Theme: Diverse Species

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Cupressus lusitanica 2006 Progeny Trial Assessment and Selections

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Leadership in forest and environmental management, innovation and research

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EXECUTIVE SUMMARY

Trees from the 2006 *Cupressus lusitanica* progeny trial at Welcome Bay (near Tauranga) were assessed for growth and stem form at age five years. A total of 2561 trees were measured across 104 families. The trial contains open pollinated material collected from the best individual from each family within the *C. lusitanica* breeding population.

There were considerable differences in estimated genetic merit between the best and worst families – 37%, 49%, 51%, 15% and 68% for DBH (diameter), STR (straightness), BR (branching), MAL (malformation) and CNK (canker) respectively.

Most traits were moderately heritable (heritability ranged from 0.25 to 0.37), indicating that genetic improvement can be made for these traits by selecting the most superior individuals based on their estimated breeding values. Malformation was not heritable (h^2 0.05).

Trees with severe malformations and canker were culled before applying a selection index combining diameter, stem straightness and branching.

The negative correlation between STR and BR with DBH (-0.33 and -0.53 respectively) made it difficult to improve all three traits simultaneously.

The best individual within each of the 104 families was selected to maintain a wide genetic base and reduce inbreeding due to the small breeding population. These selections will form the next generation of the breeding cycle.

Selection of the next generation resulted in a predicted genetic gain of 7% for DBH, 5% for STR and 2% for BR relative to the population mean. Wood properties and durability will be assessed on selected trees once heartwood develops around age 10 to determine the best trees for inclusion in future seed orchards.

The other trial in this series planted at Manawahe will be measured in the winter of 2012.
Top selections from the Welcome Bay and Manawahe trial series along with selections from the *C. lusitanica* clonal trial will be grafted into a new breeding orchard. The rankings from these trials will be used to rogue the present Proseed *C. lusitanica* seed orchard to increase genetic gain available to growers.

A list of breeding values for material assessed at Welcome Bay is available on the FFR website.

INTRODUCTION

The main cypress species grown in New Zealand are *Cupressus lusitanica* and *Cupressus macrocarpa*. Cypress canker caused by *Seiridium spp.*fungi severely attacks *C. macrocarpa* in the North Island, making *C. lusitanica* the only viable species in the region. Plantings of *C. lusitanica* in New Zealand are thought to originate largely from a small genetic base from Central America brought to Portugal around 400 years ago. *C. lusitanica* produces desirable timber with even wood properties throughout the stem making the wood very stable.

In 1984 a breeding programme for *C. lusitanica* was established with two progeny trials, planted at Gwavas and Whakarewarewa Forest (Figure 1). Trials contained the progeny of 80 trees selected from New Zealand plantings, 18 from Kenyan and 6 from Columbian seed orchards[1]. The best tree from each family was selected to form the next generation of the breeding population which was planted out at Kaingaroa and New Plymouth in 1998. The idea behind selecting the best individual in each family was to maintain the genetic base of the relatively small breeding population.

1984   **Gwavas + Whakarewarewa**
             104 Families: 80 New Zealand, 6
             Columbian, 18 Kenya

Best tree from
each family
brought forward

54 families
replanted

1998   **Kaingaroa + New Plymouth**
             Both trials suffered high mortality
             and poor growth.

50 selections
made from best
part of trial

2006   **Manawahe + Welcome Bay**

2012   Next generation selected
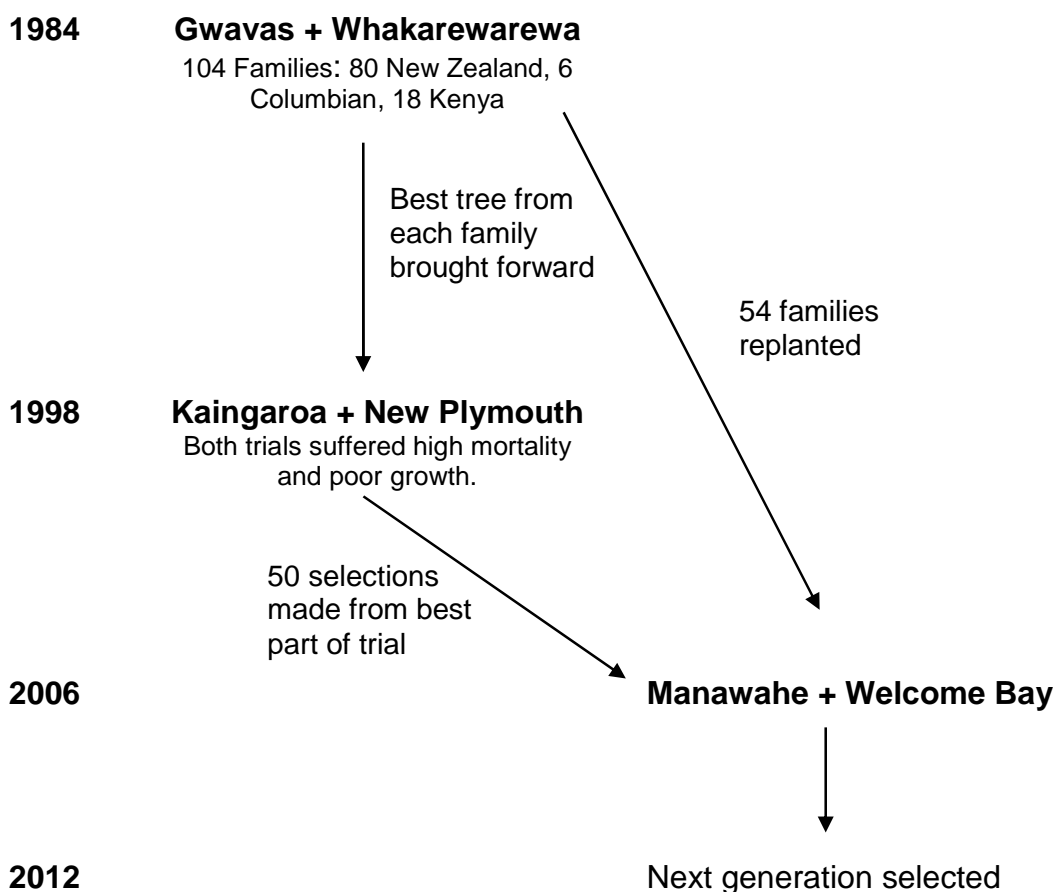
Figure 1. Flow diagram of the *C. lusitanica* breeding programme

Spray drift and nutrient deficiency resulted in poor establishment and growth at Kaingaroa. The trial at New Plymouth got off to a better start, but heavy rain caused severe flooding destroying a large section of the trial. It was decided to replant these trials. Selections from 50 of the families were made based on assessment of a third of the trial at New Plymouth that was unaffected by the flooding. These 50 second-generation selections along with the remaining 54 first-generation selections from the initial 1984 trial were replanted at two sites (Manawahe – Eastern Bay of Plenty and Welcome Bay – near Tauranga**)** in 2006[2]. Both these trials established well. Growth at Welcome Bay was relatively uniform across the site, whilst growth at Manawahe was patchier. For this reason this analysis will concentrate on the trees growing at Welcome Bay.

