E has yet been introduced. Therefore, current breeding and deployment regions cannot deliver optimal genetic gains across the whole radiata pine estate.

This study was based on the most comprehensive, genetically-connected and well-distributed network of radiata pine genetic trials maintained in Australia by the Southern Tree Breeding Association (STBA) and in New Zealand by the Radiata Pine Breeding Company (RPBC). Based on data from the trials with common genetic material, estimates of site-site genetic correlations were obtained. The patterns among these correlations were modelled against various environmental characteristics. The study was the largest effort to date to understand G×E and to obtain site classifications that account for a large proportion of G×E in Australia and New Zealand. Identification of the causal genotypic and environmental components that are driving G×E for radiata pine growth and form quality traits can be incorporated, along with bioeconomic selection indices, into breeding and deployment strategies for radiata pine.

Moreover, since genotypes are selected based on a composite trait index value rather than individual trait values (either in an index or more arbitrary independent culling), it is important to investigate if there would be G×E interaction for the index values. Although there may not be G×E for individual traits, there still may be G×E for index value, due to different economic weights for traits in different areas. Namkoong (1984) showed that when an index has different relative economic weights for component traits in different environments, genetic entries may change rankings even with the same rankings for component traits. In other words, the relative sizes of trait economic weights can influence the size and the sign of difference between genotypes in index values at different sites. In addition, genetic variances may change between sites in relation to the site means, giving different effective index weights even when the absolute weights may be the same. Therefore, it is important to quantify, in absolute terms, the expected site means and variances for productivity, form, branching and wood quality traits.

Objectives of the project

The main aim of this project was to determine the underlying geo-climatic drivers of genotype by environment interaction (G×E) across radiata pine planting environments and to define site types that would increase and come close to maximising genetic gain in productivity by matching genotypes with production environments. The outcomes of this project will facilitate optimal deployment of genetic stock to particular environments and the development of software tools for the deployment by STBA and RPBC.

The specific objectives of the study were:

- Estimate site-site genetic correlations and site-site differences in environmental (i.e. geo-climatic) variables
- Identify G×E patterns for growth, form, branching traits, and composite traits
- Determine the underlying geo-climatic drivers of G×E across planting environments in Australia and New Zealand
- Define site types that maximise genetic gain by matching genotypes with production environments
- Examine effects of climate change on breeding and deployment regions in Australia and New Zealand, and
- Ensure adoption of results by radiata pine industry

GxE analyses of STBA Trials

Summary

- This project has provided necessary information (e.g. inter-trial genetic correlations) for use in breeding value estimation by TREEPLAN® and in customised deployment tools such as SEEDPLAN®. The combination of optimal breeding and deployment of genetic stock to particular environments is likely to significantly improve radiata pine plantation productivity
- New site types were defined by grouping trial sites into clusters based on genotype performance in different environments using 'rgModel'. The first two most pronounced clusters were based on minimum temperature, representing Warm and Cool site types. The next cluster split Cool-Wet and Cool-Dry site types based on rainfall variables and further improved the model fit.
- As a result of this project, current breeding and deployment regions will be redefined in Australia. It is expected that the number of breeding regions (i.e. site types) will be reduced and this could significantly simplify management of the national breeding programme
- Genetic gains in the breeding and deployment programs will come from accounting for G×E variance, and a greater precision of selection due to larger population sizes for within-region selection hence greater selection pressure
- The framework (i.e. rgModel) has been established for future work on G×E in a suite of traits including composite traits in STBA trials, when more estimates of site-site genetic correlations are obtained

Introduction

This component study of the project was based on a comprehensive, genetically well-connected and well-distributed set of genetic trials in Australia. The study used information from all radiata pine progeny trials maintained by the Southern Tree Breeding Association (STBA). Based on data from those trials with common genetic material, estimates of site-site genetic correlations were obtained. The patterns among these correlations were modelled against various environmental characteristics. The study is the largest effort so far to understand G×E in radiata pine in Australia and to obtain site classifications that will account for a large proportion of G×E. The general aim is to facilitate optimal deployment of genetic stock to particular environments and development of software tools for deployment by the STBA. The specific objectives of the study were:

- To estimate genetic parameters such as variances (i.e. additive and dominance), heritability, and genetic correlations between trials for growth, form, branching and wood properties in the STBA trials
- To examine patterns of GxE between trial locations in southern Australia
- To identify potential geo-climatic drivers of GxE, and
- Redefine breeding and deployment zones

Methodology

Environmental variables

Climate, geological, and soil information for more than 300 STBA trial locations were obtained for the analyses. Daily climate data for the selected locations within Australia were extracted from the SILO enhanced Climate Database (http://www.longpaddock.qld.gov.au/silo). Daily climate data constructed using observations from 4600 locations across Australia for rainfall, maximum and minimum temperatures, evaporation and solar radiation based on spatial interpolation algorithms were available. The interpolation routines allow estimation of daily climate data for locations at distance from existing meteorological recording stations. The climate data sequence from planting to trial assessment was obtained, for each trial. The following variables were derived based on SILO data:

- Mean Annual Temperature (MT)
- Mean Temperature of Driest Quarter (MTDQ)
- Mean Temperature of Growing Season (MTGS)
- Mean Annual Max Temperature (MMXT)
- Max Temperature of Driest Month (MXTDM)
- Mean Annual Min Temperature (MMNT)
- Annual Precipitation (P)
- Precipitation of Driest Quarter (PDQ)
- Precipitation in Growing Season (PGS)
- Evaporation (TE)
- Potential Evapo-transpiration (PET)
- Mean Annual Solar Radiation (MRD)
- Vapour Pressure (VP)
- Relative Humidity Highest Temperature (RHHT)
- Relative Humidity Lowest Temperature (RHLT)

Growing season was defined to be from September to April based on McMurtie *et al.* 1994. A simple monthly aridity index (AIX) was calculated as a ratio of monthly mean pan evaporation rate to the total monthly rainfall. Monthly minimum AIX value for the most arid quarter was used to rank the sites in terms of aridity (Eamus *et al.* 2000). Aridity indices can also be based on precipitation and potential evapo-transpiration (PET) and are related to water balance.

Broad-scale geological (i.e. surface geology) data were obtained from Geoscience Australia (http://mapconnect.ga.gov.au/MapConnect/Geology). The Surface Geology of Australia GIS layer/surface? is a seamless national coverage of outcrop and surface geology. All map polygons have attributed geological unit name, age, and lithological composition according to the Australian Stratigraphic Units Database (Raymond and Retter 2010). Parent rock codes were categorised using a technical classification system into 11 categories (**Figure 1**). This system was developed to group forest sites according to expected volume productivity (Turner *et al.* 1990, 2001). In addition, a high-resolution weathering intensity index for the Australian continent, based on airborne gamma-ray spectrometry and digital terrain analysis was also obtained (Wilford 2012).

The Australian Soil Resource Information System (ASRIS, www.asris.csiro.au) database was used to obtain information on soil and land resources in a consistent format across southern Australia**.** ASRIS provides information at seven different scales. The first three scales provide general descriptions of soil types, landforms and regolith across the continent. The remaining four scales provide more detailed information on regions where mapping is complete. The information was obtained on soil depth, water storage, permeability, fertility, carbon content and erodibility. Most soil information is recorded at five depths. The lowest scale consists of a soil-profile database with fully characterised sites that are known to be representative of significant areas and environments.

Soil data were also available from forestry organisations and companies. For example, in the Green Triangle region of South Australia, ForestrySA maintains a GIS-based soil database developed over the last 40 years. The ForestrySA GIS soils and site productivity geographic data base is a composite of the Stephens' (1941) soil survey (CSIRO Bulletin No 142) and soil surveys conducted by the ForestrySA Research Section. Between 2007 and 2010, almost the entire ForestrySA land base in the Green Triangle Region has been field-checked for soil identification and boundaries to confirm the validity of both the original Stephens soil survey and subsequent ForestrySA soil surveys. Similarly Timberlands Pacific, also maintains a GIS database of soil data in northern Tasmania.

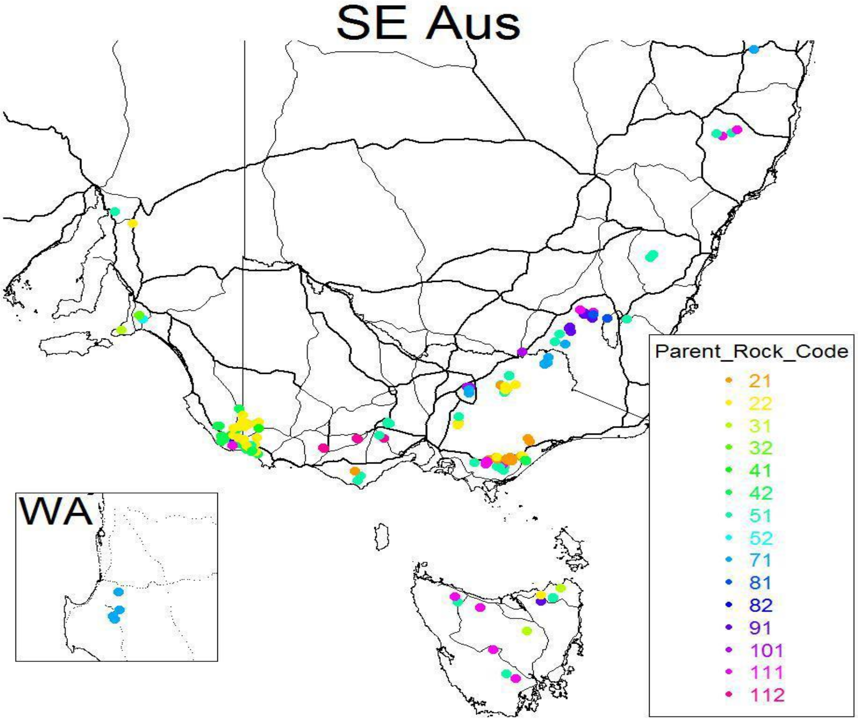


Figure 1. Parent rock codes for >200 trials from STBA DATAPLAN®

Database of genetic correlations

The following procedure was used when working with the progeny test data imported into DATAPLAN®: PPGVal® (unpublished software by G. Dutkowski) was used for data validation. PPGVal is an R language script designed to graphically validate data downloaded from DATAPLAN® (or before import into DATAPLAN®). Data validation before analysis is important because it aids the analyst in the data interpretation. Invalid data are given a reject flag (_reject field = 1) so that the data is not used for model development, variance and correlation estimation, or subsequently for TREEPLAN® breeding value estimation. TrialMAPPER® and PPGMap® programs can also be used for further validation.

Multiple stems cannot be included in spatial analyses, and for a tree with *n* stems the "equivalent diameter" defined as the quadratic mean of the measured stems calculated as:

$$Dbhq = \sqrt{Dbh_{s1}^2 + Dbh_{s2}^2 + \ldots + Dbh_{sn}^2}$$

To prepare data for spatial analysis using auto-regressive error structures all trees must be mapped to a, rectangular *xy* grid. The program PPGBlok® used row and column numbers for each tree to create a complete rectangular grid filled with missing values where there are missing trees.

For each of the trials, each trait was first analysed using a uni-variate, single site model in order to estimate the genetic variance components, individual-tree narrow-sense heritability and standard errors associated with each trait. A reduced (i.e. parental) linear mixed-effects model was fitted using ASReml software (Gilmour *et al.* 2009):

$$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Zu}_d + \boldsymbol{Zu}_f + \boldsymbol{e}$$

where $\boldsymbol{y}$ is a vector of observations, $\boldsymbol{b}$ is a vector of fixed effects (i.e. site mean and replication), $\boldsymbol{u}_d$ is a vector of random incomplete block and/or plot design features, $\boldsymbol{u}_f$ is a vector of random family effects (i.e. full-sib family), and ***e*** is a vector of random residual terms. ***X*** and ***Z*** are known incidence matrices relating the observations in ***y*** to effects in ***b***, and ***p, f,*** respectively.

Spatial data analyses were performed using a two-dimensional separable autoregressive model fitted using ASReml® (Gilmour *et al.* 2009). The spatial method partitioned the residual into an independent component (η) and a two-dimensional spatially auto-correlated component (ξ)

The raw data was adjusted for surface sum (the sum of design, spatial and extraneous terms) using PPGMap® (Greg Dutkowski, unpublished software 2012), before further analyses. After the adjustment multi-site data was combined before proceeding with bi- or multi-variate or factor analyses (Cullis et al. 2014). In bi-variate case the following model was used:

$$\boldsymbol{y_i = X_i b_i + Z_{p_i} p_i + Z_{f_i} f_i + e_i}$$

where, $\mathbf{y}_i$ is the vector of observations that is indexed (i) by the two 'traits' (i.e. parent performance of two different sites) $y_i = \begin{bmatrix} y_{site_1} \\ y_{Site2} \end{bmatrix} = \begin{bmatrix} y_1 \\ y_2 \end{bmatrix}$,

$\mathbf{b}_i$ is the vector of fixed effects representing sites (i.e. field trials) and replications within the trials and $\mathbf{X}_i$ is the incidence matrix relating the $\mathbf{y}_i$ observations to the $\mathbf{b}_i$ fixed effects; $X_i b_i = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix}$, $\mathbf{0}$ is the null matrix,

where p_i is is the vector of random open-pollinated family (GCA) effects ~MVN$(0, G \otimes A_i)$, $G = \begin{bmatrix} \sigma^2_{G_1} & \sigma_{G_{1,2}} \\ \sigma_{G_{1,2}} & \sigma^2_{G_2} \end{bmatrix}$ variances $\sigma^2_{G_i}$ for each trait and between-site genetic co-variances $\sigma_{G_{1,2}}$, and A_i is the relationship matrix that is constructed using the population's pedigree,

f_i is is the vector of random controll-pollinated family (SCA) effects ~MVN$(0, \boldsymbol{D} \otimes \boldsymbol{I}_i)$, $G = \begin{bmatrix} \sigma^2_{D_1} & \sigma_{D_{1,2}} \\ \sigma_{D_{1,2}} & \sigma^2_{D_2} \end{bmatrix}$ variances $\sigma^2_{G_i}$ for each trait and between-site genetic co-variances $\boldsymbol{\sigma_{D_{1,2}}}$, and

$\mathbf{e}_i$ is the vector of random residual terms ~MVN$(0, \boldsymbol{R} \otimes \boldsymbol{I})$ where residuals were assumed to be heterogeneous across traits, $R = \begin{bmatrix} I_1 \sigma^2_{E_1} & 0 \\ 0 & I_2 \sigma^2_{E_2} \end{bmatrix}$, $\sigma^2_{E_i}$ is the error variance for each site and I_i is the identity matrix of dimension equal to the number of observations of each trait, 0 indicates no between-site error co-variance.

For all models, Restricted Maximum Likelihood (REML) - derived variance and covariance estimates were constrained to fall within the theoretically possible range; variance components estimates were constrained to be greater than zero while covariance estimates were constrained so that correlation estimates ranged from -1 to +1. Two separate analyses were used to test for the significance of the genetic correlation between sites, where the difference between the log-likelihood estimates of a (full) model and a (reduced) model that fixed the trial-trial correlation to unity was used with a degree-of-freedom chi-squared test to estimate *p*-values (Dutkowski *et al.* 2006). The PPG ASRTools® suite of programs was also used to streamline the processing of ASReml output files and to reformat them for further analyses and reporting.

Modeling genetic correlations: rgModel

The rgModel is an R (R Development Core Team 2014) custom-made script that was used to model the database of correlations. The model of the genetic correlations gave estimates according to the formula

$Est = r_{t:t}*r_{a:a}*r_{e:e}$

where:

$r_{t:t}$ is the correlation between traits (t), when traits are used to allow for GxE by creating more than one trait, where each trait is the performance on different site types. The correlation between a trait t and itself is set to be 1 for type A (trait:trait) correlations, and for type B (site:site) can be set to 1, or estimated to give an indication of residual G×E: the correlation between sites within a site type as an expression of unexplained G×E.

$r_{a:a}$ is the age:age correlation based on parameters of the Lambeth’s (1980) correlation model. All $r_{a:a}$ are constrained to be the same value for all traits (t).

$r_{e:e}$ is the inter-environmental correlation based on an AR1 model for environmental parameter e (where present), where the values for e can be scaled so that the differences range between 0 and 10. All $r_{e:e}$ are constrained to be the same value for all traits (t) (although this restriction can be released).

Estimates of each of the parameters were found by minimising the objective function:

$Wt\ ESS = \mathrm{Sum}(W_a*W_{use}/W_{se}*W_{nPar}/W_{nUse}(Est - r_a)^2 +$

$W_b*W_{use}/W_{se}*W_{nPar}/W_{nUse}(Est - r_b)^2+W_eE)$

where:

$Wt\ ESS$ is the weighted error sum of squares

W_a is the weight given to type A correlations. Set as 1.

W_b is the weight given to type B correlations. Set as 1.

W_{use} is a flag (0/1) given by the analyst to identify whether specific type A and B estimate should be used, to avoid values in the database which are thought to be problematic.

W_{se} is the weight given to standard error of each of the type A and B estimate, to avoid giving undue weight to estimates with low standard errors. This gives more weight to values closer to 1, as values closer to 1 have lower SEs, and to a degree counter-acts the lack of estimates above 1. A maximum value of 10 was used for this weight to avoid giving correlations close to 1 a very high weight. Bounded estimates were given this value as well.

W_{nPar} is the optional weight given to each of the type a and b estimates depending on the number of parents (type A) or parents in common (type B), to give higher weights to estimates that are based on more parents. Scaled as sqrt(nPar)/100.

W_{nUse} is the weight given to number of uses of a trial for each of the type A and B estimates, to avoid giving undue weight to trials from which many estimates were derived. Scaled as sqrt($nUse$)/100 .

Est is the estimate from the model, as above.

r is the correlation estimate from the database for each of the type a and b correlations.

W_e is the weight given to the last eigen value of the $r_{t:t}$ matrix to derive estimates for trait pairs that have no or little data to support them. Set as zero apart from when trying to estimate correlations for the current site type model when not all site type correlations have correlation data to support them.

e is the last eigen value of the $r_{t:t}$ matrix.

Constraints and starting values can be added to the models. The parameters in any model are estimated by testing each possible parameter value above and below the starting or previous value, and then picking the change that best lowers the model weighted error sum of squares of all the parameters tried. This process is then repeated until no model improvement takes place, whereupon the sizes of the steps tested are reduced, and the process is repeated. After a defined set of reductions (10) with no further improvement in model fit, the estimation process stops and the final parameter values are presented. The progress of the modelling could be reviewed using the rgModel_PlotGetBestValues.r script and the resulting plot (**Figure 2**). The estimates can be checked by viewing the estimated correlations against the correlations in the database, using the script rgModelGraph.r.

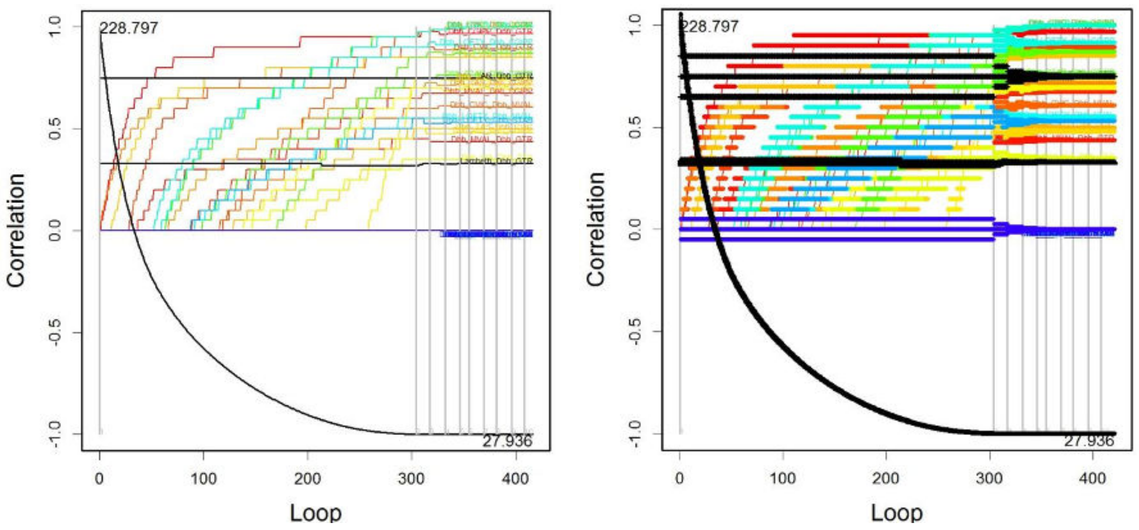


Figure 2. The progress of the estimation procedure, with the tested values shown on the right for each step: For each step of the loop, values above or below the starting or previous value are tested to see which best lowers weighted error sum of squares (black line), and the best change is set as the starting value for the next loop. Once no further reduction can be made, the size of the step above and below is halved and the process repeated 10 times until no further improvement in model fit is possible.

The base model was one where there was only a single trait (site type) for Dbh, Straightness or Branch Size. This was tried without and with residual G×E – allowing correlations between sites in a site type to be less than 1. Comparison of models proceeded only after initial estimation of the coefficient of the Lambeth age-ratio correlation model from the typeA correlations. This coefficient was then fixed in all subsequent models. The second baseline was to define traits by splitting into site types based on the current site classification used in TREEPLAN® of National Plantation Inventory regions, plus a special site type for trial that had been infected with *Dothistroma pinii*.

From the single site type baseline, each of the ordinal environmental variables was tested to see which gave the best *Wt ESS* (weighted error sum of squares) as an AR1 model. Splitting the sites into different sites type proceeded stepwise by sequentially splitting the sites into classes on the basis of the available ordinal and (non-ordinal) categorical environmental variables. For ordinal variables all possible values defined in the data were used to sequentially split out a new trait from the existing traits (initially all trials), and seeing which split value in which existing trait gave the lowest *Wt ESS* (**Figure 3&4**). The best splits were compared with those same environmental variables from the AR1 modelling. For (non-ordinal) categorical variables, each level (and unique combination of levels) was used to define a new trait and that combination which gave the lowest *Wt ESS* was chosen (**Figure 5 and 6**). All ordinal and categorical variables were thus compared and the one that gave the lowest *Wt ESS* and the split value or level combination was used. The process was repeated after the first split, with each ordinal and/or categorical variables screen for each of the existing classes.

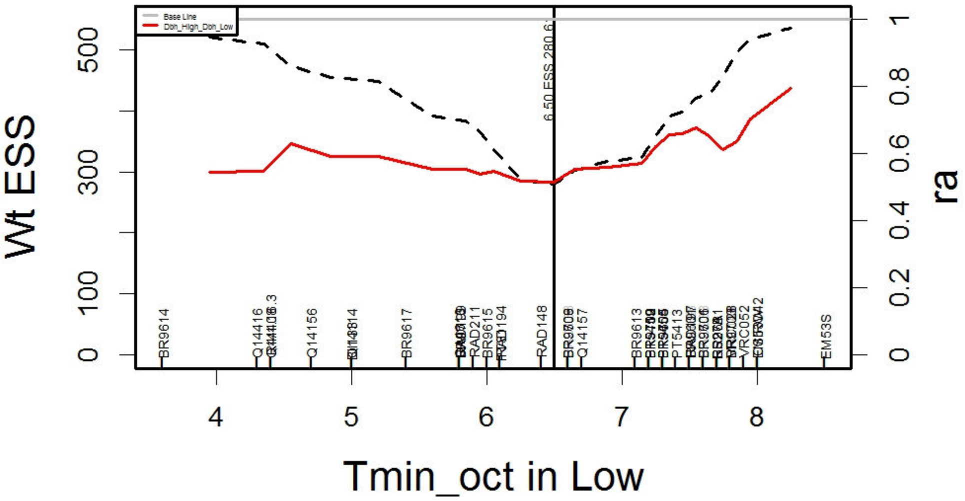


Figure 3. Splitting out a new class based on ordinal variable Tmin_oct from the initial class called "Low"

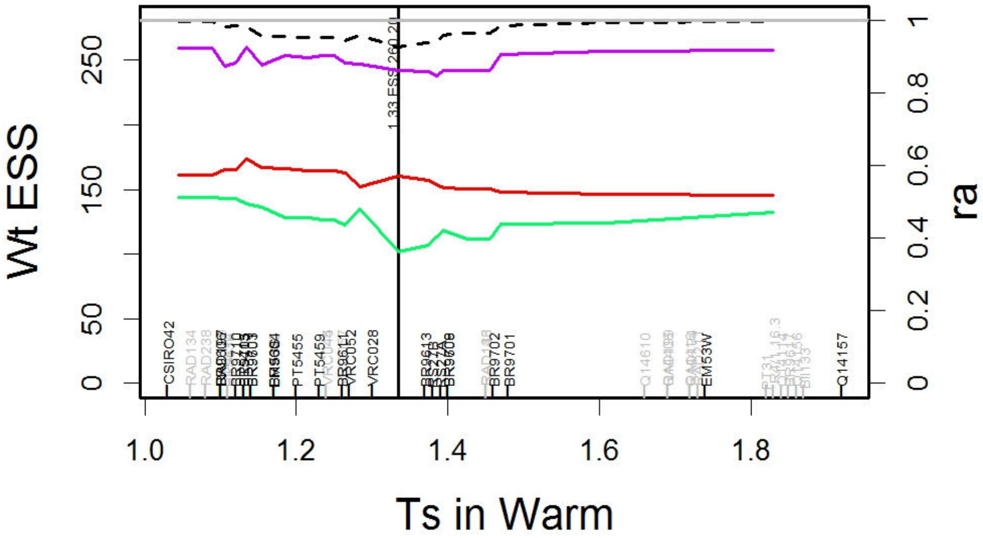


Figure 4. Splitting out a new site type based on Temperature Seasonality (Ts) after an initial split into Warm and Cool based on Tmin_oct.

