Specialty Wood Products Research Partnership

FOREST GROWERS RESEARCH

Evaluation of multi-site progeny test in *Eucalyptus fastigata*

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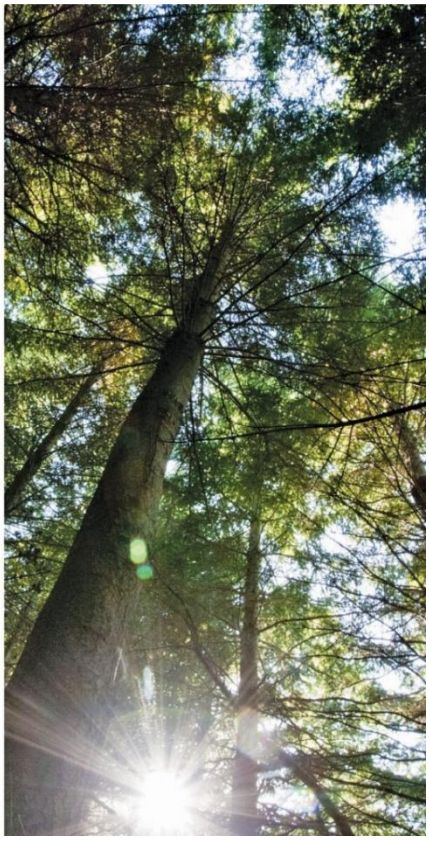

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EXECUTIVE SUMMARY

Progeny trials for *Eucalyptus fastigata* in the third cycle, planted in 2009 and 2012 in Kaingaroa (compartment 333 and 605), Waihaha and Waihapua were assessed at age of 8 for growth and form characteristics. As these trials have now reached an age when selections for the next generation can be made, it is required to acquire measurements for genetic evaluation and selection purposes prior to the thinning process.

This investigation aimed to carry out a multi-environmental genetic evaluation to estimate genetic parameters such as heritability, genetic correlations across phenotypes within sites, and genotype by environment interactions across investigated sites. Additionally, a list of breeding values was compiled for the purpose of selecting the individuals who would form the next generation of seed orchards and breeding populations.

As a result, the favourable correlation structure makes it possible to simultaneously select productive individuals that have high wood stiffness (approximated by acoustic velocity) and a favoured branching pattern. The inclusion of stem straightness (STR) and malformation (MAL) into the selection will be more restricted due to the modest but favourable genetic correlations they have with DBH.

Genotype by environment interaction (GxE) analysis showed a substantial positive genetic correlation between FR503/1 and FR503/2 across most of the studied traits. However, these two sites exhibited unfavourable genetic correlation with FR503/3, which is geographically adjacent to FR503/1. Due to FR503/3's poor site quality and lack of genetic linkage with FR503/1 and FR503/2, we presume the negative genetic correlations should be interpreted with caution. We recommend implementing multi-generational evaluation to increase the genetic connectivity of FR503/3 and FR503/4 with the rest of the breeding programme to improve the quantification of GxE.

INTRODUCTION

The breeding plan for the *Eucalyptus fastigata* tree species in New Zealand is presently in the beginning of its third cycle of selections. The breeding population is composed of individuals of Australian ancestry and seed sources originating from South Africa and New Zealand (Figure 1). During each cycle of the breeding effort, new seed sources have been tested and introduced. The goals of breeding over the cycles have been to achieve enhanced growth, form, and adaption traits such as frost resistance (Wilcox 1980, Wilcox 1982, Kennedy et al. 2011). It was predicted that there were significant genetic gains of 15% for growth and shape in the first generation, and 12% for form in the second generation. (Kennedy et al. 2011).

Eucalyptus fastigata is known to be one of the most dependable eucalypts in New Zealand's many different environments (Cannon and Shelbourne 1991). It can withstand frosts as low as -10 degrees Celsius (Miller et al. 2000), but it is sensitive to frosts that occur outside of their normal growing season (Menzies et al. 1981). Since this species has a propensity for developing wide, persistent branches, especially in open stands, achieving good shape is one of the most essential goals of breeding (Boland et al. 1984). Sawn wood, fine papers, and pulp manufacture are some of the many valued end applications for the *Eucalyptus fastigata* tree (Low et al. 2009). Wood with these characteristics is defined as being moderately hard, moderately strong, and moderately durable (Boland et al. 1984). Wood qualities have not been examined in the breeding population in the past; nevertheless, earlier studies in New Zealand have revealed that the density of the wood ranges from 450 to 600 kg m3 and that the wood's stiffness ranges from 11 to 26 GPa (gigapascal) modulus of elasticity (MOE) (Jones et al. 2010).

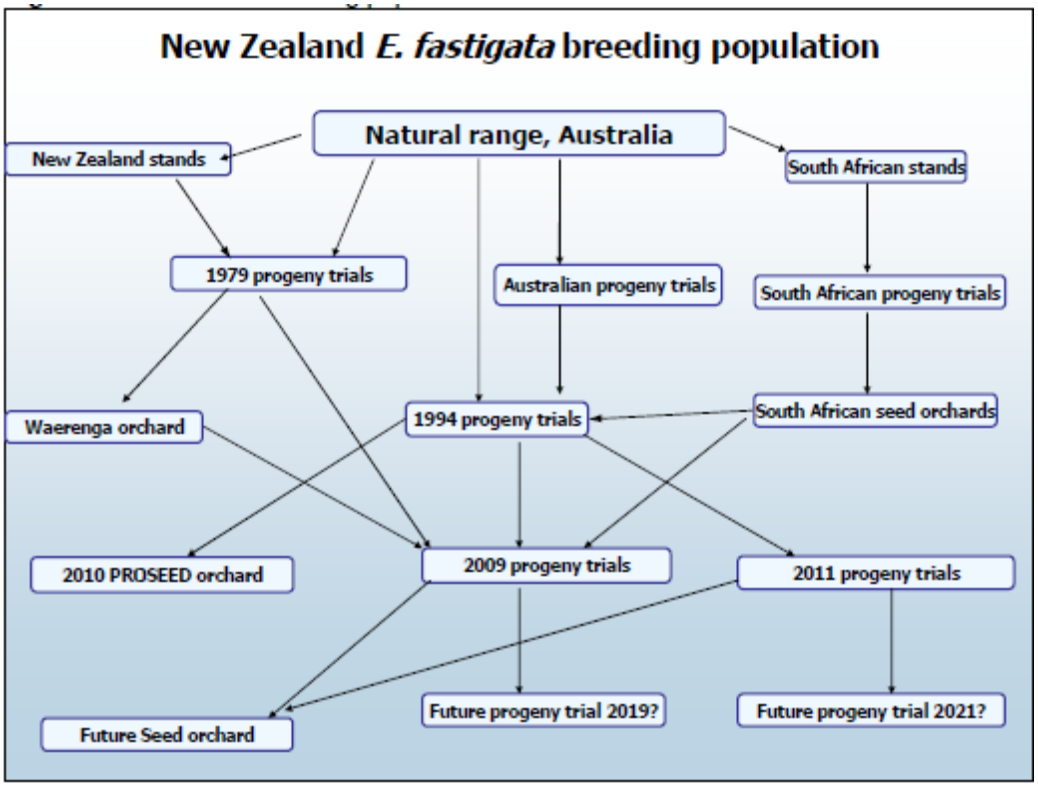

Figure 1: *Eucalyptus fastigata* breeding programme. (Figure from Low et al. 2009).