METHODS

2006 Progeny Trials

Both trials are planted in the Bay of Plenty region in the North Island (Figure 2). The trials are set out as a single tree plot incomplete block design with four blocks per replicate. Each trial contains 104 open pollinated families. Selections came from the best individual tree in each family from the initial breeding population. Welcome Bay has 30 replicates and Manawahe Road 28 replicates.

A number of control seedlots were also planted throughout each trial, but unfortunately the identities of the control seedlots were lost and could not be used in the analysis. The only one that could be identified with any certainty is the 2005/781 collection from the Amberley seed orchard. The Welcome Bay trial is planted on a former radiata pine site. The site is north to north-west facing and has a slope of 20 to 25 degrees. The Manawahe Road trial is planted on a former pasture site. The site is south facing with a slope of 20 to 25 degrees.

The Welcome Bay trial was assessed in November 2011 for the traits listed in Table 1. The trial was recently selectively pruned. A note was made of whether trees were pruned or unpruned. The Manawahe trial is growing more slowly than the Welcome Bay trial and will be assessed in the winter of 2012.

Table 1. List of traits assessed and trait description

Trait	Description
DBH	Diameter at breast height (mm)
CNK	Canker 1-4 scale (1 = none, 4 = severe)
STR	Straightness 1-8 scale (1 = bad, 8 = perfect)
BR	Branching 1-5 scale (1 = heavy , 5 = fine)
MAL	Malformation 1-9 scale (1 = multiple forking, 9 = perfect)

Figure 2. The two trial locations, Welcome Bay and Manawahe Road, both located in the Bay of Plenty.

Statistical Analysis

Cypress can be affected greatly by micro site changes, and for this reason (where significant) data were analysed spatially to remove as much of the micro site variation as possible. Genetic parameters and breeding values were estimated for traits using the following mixed model which was solved using standard genetic prediction models in the software package ASReml-3.

$$y = Xb + Z_1a + Z_2r + Z_3r.b + e$$

where: **y** is the vector of individual-tree observations on a trait, **b** is a vector of fixed effects (i.e., mean), **a** is a vector of random additive genetic effects of individual genotypes, **r** is a vector of random replicate effects, **r.b** is the random interaction between replicate and block, and **e** is a vector of random residual effects. **X**, Z_1, Z_2 and Z_3 are known incidence matrices relating the observations in **y** to effects in **b**, **a**, **r** and **r.b** respectively. Row and column were added to the design, placing each tree in a grid enabling trees to be analysed spatially

Selection of the Next Generation

Malformation and canker scores were considered as culling traits. Any tree with a canker score of two or worse and a malformation score up to four was removed from potential selections. The majority of individuals exhibited no canker or malformation (Figure 4). From the remaining trees, a selection index (*I*) was constructed for DBH, STR and BR to select the best trees within each family for these three traits simultaneously. Genetic parameters for the selection index were calculated from the culled dataset. The index was constructed as follows:

$$I = b_{DBH}X_{DBH} + b_{STR}X_{STR} + b_{BR}X_{BR}$$

where b_{DBH} is the weight given to the breeding values for X_{DBH}, and so forth.
The solution for **b** that theoretically maximises desired genetic gain for all three traits is:

$$b = P^{-1}Ga$$

where
　　　b is the column vector of index weights for DBH, STR and BR;
　　　P is the phenotypic variance-covariance matrix;
　　　G is the genotypic variance-covariance matrix;
　　　a is the column vector of technical weights.

In the absence of economic weights for cypress, technical weightings were altered to give the best predicted response for selection of the three traits. Based on the selection index, the best individual from each family was selected to form the next generation.