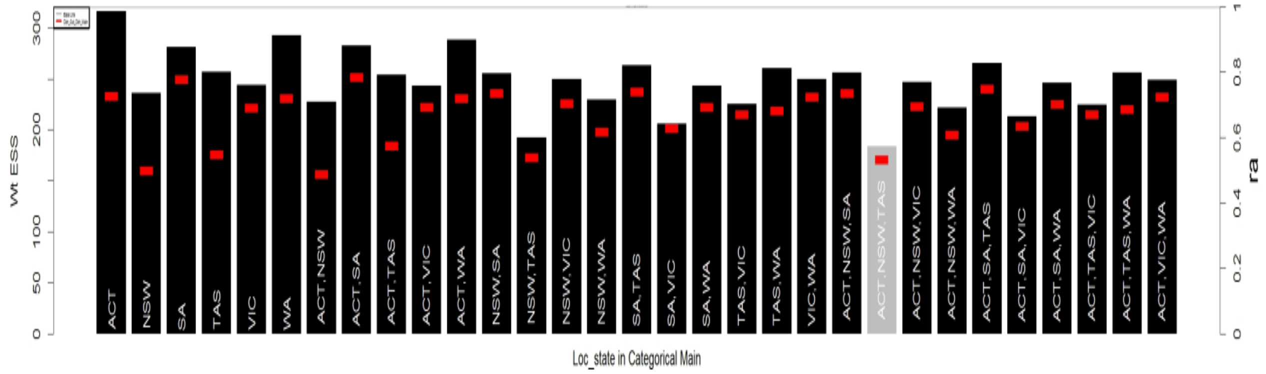


Figure 5. Splitting out a new class (state) based on a single class from a categorical variable from the initial class called "Main"

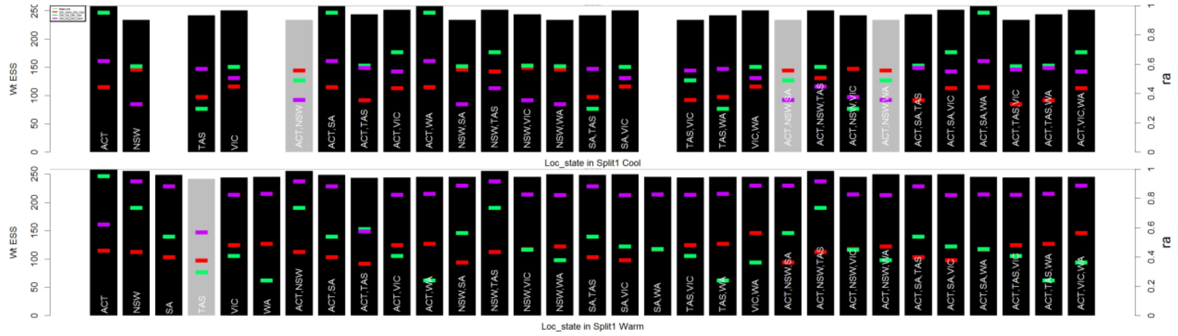


Figure 6. Splitting out a new class (state) after an initial split into Warm and Cool based on Tmin_oct.

To screen for outlier trials, all groups of trials from 1 to 3 in size were also tested as if they were categorical variables. When new traits are based on outlier trials with no clear environmental link between them, then it is likely that further splitting into site types is not warranted. Similarly no further splitting is warranted when the reduction in Wt ESS is small, or the outliers give a better model fit.

Breeding Value Prediction

For the site classification models tried, breeding values were predicted for Dbh data using TREEPLAN® (Dutkowski *et al.* 2014) and the identified site types. The estimated breeding values for each region/site type were compared in terms of variance of breeding values and correlation with *a priori* site types. The same methodology and rgModel have been applied to analyses of stem diameter (Dbh), stem straightness, and branch size (see **Appendix 1** for analyses of latter two traits).

Results

Database of genetic correlations

A database of genetic correlations was developed for this project and currently has more than 800 site-site and more than 700 trait-trait genetic correlations (between diameter at breast height, branch size, branch angle, stem straightness, wood density, wood acoustic velocity, and deformity). As more data becomes available, more correlation estimates will be included into the database of genetic correlations. Only additive genetic correlations for Dbh are presented here to demonstrate the proof of concept, but results for branch size and stem straightness can be found in **Appendix 1**. The estimates of genetic correlations were much more variable for pairs of trials with fewer than 100 parents in common and standard errors were also variable for estimates from less than 100 parents as demonstrated in **Figure 7**.

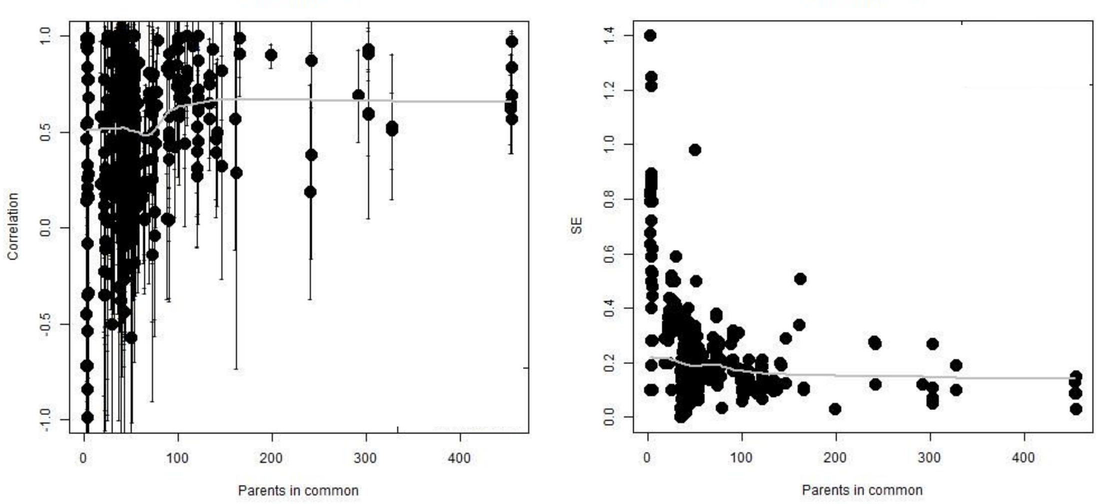


Figure 7. Site-site genetic correlations for Dbh and their standard errors (SE) (with 95%CI and smoothed loess trend) on the left. The estimates were much more variable for low numbers of parents in common and the smoothed was lower, presumably due to the lack of correlations above one. The SE of the estimates decreased for estimates close to 1, but was also lower for pairs of trials with more parents in common.

Age-age correlations

Estimation of the "age-age" parameter or "Lambeth coefficient" (Lambeth 1980) was initially done only from the trait-trait correlations and this gave a value of 0.193. Using the site-site genetic correlations led to an increase in the Lambeth coefficients (i.e. lower correlations) (**Figure 8**), especially where no G×E was allowed. As this change in Lambeth coefficients could be due to confounding of the age-age correlations with inter-site correlations less than 1, and the Lambeth coefficient of 0.193 was used for all Dbh modelling. Allowing for G×E gave a similar Lambeth coefficient to the one obtained using only trait-trait correlations.

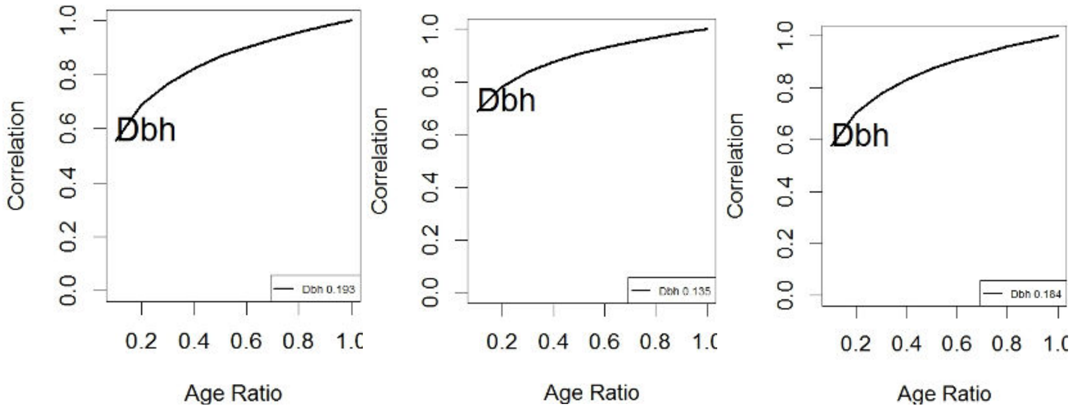


Figure 8. Lambeth Dbh age ratio model parameters and trends for trait-trait correlations (left), site-site correlations with G×E (centre) and equal weighting on both correlations (right).

Validation of the predictions from the fixed Lambeth model showed that the age:age correlations were quite well predicted. There is one low outlier, but this has been given low weight in the model.

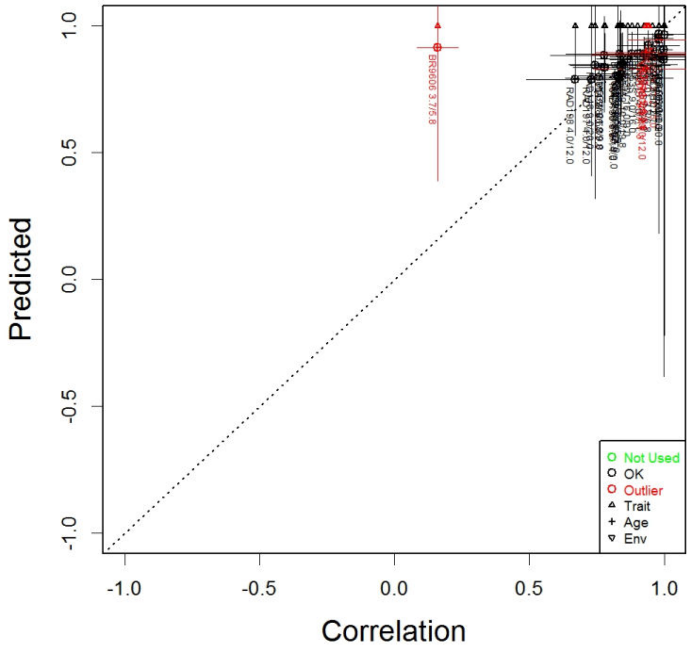


Figure 9. Diagnostic graph from single site Dbh base model with fixed Lambeth coefficient. The estimates show their 95% Confidence Interval (CI) as a vertical line. The diagonal line indicates where the model and the data are the same. Red symbols indicate that the prediction is outside the 95%CI. The horizontal lines indicate the relative weight used.

Current site classification

All the trials in STBA's DATAPLAN® are currently classified into site classes based on the National Plantation Inventory regions: Green Triangle (GTR), Central Victoria (CVIC), Central Gippsland (CGIPP), Tasmania (TAS), Central Tablelands (CTAB), Southern Tablelands (STAB), Northern Tablelands (NTAB), Murray Valley (MV) and Western Australia (WA). A "DOTHI" site type for trials with *Dothistroma* infection data (i.e. NPI_DOTHI). DOTHI trials were in NE Victoria and one trial in northern NSW (**Figure 10**).

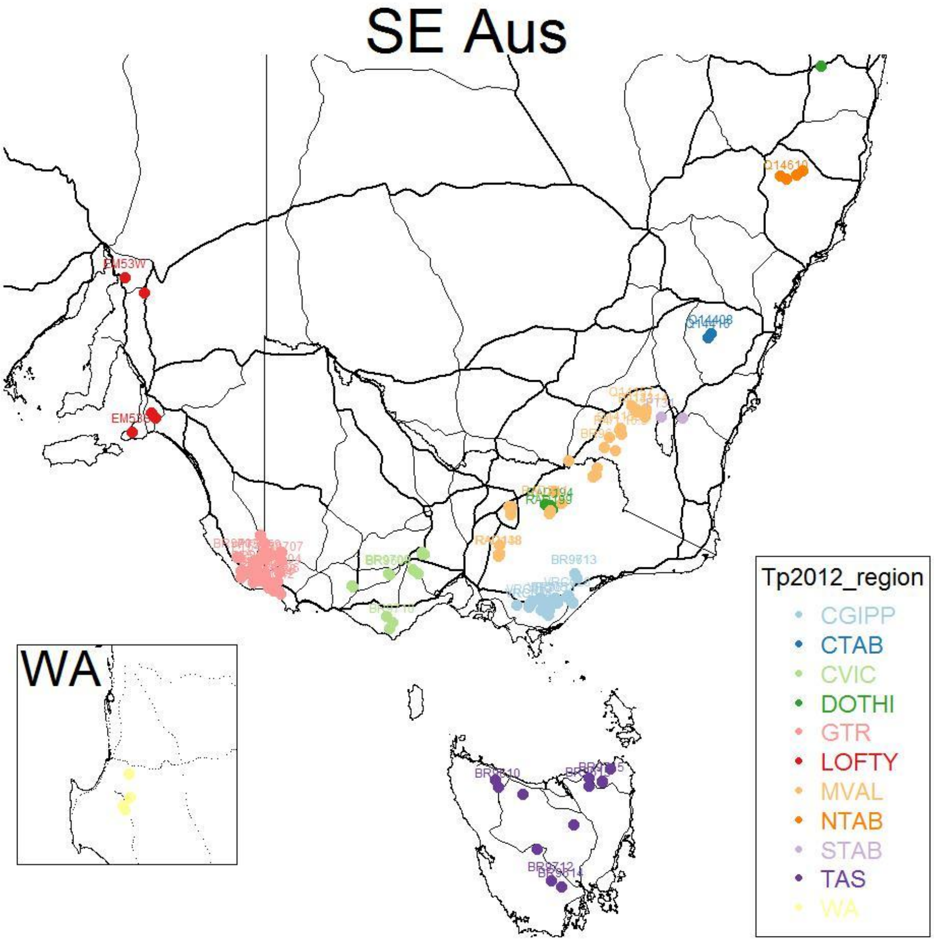


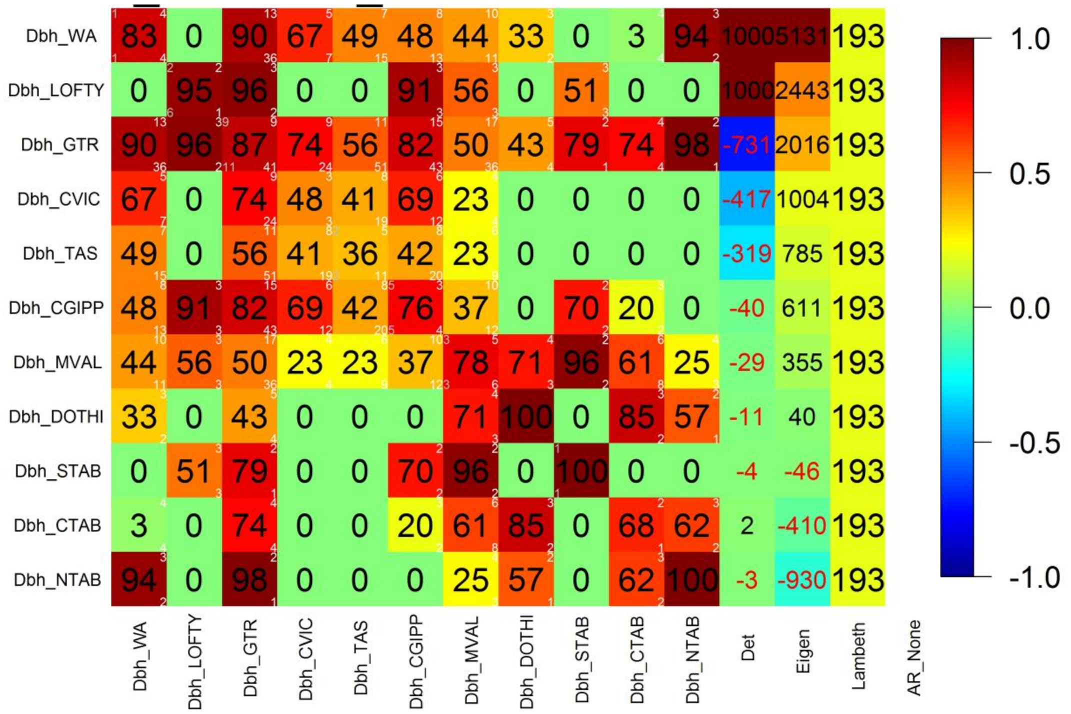
Figure 10. All DATAPLAN® trial locations classified by NPI region and DOTHI site type.

The models showed that the current *a priori* NPI_DOTHI regions and site classification and correlations were substantially better in terms of model fit (i.e. lower weighted error sum of squares - Wt ESS) than no classification, but worse than allowing for residual G×E with the No_G×E model. Within the *a priori* structure, allowing for residual G×E only marginally improved model fit. Estimating the correlations with the NPI_DOTHI structure substantially improved model fit. However, constraining the inter-trait correlation matrix to be positive definite (NPI_DOTHI_PD) led to a poorer model fit (**Table 1**).

Table 1. Results from different site classification models.

Model	*Residual GxE*	*Wt ESS*	*Residual r_a*
Baseline: No GxE	No	931.96	1
	Yes	479.90	0.66
Baseline: NPI DOTHI a priori	No	531.22	1
	Yes	480.47	0.36-0.95
Baseline: NPI DOTHI estimated	No	367.33	1
	Yes	316.59	0.36-0.95
Baseline: NPI DOTHI PD	No	468.68	1
	Yes	417.94	0.36-0.95
Split 1 Mtwetq 8.985	No	494.89	1
	Yes	364.00	Cool 0.58 Warm 0.85
AR Rain_oct	No	430.89	1
Split 1 Rain Oct 3 classes	No	513.86	1
	Yes	384.23	0.22-0.84
Split 2 Rain_march 68 in Cool	No	394.68	1
	Yes	315.78	Cool_Dry 0.75 Cool_Moist 0.18 Warm 0.85
Split 3 Temperature Annual Range in Cool_Dry	No	354.46	1
	Yes	292.09	Cool_Dry_Uniform 0.86 Cool_Dry_Variable NA Cool_Moist_0.18 Warm 0.85

Allowing for residual G×E indicated high unexplained G×E in Tasmania, however the number of trials in any of the site types were generally low (<6). Allowing for residual G×E within this structure gave a better fit, mostly due to the low between-site correlations in Tasmania (0.36-5 trials), CVIC(0.48- 3 trials) and MTAB (0.68 - 2 trials). GTR had low G×E (0.87 – 9 trials) (**Figure 11**). Estimating the correlations between these classes substantially improved model fit, however there were some site type pairs that could not have their correlations estimated due to a lack of pairs of trials in the different site types. The matrix is not positive definite (Eigen < 0) and thus cannot be used for BV prediction.



	Dbh_WA	Dbh_LOFTY	Dbh_GTR	Dbh_CVIC	Dbh_TAS	Dbh_CGIPP	Dbh_MVAL	Dbh_DOTHI	Dbh_STAB	Dbh_CTAB	Dbh_NTAB	Det	Eigen	Lambeth	AR_None
Dbh_WA	83	0	90	67	49	48	44	33	0	3	94	1000	5131	193	
Dbh_LOFTY	0	95	96	0	0	91	56	0	51	0	0	1000	2443	193	
Dbh_GTR	90	96	87	74	56	82	50	43	79	74	98	-731	2016	193	
Dbh_CVIC	67	0	74	48	41	69	23	0	0	0	0	-417	1004	193	
Dbh_TAS	49	0	56	41	36	42	23	0	0	0	0	-319	785	193	
Dbh_CGIPP	48	91	82	69	42	76	37	0	70	20	0	-40	611	193	
Dbh_MVAL	44	56	50	23	23	37	78	71	96	61	25	-29	355	193	
Dbh_DOTHI	33	0	43	0	0	0	71	100	0	85	57	-11	40	193	
Dbh_STAB	0	51	79	0	0	70	96	0	100	0	0	-4	-46	193	
Dbh_CTAB	3	0	74	0	0	20	61	85	0	68	62	2	-410	193	
Dbh_NTAB	94	0	98	0	0	0	25	57	0	62	100	-3	-930	193	

Figure 11. Genetic correlations for Dbh in NPI_DOTHI regions with G×E Model.

Constraining the matrix to be positive definite by giving weight to the last eigen value did achieve a positive definite correlation matrix. All correlations are reduced, some substantially. Clustering based on the resulting correlation matrix (**Figure 12**) showed geographically-sensible main groups for the southern mainland (CGIPP, GTR, CVIC) with TAS as an outgroup, and a southern Great Dividing Range group of MVAL and STAB, with LOFTY also as an outgroup. DOTHI and WA were outgroups relative to all of these and were grouped with CTAB and NTAB respectively. The main groups could be used to define a smaller number of site types, or the correlations between them used to improve breeding value prediction within the current site type definitions.

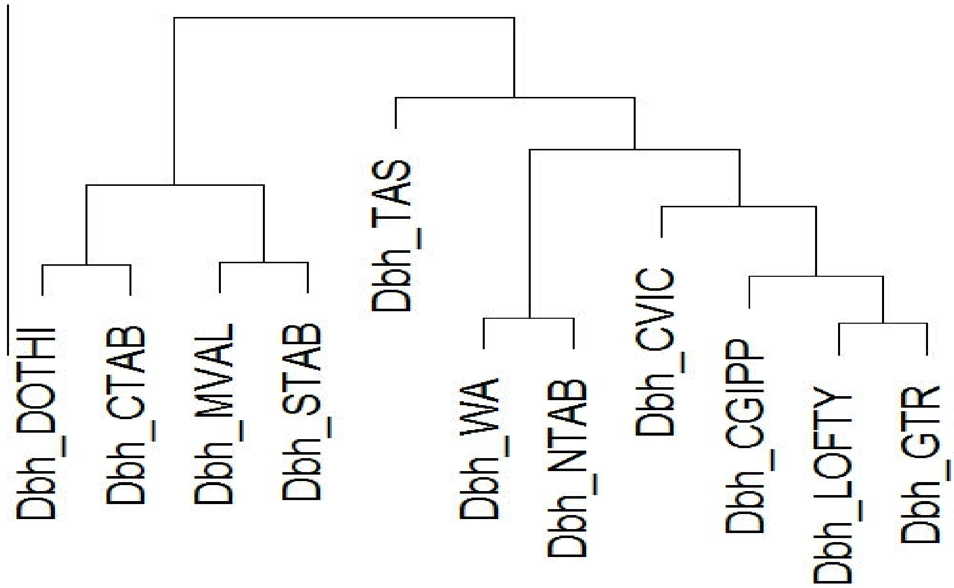


Figure 12. Dbh_NPI+DOTHI hierarchical clustering based on positive definite matrix of inter-site genetic correlations.

Site type classification based on environmental variables

The best initial split was based on mean temperature of the wettest quarter (Mtwetq). The correlation between high and low values for this temperature variable after splitting at 8.9 degrees (i.e. between Cool and Warm site types) was quite low, at *r*=0.48. However, within Cool site type, the correlations were much more dispersed, with values from the minimum allowed value of -0.5 to 1.0. There was a good scope for further splitting the Cool sites, as indicated by the high residual G×E for such site (**Figure 13**).