The third cycle progeny trials were planted in Kaingaroa (compartments 333 (FR503_1 established 2009) and compartment 605 (FR503_3 established 2011)), Waihaha (FR503_2 established 2010), and Waihapua (FR503_4 established 2012) (Figure 2). The FR503_1 experiment includes 132 open-pollinated families from 18 different provenances or seed sources. In the FR503_2 experiment, 123 open-pollinated families from 18 provenances or seed sources were used. The FR503_3 experiment consisted of 112 open-pollinated families from 14 provenances or seed sources, while the FR503_4

experiment consisted of 106 open-pollinated families from 13 provenances or seed sources. There was significant genetic overlap between FR503_1 and FR503_2, which included 123 open-pollinated families, as well as between FR503_3 and FR503_4, which included 89 open-pollinated families. However, there was limited genetic overlap between these two groups of studies, with only 17 families representing four provenances or seed sources (Appendix 2). It was reported that there had been substantial genetic advances for the early age measures (Suontama et al. 2014). These tests have now reached an advanced stage, which enables selection of genetically superior material to be taken for the future generation of the breeding cycle. Progeny trials were evaluated at the age of 7 - 9 years (FR503_1 – age of 8; FR503_2 – age of 7; FR503_3 – age of 9 and FR503_4 – age of 8) for growth, form, and adaptation.

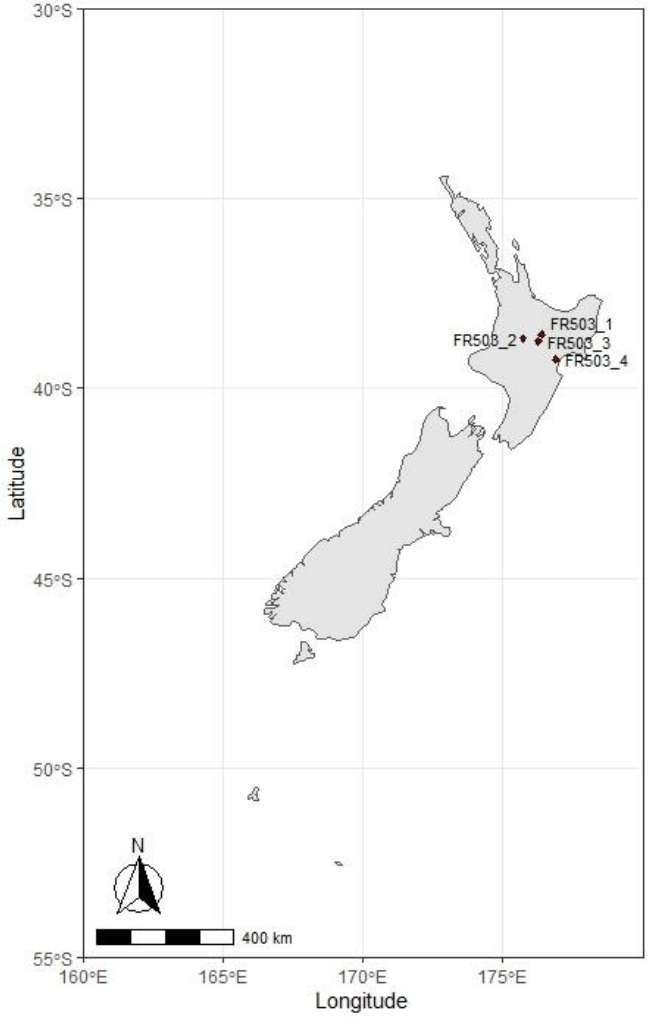

Figure 2: Map of *Eucalyptus fastigata* progeny trials

The purpose of this research was to evaluate the growth of the trees as well as their stem form at four different locations. Following the phenotypic evaluation, genetic analyses were carried out with the goals of estimating the amount of genetic variation and covariation, inferring the level of genetic correlations between studied traits, and identifying any genotype by environment interactions that existed across sites. Finally, a list of breeding values was compiled for the purpose of selecting individuals for the breeding population and the seed orchard of the next generation.

METHODS

The following characteristics of growth and form were taken into consideration while evaluating the trees: 1) Diameter at breast height (DBH), 2) Stem straightness scored on a scale from 1 to 9 where 1 is very sinuous and 9 is perfectly straight (STR), 3) Malformation scored on a scale from 1 to 9 where 1 = multiple forks and 9 = no forks (MAL), 4) branching scored on a scale from 1 to 9 where 1 = heavy branching and 9 = light branching (BRA), Acceptability scored on a scale from 0 to 1 where 0 = not acceptable and 1 = acceptable (AC). In addition, measurements of wood stiffness were taken exclusively at the Kaingaroa location (compartment 333), and the ST300 instrument was used to determine acoustic wave velocity (AVEL) as a surrogate attribute for wood stiffness.

The analysis of genetic gain was performed through mixed linear models using ASReml-R package (Butler et al.2009) as follows:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Zu} + \boldsymbol{e}$$

where ***y*** is the vector of phenotypes, ***β*** is a vector of fixed effects (intercept, replication and provenance), ***u*** is a vector of random effects (block) and additive genetic effect, ***e*** is a vector of residuals. ***X*** and ***Z*** are incidence matrices assigning the effects from ***β*** and ***u*** to the vector of phenotypes. Because eucalypt species have a propensity for self-fertilization (Griffin and Cotterill 1988), a proportion of 15% for selfing was fitted into the numerator relationship matrix in ASReml - R (Gilmour and Dutkowski 2004). On the basis of various literature references reflecting a larger proportion of selfing in natural stands than in seed orchards, this proportion was estimated as a compromise in order to get a satisfactory result (Griffin and Cotterill 1988, Moran et al. 1989, Gaiotto et al. 1997, Burczyk et al. 2002). Additionally, spatial analysis was performed to compare the effectiveness of applied experimental design to capture microenvironmental heterogeneity within each site through first order autoregression. In this case, the residual structure is divided into spatially dependent and independent part as follows:

$$R = \sigma_\gamma^2[AR1(\rho_{col}) \otimes AR1(\rho_{row})] + \sigma_\delta^2 \boldsymbol{I}$$

Where σ_γ^2 is the spatially dependent variance, AR1(ρ) is the first-order autoregressive correlation matrix, $\otimes$ is the Kronecker product and σ_δ^2 is the spatially independent residual variance.

Narrow-sense heritability was estimated as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

where σ_g^2 is the estimated additive genetic variance and σ_e^2 is the estimated residual variance.

The multi-trait analysis for the estimation of genetic correlations between traits within sites and between sites (GxE) was performed on phenotypes adjusted for design and spatial factors to simplify the multivariate models to make model convergence feasible. The optimal correction of phenotypes was decided based on Akaike's information criterion (AIC) from the single trait analysis. The accuracy of breeding values was estimated as follows:

$$r = \sqrt{1 - \frac{PEV}{(1 + F_i)\sigma_g^2}}$$

where PEV is prediction error variance (Mrode 2014) and Fi is the inbreeding coefficient of i^{th} individual. The genetic correlations between traits within site or between sites were estimated as follows:

$$r_G = \frac{\sigma_{xy}}{\sqrt{\sigma_x^2 \sigma_y^2}}$$

where σ_{xy} is the additive genetic covariance between xth and yth trait, σ_x^2 is an additive genetic variance for xth trait and σ_y^2 is an additive genetic variance for yth trait.