RESULTS

Of the 3120 trees planted (30 progeny from 104 families), 559 were too small to measure or dead, leaving 2561 trees. All families were represented by measurements from at least 20 trees. Stem diameter was normally distributed (Figure 3). Trees less than 4.5 cm diameter were not assessed as these were deemed too small to measure, and the largest trees were 22 cm in diameter. The distribution of scores for canker, malformation, stem straightness and branching across all progeny are shown in Figure 4. The majority of trees were free from stem canker (score of 1) and had no malformation (score of 9). Stem straightness and branching scores were slightly skewed to the right, likely as a result of the assessed material being second generation, scores thus clustering towards the better end of the spectrum.
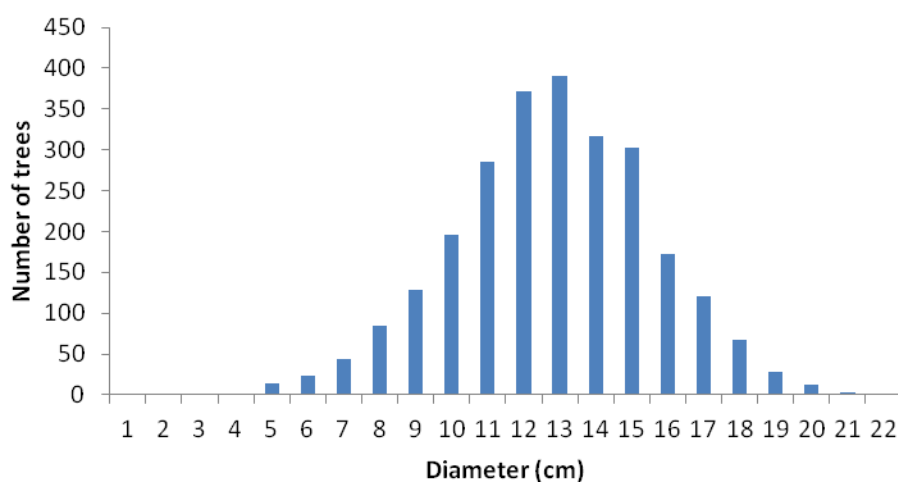
Figure 3. Distribution of DBH based on all progeny, less control seedlots.
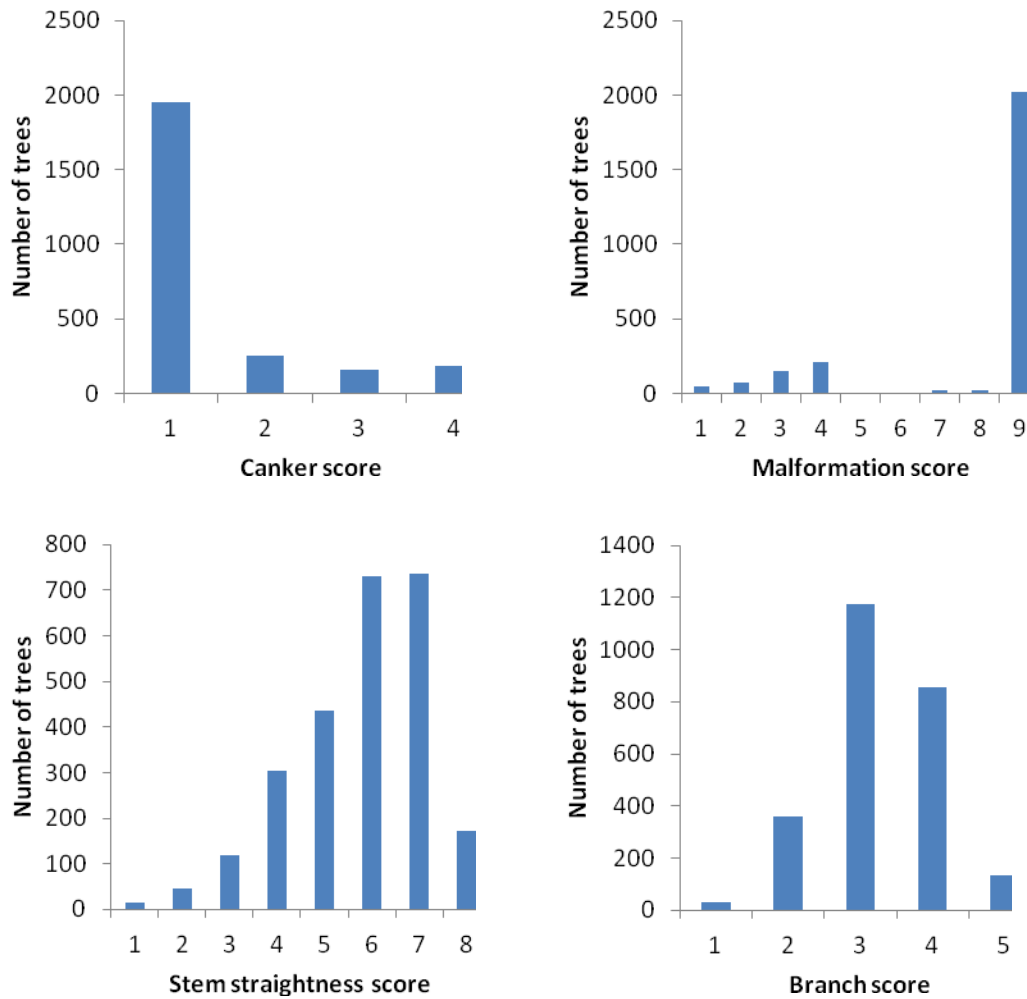
Figure 4. Distribution of score traits based on all progeny, less control seedlots. For canker score, a lower value (1) is desirable, for the other three traits, a higher score is ideal.

Genetic Parameters

A table of family breeding values is presented in Appendix 1. Breeding values are an estimate of the genetic merit for each tree for each trait. Selection decisions to choose the genetically most superior trees are based on these breeding values. The breeding values were added to the corrected population mean for each trait (Table 3). There were appreciable differences surrounding family breeding values for all traits assessed (Figure 5). The best families were 50% better for STR and BR than the worst families, and 37%, 15%, 68% better for DBH, MAL and CNK respectively. Due to the limited size of the base population (104 families), culling of the poorer families would reduce genetic variability and increase the risk of inbreeding. For this reason it was decided to select the best individual from each family to form the next generation.

Genetic parameters for each trait were estimated (Table 2). Heritabilies for DBH, STR and BR were estimated using spatial analysis which significantly improved their accuracy (Appendix 3). All traits with the exception of malformation exhibited moderate heritabilities. The low heritability (0.05) for malformation indicates little potential gain, with the majority of variation being environmental. Stem straightness, branching and malformation were all positively correlated, but all were negatively correlated with stem diameter. Canker was not strongly correlated with any other trait measured.
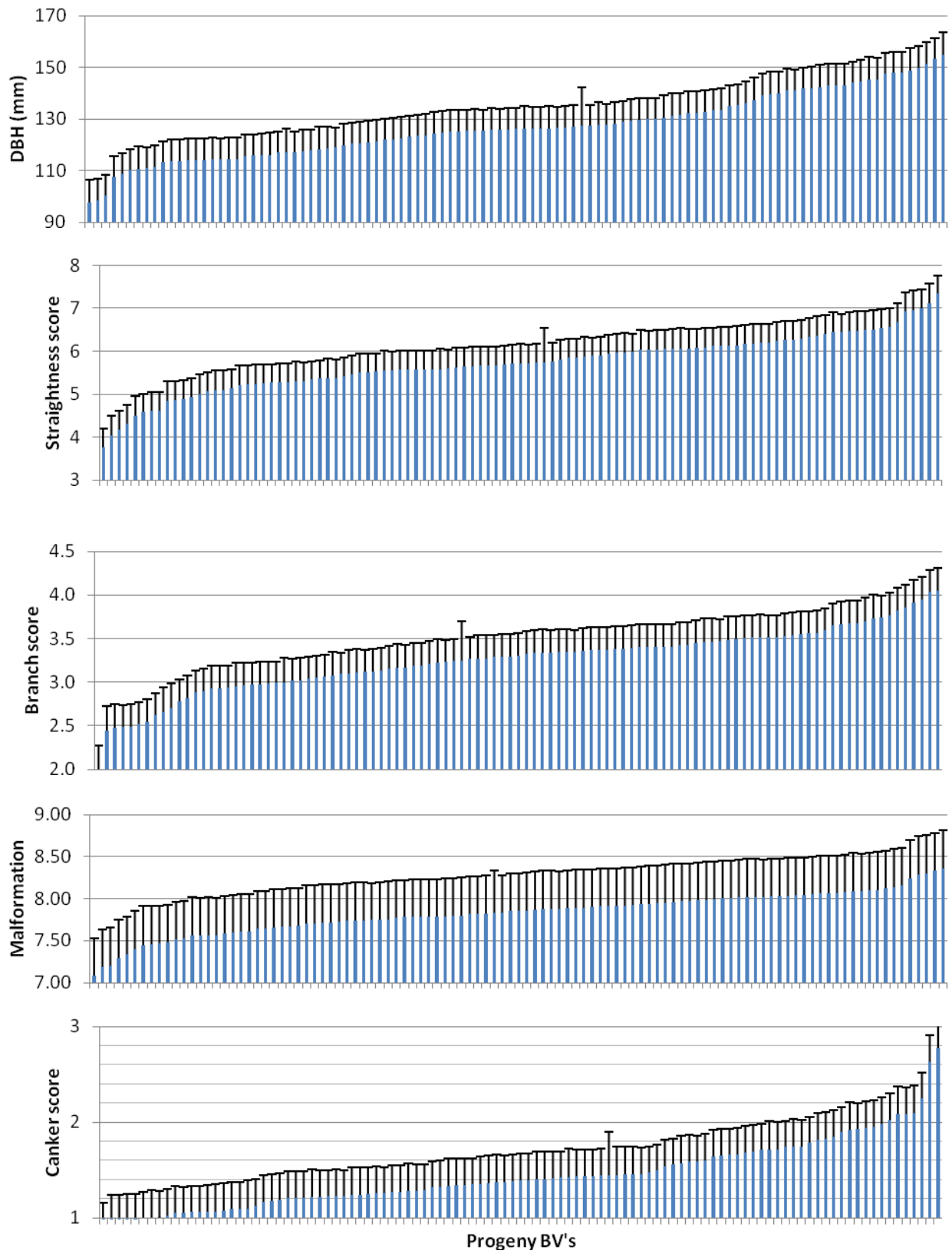
Figure 5. Distribution of family breeding values with standard errors for the five traits assessed.