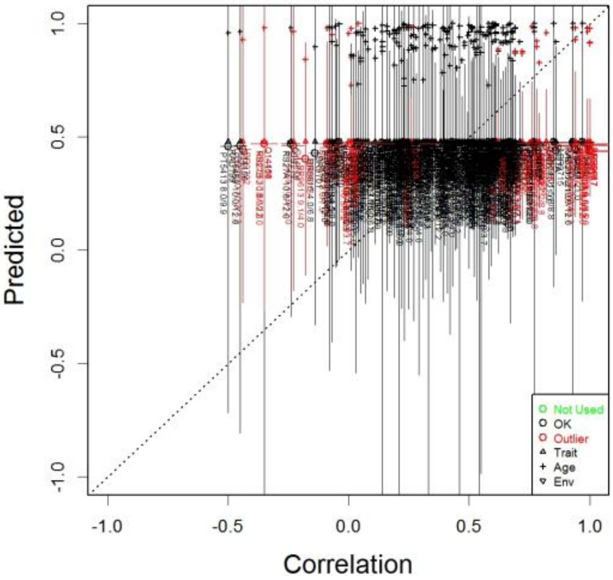


Figure 13. Additive genetic correlations between Dbh in Warm and Cool site types estimates after splitting on Mtwetq as the primary split.

The first split separated out south-eastern highland areas and most of Tasmania from WA, GTR, lowland parts of western Victoria and Gipppsland, warm sites in NE Tasmania and northern NSW. The AR model was better than splitting the trials into the two groups (as gauged by lower Wt ESS) with Rain_Oct the most informative variable. A number of other rainfall and moisture index variables had similar fit (presumably because they are correlated to rainfall) (**Figure 14**).

After splitting on Mtwetq, the AR model indicated that rainfall in October was the best predictor with a variety of other moisture variables also effective predictors. Splitting the site types indicated that rainfall in March was the best for the second split, better than the AR model, although the split only identified 4 trials in the new group at the extreme end of Rain_Mar. This variable splits out high rainfall areas in the Otway and Stzelecki ranges, parts of the Great Dividing Range, and Tasmania.

Other moisture traits all gave similar but slightly worse model fit, all within the cool sites, all giving more or less the same areas as a new site type. Three trial outliers gave the best model fit, isolating BR9610, BR9710 and Q14114, indicating that these trials have high leverage and are influencing the results for moisture as all have March rainfall >68mm. The outlier trials are however from diverse parts of the range (**Figure 14**).

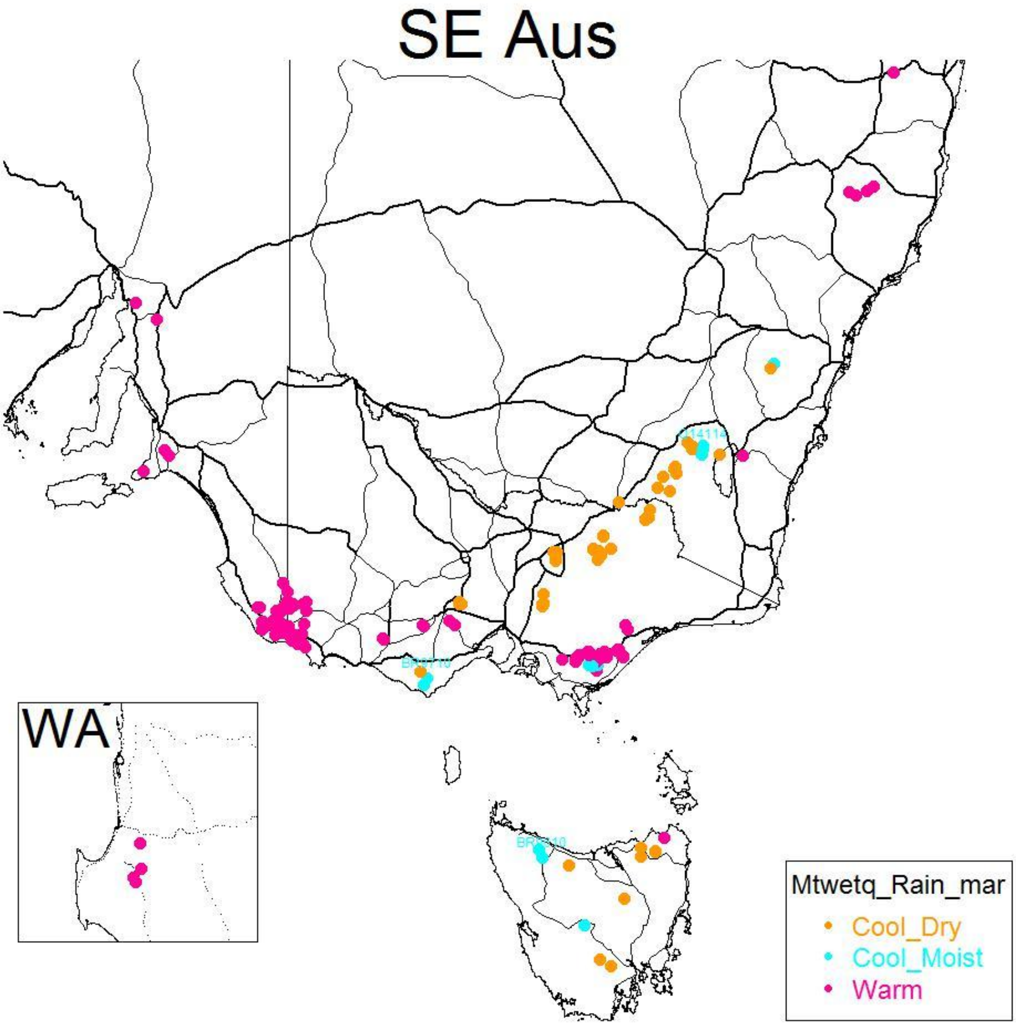


Figure 14. Map of Rainfall March within Cool sites for Mtwetq (all DATAPLAN® trials, but with outlier trials identified). DB23R

The correlations between classes were low (0.2-0.3), but they were moderate between Warm and Cool_Dry (0.5) site types. Allowing for residual G×E showed relatively high within site type correlations (>0.75) for most site types, except for the new Cool_Moist class, which had only 4 trials, and only 2 site-site correlations, with an average correlation of 0.18 (**Figure 15**).

Figure 15. Genetic correlation coefficients ×100 for the two best splits based on environmental variables.

The splits for stem straightness (Stemstr) and branch size (Brs) are described in the (**Appendix 1**). For Stemst the best split was based on environmental variable Rain September, with NFI regions CTAB, DOTHI, MVAL, NTAB next best. For branch size (Brs) the best autoregressive (AR) model was based on annual precipitation (Ap). The best split based on environmental variable was equally on identifying outlying trials BR9615, BR9710, and RAD142 and environmental variable Ap. A number of other rainfall variables, and parent rock code were not far behind as predictor variables. The correlation between Dry and Moist site types for Brs was only 0.48.

TREEPLAN® runs

TREEPLAN® runs were defined that matched with the correlation models that were tested. The runs were based on just the Dbh data which consisted of 186 trial trait measurements in 3 age classes (0-5, 6-12 and 13-14 years) from 154 trials spread across southern Australia. Only additive effects are included, and the data were scaled so that the additive variance of each of the traits was one, with each trial being given the heritability estimated from the site by allowing each trait to have a different error variance.

The BV variances (i.e. variances among breeding values) at each age were quite low (0.37-0.45) for the baseline No_GxE model. The BV variances were generally smaller for the model using NPI and *Dothistroma* regions with *a priori* (i.e. assumed) inter-region correlations (NPI_DOTHI_Apriori), although in some instances they were higher, with a general weak trend of increasing variance with the number of trials. GTR forms part of a cluster of NPI regions which now have a higher correlation with each other, than previously, so this may account for that, however the BV variance for the other regions (CGIPP and CVIC) have not changed as much. TAS and MVAL had generally lower BV variances with the PD model as these generally had lower correlations in the PD model than under the *a priori* model, suggesting inflation of the BVs (and thus gains) in these regions (**Figure 16**).

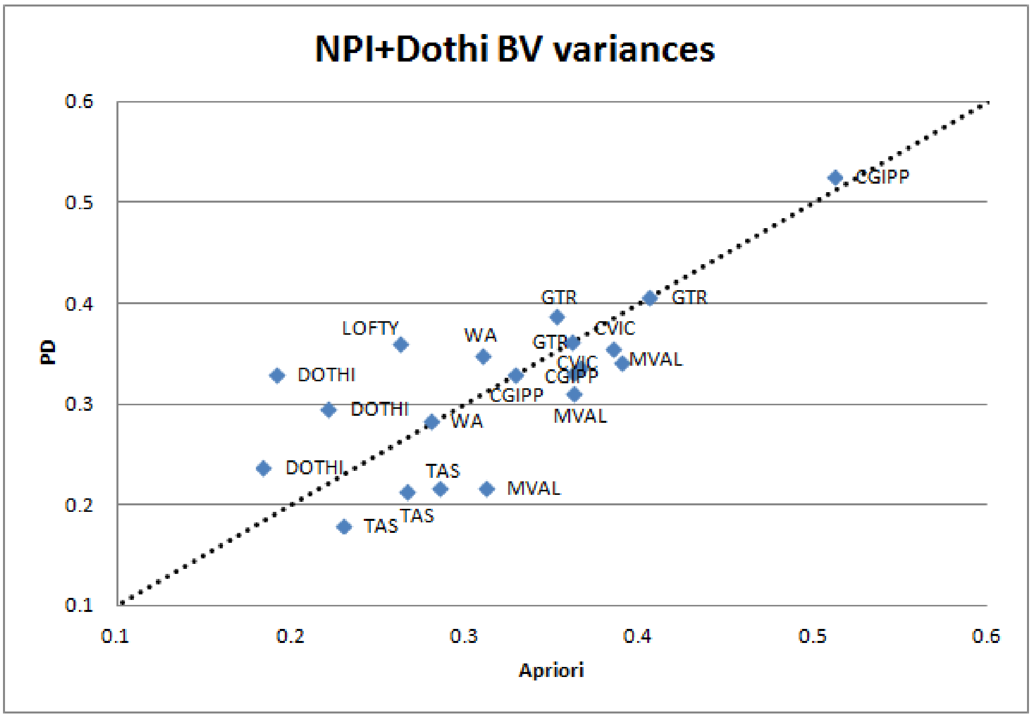


Figure 16. Comparison of BV variance from TREEPLAN® runs for current NPI and *Dothistroma* regions for positive definite (PD) and *A priori* (i.e. currently assumed) correlation matrix model (points with same label represent different age of measurement).

The correlations of the BVs between the two runs were generally high (>0.95), however they were low for the DOTHI, LOFTY, and WA which have lower correlations with the PD set than the *a priori* ones. Therefore the newly estimated correlations did make a difference. For the model based on Tmin_Oct, the BV variances for the Cool sites were much reduced (about 0.25), in line with the relatively high residual GxE in that site type. For the Warm sites the variance increased to 0.53 for the youngest age class, and was about the same for the later age classes.

Discussion

G×E analyses of STBA trials

There appeared to be a positive link between the number of parents in common between trials and genetic correlations, which was found in other studies (e.g., Apiolaza 2012). For *Pinus radiata* in Australia G×E was modelled using rgModel based on a database of genetic correlations, weighted by *t* values (i.e the ratio of estimate to its prediction error). Correlation estimates between current site types used in TREEPLAN® were updated based on the database (Dutkowski and Ivković 2014). Estimating the correlations between NPI regions substantially improved model fit, relative to current *a priori* NPI_DOTHI regions and site classification. However there were some site type pairs that could not have their correlations estimated due to a lack of pairs of trials in the different site types.

To identify new site types based on environmental variables rgModel parameters were estimated by minimising the weighted error sum of squares of each model using the genetic correlations in the database. The first split of site types was based on mean temperature in wettest quarter (Mtwetq 9.0°C). The second split was on March rainfall (Rain_march 68 mm), with a variety of other wetness variables being very similar. Only 4 trials were in a new class identified and outlier analysis indicated that only a few cool site trials were driving this difference. However, cool sites are not the primary focus of the STBA's breeding program.

This division based on environmental variables confirms drivers of G×E identified by other methods in the previous work in Australia (e.g. Baltunis *et al.* 2010, Raymond 2011, Gapare *et al.* 2012, Ivković *et al.* 2014). However, the smaller number of trials used in those studies gave variable results depending on which trials were used and what environmental variables differed between them. In addition, the historic separation of state breeding programs, which led to a lower number of genotypes in common across state boundaries for most trials, may have caused bias in the correlation estimates.

Breeding value (BV) prediction using TREEPLAN® showed that changing the correlations between currently used NPI regions to new values based on the database of genetic correlations either increased or decreased the variance among BVs. For site types which became more closely correlated than previously determined, the variance among BVs increased, which is desirable as it gives more resolution for selection. The correlation between BVs obtained on the basis of current and updated inter-NPI region correlations was generally high (>0.95), but for those regions for which the genetic correlations with other regions were now smaller, the BV correlations were lower.

Breeding value prediction using TREEPLAN® also showed that compared to a baseline model of only a single site type, splitting sites into two new site-types, cool and warm, led to reduced BV variance for cool site type, presumably due to high residual G×E. There was an increase in BV variance for the youngest age class on warm sites, however this age class had only a relatively few trials. While it had been expected that the variance of BVs would increase for models where sites were better allocated to site types, and thus conflicting performance was reduced, this was not possible to clearly see in the current data. The effect of genetic group variance and the amount of data are probably confounded with any such effects. However, this does not diminish the clear benefits of accounting for inter-region and site-type G×E based on results of the project.

Site-types determined for stem straightness (Stemstr) and branch size (Brs) are described in the (**Appendix 1**). To account for G×E in composite traits (i.e. selection index) absolute values of component (i.e. breeding-objective) traits are necessary for application in deployment tools such as SEEDPLAN®. At the same time the relationship between mean and variance for breeding-objective traits is important for scaling the breeding values of entries in TREEPLAN®. The results based on resource evaluation studies in Green Triangle Region, Western Australia (WA) and Tasmania (TAS) on the relationships between mean and variance were established are described in the **Appendix 2**.

Conclusion

As a result of this project STBA has moved from applying *a priori* (i.e. assumed) inter - NPI region genetic correlations in TREEPLAN®, to applying the best available empirical estimates. In addition, the results of current modelling and classification of trials into Warm and Cool site types, and Wet and Dry within Cool site types are currently being tested for application by the STBA's breeding and deployment programme. While it had been expected that the variance of BVs would increase for models where sites were better allocated to site types, and thus conflicting performance was reduced, this was not possible to clearly see in the current data. The effect of genetic groups (i.e. land subrace) variance and the amount of data are confounded with any such effects.

Nevertheless, the structures and approaches have been established for both the correlation modelling and the prediction of breeding values once the best models are identified. This will provide a platform for future work, when more estimates become available for inclusion in the database of genetic correlations. Additional genetic correlations will soon become available from WA trial sites, which will provide more information on G×E between warm sites and that will help to better identify causes of G×E in such areas. Breeding and optimal deployment of genetic stock to particular environments based on this knowledge is likely to significantly improve radiata pine plantation productivity.

Recommendations

1. A good framework has been established (i.e. rgModel) that should be used in future work on G×E in STBA or any other radiata pine network of trials
2. Genetic parameters (i.e. site-site, trait-trait, and age-age genetic correlations) should be deposited in a joint database of genetic parameters for radiata pine.
3. The work on G×E for GCA needs to be extended to SCA.
4. Changes in selection criteria (i.e. site type classifications) for TREEPLAN® evaluation should be further examined and implications of the results for SEEDPLAN® and site matching
5. Different weightings of the site-site genetic correlation estimates may also need to be investigated in future TREEPLAN® runs.
6. More estimates of site-site genetic correlations are needed and for that more trials are needed. Our analyses suggested that up to 100 parents in common between trials are desirable to get reliable bi-variate estimates of site-site genetic correlations.

7. For industry to fully benefit from this framework, it is important that new trials are genetically well connected to each other and to trials already in STBA DATAPLAN®.
8. For all well connected trials with genetic correlation estimates, more site-specific environmental data are also needed. Collection of fine-scale environmental data, including soil chemical, textural and depth information, for each trial is recommended.
9. Protocols should also be established so that the traits other than growth can be predicted for different deployment site types. This will help deployment based on composite index traits in deployment tools.

GxE analyses of RPBC trials

Summary

- We used one set of provenance and one set of progeny trials to predict relationships between genotype performance and environmental variables in order to determine possible drivers of genotype by environment interaction (G×E) in radiata pine grown in New Zealand.
- For provenance trials, based on analyses using multivariate regression trees (MRT), infertile clays accounted for 21% of variance and mean daily minimum temperature of the coldest month accounted for 13% of variance.
- For the progeny trials high rainfall and cold temperature are the likely drivers of G×E in New Zealand and explained 25% of G×E variance
- For deployment purposes, it is possible to group the sites into high rainfall sites (where most genotypes performed better) and cold sites, where specific parents need to be picked for deployment.
- The results from analyses such as MRT can be applied to create maps for use by breeders and forest managers to select test sites for trials as well as to match and deploy genotypes to target environments.

Inroduction

Burdon *et al.* (1997) investigated the relative performance of three mainland provenances of radiata pine (Año Nuevo, Monterey and Cambria) and three regional land-race stocks (Kaingaroa, Nelson and Southland), on different site categories. In this study, we used Dbh data from the same 21 radiata pine provenance trials planted across New Zealand in 1980, which is the subject of the publication by Burdon *et al.* (1997). We tested whether multiple regression tree (MRT) analysis could replicate the results obtained in the original study. Furthermore, we extended the analyses by combining different climate and soil attributes in order to determine the probable causes of G×E in diameter growth in New Zealand.

Second, we also applied the MRT analysis to a large data set from 48 radiata pine progeny trials, established by the Radiata Pine Breeding Company (RPBC) that are genetically connected by 28 common parents that are currently widely deployed in New Zealand. The ultimate objective was to predict relationships between parents and environmental variables in order to determine possible drivers of G×E. The identification of climatic and or environmental variables as probable causes allows us to extrapolate the performance on test sites to sites with similar characteristics and creation of site-type maps. A key question was also whether specific genotypes are needed for distinct environments or whether there are genotypes that perform uniformly well across all environments.

Methods

Environmental variables

Environmental variables that describe various aspects of New Zealand's climate, landforms and soils, were obtained from Land and Environment New Zealand (LENZ) (http://lris.scinfo.org.nz/layers) for all 112 RPBC test sites. Daily climate observations were obtained from the Virtual Climate Station Network (VCSN) from NIWA (National Institute of Water and Atmospheric Research Ltd.). The resolution was a 0.05° latitude/longitude grid, covering all of New Zealand. A thin-plate smoothing spline model based on latitude, longitude and elevation was used for spatial interpolation (Tait *et al.* 2006).

Comprehensive quantitative soil information was extracted from the S-map online database (http://www.landcareresearch.co.nz/databases/nzlri.asp). Depth to slowly permeable horizon, drainage, macroporosity at depth and at the surface, maximum salinity, minimum pH, phosphate retention, total carbon, potential rooting depth and topsoil gravel content were extracted from the National Soils Database and the New Zealand Fundamental Soil Layers (Wilde *et al.* 2000).

The climate variables used in the analyses included mean annual precipitation, temperature, radiation, and moisture indices as annual averages, max or min, or averages for different periods of the year, such as the warmest quarter or the wettest quarter. We selected climate and soil variables that were expected to have an effect, which can be measured easily and interpreted in a biologically meaningful way. In addition, it was desirable that the input variables were orthogonal with respect to each other. However, some degree of confounding or non-orthogonality was inevitable as the climatic data were predicted from the site climate location data, so factors such as radiation and temperature variables were interrelated.

Breeding values and genetic clustering

The availability of genetically-related RPBC trials planted across a wide range of environments provided genetic links and allowed estimation of across-site variance and covariance components. Unstructured site by genotype variance covariance matrices (i.e. a matrix allowing estimation of all variance and co-variance parameters among sites) can account for both scale and rank interactions, but with many environments the estimation of an unstructured covariance matrix is not usually feasible (Smith *et al.* 2001). A reduced (parental) mixed model analysis with a factor analytic (FA) variance structure for the G×E effects and separate variance for the errors for each trial were applied to RPBC trial data by Cullis *et al.* (2014). While the FA model is computationally less demanding, because fewer parameters are estimated, it also allows simultaneous estimation of all variance and covariance parameters. For reduced data dimensionality the FA*k* form uses a sparse formulation that requires *k* levels to be inserted into the mixed model equations for the *k* factors. We used breeding values estimated by Cullis and Jefferson (2012) for further analyses and clustering involving environmental described in the following section.

Clustering using multiple regression tree analyses (MRT)

Twenty one provenance trials planted across New Zealand provided the experimental basis for the first part of this study. The experimental design and detailed seed source information for Año Nuevo, Monterey and Cambria provenances and three regional land-race stocks, Kaingaroa, Nelson and Southland was described in Burdon *et al.* (1997). Since age for Dbh measurements ranged from 5 to 15 years (juvenile and transition ages), we standardised the data, so that all traits are expressed in units of standard deviations from a site mean of zero and so that they are weighted equally in MRT analysis. Although there were multiple seedlots within the native provenances compared, and the land-race stocks were single homogeneous groups, there were no significant differences in the variance of the groups after the standardisation across trials. The standardized data for each site were then analysed singly, treating provenances as fixed effects using the software ASReml (Gilmour et al. 2009) giving Best Linear Unbiased Estimates (BLUEs) for the three Californian populations and the three land races.

The second dataset used in this study contained a subset of trials that were used by Cullis *et al.* (2014) of 48 RPBC field trials. The numbers of parents and families in common varied substantially between RPBC trials and we used the empirical best linear unbiased estimates (E-BLUPs) of a subset of 24 most-tested and most-deployed parents that were tested across all 48 sites. Multivariate regression trees (MRT) are based on the same principles as Classification and Regression Trees, but extended to more than one response variable (i.e. multiple genotypes) (De'Ath 2002). The regression tree clusters are driven by the degree of genetic differentiation observed in the response dataset. These analyses were implemented with the MVpart package v1.2–6 for the R programming environment (R Development Core Team 2008).

Our approach was to start with an unconstrained clustering, using the Euclidian distance measure, so that we know the maximum variance that could be explained by G×E. Hierarchical clustering was performed with R package *hclust* using the Euclidian distance measure (R Development Core Team 2008). The result of this function is a dendrogram splitting all sites based on the distance measures. We then applied a cut off after the fourth split based on data cross-validations. All sites were assigned a group as a new categorical variable. These groups were then used as categorical predictors in the MRT analysis, in order to generate barplots representing genotype performances for the leaves and nodes in the dendrogram. Then, as an alternative, the clustering was constrained by climate and soil variables to determine which ones might be responsible for G×E. How much variance was accounted for by this latter procedure indicates the proportion of G×E that can be explained by environmental variances.

Results

Clustering of provenance trials

Our analysis of provenance trials suggests that the likely drivers of provenance by site interactions appear to be soil type and temperature. We partially replicated the results of Burdon *et al.* (1997) (**Figure 17a**). Infertile clay site types accounted for 21% of variance and mean daily minimum temperature of the coldest month (MinTCM) accounted for 13% of variance. The MRT clustering indicated that the maximum explainable G×E variance was 62%, compared to 34% explained under constraints of soil and climate variables (**Figure 17b**).