RESULTS

The investigation of phenotypic data indicated that site FR503/1 had the highest productivity (with a mean DBH of 168.7 millimetres), followed by site FR503/4 (with a mean DBH of 167.1 millimetres), and site FR503/2 had the lowest productivity (mean DBH equal to 136.8 mm). On the other hand, the sites FR503/3 and FR503/4 had the biggest standard deviation, which indicates that there are problems with the sites, such as survival, terrain profile, or microenvironmental variability (Figures 3–6). Surprisingly, the greatest performance for stem quality features (STR, BRA, and MAL) was found at the FR503/4 location, which also surpassed acceptability standards (Table 1). When compared to FR503/1 and FR503/2, FR503/3 and FR503/4 had a higher quality stem, which is most likely attributable to the fact that they were grown from different sources of seed. There are more selections from New Zealand in FR503/1 and FR503/2, while there are more selections from Australia in FR503/3 and FR503/4. The latter sites had poorer site quality, which may be another factor that contributed to the disparities in the stem quality attributes.

Table 1: Descriptive statistics of investigated traits

Variable	N	Mean	Std. Dev.	Min	Pctl. 25	Pctl. 75	Max
DBH_FR503/1	3397	168.716	37.041	96	142	195	328
STR_FR503/1	3397	7.064	1.502	1	6	8	9
BRA_FR503/1	3397	6.611	1.925	1	6	8	9
MAL_FR503/1	3396	6.304	2.626	1	4	9	9
ACC_FR503/1	3397	0.338	0.473	0	0	1	1
AVELO_FR503/1	3376	3.434	0.268	2.54	3.25	3.61	4.39
DBH_FR503/2	1472	136.826	33.683	75	111	160	256
STR_FR503/2	1472	5.06	1.685	1	4	6	9
BRA_FR503/2	1471	3.532	1.782	1	2	4	9
MAL_FR503/2	1472	2.219	1.568	1	1	3	9
ACC_FR503/2	1472	0.033	0.179	0	0	0	1
DBH_FR503/3	1451	140.174	49.564	43	101	173.5	302
STR_FR503/3	1449	5.452	3.061	1	2	9	9
BRA_FR503/3	1449	1.695	0.782	0	1	2	5
ACC_FR503/3	1448	0.21	0.464	0	0	0	9
DBH_FR503/4	2050	167.162	57.205	70	121	210	379
STR_FR503/4	2050	7.888	2.143	1	8	9	9
BRA_FR503/4	2050	2.293	1.058	1	1	3	9
ACC_FR503/4	2049	0.443	0.497	0	0	1	1