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Selection of the Next Generation

Trees with a canker score of three and above and a malformation score of four or less were culled, resulting in the elimination of 757 trees. A selection index combining DBH, STR and BR was applied to the remaining 1804 trees. The negative correlation between STR and BR with DBH limited achievable gain for all three traits. As STR and BR were already quite good across the trial index, weightings favoured improvement in DBH whilst achieving a modest gain in both STR and BR. Selection of the best individual within each family using the selection index resulted in a 7% gain in DBH, 5% in STR and 2% for BR, relative to the population mean. A list of all selections and their index ranking position are in Appendix 2.

Table 2. Genetic covariance-variance-correlation matrix between pairs of traits assessed (lower left, diagonal and upper right respectively). The mean and heritability for each trait are at the bottom of the table.

	DBH	STR	BR	MAL	CNK
DBH	204.90	-0.33	-0.53	-0.55	0.24
STR	-3.71	0.64	0.78	0.57	-0.10
BR	-3.38	0.28	0.20	0.59	-0.18
MAL	-3.95	0.23	0.13	0.26	-0.34
CNK	1.53	-0.04	-0.04	-0.08	0.20
Mean	127.20	5.74	3.25	7.83	1.45
SE	2.30	0.08	0.04	0.10	0.03
h^2	0.37	0.37	0.32	0.05	0.25

DISCUSSION

There are currently 104 families within the *C. lusitanica* breeding programme. In the absence of infusion of new genetic material, the breeding population was turned over by selecting the best individual from each family to maintain a broad genetic base and reduce inbreeding. There were large differences between the best and the worst families for each trait. Removal of these worst families would improve gains in the short term, but without the addition of new material would reduce the effective population size considerably. With the breeding population now being in its second/third generation, the provenance effects observed in the first generation will be diluted due to crossing between provenances.

Control Seedlots

Seedlots in current commercial use were obtained to form a small genetic gain trial in addition to the progeny trial. The original concept was to have the seed orchard seedlot 2005/761 represented in every block, with other seedlots also present in every fourth block.

Unfortunately, the vital piece of paper relating seedlot codes to seedlot numbers was lost. If we had a means of DNA fingerprinting we could resolve this as seedlots from Gwavas and the CP seedlot had known mothers, but the identity of the seed orchard seedlot is the only one that is true to label. This seedlot has outstanding growth as might be expected from a seedlot with both parents selected, while all other seedlots had a less select pollen cloud.

Spatial Analysis

The data were analysed conventionally using replicates to identify environmental differences, and spatially where values were adjusted by correlations with neighbours. The spatial analysis improved heritability about 10% for diameter, straightness and branching, but made no difference for malformation and canker. This was a similar finding to that of other studies[3] and confirms that the fussy nature of cypresses requires spatial analysis to adjust for microsite differences.

Malformations

Malformation is not considered as a continuous trait with different scores representing different malformations, although ordered from most severe through to least severe. Scores of one and two represent forking and three and four shifts in the leader. Both these types of malformation will severely compromise the amount of utilisable timber that can be extracted from a tree. Malformation as a trait was not heritable, suggesting that malformations are mainly caused by environmental factors. The diverse nature of this trait could mask genetic effects. For this reason any badly malformed trees were not selected.

Moving Forward

Cupressus lusitanica is one of the two core species of the cypress development plan for FFR[4]. This species will continue to be improved through multiple generations, using a combination of control pollination and open-pollination. Control pollination will be undertaken in the new breeding orchard, to be established on land provided by Proseed.

The results from this analysis will be used directly to advance the breeding and deployment programmes:

- The Manawahe trial will be measured in the winter of 2012.

- The top selections from this trial series (Manawahe and Welcome Bay) and the *C. lusitanica* clonal trial[3] will be grafted to the new breeding orchard. Grafting will commence in winter 2012 with selections from Welcome Bay.
- Once established, the *C. lusitanica* grafts will be used for :
  - o Establishment of the cypress breeding orchard;
  - o Control pollination to create new hybrid germplasm.

The rankings from the trials will be used to rogue the Proseed *C. lusitanica* seed orchard to increase the genetic gain available to growers. This will be done in consultation with Proseed.

ACKNOWLEDGEMENTS

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2   Stovold, G. Fleet, K. (2007) 2006 establishment report for C. lusitanica breeding population trial on two sites. Output 41081

3   Dungey, H., Russell, J, Low, C., Stovold, G., Fleet, K. (2009) Results from *Cupressus lusitanica* clonal test across three sites in New Zealand. FFR report number FFR-DS011

4   Dungey, H., Russell, J., Low, C., Stovold, G. (2010) Updated development plan for cypresses in New Zealand. FFR report number FFR- DS031

APPENDICES

Appendix 1 – Family breeding values followed by their standard errors

Families and controls are ranked according to DBH and STR. Only the collection from the Amberley seed orchard (2005/781) is known: the other controls are labelled 302-305 as their exact identity cannot be confirmed.