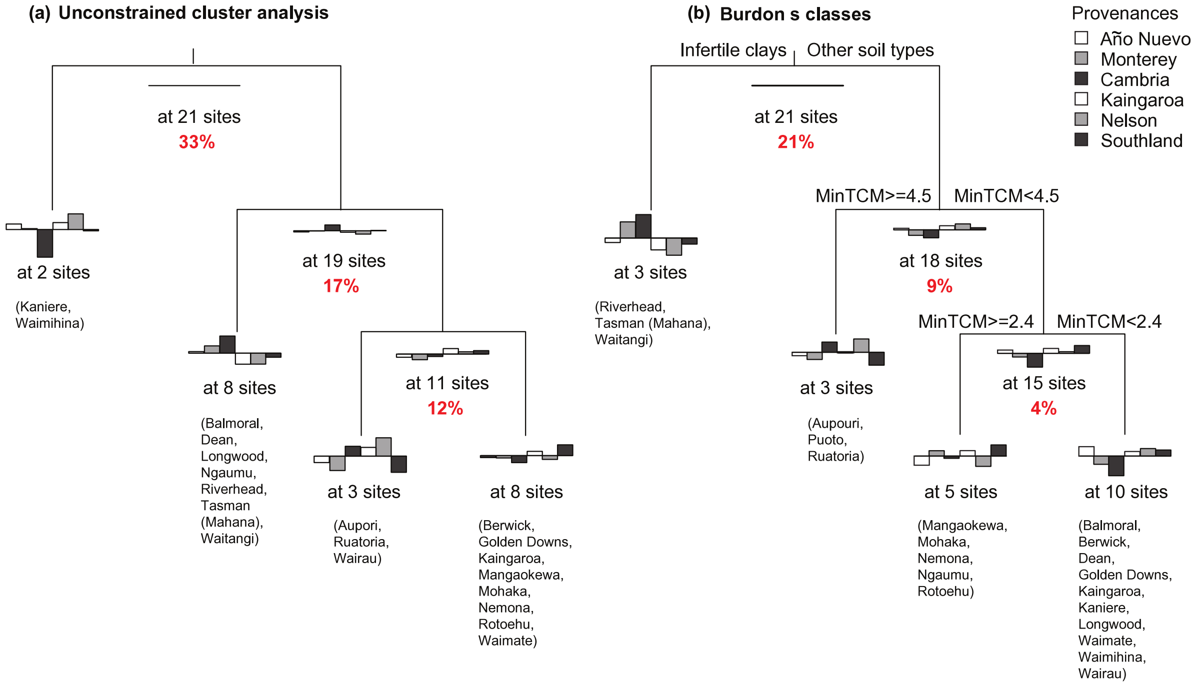


Figure 17 Unconstrained (**a**) and constrained cluster (**b**), grouping 21 planting sites according to the performance of Año Nuevo, Monterey and Cambria provenances and three regional land-race stocks, Kaingaroa, Nelson and Southland. The same order of provenances used for legend (vertical order of listing) is also used for the histograms (horizontal order). Variances in breeding values explained by each node of the cluster are indicated in red. In gray scale colored bars represent group means expressed in deviation from an overall mean of zero (horizontal line). Site names are given below each group.

Clustering of progeny trials

The unconstrained clustering analysis based on Euclidean distance of genotypic performance of the 24 parents tested at 48 RPBC progeny trials revealed four groups (A to D) (**Figure 18**). Group A with nine sites comprised the overall top-performing genotypes, while group B was characterised by a relatively poor performance of the same parents at 16 sites. The remaining 23 sites were split into groups C and D with mixed performance of the parents. The total variance in breeding values explained by the clustering was 58% and the breakdown in variances in breeding values explained by each node of the cluster were 31%, 17% and 10% (**Figure 18**).

Imposing constraints by climate variables – mean annual precipitation (MAP), mean minimum temperature coldest month (MinTCM), we obtained similar groupings (**Figure 19**). The first split was by MAP, identifying 11 wet sites with MAP above 1670 mm. It is on these 11 wet sites where the good performers did better (as in Group A in **Figure 18**). Interestingly, the estimated BV values for individual parents were almost the same across these 11 sites as they were for the nine sites of group A in the unconstrained cluster, even though the unconstrained clustering accounted for much more observed variance (31% vs. 9%). The remaining 37 sites were split into two groups based on MinTCM (<1.6), the split being similar to the one in the unconstrained analysis, separating group B from C and D. When clustering was constrained by climatic variables, total variance in predicted breeding values explained by the clustering was 15% (or 26% of G×E variance). We used the results from the constrained clustering to produce a map (**Figure 20**) showing location of trials in each group. We also show radiata pine plantation areas in NZ Central North Island with minimum temperature coldest month less than 1.6, where a high degree of GxE can be expected (**Figure 21**). Such maps may be used by tree breeders and forest managers to select sites for breeding trials as well as match genotypes to target environments.

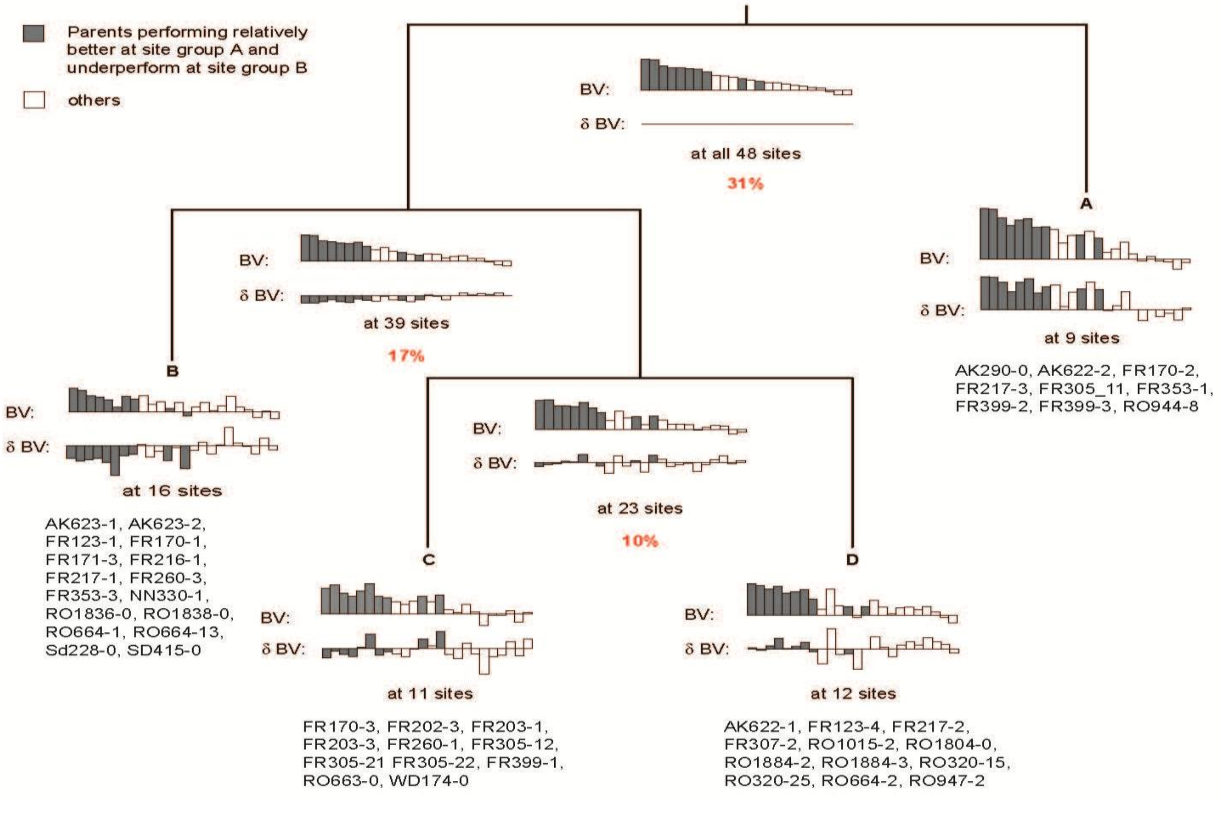


Figure 18. Unconstrained cluster analysis: grouping of 48 planting sites according to the performance of 24 parental genotypes. Genotypes are ordered from left to right by breeding value (BV), and the lower bar chart displays how genotypes deviate from their average breeding values at a particular group of sites (δBV). Variances in breeding values explained by each node of the cluster are indicated in red. The parental genotypes coded 1 to 24 from left to right. Site codes are shown below each group.

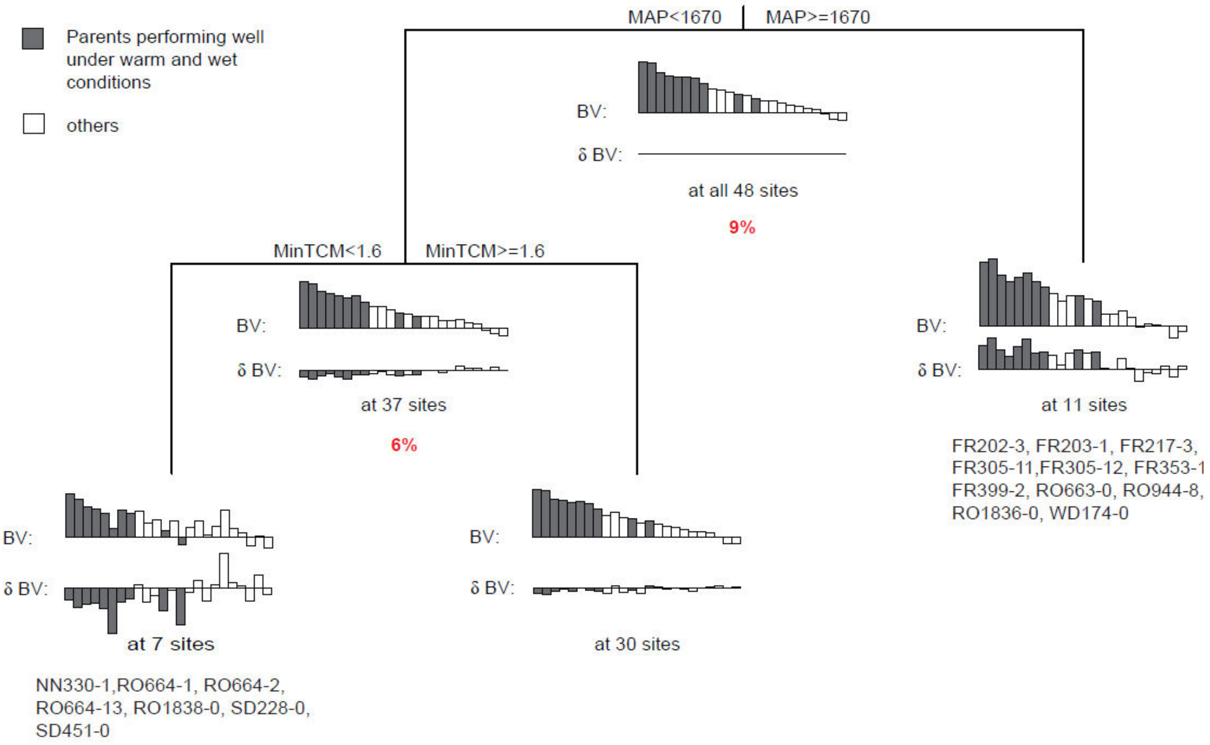


Figure19. Constrained cluster analysis: grouping of 48 planting sites according to the performance of 24 parental genotypes, constrained by mean annual precipitation (MAP) and minimum temperature of the coldest month (MinTCM).when performance of 24 parental genotypes is constrained by mean annual precipitation (MAP) and minimum temperature of the coldest month (MinTCM). Genotypes are ordered from left to right by breeding value (BV), and the lower bar chart displays how genotypes deviate from the average breeding value at a particular group of sites (δBV). Variances in breeding values explained by each node of the cluster are indicated in red. The parental genotypes coded 1 to 24 from left to right. Site codes are shown below each group.

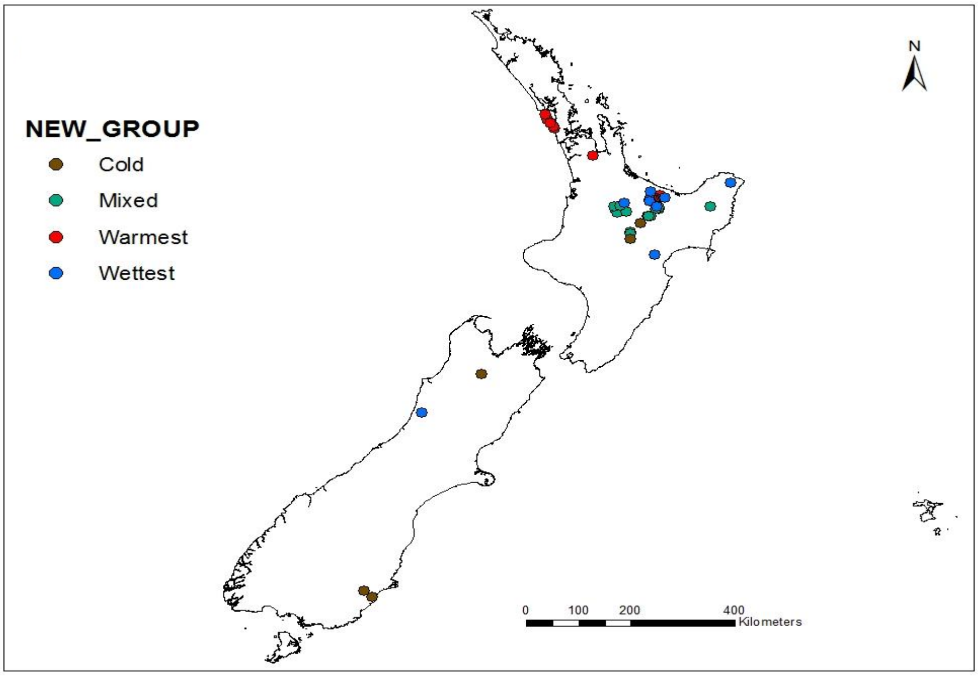


Figure 20. Grouping of 48 trial sites (●) in New Zealand based on mean annual precipitation (MAP) and minimum temperature cold month (MinTCM) (based on clustering in Figure 19);

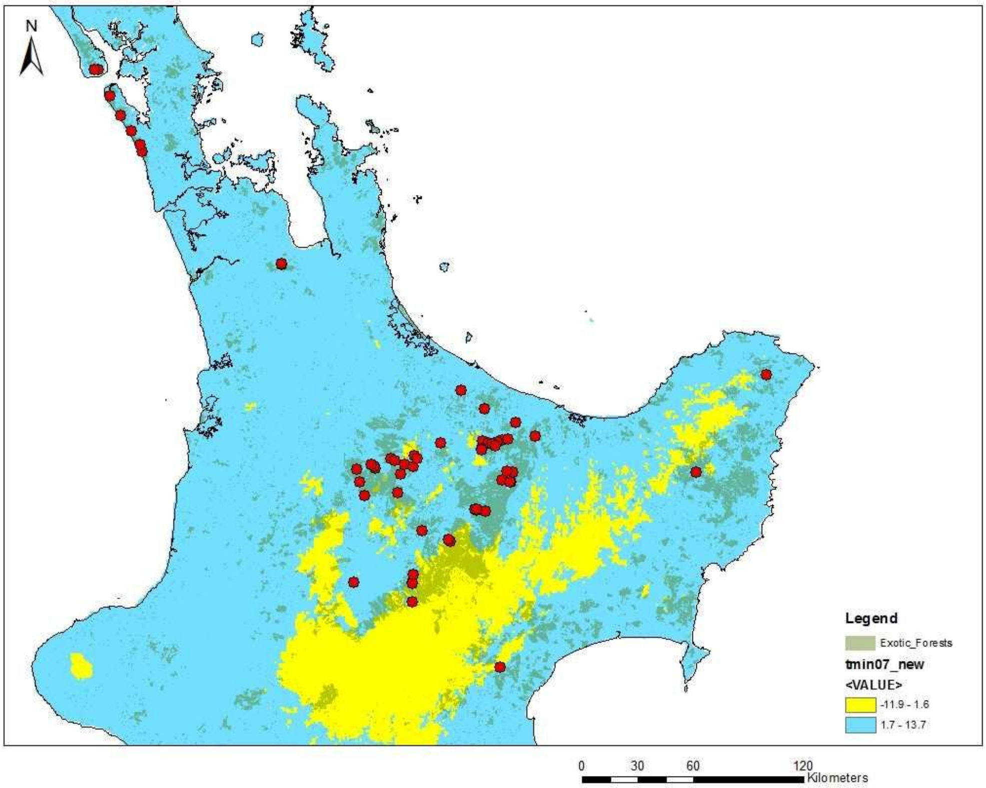


Figure 21. Radiata pine plantation areas (overlap of green and yellow) in NZ Central North Island with minimum temperature coldest month less than 1.6°C, where cross-over G×E can be expected.

Discussion

Clustering without and with environmental constraints

Using the soil variables collated from Land and Environment New Zealand (LENZ) layers we could not replicate the results of Burdon *et al.* (1997), and the split of trials on infertile clays, which previously explained a substantial amount of G×E for the provenance data. This suggests that in addition to soil types and temperature, there are other management or environmental variables contributing to the observed G×E in DBH. Susceptibility to *Dothistroma* needle blight may also have a differential effect on provenance performance, as it has previously been shown to affect Cambria provenance negatively. Gapare *et al.* (2011), for example, found negative genetic correlations between *Dothistroma* defoliation and DBH as well as between defoliation and survival in radiata pine provenances (Gapare et al. 2011).

A study by Watt *et al.* (2010) reported that variables driving productivity in New Zealand included mean annual temperature, available root zone water storage, mean annual wind speed, length and slope factor and major soil parent material. MacDonald (2009) applied multiple regression to resemblance matrices for Dbh and a number of environmental matrices, finding G×E to be driven by extreme maximum temperatures and altitude. The effect of these two climatic variables may also be proxies for moisture availability. However, in our case, none of the other climatic and environmental predictors could explain as high a proportion of G×E variance as was explained by mean annual precipitation (MAP) and minimum temperature coldest (MinTCM).

This study has confirmed the presence of G×E in New Zealand for Dbh in contrast to traits related to stem form and wood quality which have shown little or no evidence of G×E (e.g. Johnson and Burdon 1990, MacDonald 2009, Gapare *et al.* 2010, Apiolaza 2012). We characterised the role of environments and identified specific environmental variables responsible for generating a proportion of the G×E interaction. More detailed environmental variables and better connected trials may enable us in the future to explain a larger proportion of the G×E for growth in New Zealand, and may allow us to develop a regionalisation strategy to deal with the issue (Cullis *et al.* 2014).

Conclusions

Analyses here demonstrated relationships between genotype performance and the environmental variables as drivers of G×E in radiata pine grown in New Zealand. The analyses of progeny trial data showed that extreme rainfall and cold temperature are the likely drivers of G×E in New Zealand. Second-generation genotypes behaved more consistently than first-generation provenance material across a wide variety of site and climate conditions. The best genotypes performed above average on wettest sites. They only rarely significantly changed ranks with other genotypes at other sites, except as cold sites. Our analyses suggests, that significant rank changes can be expected on cold sites with minimum temperature of the coldest month less than 1.6 °C (i.e. Southland- Otago and Nelson regions, and high elevation sites in Waikato region)

Currently the same set of genotypes are deployed throughout New Zealand, and it is believed that little could be gained by a strategy of matching particular genotypes to environments to which they may be best adapted. Assuming that we want to deploy 10 of 24 parents examined in MRT analyses, there are two options: 1) a ‘Single Population’ strategy, to select genotypes which perform well across all environments, and 2) a ‘Regionalisation’ strategy, to select two clusters, which have genotypes more specifically adapted to each of the two environments. If selection is based on breeding values derived from BLUPs, percent gain for a single population strategy, DBH genetic gain was in the order of 8%. Genetic gains for wet and cold sites separately were 3% and 20%, respectively. This suggests that it is feasible to increase plantation productivity and realise genetic gain through targeted deployment.

While results from our analyses point to the fact that G×E is of practical importance, more data from new, genetically well-connected trials and more precise information on environmental variables (in particular soils) are needed to quantify the G×E effects and extend predictive ability. That will enable RPBC to make better-informed decisions on how genotypes may be allocated to specific sites in order to maximise productivity. It will also allow development of adapted genotypes for deployment in specific environments to achieve stable and high productivity. For deployment purposes, it will be possible to create maps for tree breeders and forest managers to select test sites that are representative of specific target planting zones for genetic trials as well as match genotypes to target environments (eg. **Figure 21**).

Recommendations

1. A substantial amount of G×E interaction was found in RPBC trials that may be exploited for better gains.
2. A site matching approach has been proposed, where new target environments can be matched with environments in the MET dataset.
3. In particular genetic gains for deployment to cold sites separately are expected to increase plantation productivity and realise genetic gain through targeted deployment.
4. A framework (Cullis *et al.* 2014) for future work on G×E in RPBC trials has been established, however, more estimates of site-site genetic correlations are needed. For that more well-connected trials are needed.
5. In addition, more site-specific environmental data at a finer scale are also needed, for the RPBC trials.
6. The work on G×E needs to be extended to specific combining ability (SCA) and to other traits, including selection indices.
7. Deciding on future planting sites should consider future climate and therefore the locations of genetic trials should also be representative of those climates.
8. Based on variability of climate predictions, determine which site types may need more diverse genetic material.
9. A diverse portfolio of genotypes for deployment should be established to mitigate the effects of climate change, and this issue should be examined in future studies.
10. Protocols should also be established so that the traits other than growth can be predicted for different deployment site types. This will help deployment based on composite index traits in deployment tools.

Effects of climate change on breeding and deployment zones in Australia and New Zealand

Summary

- We analysed long-term average climate for National Plantation Inventory (NPI) regions in Australia and districts in New Zealand, and evaluated how well represented the climate of plantation areas by the existing genetic field trials
- Representation by trials of the historic climate (i.e. average of period from 1961-1990) in Australia and New Zealand was variable, with some regions and districts not being covered at all, and some only partially covered
- We also examined future climate scenarios to identify field trials that may not be representative of future climates in their area, and to identify areas where these currently well-tested climates may occur in the future
- Typical climates where radiata pine is currently managed are predicted to shift relative to the climate at test sites during trial periods. The shifts according to the HadGEM2–ES model for the year 2050 were significant both in Australia and New Zealand
- A significant predicted shift will result in Tasmania becoming more like Central Victoria and Central Gippsland. Murray Valley and parts of Western Australian estate are predicted to move into a non-analogous climate, which may be a reason for concern. The Green Triangle region is predicted to become warmer and drier similar to the current climate of the MtLofty-Kangaroo Island region
- Similarly, according to the HadGEM2–ES model, by year 2050 in New Zealand temperature will increase approximately by 1.9°C and precipitation will decrease 2%. The future climate of radiata pine plantation areas in New Zealand is predicted to shift significantly relative to the climate during the current trial period. The northern South Island plantation estate is predicted to become climatically similar to the southern North Island plantation region of the present. West Coast and parts of Otago-Southland estate is predicted to become more like current Bay of Plenty
- Most of the existing test sites in the Central North Island are not well aligned with the climate of future plantation areas which suggests new tests should be established in new areas.

Introduction

It has been long recognised that G×E in radiata pine is driven by climate (e.g. Wu and Matheson 2005, Gapare *et al.* 2010, Baltunis *et al.* 2010, Raymond 201, Gapare *et al.* 2012). The previous studies highlight the importance of climatic drivers of G×E and therefore the importance of considering climate change in defining future breeding and deployment zones. Anticipating future changes in climate is particularly important as radiata plantations are managed on a 25-35 year crop rotation. The recent State of the Climate Report by Bureau of Meteorology and CSIRO (2014) reported that Australia's climate has warmed by 0.9°C since 1910, and that frequency of extreme weather has changed, with more extreme heat and fewer cool extremes. Australian temperatures are projected to continue to increase, with more extremely hot days and fewer extremely cool days. Autumn and early winter rainfall has mostly been below average in the southeast since 1990 and average rainfall in southern Australia is projected to decrease.

In New Zealand, based on the projections by the Ministry for the Environment (2014) (https://www.climatechange.govt.nz/science/), temperature is expected to increase throughout the country. For example, temperature in the Bay of Plenty, one of the largest contiguous plantation areas of radiata pine in New Zealand, is likely to be at least 0.9˚C warmer by 2040 and 2.1˚C warmer by 2090, compared to 1990, with about 30–60 extra days exceeding 25˚C and 20 fewer frosts per year. Rainfall is expected to decrease throughout most of the North Island and northern South Island but to increase in West Coast, Otago, and Southland.