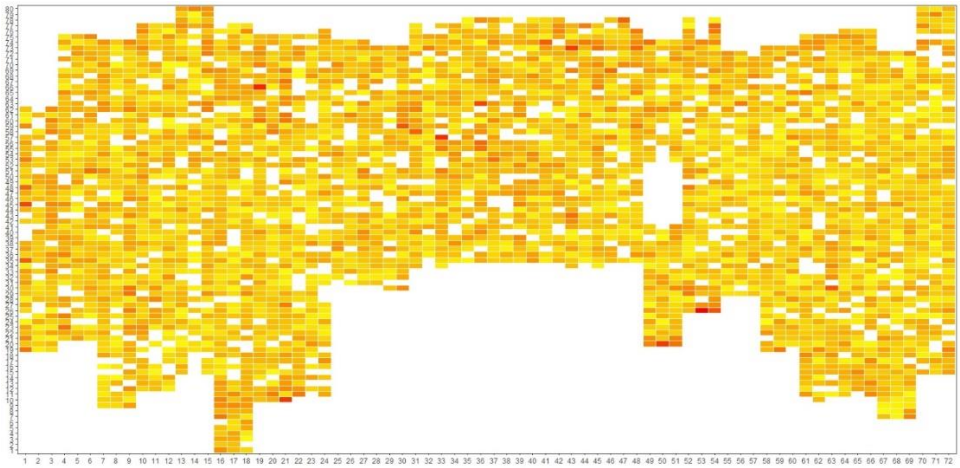

Figure 3: Spatial distribution of DBH at FR503/1

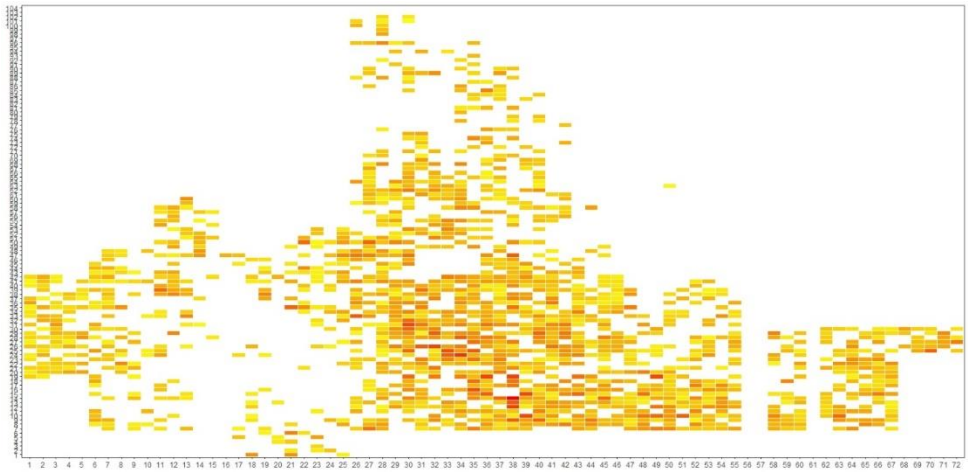

Figure 4: Spatial distribution of DBH at FR503/2

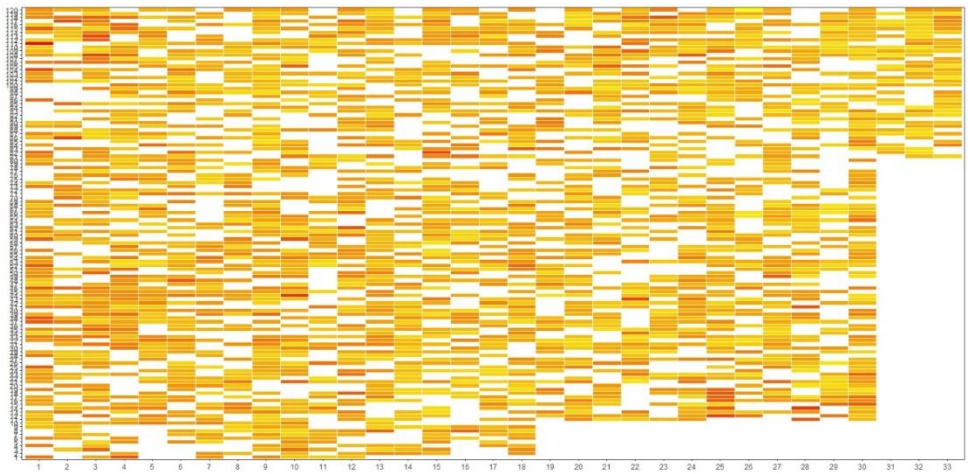

Figure 5: Spatial distribution of DBH at FR503/3

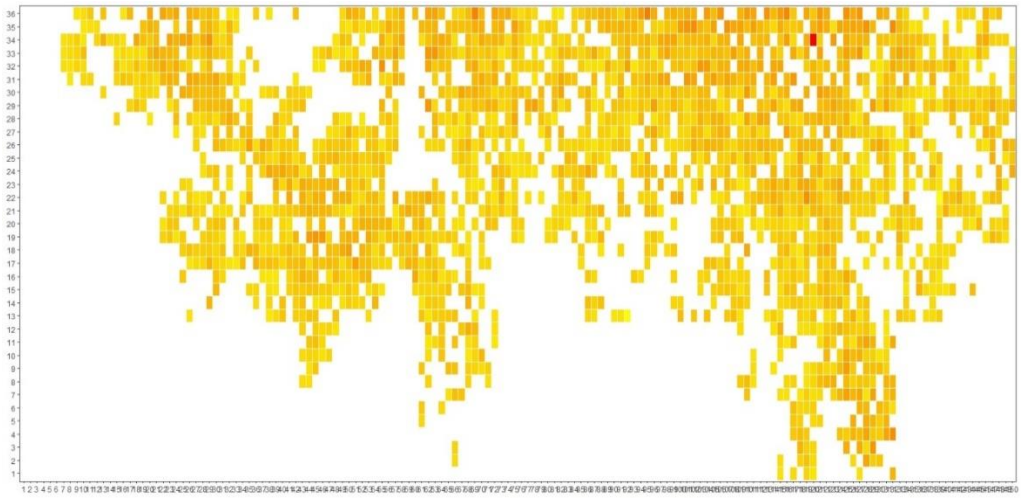

Figure 6: Spatial distribution of DBH at FR503/4

From the study of genetic parameter estimates, the levels of heritability estimated at FR503/1 and FR503/2 are greater than those estimated at FR503/3 and FR503/4. For instance, the heritability of DBH ranged from 0.17 and 0.18 at sites FR503/1 and 2, however, the range was 0.04 and 0.07 at sites FR503/3 and 4. A similar trend was detected in all the other qualities that were evaluated. Within the category of stem quality characteristics, STR was shown to have the highest heritability, followed by BRA and MAL. Acoustic velocity (AVEL) had a heritability of 0.37, which is moderate. According to the AIC criterion that was utilised in this work, the spatial analysis that was performed with the intention of capturing spatial patterns in microenvironmental heterogeneity was only successful at FR503/1 and FR503/2, respectively. This may be due to the complexity of the terrain profiles or the overall deficiency of the FR503/3 and FR503/4 locations, respectively. The accuracy of breeding values ranged from 0.174 to 0.544, and they were correlated with heritability estimates. The highest EBV accuracy was achieved in AVEL. In the stem quality traits, the highest EBV accuracy was achieved in STR, with values ranging from 0.237 to 0.542, while the EBV accuracy of the MAL was found to be the lowest, with values ranging from 0.254 to 0.414 (this trait was not scored at FR503/3 and FR503/4, which showed generally lower values). The accuracy of DBH EBV measurements ranged from 0.207 to 0.434. The utilisation of spatial analysis resulted in just a marginal enhancement to the accuracy of the EBV. This was more obvious at FR503/1 and FR503/2, following the pattern in the AIC criterion changes.

Table 2: Genetic parameter estimates for sites FR503/1 and FR503/2

Site	FR503_01					FR503_02			
Param.	**DBH**	**STR**	**BRA**	**AVEL**	**MAL**	**DBH**	**STR**	**BRA**	**MAL**
Add. Gen. Var.	218.5 (40.560)	0.45 (0.074)	0.56 (0.099)	0.02 (0.003)	0.96 (0.183)	174.2 (46.090)	0.78 (0.168)	0.58 (0.144)	0.19 (0.078)
Block var.	7.8 (7.590)	0.01 (0.007)	0.02 (0.015)	0.00 (0.000)	0.03 (0.033)	4.59 (5.969)	0.01 (0.013)	0.00 (0.011)	0.03 (0.029)
Resid. var.	1084 (43.650)	1.41 (0.069)	2.44 (0.103)	0.04 (0.003)	5.11 (0.201)	807.5 (52.050)	1.75 (0.158)	2.02 (0.149)	1.98 (0.108)
AIC	27647.970	5529.007	7188.041	-6288.554	9574.819	11506.940	2887.972	2935.353	2693.668
h^2	0.17 (0.036)	0.24 (0.049)	0.19 (0.046)	0.37 (0.051)	0.16 (0.053)	0.18 (0.076)	0.31 (0.094)	0.22 (0.077)	0.09 (0.042)
r	0.423	0.485	0.443	0.544	0.414	0.434	0.542	0.476	0.254
Add. Gen. var.	238.1 (41.810)	0.46 (0.076)	0.53 (0.095)	0.02 (0.003)	0.95 (0.181)	171.5 (44.580)	0.77 (0.162)	0.55 (0.131)	0.15 (0.070)
Block var.	3.57 (5.260)	0.01 (0.007)	0.02 (0.018)	0.00 (0.000)	0.03 (0.035)	1.33 (4.076)	0.00 (0.000)	0.00 (0.000)	0.00 (0.008)
Spat. var.	513.9 (131.930)	0.15 (0.036)	0.23 (0.053)	0.01 (0.001)	0.42 (0.131)	191.0 (59.470)	1.24 (0.436)	1.22 (0.338)	0.51 (0.266)
Resid. var.	885.4 (43.220)	1.27 (0.075)	2.28 (0.102)	0.03 (0.003)	4.86 (0.204)	697.4 (51.860)	1.43 (0.149)	1.43 (0.130)	1.89 (0.103)
AIC	27466.290	5498.817	7122.622	-6362.919	9550.296	11457.140	2786.987	2705.080	2658.524
h^2	0.21 (0.036)	0.27 (0.042)	0.19 (0.033)	0.39 (0.054)	0.16 (0.030)	0.19 (0.050)	0.35 (0.069)	0.28 (0.063)	0.07 (0.035)