Grandma	Mother	DBH	SE	STR	SE	BR	SE	MAL	SE	CNK	SE	Rank
893.404	2004.243	141.76	8.05	7.33	0.43	3.74	0.25	8.09	0.44	1.06	0.27	2
	893.401	145.28	8.27	6.67	0.44	3.38	0.26	7.48	0.45	1.09	0.28	4
	897.752	144.53	8.28	6.39	0.44	3.30	0.26	7.87	0.45	2.63	0.28	5
890.136	2004.254	141.04	8.39	6.53	0.45	3.94	0.26	8.10	0.45	1.36	0.28	6
	893.429	153.12	8.27	5.45	0.44	2.97	0.26	7.74	0.45	1.74	0.28	8
	897.773	130.00	8.05	7.00	0.43	3.51	0.25	7.90	0.44	1.26	0.27	9
	893.435	139.99	8.39	6.26	0.45	3.13	0.26	7.72	0.45	1.21	0.28	10
893.430	2004.235	141.99	8.39	6.08	0.45	2.96	0.26	7.59	0.45	1.21	0.28	11
	893.418	147.97	7.96	5.58	0.42	3.09	0.25	7.78	0.44	1.55	0.27	12
	897.758	139.76	8.63	6.13	0.46	3.12	0.27	7.94	0.45	1.24	0.29	13
	893.410	126.40	8.63	6.94	0.46	3.39	0.27	7.86	0.45	1.41	0.29	14
	897.731	135.38	8.06	6.27	0.43	3.65	0.25	7.83	0.45	1.40	0.27	15
	897.766	143.09	8.18	5.71	0.43	3.02	0.25	7.88	0.45	1.95	0.27	16
893.414	2004.207	125.84	8.07	6.94	0.43	3.56	0.25	8.07	0.44	1.45	0.27	17
	897.762	147.95	7.95	5.34	0.42	2.62	0.25	7.61	0.44	1.42	0.27	18
	897.733	148.89	8.51	5.24	0.45	2.93	0.26	7.40	0.45	1.38	0.28	19
	897.760	147.54	8.17	5.31	0.43	2.78	0.25	7.91	0.45	1.66	0.27	20
	897.734	143.18	8.28	5.57	0.44	3.41	0.26	7.79	0.45	1.68	0.28	21
	897.710	151.46	8.17	4.90	0.43	2.49	0.25	7.78	0.45	1.65	0.27	22
	897.728	129.19	8.51	6.48	0.45	2.96	0.26	8.01	0.45	1.02	0.28	23
	897.739	136.19	8.29	5.90	0.44	3.43	0.26	7.85	0.45	2.08	0.28	24
	893.412	141.12	7.87	5.53	0.42	2.99	0.24	8.00	0.44	1.89	0.27	25
893.413	2004.209	118.64	8.39	7.12	0.45	4.05	0.26	8.00	0.45	1.36	0.28	26
	897.776	130.05	8.06	6.29	0.43	3.06	0.25	8.03	0.44	1.49	0.27	27
	897.767	154.82	8.90	4.49	0.47	1.99	0.28	7.45	0.46	1.45	0.30	28
	897.723	131.73	8.39	6.07	0.45	3.37	0.26	7.67	0.45	1.81	0.28	29
	897.708	125.68	8.39	6.47	0.45	3.86	0.26	8.09	0.45	1.00	0.28	30
	890.126	132.64	8.52	5.93	0.45	3.21	0.26	7.67	0.45	1.43	0.28	31
	890.174	125.06	8.52	6.44	0.45	3.67	0.26	7.71	0.45	1.33	0.28	32
897.768	2004.229	124.32	8.27	6.48	0.44	3.40	0.26	7.78	0.45	1.64	0.28	33
	897.725	144.01	8.28	5.06	0.44	2.52	0.26	8.13	0.45	1.09	0.28	34
	893.422	128.85	7.96	6.13	0.42	3.24	0.25	8.33	0.44	1.29	0.27	35
893.415	2004.245	142.84	8.53	5.09	0.45	3.53	0.26	8.02	0.45	1.22	0.28	36
	897.715	133.49	8.17	5.73	0.43	3.27	0.25	8.00	0.45	0.88	0.27	38
	893.425	145.25	8.76	4.84	0.47	2.48	0.27	7.29	0.46	2.09	0.29	39
	897.756	126.22	8.28	6.20	0.44	3.19	0.26	7.74	0.45	1.28	0.28	40
	897.720	135.02	8.06	5.56	0.43	2.97	0.25	7.65	0.44	1.59	0.27	41
	897.736	137.41	8.64	5.36	0.46	3.27	0.27	7.82	0.45	1.45	0.29	42
897.747	2004.241	125.39	8.17	6.20	0.43	3.37	0.25	8.04	0.45	1.13	0.27	43
897.732	2004.210	125.43	8.40	6.18	0.45	3.08	0.26	7.75	0.45	1.05	0.28	44
	897.709	133.52	8.17	5.60	0.43	3.67	0.25	8.04	0.45	1.66	0.27	45
	897.755	123.04	8.26	6.33	0.44	3.83	0.26	8.30	0.45	1.53	0.28	46
	897.777	126.91	8.39	6.04	0.45	3.51	0.26	7.78	0.45	1.20	0.28	47