The above findings indicate that climate change has to be considered when planning future site type classification for genetic evaluation trials. Therefore, the general objective of this study was to evaluate the effects climate change on the breeding and deployment zones and on the representativeness of historic genetic trials in relation to plantations of radiata pine in Australia and New Zealand. The specific objectives were to:

- Analyse long-term average climate for National Plantation Inventory (NPI) regions in Australia and districts of New Zealand and determine how well is the climate of current plantation areas represented by the existing genetic field trials
- Analyse future climate scenarios and identify field trials that may not be representative of future climates in their area
- Determine how representative are current progeny tests of the radiata pine plantation areas in Australia and New Zealand
- Can we use current information from progeny test to select well adapted genotypes for the future
- Identify new areas in which field trials should be currently planted so that they will be representative of the future climate

Methods

Geographic coordinates were available for 307 and 112 genetic trials in Australia and New Zealand, respectively. Those trials have measurements data stored in the DATAPLAN data management system of the Southern Tree Breeding Association (STBA) in Australia, and exSITEz data management system of Radiata Pine Breeding Company (RPBC) in New Zealand. Coordinates for grid centroids for radiata pine plantation areas were obtained from Department of Agriculture, Land use in Australia (http://data.daff.gov.au/anrdl/metadata_files/pa_luav4g9abl07811a00.xml) and from Land Resource Information Systems Portal (LRIS) website for exotic forest in New Zealand (https://lris.scinfo.org.nz/layer/401-lcdb-v33-land-cover-database-version-33/).

Climate data used in the analyses for this report were obtained from the WorldClim, Version 1.4 (Release 3) (Hijmans *et al.* 2005). WorldClim is a set of global climate layers (climate grids) with a spatial resolution of about 1 square kilometre. The data available were climate projections from 20 global climate models for four representative CO_2 concentration pathways (RCPs). These are the most recent climate projections that are used in the Fifth Assessment IPCC report (IPCC 2013). The output was downscaled and calibrated (bias corrected) using as baseline long-term average climate. The variables included are monthly minimum and maximum temperature, precipitation, and 19 “BIOCLIM”variables derived from these 36 monthly values (see Xu and Hutchinson 2014, Booth *et al.* 2014).

Choice of global circulation model and climate scenario

Changes in predicted temperature and precipitation vary substantially, particularly when projected over long time frames. The scenarios of the fifth phase of the Coupled Model Inter-comparison Project (CMIP5) provide a multi-model context for assessing the mechanisms responsible for model differences. The range of GCM using RCP4.5 scenario outputs from WorldClim for the radiata pine plantation estate in Australia and New Zealand expressed in terms of mean annual temperature (MAT) and mean annual precipitation (MAP) are shown in **Figure 22.**

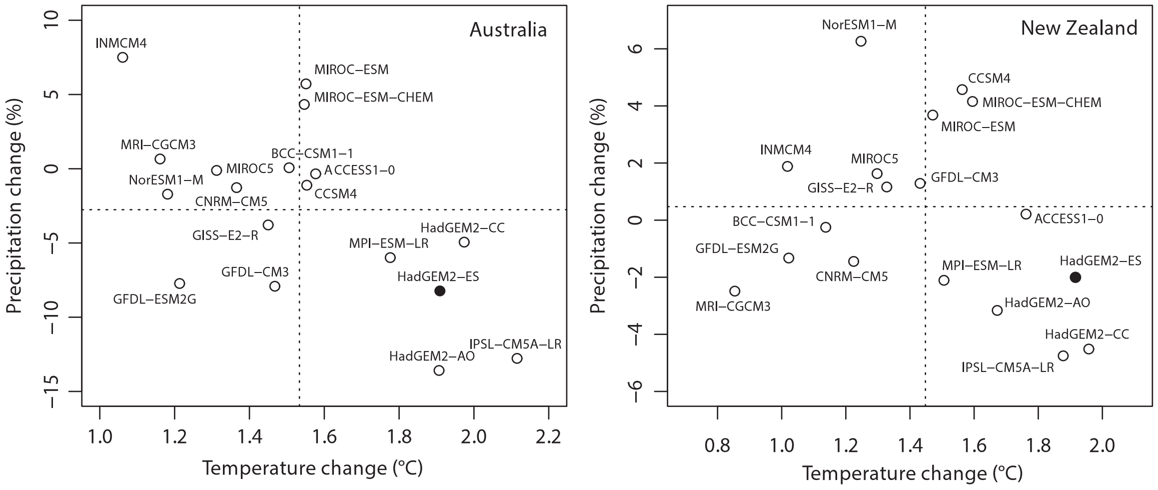


Figure 22. Climate change projections (CMIP5, RCP 4.5, 2050) for radiata pine estate in Australia (left) and New Zealand (right). The scenario HadGEM2-ES chosen for this study is represented by filled circles, the open circles represent other models.

There are a number of GCMs that can be used to develop projections of future climates for Australia and New Zealand. It is possible to use an average of all available models, but combining models requires the addition of errors associated with each model, leading to very high levels of uncertainty. Therefore, for this initial analysis, the Hadley Global Environment Model 2 - Earth System (HadGEM2 –ES) was chosen. This model was selected to allow us to consider a relatively hot and dry future climate. The model has been used for operational weather forecasting and for previous climate change studies of plantation forests (e.g. Battaglia *et.al.* 2009, Kirschbaum *et al.* 2012). As with many climate change projection models and analyses on future climate envelopes for species, the target year could be reduced to lessen the impact of the climate model; in this project, we were exploring the pattern of changes expected rather than the absolute regions that consensus projections could provide.

Variability of climate change predictions

Rainfall is one of the most difficult phenomena to predict, but climate projections predict decreased rainfall in the mid-latitudes around 25–30°S in southern Australia (IPCC 2013). All the GCMs generally agree on this, although different models draw the boundaries at slightly different latitudes. Climate models indicate that there is likely to be less rainfall in southern areas of Australia, especially in winter, and in southern and eastern areas in spring, caused by the contraction in the rainfall belt towards the higher (more southern) latitudes (**Figure 23**). It is also likely that the most intense rainfall events in most locations will become more extreme, driven by a warmer, wetter atmosphere. Temperature predictions have a higher degree of confidence than rainfall predictions. The main uncertainty in temperature projections relates to how much CO2 and other greenhouse gases will be emitted between now and the latter part of this century.

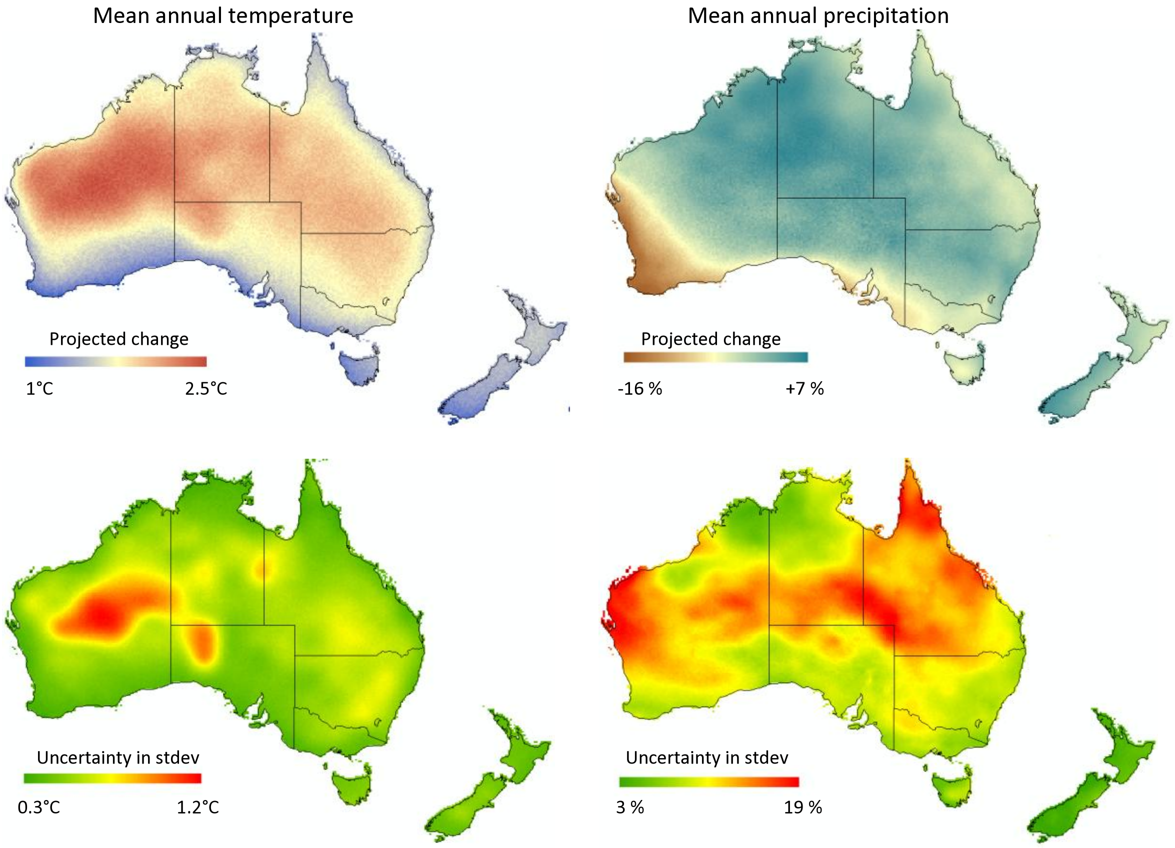


Figure 23. CMIP5 multi-model projections corresponding to the IPPC Assessment Report 5 (IPCC 2013). The top images show the average projected change of 19 models for the RCP 4.5 scenario. The bottom images show the associated uncertainty in units of standard deviations, 68% of the models fall within +/- the specified (color-coded) uncertainty.

Ordination of long-term average and future climate

Canonical discriminant analysis (CDA) was used for pattern recognition classifications and dimensionality reduction (Venables and Ripley 2002). CDA was used to represent plantation regions (**Appendix 3**) and trials in a multivariate climate space. The CDA for the current report was performed using the '*candisc*' package in R V3.02 (R Development Core Team 2013). In Australia, 11 National Plantation Inventory regions were used as categorical dependent variables: Tasmania, Western Australia, Mount Lofty Ranges and Kangaroo Island, Green Triangle, Northern Tablelands, Central Tablelands, Southern Tablelands, Murray Valley, Central Victoria, Central Gippsland, Bombala-East Gippsland.

In New Zealand, the 11 following districts were used as categorical variables: Auckland, Bay of Plenty, Canterbury, Gisborne, Hawke's Bay, Nelson-Marlborough, Northland, Otago-Southland, Southern North Island, Waikato, and West Coast.

Independent variables used to explore long-term average and future (2050) climate were mean annual temperature (MAT), Maximum Temperature Warmest Month (MaxTWM), Minimum

Temperature Coldest Month (MinTCM), Annual Temperature Difference (TD), Precipitation November to March (PrecNM), Crop Moisture Index December to February (CmiDF), Annual Sum (i.e. difference) of Climate Moisture Index (CMI, Hogg 1997). CMI represents precipitation minus potential evapo-transpiration estimated using the simplified Penman–Montieth method. These variables were chosen as they have proved useful for distinguishing between regions in previous analyses (e.g. Battagila *et al.* 2009, Kirschbaum and Watt 2011, Worrall *et al.* 2013).

Results

Analyses of long-term average climate in Australia and New Zealand

GIS maps were used to examine the long-term average climate in different NPI regions and districts in Australia and New Zealand, respectively (**Figure 24**). Locations where about 90% by area of major commercial radiata pine plantations exist are approximately: mean annual temperatures between 8°C and 18°C and rainfall between 500mm and 2250mm (Booth and McMurtie 1988, Battaglia *et al.* 2009). Analyses of long-term average climate showed a generally wider range of climate conditions in Australia then in New Zealand, especially considering dry periods in certain regions. In Australian radiata plantation regions MAT ranged from 10.8°C to 16.4°C and MAP from 729mm to 1130mm. Wet periods were more widespread in New Zealand, and MAT ranged from 9.0°C to 15.2°C and MAP from 866mm to 3360mm. The average extreme temperatures maximum temperature warmest month (MaxTWM) and minimum temperature coldest month (MinTCM) ranged in Australia from = 29.7°C to MinTCM=-0.6°C, and in New Zealand from MaxTWM = 23.9°C to MinTCM=-0.5°C.

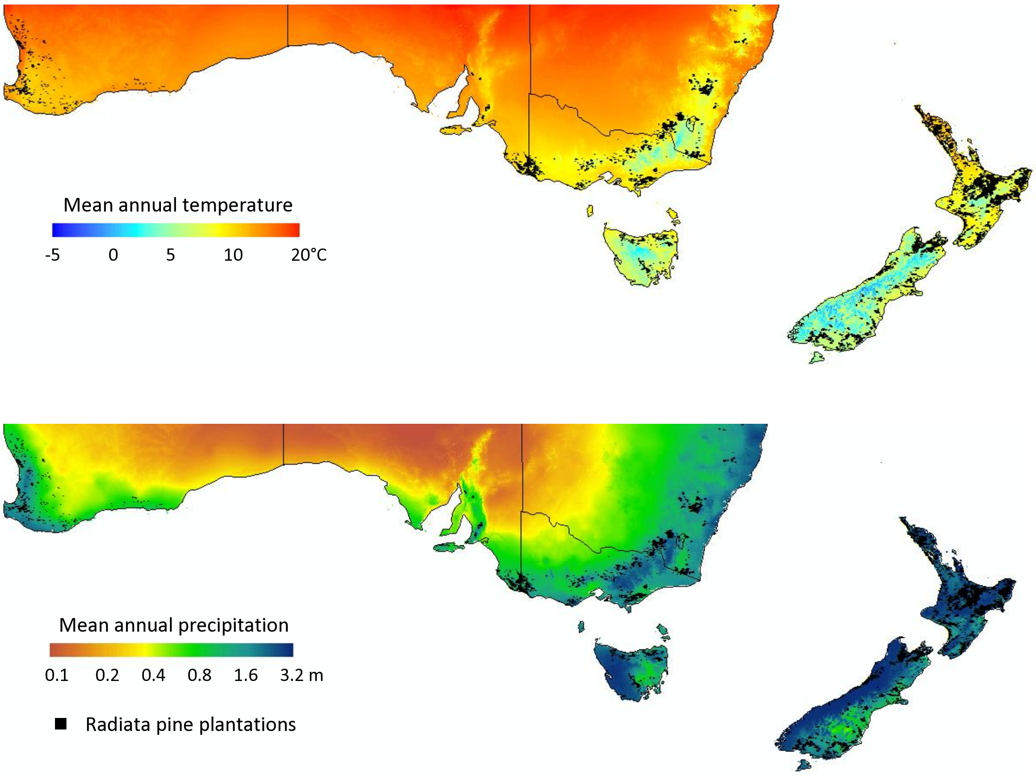


Figure 24. Mean annual temperature (top) and mean annual precipitation (bottom), where radiata pine has been planted in Australia and New Zealand.

The plot of Canonical Discriminant climate variables in **Figure 23** (left plot) shows the long-term average plantation estate and the climate during trial periods (i.e. time from palnting to measurement) in Australia. The higher vertical axis means drier and warmer summers (i.e. increase in maxTWM); the left direction means warmer winters (i.e. increase in minTCM) and slightly drier overall. The top right part of the plot represents a more continental climate (i.e. increase in annual temperature difference – TD), while the lower left means more maritime climate. The upper-left indicated desert, while the lower right indicates montane climates. The cover of the climate space by trials was variable, with some regions not currently being covered at all (i.e. Bombala-East Gippsland) and some regions (i.e. Northern, Central and Southern Tablelands, Central Victoria, Mount Lofty and Kangaroo Island, and Western Australia) only partially covered.

The plot of Canonical Discriminant climate variables of the trials in New Zealand shows the long-term average plantation estate and the climate in **Figure 24** (upper plot). The left part of the plot means generally warmer temperatures (i.e. increase in maxTWM and mean annual temperature MAT), the upper left part in the plot represents warmer winters (i.e. minTCM) and drier overall. Right part of the plot represents colder and drier climate. The cover of the climate space by trials was variable with some regions being poorly covered (i.e. Southern Northern Island, Waikato, Hawkes Bay).

Analyses of future climate in Australia and New Zealand

The plot of canonical discriminant variables in **Figure 23** (lower right panel) shows how the future climate of radiata pine plantation areas in Australia will shift relative to the climate during trial periods. The trial positions (triangles) in the Canonical Discriminant Analyses (CDA) coordinate system are fixed because they relate to historic time periods. However, the plantation areas (dots) will experience a shift in the climate.

The shifts according to HadGEM2–ES model 2050 were significant. The most significant shift was of Tasmania becoming more like Central Victoria and Central Gippsland. The Green Triangle region moved towards warmer and drier space similar to the current climate of the Mt Lofty-Kangaroo Island region. Northern, Central and Southern Tablelands and parts of the Western Australian estate moved into a new currently unrepresented climate space, which may be a reason for concern. Two trial sites that are the sole representatives of genetic trials for many plantation locations (the red Central Tablelands cluster) under climate change remain the most relevant to the Central Tablelands, but will also become representative of the Bombala-East Gippsland (blue cluster).

The plot of canonical discriminant variables in **Figure 25** (lower-left) shows how the future climate of radiata pine plantation areas in New Zealand will shift relative to the climate during the trial periods. The shifts according to the HadGEM2 –ES model, 2050 were strong, reflecting mostly the large increase in MAT. For example, the Northern South Island plantation estate will move towards the climate space currently occupied by the Southern North Island plantations. West Coast and parts of Otago-Southland estate will become more like current Bay of Plenty. Generally, most of the existing range of test sites will be not representative of the climate in the plantation areas.

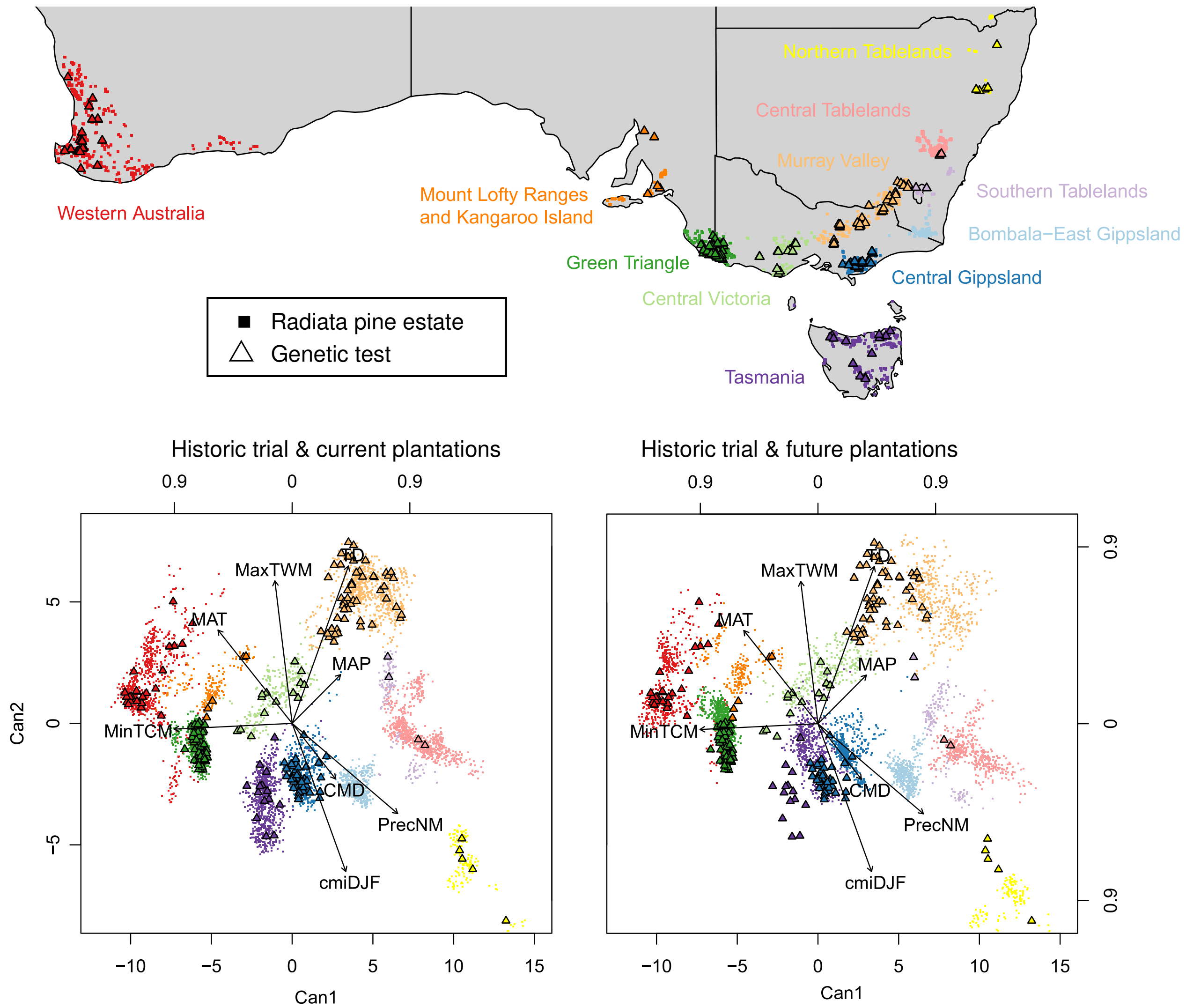


Figure 25. Canonical discriminant analysis of long-term average climate (lower-left panel) and future (lower-right panel) in Australian plantation areas (dots) and genetic trial locations (triangles). Direction abbreviations mean annual temperature (MAT), Maximum Temperature Warmest Month (MaxTWM), Minimum Temperature Coldest Month (MinTCM), Annual Temperature Difference (TD), Precipitation November to March (PrecNM), Crop Moisture Index December to February (CmiDJF), Annual Sum (i.e. difference) of Crop Moisture Index (CMD). The colours in the charts below refer to the colours of different regions on the map above.

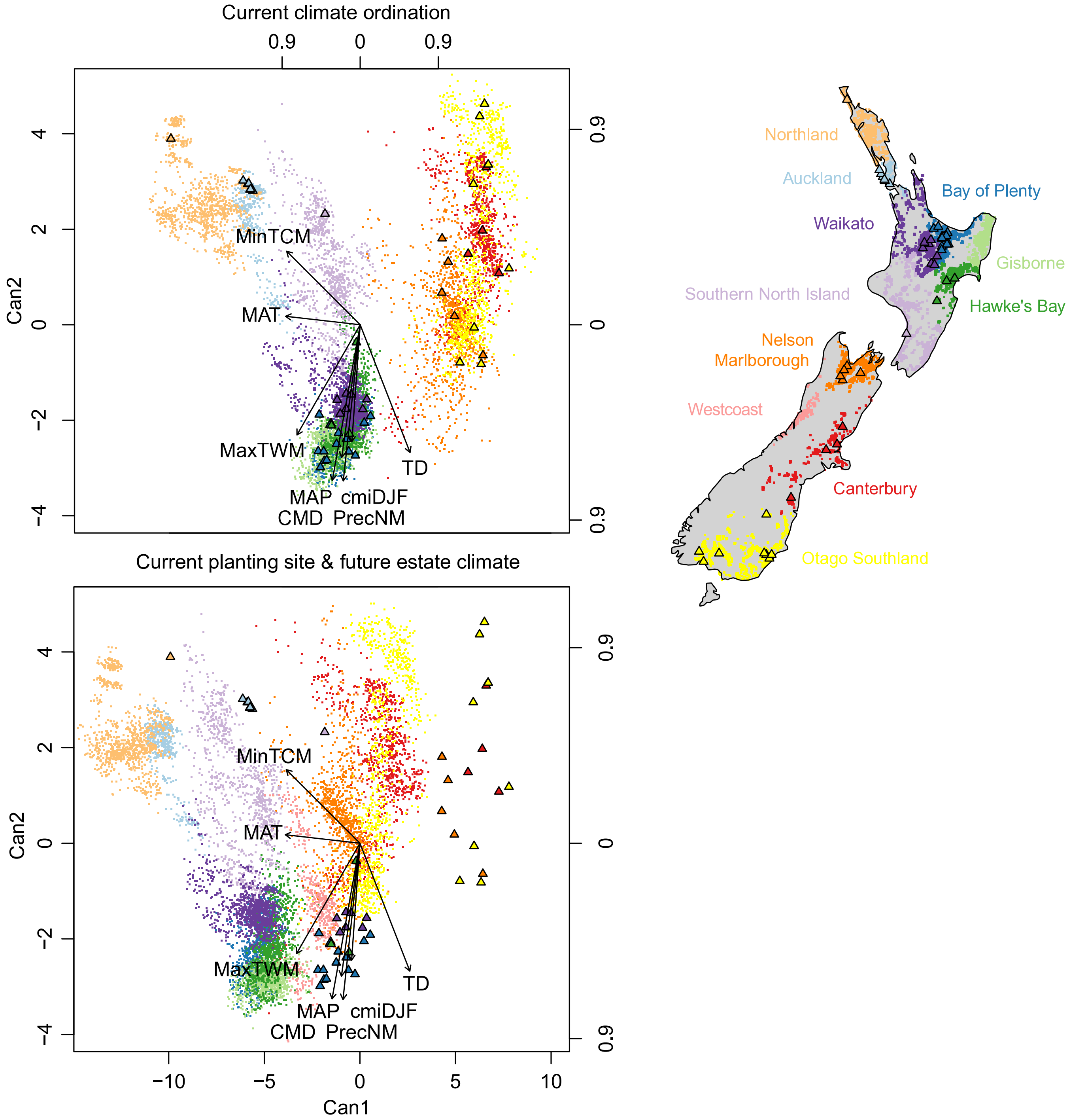


Figure 26. Canonical discriminant analysis of long-term average climate (upper panel) and future (lower panel) in New Zealand plantation areas (dots) and genetic trial locations (triangles). Direction abbreviations mean annual temperature (MAT), Maximum Temperature Warmest Month (MaxTWM), Minimum Temperature Coldest Month (MinTCM), Annual Temperature Difference (TD), Precipitation November to March (PrecNM), Crop Moisture Index December to February (CmiDJF), Annual Sum (i.e. difference) of Crop Moisture Index (CMD). The colours in the charts left refer to the colours of different regions on the map right.