r	0.461	0.498	0.443	0.546	0.414	0.438	0.551	0.492	0.252

Table 3: Genetic parameter estimates for sites FR503/3 and FR503/4

Site	**FR503_03**			**FR503_04**		
Parameter	**DBH**	**STR**	**BRA**	**DBH**	**STR**	**BRA**
Add. Gen. Var.	143.6 (52.15)	0.26 (0.173)	0.05 (0.016)	99.8 (53.36)	0.16 (0.094)	0.06 (0.025)
Block var.	40.5 (22.99)	0.78 (0.189)	0.01 (0.006)	469.6 (106.3)	0.08 (0.053)	0.07 (0.021)
Resid. var.	1870.6 (77.11)	8.39 (0.318)	0.50 (0.022)	2444.3 (95.08)	4.48 (0.173)	0.97 (0.040)
AIC	18687.03	7010.27	1034.767	18426.81	5375.956	2337.273
h^2	0.07 (5.123)	0.03 (0.026)	0.09 (0.030)	0.04 (3.597)	0.04 (0.024)	0.06 (0.026)
r	0.207	0.257	0.256	0.256	0.237	0.174
Add. Gen. var.	141.3 (51.74)	0.28 (0.175)	0.05 (0.016)	108.04 (51.11)	0.18 (0.095)	0.07 (0.026)
Block var.	41.1 (22.98)	0.76 (0.191)	0.01 (0.006)	0.00 (0.000)	0.02 (0.063)	0.00 (0.000)
Spatial var.	33.9 (37.29)	8.39 (0.320)	0.13 (0.188)	1052.5 (165.6)	1.21 (0.506)	0.18 (0.041)
Resid. var.	1839.9 (83.29)	0.00 (0.000)	0.37 (0.189)	1969.9 (99.18)	3.33 (0.532)	0.88 (0.044)
AIC	18692.15	7012.368	1034.302	18313.64	5356.839	2315.448
h^2	0.07 (0.026)	0.99 (0.000)	0.12 (0.065)	0.05 (0.025)	0.05 (0.028)	0.07 (0.027)
r	0.207	NA	0.274	0.258	0.239	0.176

The analysis of genetic correlations identified two main clusters within the investigated traits. The first cluster is formed by acoustic velocity and DBH at FR503/1, while the other cluster is formed purely by stem quality traits. While there were positive but statistically non-significant positive genetic correlations between DBH and STR and DBH and MAL (0.159 and 0.179), there was a strong statistically significant negative genetic correlation between DBH and BRA (-0.553). A similar pattern was observed at FR503/2. As a result, the favourable correlation structure makes it possible to simultaneously select productive individuals that have high wood stiffness (AVEL) and a favoured branching pattern (BRA). The inclusion of STR and MAL into the selection will be more restricted due to the modest but favourable genetic correlations they have with DBH. The sites FR503/3 and FR503/4 resulted in positive genetic correlations between DBH and BRA, probably due to the low level of heritability estimated these sites (Table 4, Figure 7).

Table 4: Pair-wise genetic correlations between traits within each site

Traits	**FR503/1**	**FR503/2**	**FR503/3**	**FR503/4**
DBH - STR	0.159 (0.118)	0.269 (0.155)	0.365 (0.341)	0.032 (0.386)
DBH - BRA	-0.553 (0.087)	0.012 (0.176)	0.695 (0.120)	0.769 (0.134)
STR - BRA	0.427 (0.104)	0.889 (0.070)	0.593 (0.299)	-0.002 (0.333)
DBH - AVEL	0.257 (0.109)	NA	NA	NA
STR - AVEL	-0.140 (0.110)	NA	NA	NA
BRA - AVEL	-0.632 (0.083)	NA	NA	NA
DBH - MAL	0.179 (0.129)	0.236 (0.229)	NA	NA
STR - MAL	0.864 (0.054)	0.885 (0.155)	NA	NA
BRA - MAL	0.492 (0.108)	0.737 (0.185)	NA	NA
AVEL - MAL	-0.264 (0.114)	NA	NA	NA

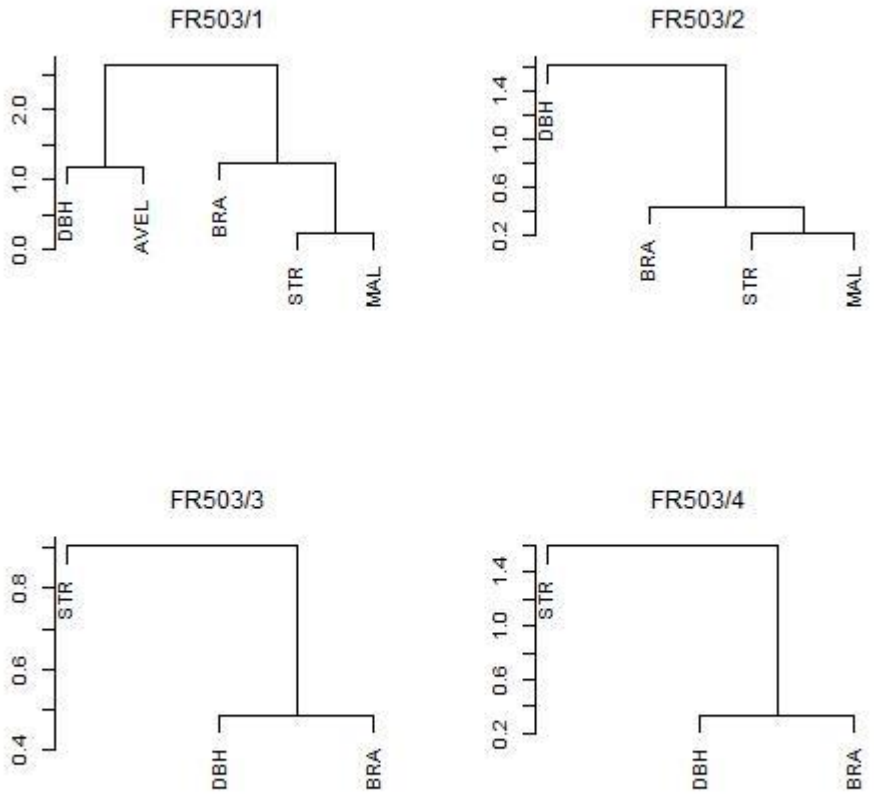

Figure 7: Histograms representing clusters of traits based on genetic correlation analysis.

The genotype by environment interaction (GxE) analysis indicated a significant positive genetic correlation between FR503/1 and FR503/2 (0.63 in DBH, 0.97 in STR, and 0.74 in BRA). Conversely, these two locations also displayed negative genetic connections with FR503/3 (-0.47 and -0.49 in DBH, -0.05 and 0.15 in STR, and -0.39 and -0.12 in BRA), which is geographically close to FR503/1 (Figure 1). We assume that the negative genetic correlations should be considered with caution due to the inferior site quality at FR503/3 and the lack of genetic connectivity between FR503/3 and both FR503/1 and FR503/2. There are no open-pollinated families in common between these sites; there are only 5 provenances represented across all investigated sites, but with different OP families). As a result of these factors, we have conclude that the negative genetic correlations should be considered with caution (Figure 8). We were not able to quantify the genetic association of FR503/4 with any other sites, because of problems with the inferiority of the site and the absence of genetic connectedness.