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	897.706	130.27	8.76	5.80	0.47	3.17	0.27	8.04	0.46	1.37	0.29	48
897.704	2004.242	131.32	8.51	5.71	0.45	3.37	0.26	8.14	0.45	0.96	0.28	49
	890.127	125.58	8.06	6.12	0.43	3.92	0.25	8.06	0.44	2.25	0.27	50
893.437	2004.250	126.66	8.17	5.97	0.43	3.41	0.25	7.66	0.45	1.71	0.27	51
	897.763	149.89	8.17	4.31	DS043	2.55	0.25	7.97	0.45	1.85	0.27	52
	897.741	124.69	8.39	6.08	0.45	3.36	0.26	7.51	0.45	1.26	0.28	53
897.722	2004.203	126.20	8.64	5.98	0.46	3.46	0.27	7.91	0.45	1.24	0.29	54
897.714	2004.216	125.11	8.51	6.03	0.45	3.10	0.26	7.70	0.45	1.60	0.28	55
897.716	2004.249	127.49	7.97	5.77	0.42	3.52	0.25	7.75	0.44	1.05	0.27	56
	893.433	127.20	14.93	5.74	0.79	3.25	0.45	7.83	0.51	1.45	0.45	57
897.729	2004.227	122.18	8.26	6.05	0.44	3.68	0.26	7.93	0.45	1.39	0.28	58
	897.701	116.11	8.63	6.48	0.46	3.48	0.27	7.95	0.45	1.40	0.29	59
	897.705	120.85	8.39	6.03	0.45	3.54	0.26	7.89	0.45	2.02	0.28	60
	893.408	126.24	8.28	5.56	0.44	3.04	0.26	7.08	0.45	1.98	0.28	61
	897.757	132.31	8.41	5.10	0.45	2.89	0.26	7.19	0.45	1.82	0.28	62
	897.727	113.25	7.96	6.44	0.42	2.88	0.25	8.03	0.44	1.93	0.27	63
893.434	2004.231	118.42	8.76	6.06	0.47	3.46	0.27	8.02	0.46	1.43	0.29	64
	893.421	111.10	8.06	6.56	0.43	3.59	0.25	7.98	0.45	1.07	0.27	65
	890.152	129.70	8.17	5.23	0.43	3.41	0.25	7.58	0.45	1.22	0.27	66
	897.703	120.39	8.07	5.89	0.43	3.13	0.25	7.73	0.44	1.35	0.27	67
890.133	2004.246	120.57	8.52	5.84	0.45	3.77	0.26	7.82	0.45	1.74	0.28	68
	897.772	122.45	8.28	5.68	0.44	3.17	0.26	7.99	0.45	1.59	0.28	69
	897.743	128.04	8.40	5.28	0.45	2.93	0.26	7.46	0.45	1.92	0.28	70
890.151	2004.255	116.02	8.28	6.13	0.44	3.45	0.26	7.93	0.45	1.94	0.28	71
897.764	2004.226	125.97	8.27	5.36	0.44	2.94	0.26	7.94	0.45	1.34	0.28	72
	897.775	118.81	7.96	5.86	0.42	3.35	0.25	8.02	0.44	1.79	0.27	73
	897.737	121.43	8.39	5.67	0.45	3.33	0.26	8.16	0.45	0.95	0.28	74
890.137	2004.221	114.02	8.27	6.18	0.44	3.51	0.26	8.24	0.45	1.19	0.28	75
893.423	2004.257	123.43	8.28	5.50	0.44	3.31	0.26	7.77	0.45	1.74	0.28	76
893.409	2004.202	126.61	8.06	5.27	0.43	3.23	0.25	7.57	0.44	1.06	0.27	77
890.123	2004.223	111.22	8.50	6.36	0.45	3.70	0.26	8.29	0.45	1.28	0.28	78
	897.753	117.30	8.51	5.88	0.45	3.23	0.26	7.75	0.45	1.22	0.28	79
	897.765	142.24	8.91	4.03	0.47	2.45	0.28	7.66	0.46	2.08	0.30	80
897.735	2004.237	126.14	8.16	5.14	0.43	3.05	0.25	7.34	0.45	1.32	0.27	81
	897.761	127.58	8.89	4.99	0.47	2.71	0.28	7.19	0.46	1.00	0.30	82
	893.419	132.45	8.18	4.61	0.43	3.12	0.25	7.57	0.45	1.38	0.27	83
	893.432	108.60	8.30	6.23	0.44	3.56	0.26	7.97	0.45	1.25	0.28	84
	897.749	115.95	8.17	5.68	0.43	3.52	0.25	8.10	0.45	0.97	0.27	85
	897.750	117.07	9.04	5.58	0.48	2.66	0.28	7.89	0.46	1.71	0.30	86
	897.754	114.40	8.28	5.70	0.44	3.35	0.26	8.06	0.45	1.43	0.28	87
	897.707	115.45	8.63	5.61	0.46	3.74	0.27	7.79	0.45	1.45	0.29	88
	893.436	117.81	8.17	5.42	0.43	3.34	0.25	7.53	0.45	2.77	0.27	89
	897.769	113.98	8.51	5.64	0.45	3.19	0.26	7.85	0.45	1.69	0.28	90
897.712	2004.238	113.69	8.52	5.64	0.45	3.42	0.26	7.74	0.45	1.07	0.28	91
	897.740	114.59	8.19	5.57	0.43	3.34	0.25	7.64	0.45	1.27	0.27	92
	893.406	119.68	8.63	5.20	0.46	3.27	0.27	7.72	0.45	1.08	0.29	93
893.405	2004.258	114.43	8.39	5.57	0.45	3.35	0.26	7.61	0.45	1.45	0.28	94
	897.742	127.70	7.97	4.59	0.42	2.98	0.25	7.82	0.44	1.48	0.27	95
	897.711	123.75	8.29	4.86	0.44	3.02	0.26	7.78	0.45	1.44	0.28	96
	893.427	139.07	8.51	3.75	0.45	2.82	0.26	7.91	0.45	1.17	0.28	97
893.417	2004.228	107.40	8.08	5.98	0.43	4.03	0.25	7.88	0.44	1.34	0.27	99

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	893.431	121.92	8.16	4.93	0.43	3.47	0.25	7.47	0.45	1.22	0.27	100
	897.713	113.95	8.39	5.50	0.45	3.55	0.26	8.05	0.45	1.16	0.28	101
	893.433	117.09	8.17	5.27	0.43	3.16	0.25	8.36	0.45	1.42	0.27	102
890.141	2004.230	110.09	8.27	5.66	0.44	3.40	0.26	7.89	0.45	0.99	0.28	103
893.433	2004.232	110.50	8.90	5.54	0.47	3.00	0.28	7.96	0.46	1.56	0.30	104
	893.411	113.65	8.40	5.24	0.45	3.50	0.26	7.80	0.45	0.96	0.28	105
893.426	2004.218	97.48	8.77	6.05	0.47	3.34	0.27	7.56	0.46	1.10	0.29	106
	897.746	117.05	8.18	4.61	0.43	2.48	0.25	7.56	0.45	1.32	0.27	107
	897.718	100.16	8.18	5.36	0.43	3.39	0.25	8.08	0.45	1.23	0.27	108
	897.770	114.42	8.17	4.18	0.43	3.29	0.25	7.88	0.45	1.27	0.27	109
897.721	2004.256	98.34	8.40	5.31	0.45	3.30	0.26	7.91	0.45	1.72	0.28	110
	2005/781	163.19	6.30	5.72	0.28	3.07	0.14	6.95	0.51	2.02	0.22	3
	302	144.81	7.91	6.24	0.33	3.18	0.15	7.62	0.62	2.13	0.28	7
	303	114.70	11.09	5.48	0.43	3.28	0.17	7.14	0.79	1.37	0.38	98
	304	130.78	9.98	5.95	0.40	3.20	0.16	7.75	0.73	1.24	0.34	37
	305	158.93	9.99	6.80	0.40	3.36	0.16	8.90	0.73	0.94	0.34	1
	mu	127.20	2.30	5.74	0.08	3.25	0.04	7.83	0.10	1.45	0.03	

Appendix 2 – Best individual from each family along with index ranking

Note CNK and MAL are not breeding values and actual tree scores.