Discussion

Our current research on G×E has shown that site type definition for breeding and deployment of genetic stock in Australia depends on climate variables. This also confirms the results about the climatic drivers of G×E from the literature (e.g. Gapare *et al.* 2010, Raymond 2011). Similarly, analyses of trials in New Zealand resulted in two major groups being significantly different for a number of climate variables, including mean annual precipitation and minimum temperature coldest month (Cullis *et al.* 2014, Gapare *et al.* 2014). Those results have highlighted the importance of climate variables as drivers of G×E in both Australia and New Zealand.

The HadGM2-ES was chosen as a future climate model for the analysis of effects of climate change, because it is one of the most advanced models and it combines atmospheric, ocean and earth systems. Although this Global Circulations Model (GCM) is relatively drier and warmer than the median of other model predictions for Australia and New Zealand, the representative concentration patterns scenario (RCP 4.5) was relatively moderate (Meinshausen *et al.* 2011). The combination of GCM and RCP is an example of what can potentially occur in the future, and regardless of the exact magnitude of climate change by 2050, it is the relative shift in the plantation estate that is of interest here.

Acording to the HadGEM2–ES model, by year 2050 in Australia temperature will increase approximately by 1.9°C and precipitation will decrease 8%. However, the climate shifts are predicted to be significant in some regions, but more subtle in other regions of Australia. For example, a significant predicted shift is for Tasmania to become more like Central Victoria and Central Gippsland. Murray Valley and parts of Western Australian estate are predicted to move into a new climate space, which may be a reason for concern. Green Triangle region is predicted to move towards warmer and drier space similar to the current climate of MtLofty-Kangaroo Island region.

Similarly, according to the HadGEM2–ES model, by year 2050 in New Zealand temperature will increase approximately by 1.9°C and precipitation will decrease 2%. The future climate of radiata pine plantation areas in New Zealand is predicted to shift significantly relative to the climate during the current trial period. The northern South Island plantation estate is predicted to move towards the climate space currently occupied by the southern North Island plantations. West Coast and parts of Otago-Southland estate is predicted to become more like current Bay of Plenty. Most of the existing range of test sites are not predicted to be representative of the climate in the plantation areas. This could be alarming, although the predicted future climate scenario is more extreme (i.e. relative to the present variation) in New Zealand than in Australia (CSIRO 2011).

Although the geographic extent of the plantation estate may not move much, the climate will highly likely change. Some new plantation areas may be required to offset reduced productivity (e.g. Pinkard and Bruce 2011, Battaglia *et al.* 2009, Kirschbaum and Watt 2011, Pinkard *et al.* 2014). This paper deals exclusively with how the existing trials are representative of their regions in term of climate and does not address the issue of productivity of different locations in the future. This study helps determine where to establish new trials that will be representative of future climates.

Conclusions

Our research on G×E has shown that site type definition for breeding and deployment of genetic stock in Australia and New Zealand depend largely on climate variables. However, the future climate of radiata pine plantation areas will shift relative to the climate during the lifetime periods of existing trials. Acording to HadGEM2–ES model by year 2050 in Australia temperature will increase approximately by 1.9°C and precipitation will decrease 8%. Similarly, according to HadGEM2–ES model, by year 2050 in New Zealand temperature will increase approximately by 1.9°C and precipitation will decrease 2%. The scenario is just an example of what can potentially occur in the future, and regardless of the exact magnitude of climate change by 2050, it is the relative shift in the plantation estate that is important.

Although the plantation estate may not move much physically, the climate space will certainly change. Some new plantation areas may be planted because the issue of productivity will also come into play. We showed that existing trials are not representative of their regions in terms of future climate, and that we can determine where to establish new trials that will be representative of future climates.

Recommendations

1. The analysis of future climate across radiata pine estate presented here suggests that additional climate projections should be evaluated to obtain a more complete and balanced representation of the effects of climate change on the radiata pine estate in Australia and New Zealand. Such a so called "consensus" model should be used for more exact breeding and deployment region delineations that would allow sensitivity analysis.
2. Decisions on future planting sites should take into consideration future climate and therefore the locations of genetic trials planted today should also be representative of those future climates.
3. Depending on the variability of climate predictions, some site types may require more diverse genetic material to cover the full range of possible scenarios. A diverse portfolio of genotypes for deployment should be established to mitigate the effects of climate change, and this issue should be examined in future studies (Matheson et al. 2007).

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The significance and benefits of the outcomes of the project were documented in detail in 9 technical reports delivered to funding organisations and industry clients, and in 5 scientific papers.

List of peer reviewed publications:

1) Miloš Ivković, Washington Gapare, Huixiao Yang, Gregory Dutkowski, Peter Buxton and Harry Wu (2014) Pattern of genotype by environment interaction for radiata pine in southern Australia. Annals of Forest Science, DOI10.1007/s13595-014-0437-6

2) Washington J. Gapare, Miloš Ivković, David Pilbeam, Harry X. Wu (submitted to Australian Forestry) Genetic parameters and genotype × environment interaction in a series of radiata pine progeny trials in southeastern Australia

3) Washington J. Gapare, Miloš Ivković, Paul Jefferson, Charlie B. Low, Katharina J. Liepe, Andreas Hamann (In review Tree Genetics and Genomes) Identification of drivers of genotype by environment interaction in radiata pine using multivariate regression trees

4) Miloš Ivković, Andreas Hamann, Washington Gapare, Tom Jovanovic and Alvin Yanchuk (draft to be submitted to Regional Environmental Change) Potential effects of climate change on the representativeness of genetic evaluation trials in raditata pine relative to the current plantation areas in Australia and New Zealand

5) Dutkowski GW, Ivkovic M, Hamann A (draft to be submitted to Tree Genetics and Genomes) Genetic correlation modelling and breeding value prediction for *Pinus radiata* using TREEPLAN®.

Appendix 1. Genetic correlation modeling and BV prediction for *Pinus radiata* using TREEPLAN® - traits other than Dbh growth

Modelling genetic correlations for stem straightness (Stemst)

Correlation database version 23R was used. There were no additive correlations below zero. Different stem straightness traits from different organisations collected over time were amalgamated into a single trait. There was more variability of Type b correlations with less parents in common, especially < 100. However, there were no trial pairs with more than about 160 parents in common, in contrast to DBH, where there were trial pairs with up to 450 parents in common. Trial pairs with low number of parents in common (<20) had very high standard errors associated with the estimates (**Figure A1.1).**

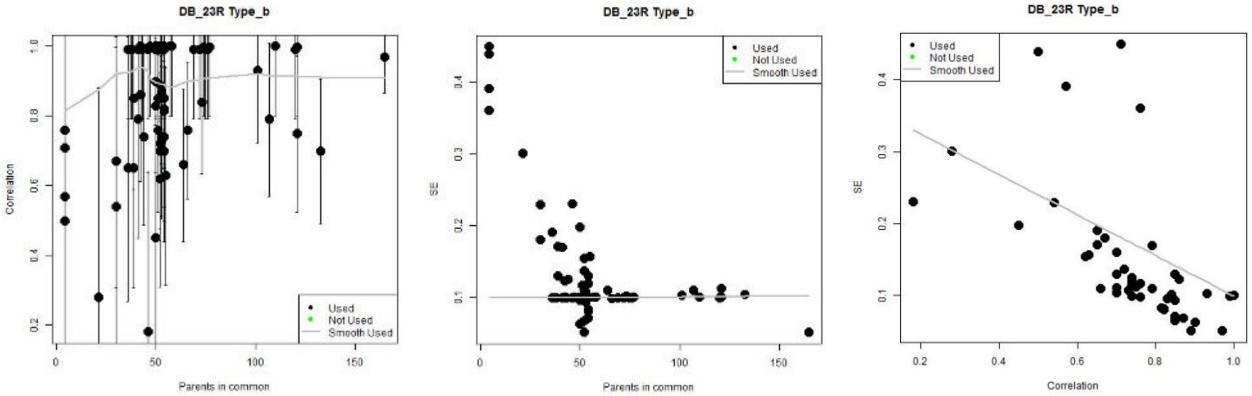
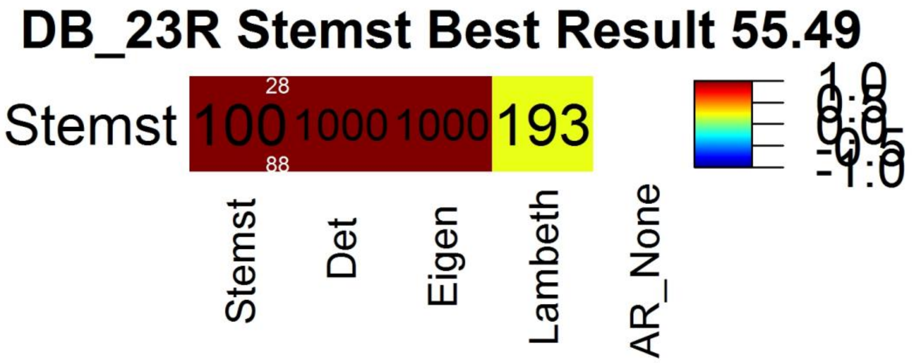


Figure A1.1 Type b correlations for Stemst (with 95% CI and smoothed loess trend).

There were no measurements of stem straightness at different ages, so the DBH Lambeth age:age correlation model coefficient of 0.193 was assumed. There was a low level of GxE with the residual correlation of 0.93. Model results from Stemst models are given in **Tables A1.1, A1.2** and **Figure A1.2**.

Table A1.1 Model results from Stemst models DB23R.

Model	*Residual GxE*	*Wt ESS*	*Residual ra*	*Model No.*
Baseline: No GxE	No	55.49	1	20.1
	Yes	47.35	0.93	20.2
AR – Temperature seasonality (Ts)	No	44.33	1	22.2
SplitVarb:Rain_sep	No	38.24	1	24
	Yes	33.33	Dry: 0.95 Moist:NA	24.1



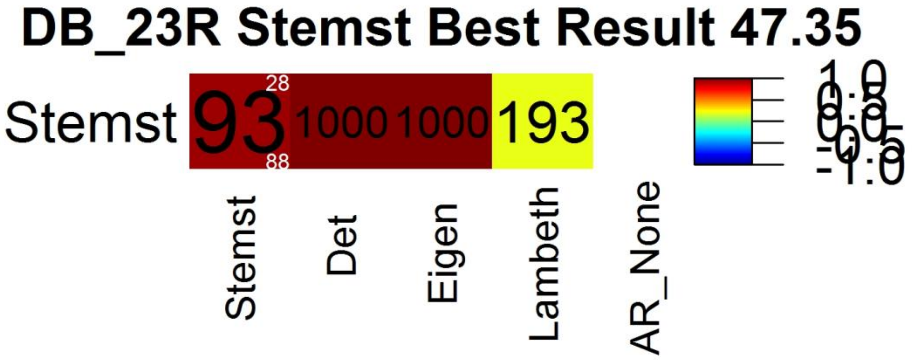


Figure A1.2 Stemst base model without GxE (top) and with GxE (bottom).

Table A1.2 Stemst AR models and split on environmental variables, with the best groups of outlier trials (with values of the best split variables shown).

Env Variable	*Wt ESS AR 1*	*Wt ESS Split 1*	*Split 1*	*Wt ESS AR 2*	*Wt ESS Split 2*	*In*
Trial_id		40.92	RAD148			
Trial_id 2		**35.69**	PT5413,PT5455			
Trial_id 3		**34.57**	PT5413,PT5455,RAD211			
Latitude	53.42	47.82	-37.517			
Longitude	54.28	47.96	147.717			
Si_mon_c_2	50.85	47.48	71.5			
Elev	47.76	47.25	367.5			
Amt	53.77	48.30	13.605			
Mdr	50.31	49.33	13.435			
Ist	46.28	39.91	0.475			
Ts	**44.33**	45.79	1.57			
Mtwp	52.74	49.34	26.595			
Mtcp	48.91	48.50	0.775			
Tar	47.70	46.39	25.745			
Mtwetq	47.03	48.59	9.605			
Mtdq	52.21	48.72	18.38			
Mtwq	53.70	50.53	18.05			
Mtcq	50.39	47.92	8.72			
Ap	46.38	42.99	1105.985			
Pwp	51.81	49.90	29.15			
Pdp	50.63	47.46	10.135			
Ps	53.85	51.33	18.68			
Pwetq	51.17	49.90	336.77			
Pdq	50.57	49.90	144.765			
Pwq	49.95	48.56	161.47			
Pcq	51.34	50.62	347.395			
Amr	53.09	51.66	15.48			
Hpr	52.35	49.87	25.66			
Lpr	52.48	51.59	5.915			

Rs	51.60	50.98	42.73			
Rwetq	52.37	51.77	18.44			
Rdq	50.57	51.41	24.16			
Rwq	53.07	51.27	23.395			
Rcq	52.64	51.58	7.71			
Ammi	50.60	50.24	0.71			
Hpmi	54.29	53.40	0.97			
Lpmi	51.82	48.94	0.265			
Mis	50.88	49.90	44.505			
Mmihq	54.65	52.78	0.955			
Mmilq	51.22	49.90	0.27			
Mmiwq	50.99	49.90	0.305			
Mmicq	52.34	48.99	0.985			
Tmax_jan	52.57	49.34	25.4			
Tmax_feb	52.66	48.93	26.35			
Tmax_mar	53.20	48.68	23.55			
Tmax_apr	53.44	48.49	20.25			
Tmax_may	53.01	49.74	16			
Tmax_jun	51.39	47.92	13.1			
Tmax_jul	50.43	47.46	11.55			
Tmax_aug	51.35	47.92	13.85			
Tmax_sep	52.62	47.31	15.85			
Tmax_oct	52.56	48.15	18.5			
Tmax_nov	52.64	47.23	21.2			
Tmax_dec	53.04	50.02	23.5			
Tmin_jan	54.51	51.03	11.55			
Tmin_feb	54.68	51.03	11.85			
Tmin_mar	53.22	47.28	10.75			
Tmin_apr	50.85	48.85	8.5			
Tmin_may	49.95	48.85	6.9			
Tmin_jun	49.72	49.50	4.5			
Tmin_jul	49.09	48.50	0.95			
Tmin_aug	49.53	49.50	4.05			
Tmin_sep	50.50	49.31	5.2			
Tmin_oct	51.96	48.40	6.9			
Tmin_nov	53.65	47.28	8.8			
Tmin_dec	54.22	48.07	10.35			
Rain_jan	49.40	42.48	65.6			
Rain_feb	50.10	48.96	43.05			
Rain_mar	50.23	49.90	46.8			
Rain_apr	49.74	49.32	83.9			
Rain_may	50.76	49.51	76.7			
Rain_jun	52.51	50.62	111.3			
Rain_jul	52.23	50.62	113.4			
Rain_aug	49.53	45.01	142.35			
Rain_sep	45.66	**38.24**	128.15			
Rain_oct	48.19	45.01	104.4			
Rain_nov	48.80	39.64	93.3			
Rain_dec	50.35	39.64	86.55			
Loc_state		47.96	NSW			
Tp2012_region		38.80	CTAB,DOTHI,MVAL,NTAB			
Parent_Rock_Code		49.69	51			
Parent_Rock_Class		49.69	Argillaceous Group			

The best AR trait was Ts (Temperature Seasonality). The best split was on identifying outlying trials PT5413 and PT5455, with RAD211. The best environmental variable was almost as good using Rain September, with NFI regions CTAB, DOTHI, MVAL, NTAB next best, and then a few more monthly rainfall variables. Rain_sep pulls out three high rainfall trials as different (Q14156, RAD199 and RAD148). The other rainfall variables also pull out RAD148, which is the single outlier trial identified. The correlation between Dry and Moist site types for Stems is only 0.40. There are no trial pairs within the moist class however, so the approach is only pulling out outliers trials that share a common high environmental value. There is no way to check if these trials are actually well correlated with each other.

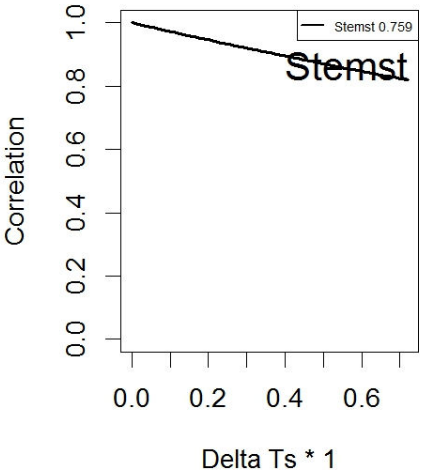


Figure 2 Best AR model for Stemst.

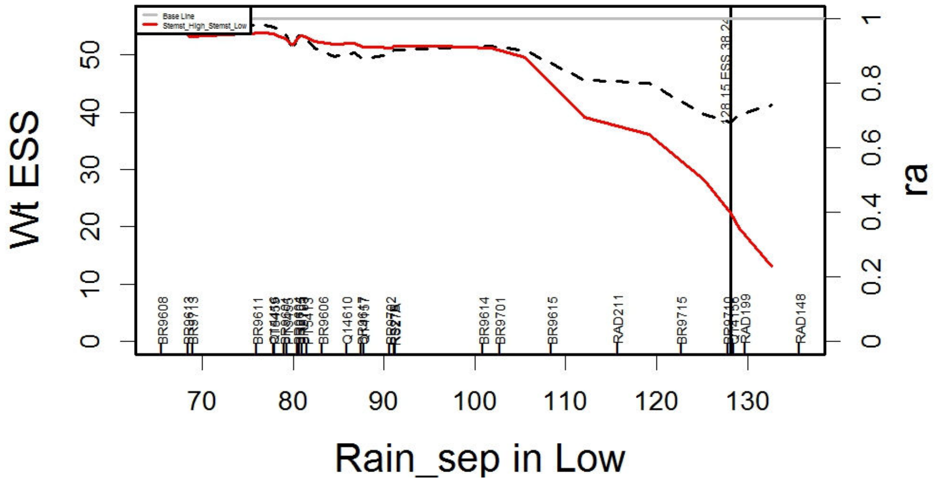
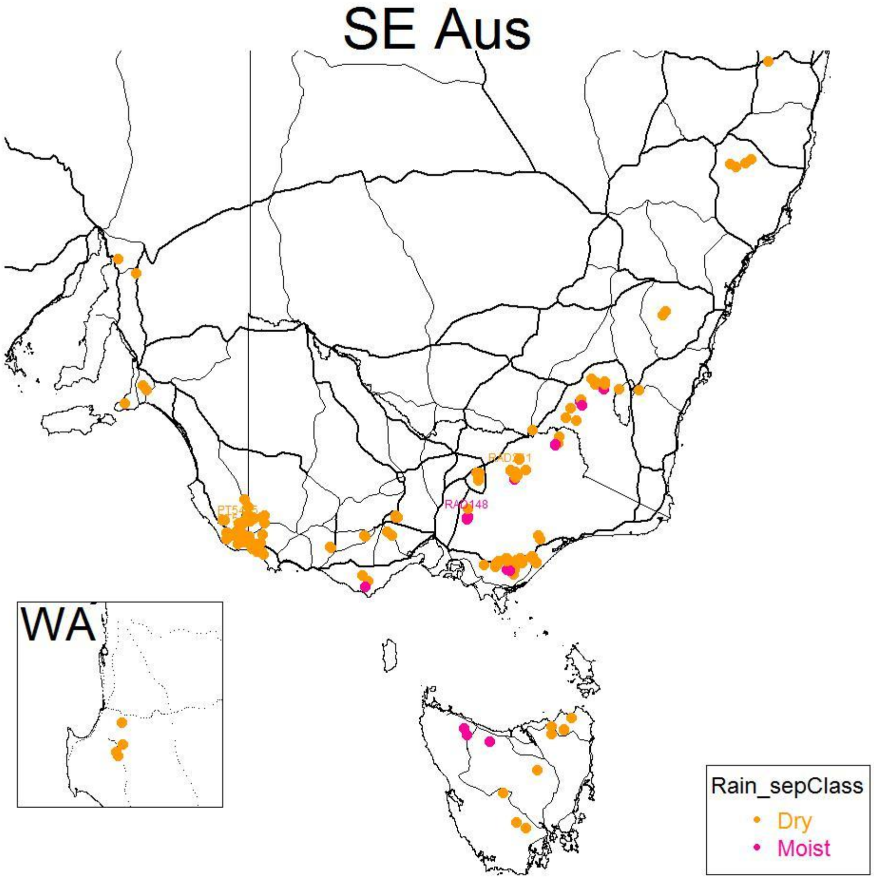


Figure A1.4 Split variables for Stemst based on DB23R.



FigureA1.5 Map of first split for Stemst and outlier trials.

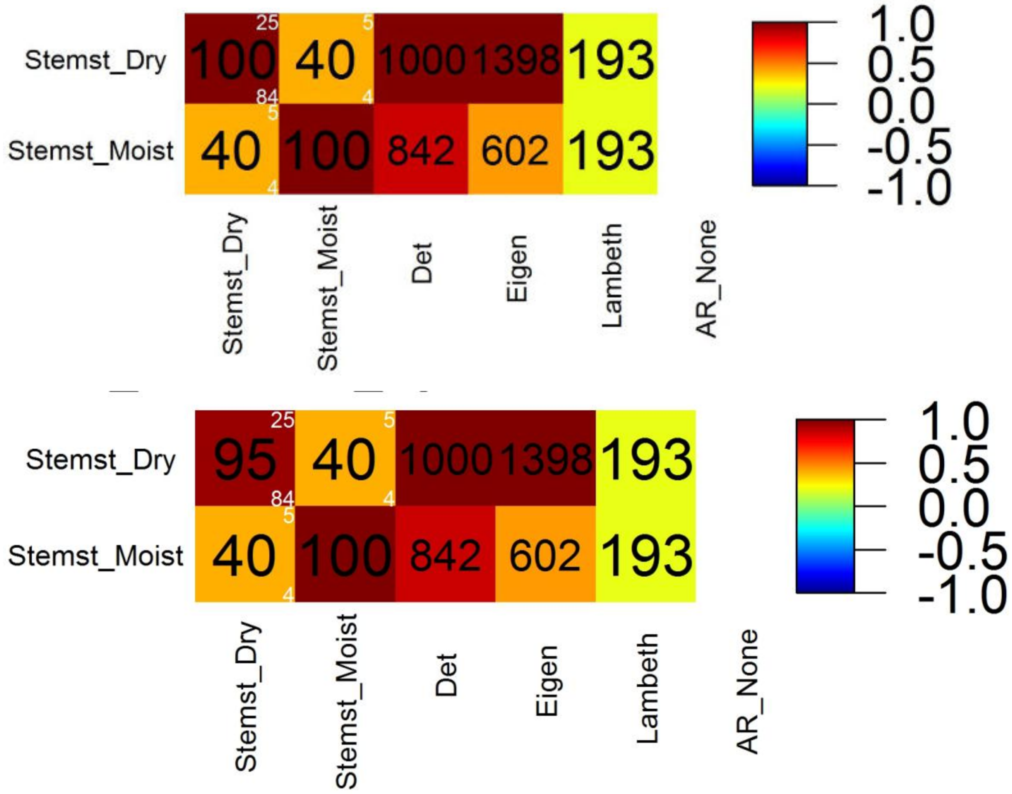


Figure A1.6 Stemst Split on Rain_sep parameters without GxE (top) and with GxE (bottom).