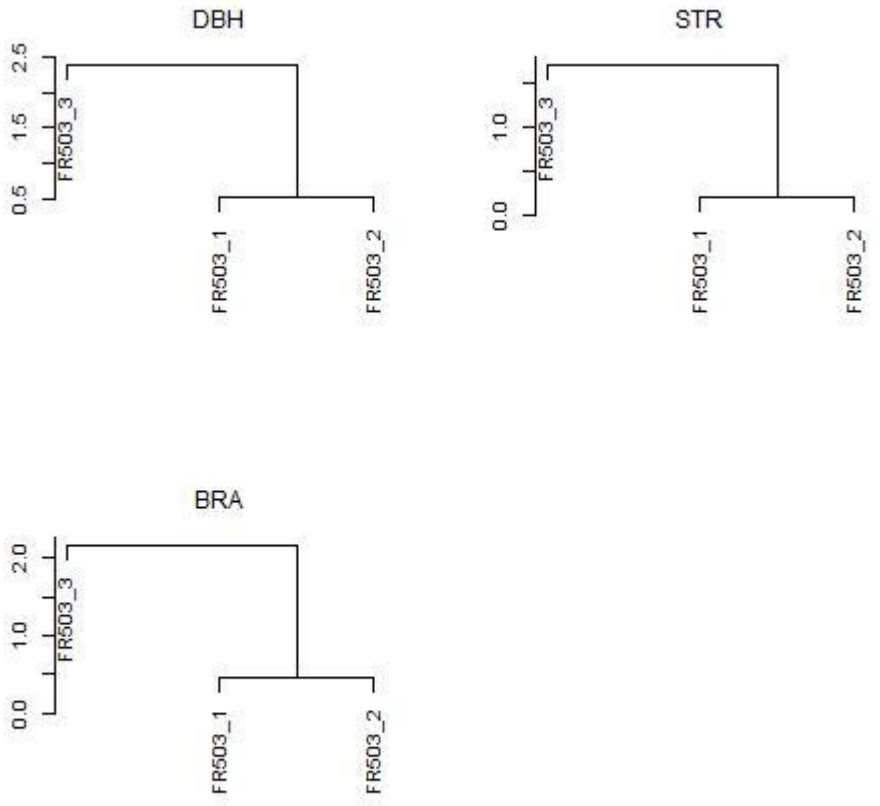

Figure 8: Histograms representing clusters of sites based on genetic correlation analysis.

Comparison of estimated breeding values determined that families originating from the selections at Marlborough and Tikitere seem to perform best in DBH at sites FR503/1 and FR503/2 (Figures 9 and 10), while material from provenances Bombala and Tallaganda (NSW) showed superiority in DBH at sites FR503/3 and FR504/4 (Figures 11 and 12). Plant material originating from the provenances Barrington Tops and Yetholme at FR503/1 and R503/2, as well as plant material originating from the provenances Nitens Road (Glenbog) and Riamukka State Forest at FR503/3 and FR503/4, exhibited the lowest performance in DBH. Since BRA showed a significant genetic association with DBH, the same provenances, namely Marlborough and Tikitere, demonstrated superior performance in both FR503/1 and FR503/2. The same was true for the provenances with the lowest quality (Barrington Tops). However, the opposite pattern in genetic correlations was observed at FR503/3 and FR503/4, which resulted in the superior performance of material originating from the Nitens Road (Glenbog) and Riamukka State Forest provenances, even though these provenances performed poorly in terms of productivity at these sites. The best-performing material in terms of stem quality attributes came from the provenances Tikitere, E. Transvaal, Barrington Tops, and Marlborough at FR503/1 and FR503/2, as well as from the provenances Monga State Forest and Riamukka State Forest at FR503/3 and FR503/4. On the other hand, the worst performers were those that came from Oakura, Rotorua, Oberon, and Marlborough provenances at FR503/1 and FR503/2, as well as Coolangubra State Forest and Bombala provenances at FR503/3 and FR503/4.

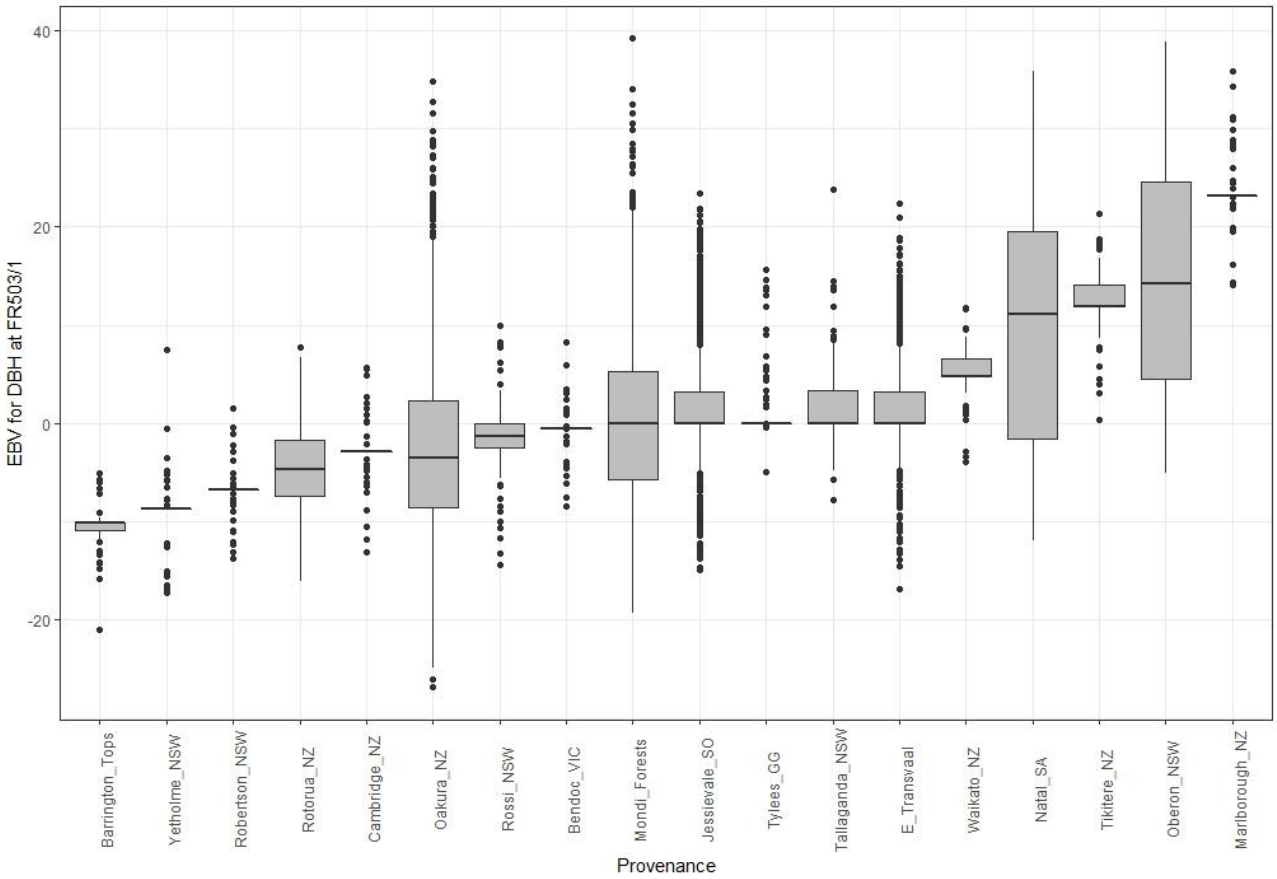

Figure 9: Ranking of seed sources according to breeding values for DBH at FR503/1