Grandma	Mother	DBH$_{BV}$	SE	STR$_{BV}$	SE	BR$_{BV}$	SE	CNK	MAL	Tree	Blk	Rank
	897.734	146.88	11.42	6.36	0.60	3.68	0.35	1	9	15	95	1
893.404	2004.243	142.29	11.37	6.92	0.60	3.62	0.35	1	9	16	108	2
	897.731	151.45	11.38	6.25	0.60	3.33	0.35	2	9	16	3	3
890.136	2004.254	147.17	11.40	6.44	0.61	3.48	0.35	1	9	17	101	4
	893.429	156.76	11.40	5.75	0.61	3.09	0.35	1	9	9	93	6
	893.401	142.67	11.39	6.72	0.60	3.49	0.35	1	9	20	2	8
	893.435	148.16	11.41	6.39	0.61	3.23	0.35	1	9	11	17	9
	897.766	154.02	11.37	5.50	0.60	3.29	0.35	1	9	20	74	14
893.413	2004.209	139.00	11.42	6.94	0.61	3.53	0.35	1	9	24	7	15
	897.752	146.79	11.40	6.45	0.61	3.22	0.35	1	9	16	24	17
	893.418	145.41	11.38	6.26	0.60	3.36	0.35	1	9	6	112	21
	897.708	141.15	11.40	6.26	0.61	3.62	0.35	1	9	22	72	25
	897.733	157.70	11.42	5.54	0.61	2.78	0.35	1	7	5	79	30
893.414	2004.207	138.30	11.37	6.57	0.60	3.57	0.35	1	9	20	23	31
	890.126	144.87	11.44	6.39	0.61	3.19	0.35	2	9	7	6	32
	897.709	143.76	11.40	6.27	0.61	3.34	0.35	1	9	7	60	33
	897.758	147.24	11.43	6.22	0.61	3.11	0.35	1	9	11	61	34
893.430	2004.235	141.19	11.42	6.49	0.61	3.33	0.35	1	9	8	97	41
	893.410	137.44	11.44	7.02	0.61	3.25	0.35	1	9	14	10	46
	890.174	140.83	11.43	6.28	0.61	3.35	0.35	1	9	10	115	54
	897.763	154.40	11.41	5.29	0.61	2.94	0.35	1	9	22	118	56
	890.127	131.71	11.37	6.39	0.60	3.85	0.35	1	9	23	75	64
	897.736	141.77	11.41	5.89	0.61	3.41	0.35	1	9	9	30	65
893.415	2004.245	137.67	11.41	5.67	0.61	3.82	0.35	1	9	20	67	67
	897.706	141.61	11.43	5.94	0.61	3.39	0.35	1	9	12	64	68
	893.412	142.59	11.37	6.30	0.60	3.07	0.35	1	9	7	37	73
	897.723	142.98	11.40	6.10	0.61	3.16	0.35	1	9	8	63	75
893.423	2004.257	138.86	11.41	6.02	0.61	3.48	0.35	1	9	8	23	79
	893.408	143.19	11.38	6.09	0.60	3.12	0.35	1	9	11	109	81
	897.755	135.50	11.38	6.49	0.60	3.42	0.35	1	9	9	105	84
897.704	2004.242	145.74	11.42	5.94	0.61	2.99	0.35	1	9	15	45	86
890.133	2004.246	139.31	11.42	5.68	0.61	3.59	0.35	1	9	4	78	91
	897.773	138.39	11.37	6.39	0.60	3.25	0.35	1	9	6	43	94
890.151	2004.255	130.31	11.42	6.44	0.61	3.77	0.35	1	9	10	13	102
	897.737	144.41	11.38	5.69	0.60	3.18	0.35	1	9	11	43	103
	897.760	141.67	11.39	5.85	0.60	3.27	0.35	1	9	21	78	109
	897.776	136.91	11.37	6.68	0.60	3.12	0.35	1	9	12	59	114
	897.720	138.38	11.35	6.17	0.60	3.30	0.35	1	9	11	78	119
	897.762	140.99	11.36	5.91	0.60	3.20	0.35	1	9	13	14	138
	897.775	139.19	11.40	6.04	0.61	3.24	0.35	1	9	3	115	143
897.732	2004.210	134.43	11.40	6.46	0.61	3.33	0.35	1	9	12	106	147
897.747	2004.241	130.97	11.39	6.59	0.60	3.49	0.35	2	9	10	103	150
	897.728	132.36	11.44	6.65	0.61	3.35	0.35	1	9	7	93	151
	897.715	138.29	11.41	6.12	0.61	3.22	0.35	1	9	16	92	155
	890.152	143.68	11.38	5.42	0.60	3.23	0.35	1	9	4	71	158
	897.703	134.68	11.39	6.28	0.60	3.36	0.35	1	9	18	16	164