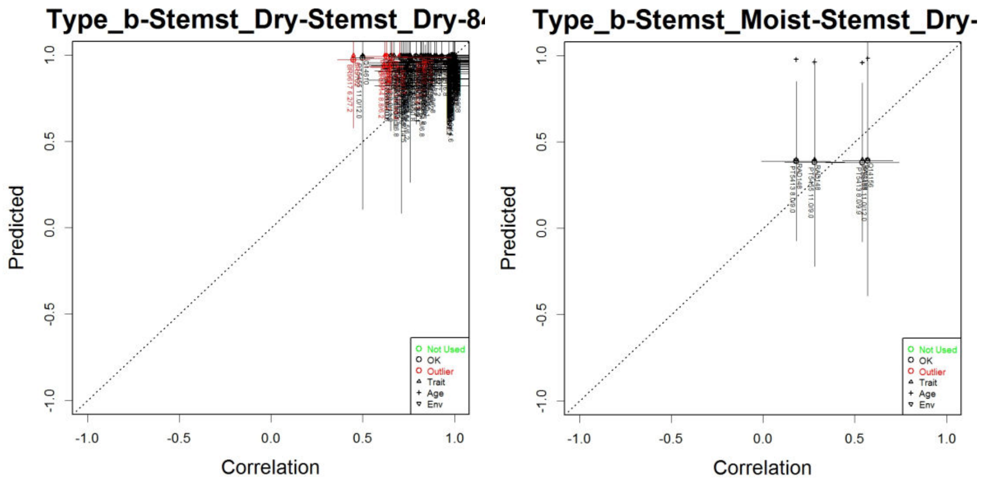


Figure A1.7 Modelled Stemst correlations (y-axis) compared to database correlations for Rain_sep split 1.

Modelling genetic correlations for branch size (Brs)

Correlation database version 23R was used. There were no additive correlations below zero. Different branch size traits from different organisations collected over time were amalgamated into a single trait. There was more variability of type b correlations with less parents in common, especially < 100. However there were no trial pairs with more than about 160 parents in common, in contrast to DBH, where there were trial pairs with up to 450 parents in common. The correlation was not related to the number of parents in common, but the SE did go down as the correlations approached one (**Figure A1.8**.

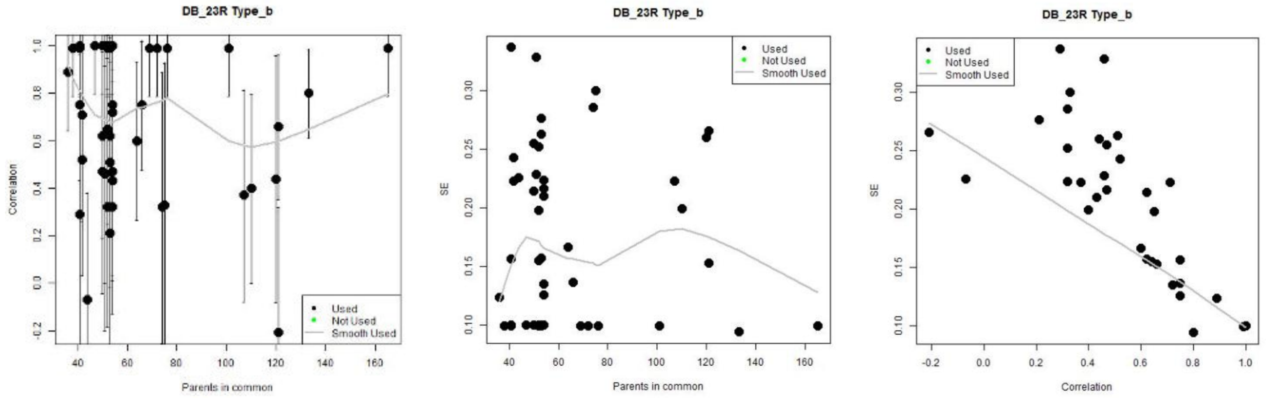


Figure A1.8 Type b correlations for Brs (with 95%CI and smoothed loess trend).

There was only 1 trial with measurements of branch size at different ages, so the DBH Lambeth age:age correlation model coefficient of 0.193 was assumed. There were only 51 correlations involving 15 trials.There was some level of GxE with the residual correlation of 0.85.

Table 2 Model results from Brs models.

Model	*Residual GxE*	*Wt ESS*	*Residual ra*	*Model No.*
Baseline: No GxE	No	100.65	1	30.1
	Yes	78.90	0.85	30.2
AR – Annual Precipitation (Ap)	No	66.08	1	32.2
SplitVarb:Ap	No	70.09	1	34
	Yes	61.40	Dry: 0.90 Moist: Na	34.1

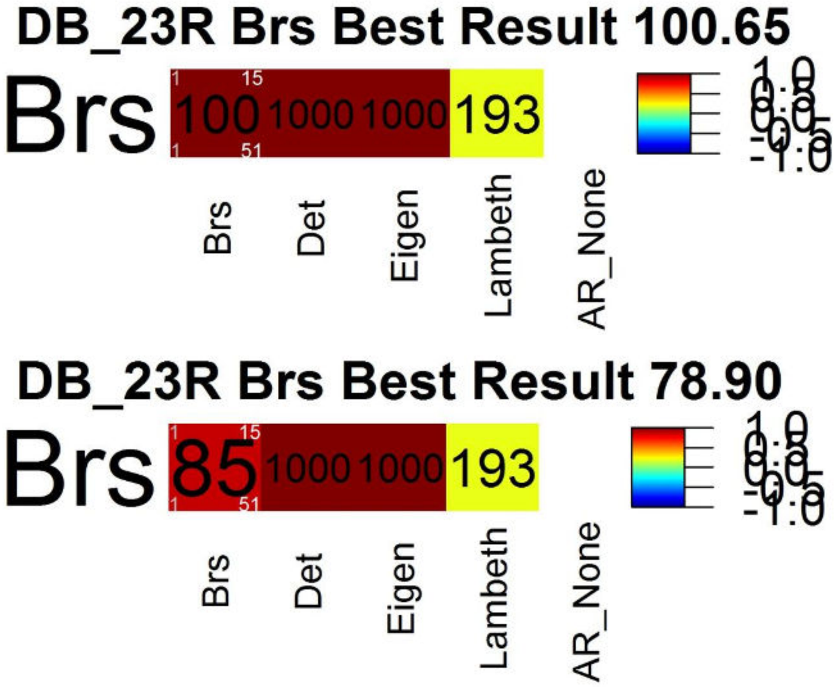


Figure 39 Brs base model without GxE (top) and with Gxe (bottom).

Table A1.4 Stemst AR models and split on environmental variables, with the best groups of outlier trials (with values of the best split variables shown).

Env Variable	*Wt ESS AR 1*	*Wt ESS Split 1*	*Split 1*	*Wt ESS AR 2*	*Wt ESS Split 2*	*In*
Trial_id		78.57	BR9615			
Trial_id 2		70.09	BR9615,BR9710			
Trial_id 3		70.09	BR9615,BR9710,RAD142			
Latitude	82.74	73.65	-38.411			
Longitude	95.26	77.20	147.295			
Si_mon_c_2	87.72	81.98	71.5			
Elev	82.47	77.72	63.5			
Amt	84.36	73.65	12.8275			
Mdr	82.91	73.65	10.275			
Ist	84.52	85.79	0.505			
Ts	83.83	83.57	1.155			
Mtwp	79.62	73.65	24.39			
Mtcp	81.95	75.62	4.865			
Tar	81.88	73.65	20.11			
Mtwetq	83.69	76.56	8.985			
Mtdq	88.27	76.96	17.29			
Mtwq	81.97	73.65	17.315			
Mtcq	83.14	81.54	8.05			
Ap	**66.08**	**70.09**	1031.14			

Pwp	88.81	84.02	26.685			
Pdp	81.82	76.56	9.505			
Ps	90.67	87.57	43.15			
Pwetq	88.75	85.91	347.395			
Pdq	82.88	73.65	160.495			
Pwq	83.77	76.96	162.28			
Pcq	88.23	85.91	347.395			
Amr	79.12	73.65	14.5225			
Hpr	78.71	73.65	24.2025			
Lpr	84.14	73.65	5.265			
Rs	80.29	73.65	47.5775			
Rwetq	90.93	**70.09**	7.1475			
Rdq	88.94	82.19	19.665			
Rwq	77.59	73.65	22.025			
Rcq	83.60	73.65	6.9725			
Ammi	77.02	73.65	0.78			
Hpmi	99.92	99.23	0.99			
Lpmi	82.40	76.96	0.285			
Mis	81.57	73.65	31.675			
Mmihq	98.22	96.39	0.995			
Mmilq	80.61	73.65	0.4			
Mmiwq	80.15	73.65	0.435			
Mmicq	89.20	82.01	0.99			
Tmax_jan	80.82	73.65	23.4			
Tmax_feb	79.56	73.65	24.05			
Tmax_mar	82.67	73.65	21.8			
Tmax_apr	84.35	73.65	18.675			
Tmax_may	85.49	73.65	15.15			
Tmax_jun	85.45	76.56	12.35			
Tmax_jul	84.53	76.56	11.7			
Tmax_aug	83.59	73.65	12.6			
Tmax_sep	83.80	73.65	14.675			
Tmax_oct	81.02	73.65	17.475			
Tmax_nov	81.28	73.65	19.55			
Tmax_dec	80.67	73.65	21.6			
Tmin_jan	85.41	73.65	11.25			
Tmin_feb	85.38	76.82	11.7			
Tmin_mar	84.42	81.54	9.925			
Tmin_apr	84.48	81.54	7.625			
Tmin_may	83.89	81.54	5.775			
Tmin_jun	82.92	75.62	5.85			
Tmin_jul	82.21	75.62	5.05			
Tmin_aug	82.82	75.62	5.5			
Tmin_sep	82.06	75.62	6.55			
Tmin_oct	83.26	81.54	6.3			
Tmin_nov	84.88	79.39	7.9			
Tmin_dec	84.70	79.39	9.55			
Rain_jan	83.17	76.96	57.45			
Rain_feb	83.34	79.13	40.75			
Rain_mar	82.92	80.00	50.25			
Rain_apr	69.42	**70.09**	79.175			
Rain_may	84.20	78.70	109.7			
Rain_jun	87.55	85.91	111.3			
Rain_jul	90.27	84.02	101.95			
Rain_aug	85.90	72.18	129.95			
Rain_sep	69.05	**70.09**	105.55			
Rain_oct	73.09	73.65	87.9			
Rain_nov	81.99	76.96	76.4			
Rain_dec	83.56	73.65	67.9			
Loc_state		79.39	TAS			
Tp2012_region		79.39	TAS			
Parent_Rock_Code		70.38	51,91			

Parent_Rock_Class		70.38	Argillaceous Group,Feldspathic - Micaceous Group			

The best auto-regressive (AR) trait was Ap (Annual Preccipitation), with a number of other rainfall variables close behind. The best split was equally on identifying outlying trials BR9615, BR9710, and RAD142 and environmental variable annual precipitation (Ap) and a number of other rainfall variables, with parent rock code not far behind. Ap pulled out the same three high rainfall trials identified as outliers. The correlation between Dry and Moist site types for Brs is only 0.48. There are no trial pairs within the moist class, however, so the approach is only pulling out outliers trials that share a common high environmental value. There is no way to check if these trials are actually well correlated with each other.

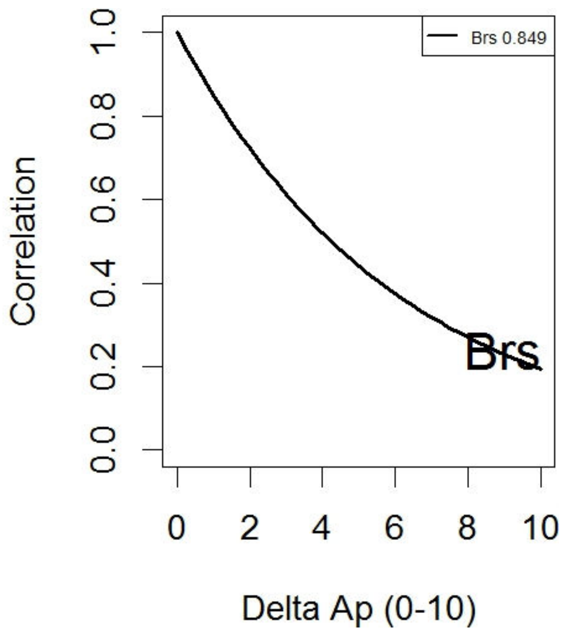


Figure A1.10 Best AR model for Brs.

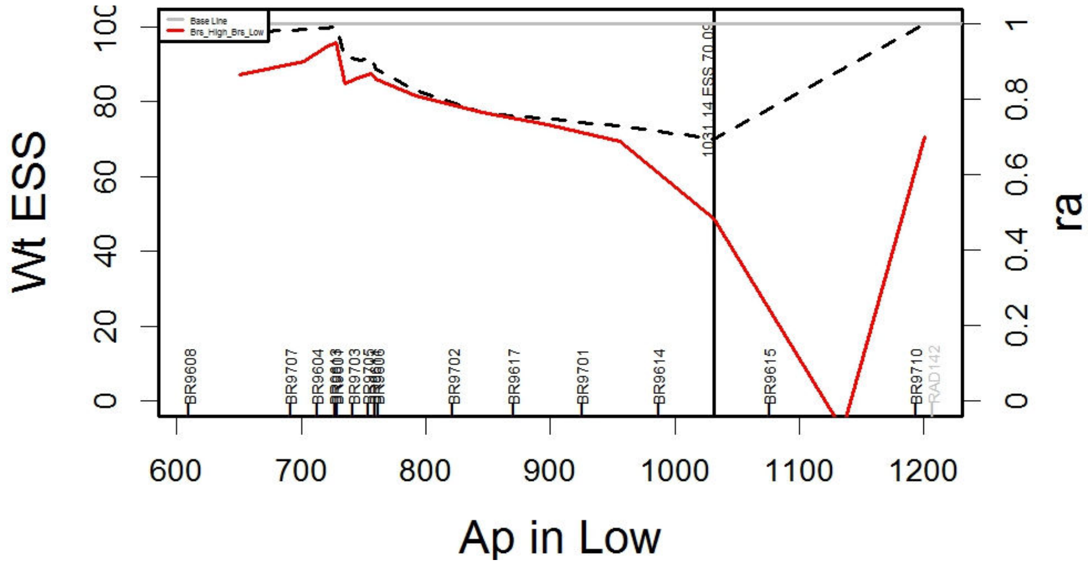


Figure A1.10 Split variable annual precipitation (Ap) for Brs. (RAD142 is grayed as it has no type b correlations, only type a).

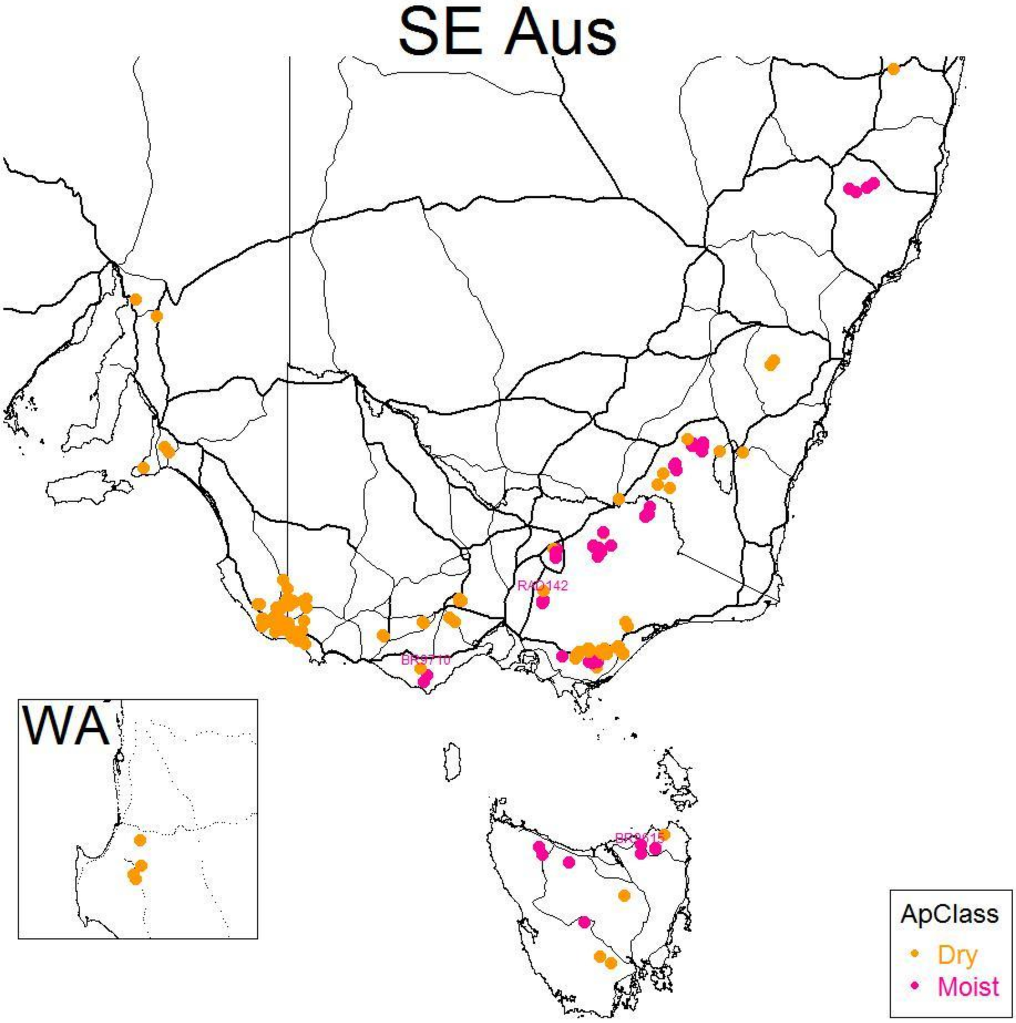


Figure A1.11 Map of first split for Brs and outlier trials.

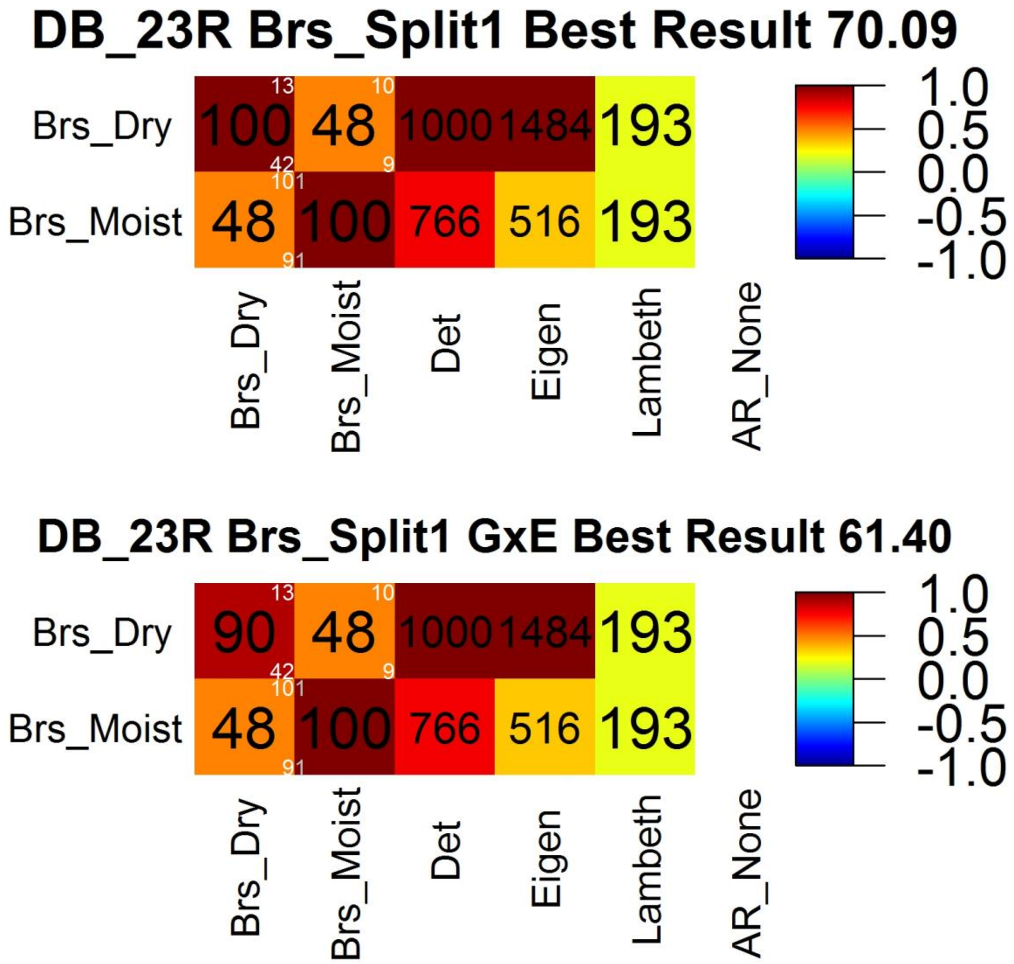


Figure A1.12 Brs split on Ap parameters without GxE (top) and with GxE (bottom).

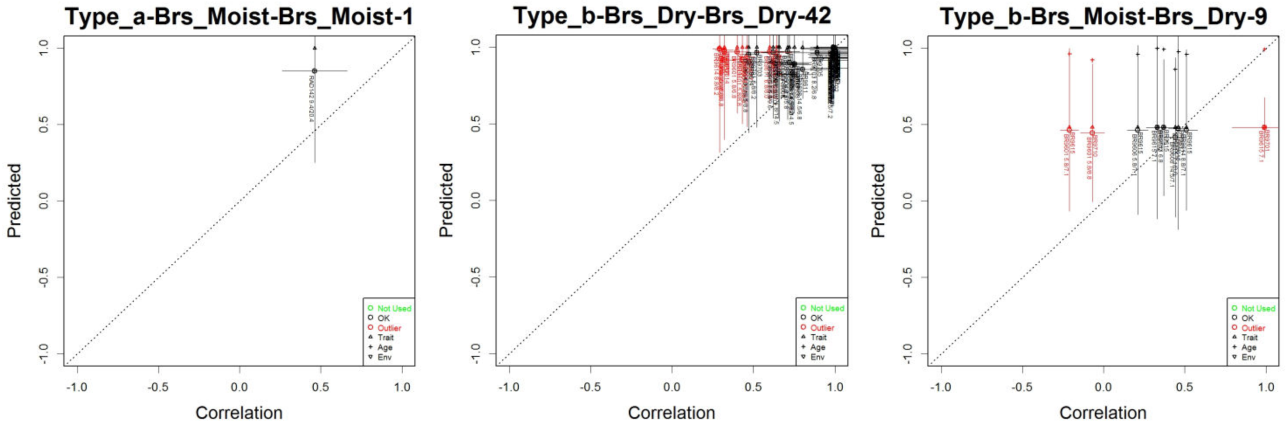


Figure A1.13 Modelled brs correlations (y-axis) compared to database correlations for Ap split 1.

Appendix 2

G×E for compound traits: relationship between mean and variance for traits other than growth

Summary

- To account for G×E in composite traits (i.e. selection index) absolute values of component (i.e. breeding-objective) traits are necessary for application in deployment tools such as SEEDPLAN®
- At the same time the relationship between mean and variance for breeding-objective traits is important for scaling the breeding values of entries in TREEPLAN®
- Based on resource evaluation studies in Green Triangle Region, Western Australia (WA) and Tasmania (TAS) the relationships between mean and variance were established, as follows:
  - Sweep had strong positive relationship between mean and variance that did not differ much between log height-classes
  - Maximum Branch Size measured on logs (GTR study) differed markedly between log height classes, ranging from: negative for 1st log to positive upper logs. Visually assessed Branch Size or Branch Index (WA and TAS studies) had an overall curvilinear relationship, mainly due to lower variance estimates for upper logs (possibly biased).
  - Stiffness estimated on logs using HM200 – Hitman instrument differed markedly between log height classes, ranging from: negative for to slightly positive for upper logs (GTR and TAS studies). Stiffness on standing trees estimated using ST300-Director instrument (WA study) the relationship between the mean and variance behaved similarly to HM200 measurements taken on 1st logs.
- Protocols should be established so that the traits other than growth can be routinely measured and predicted for different site types.