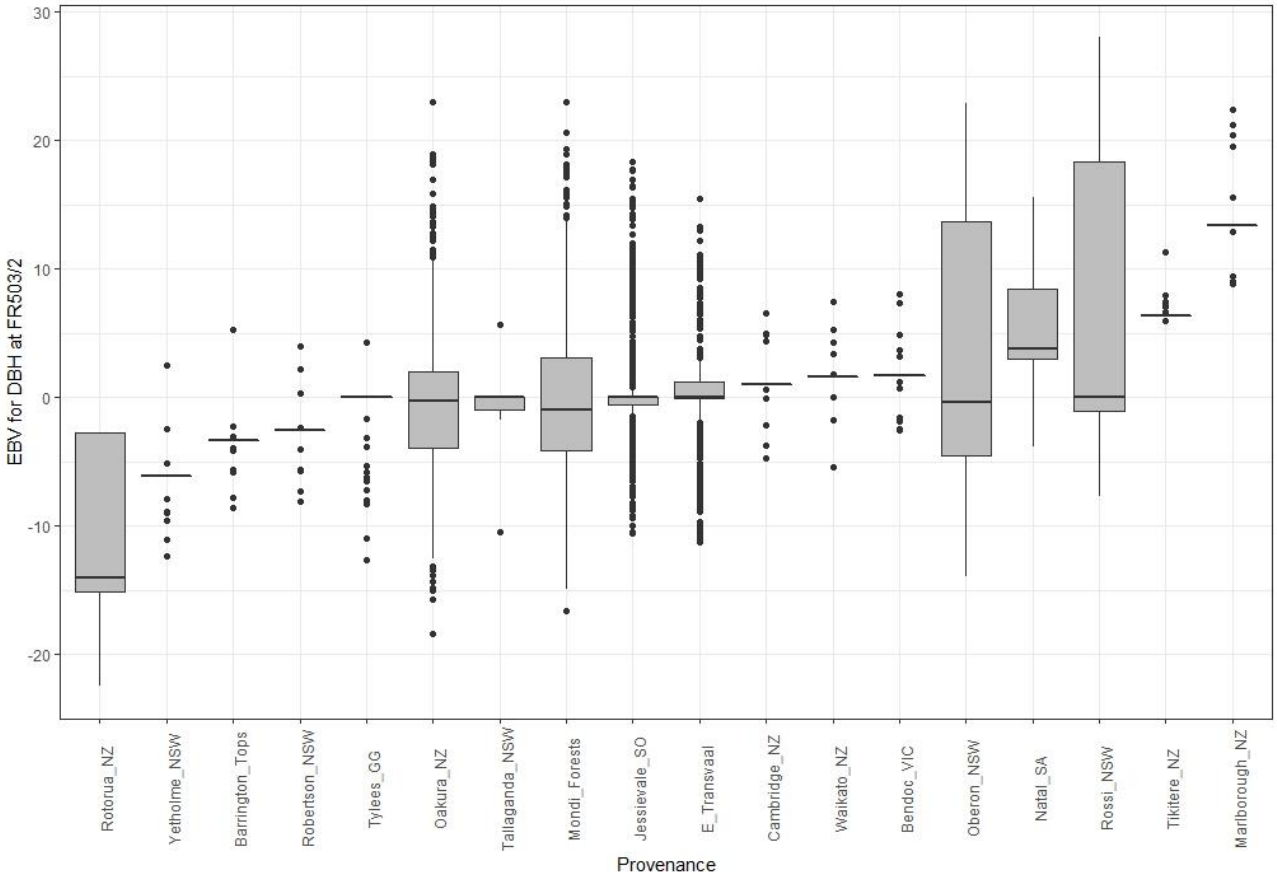

Figure 10: Ranking of seed sources according to breeding values for DBH at FR503/2

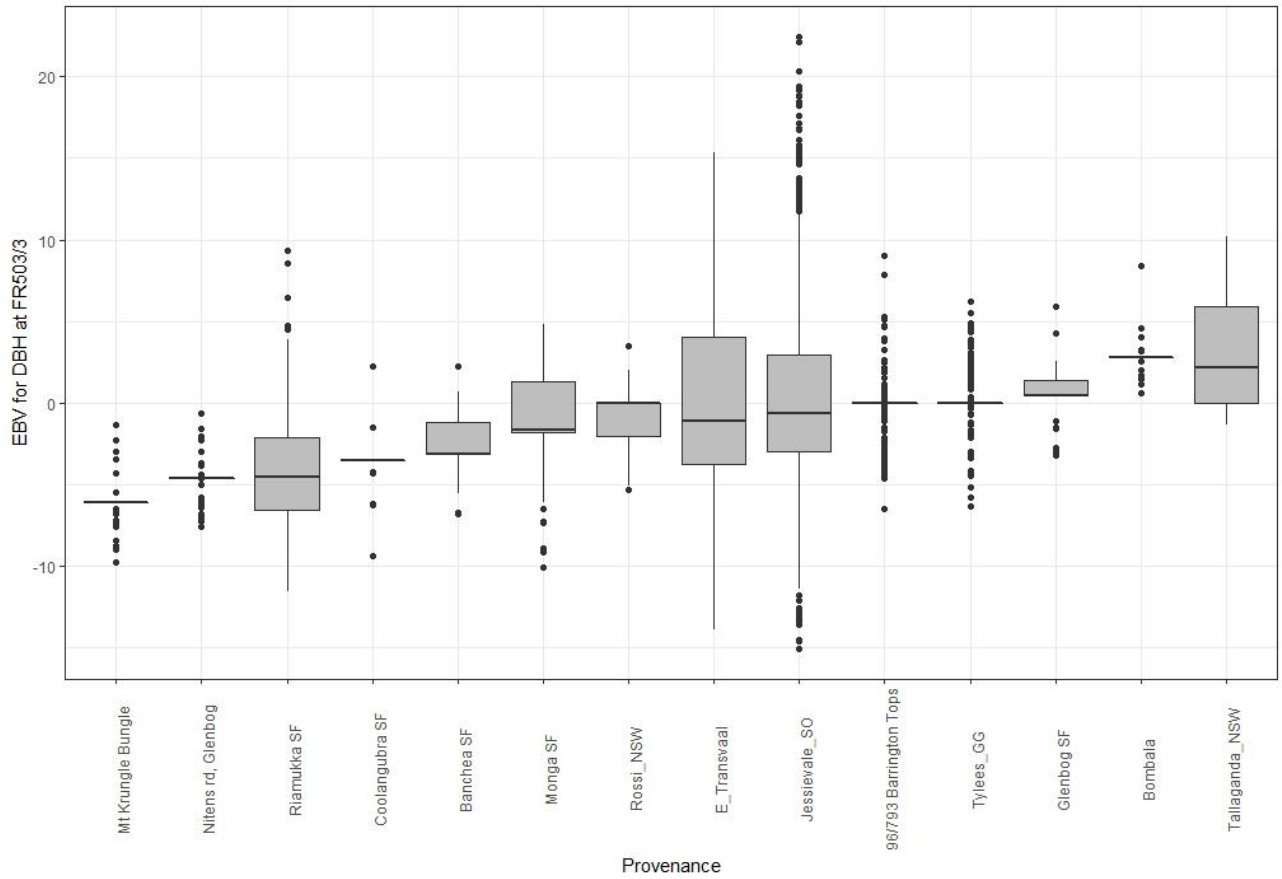

Figure 11: Ranking of seed sources according to breeding values for DBH at FR503/3