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	897.756	133.85	11.38	6.34	0.60	3.38	0.35	1	9	20	94	168
	897.707	132.72	11.45	6.00	0.61	3.64	0.35	1	9	25	66	174
	897.710	146.47	11.40	5.63	0.60	2.86	0.35	2	9	4	62	180
	897.725	152.77	11.39	5.23	0.60	2.63	0.35	1	7	23	100	184
	897.777	130.07	11.41	6.43	0.61	3.54	0.35	1	9	26	3	198
897.714	2004.216	129.10	11.45	6.40	0.61	3.61	0.35	1	9	7	100	202
	893.422	134.79	11.37	6.29	0.60	3.25	0.35	2	9	9	90	217
897.722	2004.203	133.27	11.44	5.95	0.61	3.54	0.35	1	9	17	35	224
	897.713	127.54	11.43	6.13	0.61	3.83	0.35	1	9	21	10	227
897.764	2004.226	141.07	11.39	5.82	0.60	3.03	0.35	1	9	8	71	235
	897.739	135.88	11.39	5.72	0.60	3.45	0.35	1	9	7	81	239
	897.772	138.93	11.39	5.91	0.61	3.12	0.35	1	9	11	5	245
897.716	2004.249	140.74	11.40	5.83	0.61	3.03	0.35	1	9	11	35	246
893.437	2004.250	127.26	11.38	6.35	0.60	3.69	0.35	1	9	23	71	248
897.768	2004.229	132.07	11.39	6.54	0.60	3.23	0.35	2	9	20	78	252
	897.701	131.22	11.43	6.54	0.61	3.27	0.35	1	9	13	108	258
	897.767	144.63	11.45	5.48	0.61	2.92	0.35	1	9	25	63	260
897.729	2004.227	139.24	11.40	5.41	0.61	3.35	0.35	1	9	12	22	262
	897.741	132.26	11.39	6.53	0.61	3.19	0.35	1	9	24	94	268
893.417	2004.228	126.51	11.39	6.28	0.60	3.74	0.35	1	9	22	53	269
893.434	2004.231	134.04	11.43	6.11	0.61	3.28	0.35	1	9	17	58	282
	897.757	139.99	11.41	5.82	0.61	3.02	0.35	1	9	16	100	284
	897.761	143.33	11.47	5.43	0.61	2.98	0.35	1	9	6	60	296
	897.742	138.60	11.37	5.36	0.60	3.32	0.35	1	9	15	100	328
897.735	2004.237	138.79	11.40	5.73	0.60	3.09	0.35	1	9	21	19	329
	897.705	130.25	11.41	6.47	0.61	3.27	0.35	1	9	25	38	336
	897.765	146.71	11.48	5.12	0.61	2.86	0.35	2	9	3	16	340
	893.425	148.01	11.43	4.88	0.61	2.90	0.35	1	9	11	105	350
	897.754	131.50	11.38	6.42	0.60	3.18	0.35	1	9	26	94	360
	897.753	129.55	11.47	6.19	0.61	3.45	0.35	1	9	3	26	369
	893.421	126.76	11.37	6.26	0.60	3.58	0.35	1	9	25	14	398
	897.711	137.49	11.44	5.80	0.61	3.06	0.35	2	9	14	21	407
890.123	2004.223	122.52	11.43	6.63	0.61	3.62	0.35	1	9	21	115	440
	893.419	128.51	11.39	5.88	0.60	3.61	0.35	1	9	27	85	455
	897.769	137.63	11.51	5.50	0.61	3.17	0.35	2	9	13	19	456
890.137	2004.221	125.80	11.42	6.40	0.61	3.50	0.35	1	9	25	16	458
	893.427	142.01	11.41	5.11	0.61	3.07	0.35	1	9	27	86	471
	897.749	125.45	11.41	6.31	0.61	3.55	0.35	1	9	14	13	478
	893.411	133.04	11.40	5.82	0.61	3.25	0.35	1	9	17	60	503
	897.740	126.84	11.41	6.12	0.61	3.49	0.35	1	9	7	88	528
	897.727	123.14	11.36	6.50	0.60	3.53	0.35	1	9	26	8	540
897.712	2004.238	130.18	11.40	6.01	0.61	3.29	0.35	1	9	10	50	556
893.409	2004.202	133.89	11.38	5.71	0.60	3.19	0.35	1	9	24	67	564
	893.431	130.84	11.37	5.47	0.60	3.54	0.35	1	9	12	83	577
893.433	2004.232	134.63	11.46	5.77	0.61	3.07	0.35	1	9	17	22	605
890.141	2004.230	130.56	11.39	5.94	0.61	3.24	0.35	1	9	19	88	626
	893.436	126.93	11.38	5.96	0.60	3.47	0.35	1	9	8	108	650
893.405	2004.258	121.79	11.40	6.12	0.60	3.73	0.35	2	9	8	54	670
	893.432	125.84	11.41	6.29	0.61	3.31	0.35	1	9	24	88	712
	893.406	128.03	11.42	5.72	0.61	3.44	0.35	1	9	17	107	755
	897.743	126.53	11.40	6.12	0.61	3.29	0.35	1	9	15	30	776

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	897.718	125.26	11.39	5.84	0.60	3.46	0.35	1	9	16	60	862
	897.770	130.29	11.41	5.50	0.60	3.25	0.35	2	9	1	11	906
	897.750	124.47	11.46	6.13	0.61	3.22	0.35	1	9	20	58	983
893.426	2004.218	116.95	11.47	6.08	0.61	3.42	0.35	1	9	3	8	1339
897.721	2004.256	115.31	11.41	5.89	0.61	3.42	0.35	1	9	15	48	1502
	897.746	122.68	11.42	5.46	0.61	2.95	0.35	1	9	27	17	1597

Appendix 3 – Variance components for all five traits estimated using spatial analysis where significant

| | DBH | | | | STR1 | | | | BRCH1 | | | |
| | Spatial | | Non-spatial | | Spatial | | Non-spatial | | Spatial | | Non-spatial | |
	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE
LogL	-10324.30		-10365.80		-2210.80		-2230.60		-770.53		-780.23	
Replicate	-0.30	7.60	39.75	16.85	0.054	0.027	0.082	0.030	0.00045	0.0041	0.0074	0.0049
Replicate.Block	18.70	10.22	63.10	13.69	-0.016	0.018	0.042	0.018	-0.00037	0.0062	0.015	0.0063
Additive variance	222.80	44.83	219.27	44.57	0.62	0.13	0.63	0.12	0.20	0.042	0.19	0.040
Independent residual	385.23	39.35	******	******	1.07	0.12	******	******	0.42	0.038	******	******
AR1 (row)	0.88	0.04	******	******	0.71	0.074	******	******	0.79	0.091	******	******
AR1 (column)	0.85	0.04	******	******	0.69	0.081	******	******	0.83	0.071	******	******
Variance	129.70	24.94	439.75	38.57	0.27	0.059	1.25	0.11	0.048	0.015	0.46	0.036
h^2	0.37		0.33		0.37		0.33		0.32		0.29	

| | CNK1 | | MALF | |
| | Non-spatial | | Non-spatial | |
	Estimate	SE	Estimate	SE
LogL	-1090.62		-3730.48	
Replicate	******	******	0.19	0.069
Replicate.Block	0.0033	0.0050	0.048	0.043
Additive variance	0.20	0.045	0.26	0.16
Variance	0.61	0.042	5.11	0.21
h2	0.25		0.05	

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