Introduction

Since genotypes are selected based on a composite index value rather than individual trait values (either on an index or more arbitrary independent culling), it is important to investigate if there would be GxE interaction for the index values. Although there may not be GxE for individual traits, there still may be G×E for index value, because of different economic weights for traits for different sites. The relative sizes of trait economic weights can influence the size and the sign of difference between genotypes in index values at different sites (Namkoong 1984, Gapare *et al.* 2009). In addition, genetic variances may change between sites in relation to the site means, giving different effective index weights even when the absolute weights may be the same. Therefore, it is important to quantify, in absolute terms, the expected site means and variances for productivity, form, branching and wood quality traits.

If breeding objective traits (i.e. mean annual increment, stem straightness, branch size, and wood stiffness) are scaled to an average site type, then gains are likely to be overestimated for low quality sites, or underestimated for higher productivity sites. Thus it is important for users of SEEDPLAN® to scale breeding objective traits according to the site types used in their organisation. We reviewed models that can predict form, branching and wood quality based on measured data in stands. Input data requirements vary between different models, but rapid development new data acquisition technologies make these requirements feasible.

At the same time, TREEPLAN® system defines variances on a unit additive genetic standard deviation scale. Breeding objective trait values are transformed onto an observed scale at the point of retrieval, or when a new selection index is created. The scaling factor typically cannot be estimated directly, due to the absence of pedigreed, harvest age data. However, the scaling factor can be estimated as a function of the site phenotypic mean and variance. The purpose of this section is to 1) determine the relationship between mean and variance for breeding objective traits, in particular, form (sweep), branching and wood quality; and 2) make recommendations regarding data acquisition for breeding objective traits other than growth increment.

Methodology

We used data from the resource evaluation studies to evaluate variability in site means and to develop models of relationship between site mean and variance (McKinley *et al.* 2003, Cown *et al.* 2006, Blakemore *et al.* 2010). The major objectives of the resource evaluation studies were to assess Australian (i.e. Green Triangle Region, Tasmania and Western Australia) and New Zealand softwood plantation to determine the extent of variation in stem and wood quality characteristics. The studies also attempted to link such variations to site and/or silvicultural practices. The studies used standing tree tools (i.e. increment cores for wood density, ST300 for acoustic velocity, visual branch and resin assessment) to document within-stand and between stand variation and provide data to assist prediction of timber quality. A subsequent processing study related stem and log features to grade recovery and value. These studies were used here to estimate relationship (i.e. linear and non-linear regression) between mean and variance for breeding-objective traits close to harvest age.

Resource evaluation study in Green Triangle Region

An outerwood density survey was undertaken across 58 sites in the Mt Gambier region, (McKinley *et al.* 2003) involving forest plantations owned by Auspine, Forestry SA, Green Triangle Forest Products and Hancock Victorian Plantations. 30 individual trees were identified at each site and assessed for tree characteristics (Dbh, branching and internodes) and sampled for an outerwood density core.

Ten sites were selected (2 or 3 per company) for a joint study of wood properties and sawing recoveries. Site selection aimed to include the range of regional variability in outer-wood density and assessed tree characteristics (Dbh, branch size and internodes). Six of the sites were chosen to represent the low and high outer-wood density extremes (<450kg/m3 and >500 kg/m3 respectively) and four sites for medium outer-wood density (451kg/m3 to 499kg/m3). The sample sites were also chosen to represent an age range from < 25 years to > 35 years (**Table A2.1**).

Table A2.1 Summary of 10 selected sites with their age and density class selected for detailed wood property survey from McKinley *et al.* (2003)

	Outerwood density class (kg/m^3)		
Age (years)	Low (≤ 450)	Medium (451 – 499)	High (≥ 500)
≤ 25	**L (23)** - HVP Porter's	**M (25)**- Auspine Nangeela	NA
26 - 30	**L (26)** - HVP Emerson's	**M (28)** - GTFP Kongorong	**H (27)** - Auspine Byduke
31 - 35	**L (33)** -GTFP Myora HQ	**M (31)** - GTFP Kentbruk	**H (32)** - FSA McGillivray's
≥ 36	NA	**M (37)** - FSA Long's	**H (44)** - FSA Caroline HQ

Based on tree characteristic information collected during the outerwood density survey, 9 to 16 trees were selected per site. The selected trees were felled, and the whole stem length was recorded and a DIRECTOR HM200 acoustic measure was made prior to sectioning the stem into 4.9m logs for the sawing study, and collecting discs for measurement of wood properties. One complete set of discs from all sampling heights (0m, 5m and subsequent 5m intervals down to a SED of approximately 100mm) was removed for basic density and spiral grain assessment

Resource evaluation study in Western Australia

Results of the forest survey of wood quality in Western Australian radiata pine, including information on Dbh, branching, outerwood density, and standing tree acoustics are given in Blakemore et al. (2010). The survey was conducted in the south-west of Western Australian, encompassing major site types, silvicultural regimes and crop ages. This approach is similar to that used in the Green Triangle and Tasmanian studies (McKinley *et al.* 2003; Cown *et al.* 2006). The Western Australian softwood resource was divided into eight distinct regions (Sunklands, Harvey Coast, Hills, Blackwood Valley, Grimwade, Warren) from north of Perth to Pemberton and 42 *P. radiata* stands were assessed for sampling purposes. The sites sampled were selected from mid-rotation (17 – 24 years-old) and mature stands (25+years-old).

At each location, 30 standing "crop" trees were selected (avoiding severely suppressed, severely swept, malformed, double leaders and dead trees). The following stem characteristics were assessed:

- Dbh – Diameter at breast height over bark was measured (mm)

- Outerwood density - Two 5mm outerwood cores, 50mm in length, were collected at breast height
- Standing tree acoustics - Two measurements per tree were undertaken using an ST300 time-of-flight tool.
- Branch Size - Thirty stems per plot were visually scored for branching in the butt, second, third and fourth logs assuming 5m log lengths using 0 (0), 1 (<3cm),2 (3-6cm), 3(6-9cm) and 4(>9cm) scores

Twelve trees were selected from each of four plots representing two mid-rotation and two late-rotation stands with contrasting branch size classification, based on Dbh and ST300 classifications. In each plot, the total height of the tree, height to crown base, pruned height and stump height were measured on each of the selected trees after they were felled. Acoustic velocity of the whole stem was measured using the HM200 (FibreGen, Auckland, New Zealand) before logs, 4.85 m long, were prepared and discs were cut at the base and at the top of each log to allow density determinations. Knots were avoided where possible. Acoustic velocity was again measured with a HM200 tool on each log before maximum branch size and location was recorded.

Benchmarking study in Tasmania

The major objective of this study was to identify the sources of variation in wood properties affecting structural lumber recoveries across Tasmania (within and between sites) in crops within 10 years of harvest. The sources of variation sampled were environmental effects (latitude, altidude, rainfall, soil type) and between and within stem variation.

Twenty-six sites of the two major companies, Rayonier and Norske Skog within ten years of harvest (20 to 31 years old) were selected for non-destructive field sampling across the main plantation forest areas of Tasmania. The assessments of 30 trees per site included visual observations of crown characteristics (branch size and distribution) and breast height diameter, standing tree acoustics (ST300 and IML Hammer) and wood density cores (5mm). Across twenty sites, a sample of five stems was felled for the measurement of stem and log acoustics (5m logs). In addition, wood discs (from breast height and 5m intervals from the butt to 100mm top diameter) were collected.

Results and Discussion

Mean-variance relationship

The detailed results on variability of the stand means and the relationship between the mean and the variance in the Green Triangle Region (GTR), Tasmania (TAS) and Western Australia (WA) were given in the confidential report for the Milestone 7 of this project. Strong positive relationship between mean and variance was observed for sweep, and the relationship did not differ between log height-classes. Overall relationship was y=6.3x+5.2 in the GTR study. Maximum Branch Size measured on logs (GTR study) differed markedly among log height classes, ranging from: negative for 1st log to positive upper logs. Visually assessed Branch Size or Branch Index (WA and TAS studies) had an overall curvilinear relationship, mainly due to lower variance estimates for upper logs (possibly biased). Stiffness estimated on logs using HM200 – "Hitman" instrument differed among log height classes, ranging from: negative for to slightly positive for upper logs (GTR and TAS studies) (**Figure 20**).

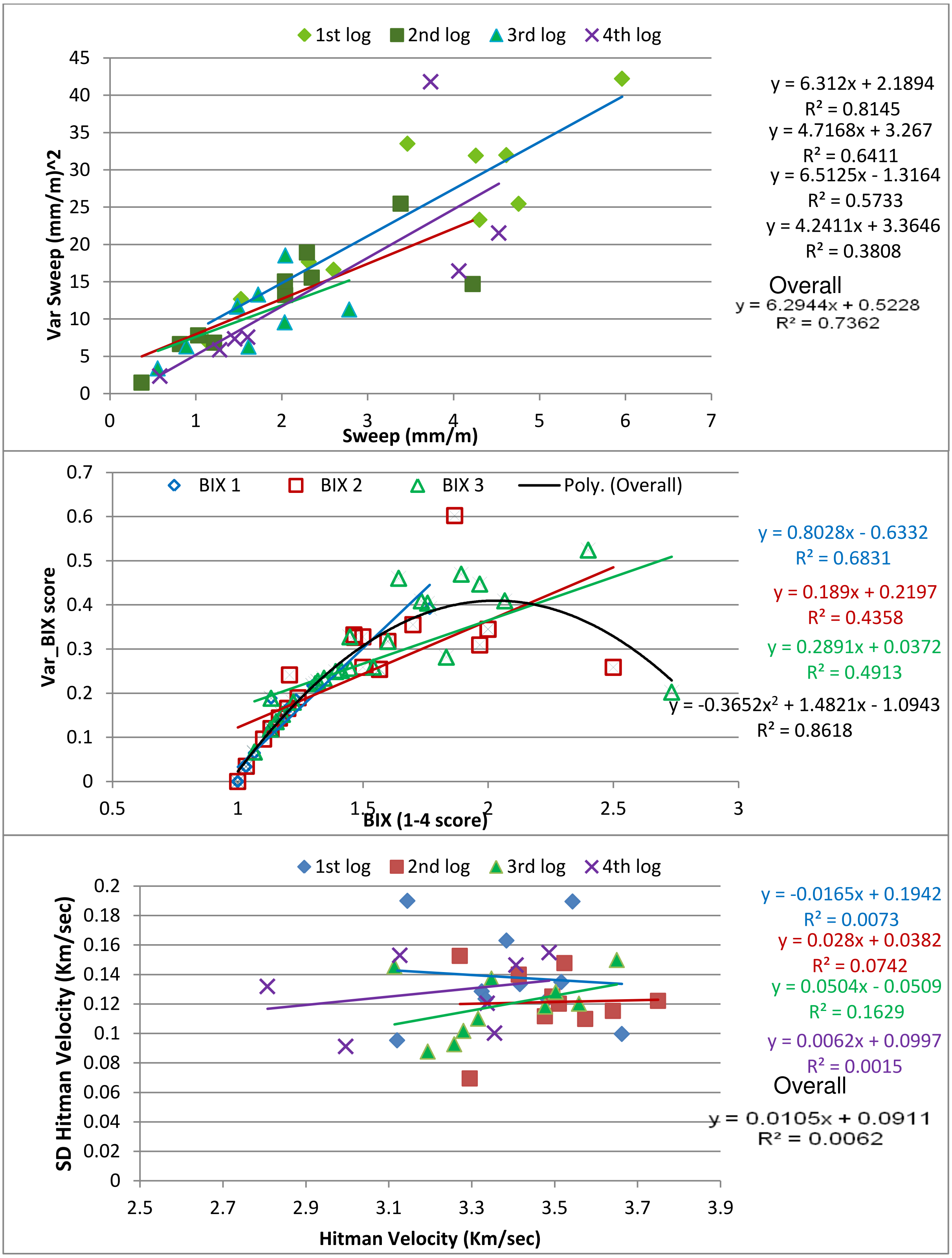


Figure A2.1 Relationship between phenotypic mean and variance for sweep in GTR study (upper), branch size score in WA study (middle), and Hitman velocity in TAS study (lower panel).

Data acquisition for breeding objective traits other than growth increment

Stem form is routinely assessed visually, as a 4 or 6 point score, but absolute scale measurement of stem shape can be obtained using laser, theodolite or digital camera systems. The photographic system gives a quick and reliable measure of the three dimensional (3D) stem profile. However, the new 'Zebedee' 3D mapping device developed by CSIRO (https://wiki.csiro.au/display/ASL/Zebedee) is an accurate handheld laser device. Zebedee enables a user to generate a 3D map simply by walking through a desired location. Using 3D profiles of trunks, a series of indicators which characterize the form in the longitudinal direction can be developed.

Branching traits in genetic trials are routinely assessed visually, as a score or as a branch cluster frequency to a certain height along the stem. In the past MARVL was routinely used in pre-harvest assessments of plantations. In new tools such as ATLAS Cruiser® tree description method takes stem assessment from a subjective to objective, and features of the stem are recorded quantitatively. Branch size is modelled over time using branch data from the assessments to obtain repeatable and consistent estimates. Absolute-scale of branch size is obtained, the probable error limits are reported for all estimates.

More recently, new remote sensing measurements on trees and stands can provide previously unavailable data for site characterisation, precision silviculture and genetic deployment. For example, LIDAR can create topographical maps and reveal the slopes and sun exposure of land. Topographical information can be matched with the yield results. From this information, and using information on GF rating in New Zealand (Dungey *et al.* 2013), the land is categorized into high-, medium-, or low-yield zones. This technology is valuable to forestry managers because it also can indicate which areas can achieve the highest crop yield, or which areas are susceptible to pests and diseases.

In addition to laser technology, measurement on logs at harvesting, including harvester data, or before processing (log scanners) can provide detailed information for site characterisation. Information on sweep can also be sourced from optical log scanner data. For example Ivkovic *et al.* 2006 obtained data from Tarpeena Sawmill (Auspine, Mount Gambier SA). The data sets included logs scanned in October and November 2003, and contained pattern-sorted logs and associated recovery, from logs of two lengths: 4.8 m and 6.0 m. All logs originated from clear-fall operations at two sites: Byjuke and Kongorong.

Wood quality information can also be obtained from harvesters equipped with acoustic measurement of MoE (Dungey *et al.* 2013). Log yard measurements that are used for classification of logs can also be used for site characterisation, if the log site of origin is traced. Using all available data breeding and deployment zones (i.e. site types) can be defined for growth, form, branching and wood quality and the information supplied into optimisation tools such as SEEDPLAN® (STBA) or ATLAS®, Genotype Deployment (RPBC).

Conclusions

Based on the resource evaluation studies the relationship between mean and variance for breeding objective traits can be summarised: 1) The strongest positive linear relationship between mean and variance was found for sweep; 2) the relationship for maximum branch size was positive, but for visually scored branch size it was weak (and possibly biased) for upper logs, and 3) the relationship for Hitman velocity was generally weak, but slightly negative for the first log and weakly positive for logs 2-4.

Management tools can be used to predict impacts of site, silviculture and genetics on tree growth, branching, wood properties, and hence on aggregated wood value. The predictive models can project not only the size of individual stems, but also quality factors such as wood density, and position and size of branches. These models can be calibrated using actual measurements obtained from inventories. Several models to predict radiata pine properties other than growth were reviewed, and relationships between means and variance over a range of site types have been established. Such models are necessary for breeding (i.e. TREEPLAN®) and deployment tools (i.e. SEEDPLAN® and ATLAS®, Genotype Deployment).

Recommendations

1. Protocols should be established so that the traits other than growth can be predicted for different deployment site types
2. For standing tree form and branching ground based laser measurements will soon be feasible
3. For wood quality acoustic stiffness measurements on logs at harvesting or in log yards are possible
4. This information should be used in customised breeding value estimation by TREEPLAN® and site matching based on composite index traits in deployment tools such as SEEDPLAN®

Appendix 3. Description of regional climates in Australia and New Zealand

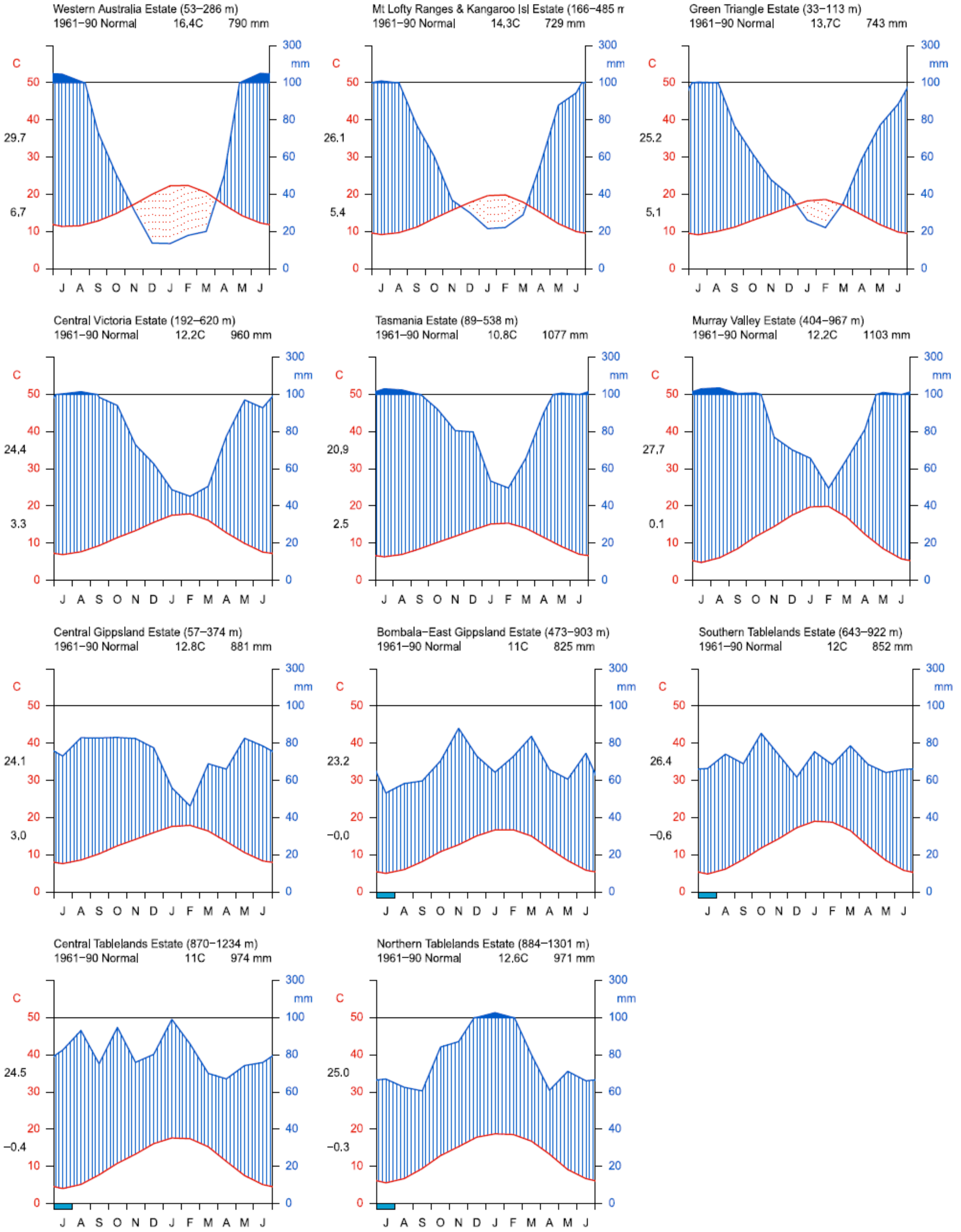


Figure A3.1 Walter & Lieth climate diagrams of radiata pine plantations in Australia. The plots report region and the 10th to 90th percentile of the elevation range of plantations in the title. Below the title, mean annual temperature (MAT) and mean annual precipitation (MAP) are reported. Mean maximum temperature of the warmest month (MaxTWM) and mean minimum temperature of the coldest month (MinTCM) are shown next to the y-axis.

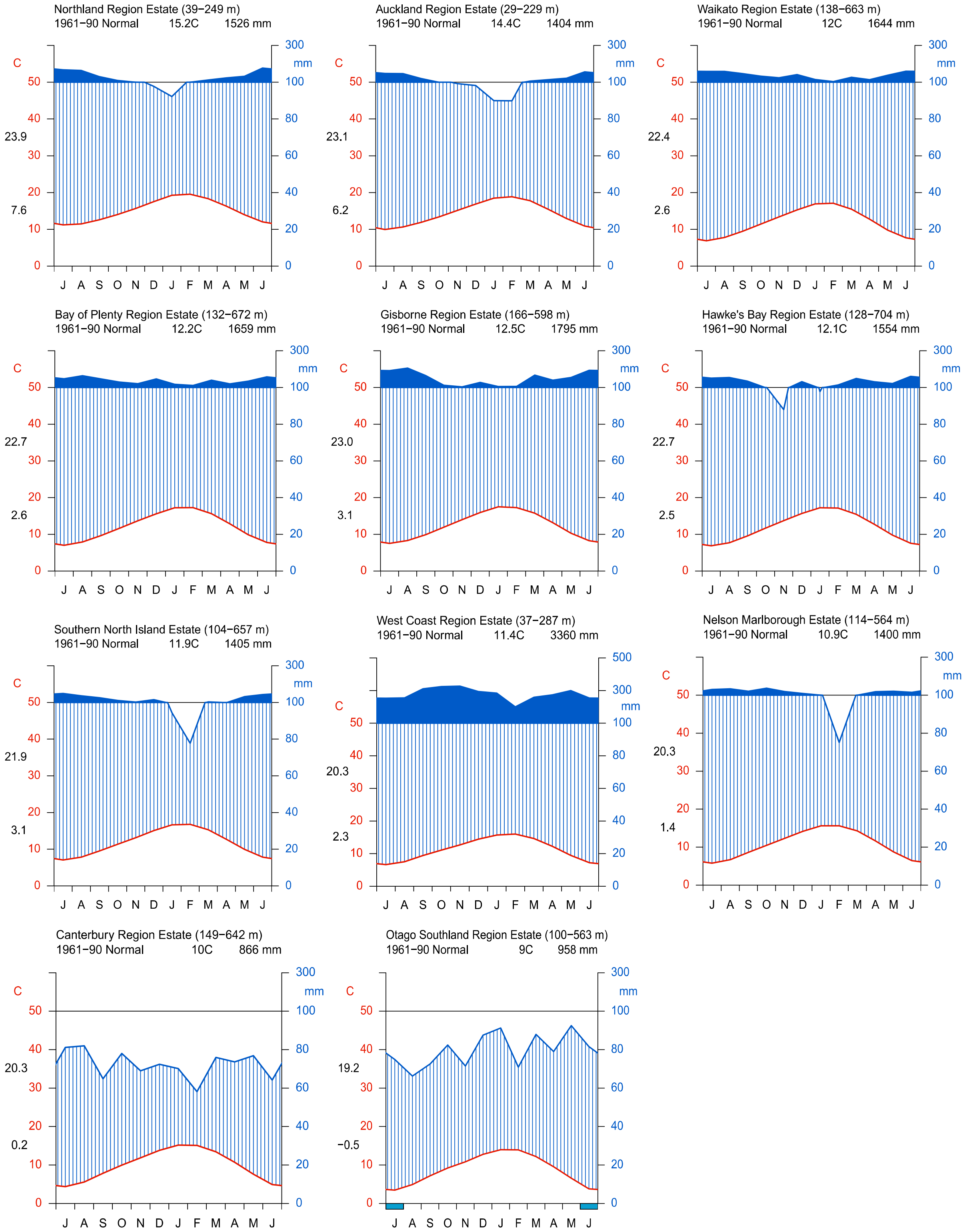


Figure A3.2 Walter & Lieth climate diagrams of radiata pine plantations in New Zealand. The plots report region and the 10th to 90th percentile of the elevation range of plantations in the title. Below the title, mean annual temperature (MAT) and mean annual precipitation (MAP) are reported. Mean maximum temperature of the warmest month (MaxTWM) and mean minimum temperature of the coldest month (MinTCM) are shown next to the y-axis.