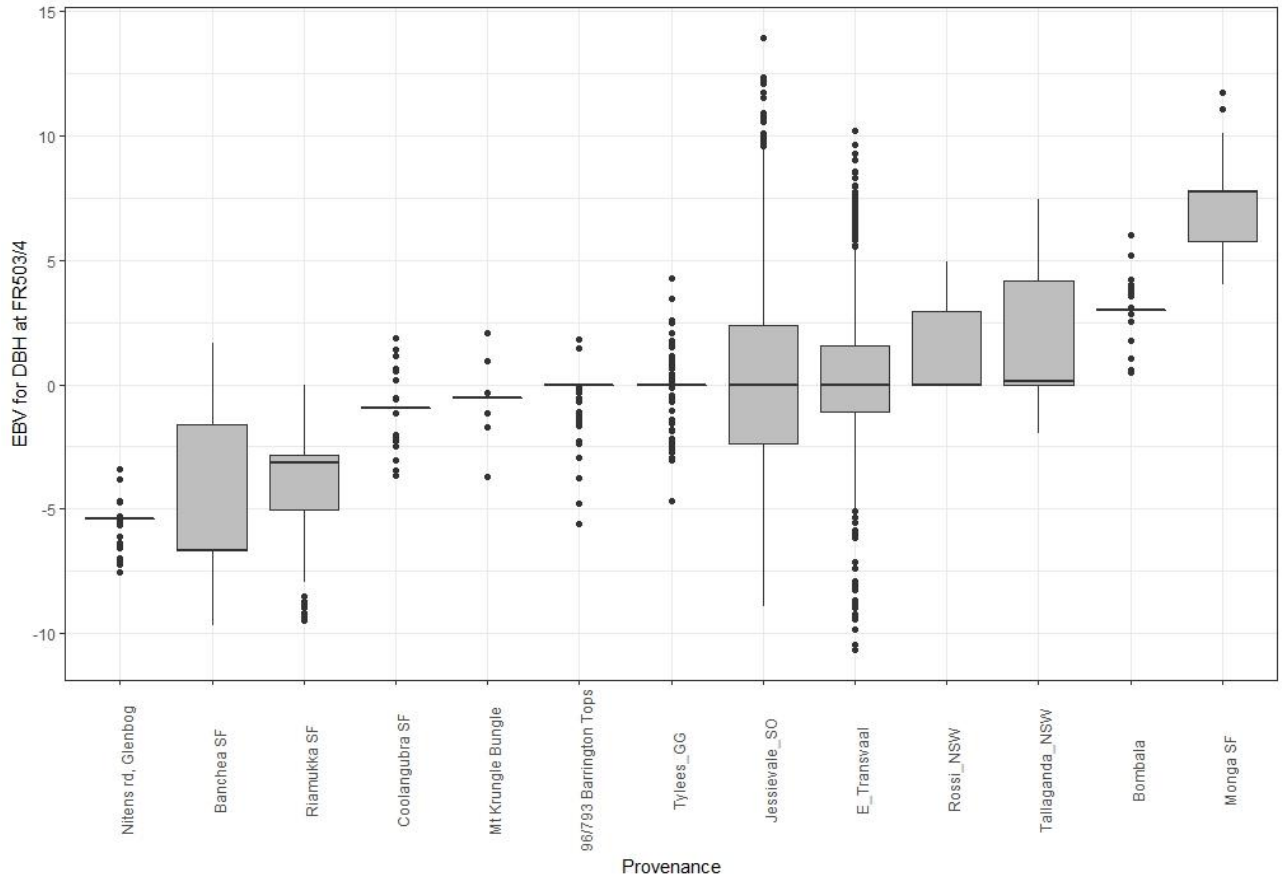

Figure 12: Ranking of seed sources according to breeding values for DBH at FR503/4

CONCLUSION

It was possible to estimate narrow-sense heritability for each investigated trait at each site. However, sites FR503/3 and FR503/4 showed relatively smaller estimates compared to sites FR503/1 and FR503/2. These poor results might be related to the inferior growing conditions at FR503/3 and FR503/4 sites. The implementation of spatial analysis improved the model fit only for FR503/1 and FR503/2 while no or rather negative impact was observed for FR503/3 and FR503/4. We assume, that the terrain complexity and overall site's inferiority was the major factor contributing to such an outcome.

The genetic correlation study revealed two major clusters within the analysed characteristics. The first cluster is generated by acoustic velocity and DBH at FR503/1, but the second cluster is produced only by stem quality characteristics. At FR503/2, a similar trend was seen. This favourable correlation structure enables the simultaneous selection of productive individuals with high wood stiffness (AVEL) and a favourable branching pattern (BRA). Due to the weak but positive genetic connections between STR and MAL and DBH, their inclusion in the selection process will be restricted. Interestingly, the sites FR503/3 and FR503/4 produced positive genetic correlations between DBH and BRA, most likely due to the overall low amount of heritability attained in these sites.

Genotype by environment interaction (GxE) analysis showed a substantial positive genetic correlation between FR503/1 and FR503/2 across most of the studied traits. However, these two sites exhibited an unfavourable genetic correlation with FR503/3, which is geographically adjacent to FR503/1. Due to FR503/3's poor site quality and lack of genetic connectedness with FR503/1 and FR503/2, we presume the negative genetic correlations should be interpreted with caution. There are no open-pollinated families in common between these sites and there are only 5 provenances represented across all investigated sites but with different OP families. FR503/4's inferiority and lack of genetic connection prevented us from quantifying its genetic correlations with other sites. We recommend implementing multi-generational evaluation to increase the genetic connectivity of FR503/3 and FR503/4 with the rest of the breeding programme to improve the quantification of GxE.

Families from the selections at Marlborough and Tikitere performed best in DBH at FR503/1 and FR503/2, whereas material from provenances Bombala and Tallaganda (NSW) performed best at sites FR503/3 and FR503/4. The provenances Barrington Tops, Yetholme, Nitens Road (Glenbog), and Riamukka State Forest have the lowest DBH. As BRA revealed a substantial genetic link with DBH, Marlborough and Tikitere performed better at FR503/1 and FR503/2. Poor provenances were the same (Barrington Tops). Conversely, in FR503/3 and FR503/4, material from Nitens Road (Glenbog) and Riamukka State Forest provenances, which fared poorly at these locations, performed better. In stem quality attributes, Tikitere, E. Transvaal, Barrington Tops, and Marlborough at FR503/1 and FR503/2, and Monga State Forest and Riamukka State Forest at FR503/3 and FR503/4, performed best. Nevertheless, Oakura, Rotorua, Oberon, and Marlborough provenances at FR503/1 and FR503/2, and Coolangubra State Forest and Bombala provenances at FR503/3 and FR503/4 performed poorly.

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APPENDICES

Appendix 1: List of individual breeding values, their standard errors, and accuracies.
Appendix 2: Genetic composition of field experiments

Please contact Marco Lausberg for the datasets if required.