Funded by
Te Uru Rākau New Zealand Forest Service

Selection and deployment of elite *E. bosistoana* for short rotation hardwood forestry

MPI Technical paper: 03

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ISBN No: (contact the Design team)
ISSN No: (contact the Design team)

September 2025

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Abstract

NZDFI is advancing genetic improvement of *Eucalyptus bosistoana*, a naturally durable eucalypt, to produce superior genetic material for large-scale forestry deployment. The focus is on planting short rotation forests to lead to the establishment of a significant new hardwood supply chain in New Zealand.

Extensive Australian natural (unimproved) populations were deployed to establish NZDFI's broad-based breeding populations. These replicated trials have tested many families over multiple environments and stable genotypes have been identified with minimal genetic x environment variability. This has enabled selection of diverse elite genotypes for commercial deployment, and for deployment in second generation breeding populations to advance improvement.

The current availability of seed of improved genetic quality has resulted from advances made by NZDFI's tree breeding programme. Having a secure supply of genetically improved seed makes it possible for these gains to be available for commercial-scale seedling production and planting.

The 2012 progeny trials established at Dillon, Marlborough and McNeill, Hawkes Bay, were evaluated for growth, form and wood property traits between December 2024 and May 2025. Breeding values (BVs) were calculated for each family to rank the 87 families in the trials. An equal weighting across diameter at breast height (DBH), heartwood development, extractive content and overall stem acceptability was applied to produce a ranking of family performance.

The top 24 families across both sites were selected and the best 1-3 individual trees at each site have been identified.

In addition, a DNA analysis of the genetic structure of the families in the NZDFI breeding populations completed in 2023 identified errors in the species and origin of parent trees among the families established in the 2010 progeny trials. These have been corrected and 9 trees from 6 families have been selected.

Proseed will collect scion material in December 2025 and graft these new elite individual trees for planting in their Amberley clonal seed orchard in spring 2026.

Including elite selections from these families will expand NZDFI's clonal seed orchard and the commercial production of high-quality XyloGene®-branded *Eucalyptus bosistoana* seed supply to nurseries and forest growers.

1 Introduction

Durable eucalypts offer a short rotation option to forest growers and farm foresters in Marlborough and many North Island regions[1]. New Zealand Dryland Forests Innovation (NZDFI) is promoting a vision to plant 60,000 ha of durable hardwood forests by regional planting programmes sustained over 25-30 years. The scale of these regional planting programmes requires establishing around 2,000 ha annually and will require national production of 2 - 3 million seedlings annually. Growers need to have confidence that their investment in new planting is going to be economically rewarding. Success is underpinned by planting high-quality nursery stock of improved genetics - plants of proven potential.

NZDFI's major investment in tree breeding is designed to produce superior genetic material for large-scale forestry deployment, leading to the establishment of a significant new hardwood supply chain in New Zealand.

Before NZDFI's breeding programme began, durable eucalypts planted in New Zealand were unimproved, i.e. they were grown from seed collected from natural Australian forests or were the progeny of early New Zealand plantings.

Eucalyptus bosistoana, coast grey box, was selected by NZDFI for genetic improvement as it has proven adaptability in many NZ regions[2,3] and produces class 1 durable timber (expected in-ground service-life of 25-plus years) with excellent strength[4]. The tree breeding cycle can take up to 20 years from testing a new forestry species through to commercial production of 1st generation improved seed.

There is considerable genetic diversity in all eucalypt species so significant gains in selected traits are possible. NZDFI established extensive progeny trials from 2009 onwards to provide the foundation for a robust tree breeding programme that applies well-proven scientific methods, combined with innovative technology to deliver genetic gain across tree growth, form and wood quality traits for *E. bosistoana*.

Figure 1 shows how, since 2003, NZDFI has made progress through the first cycle of tree improvement of *E. bosistoana.*

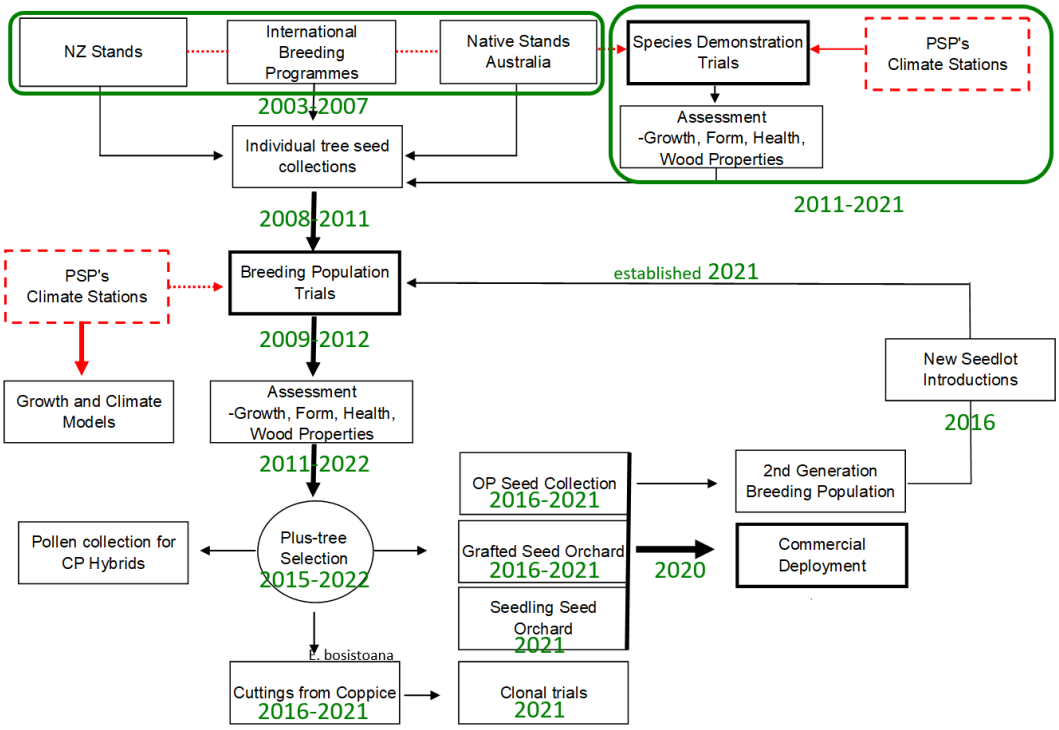

Figure 1: NZDFI's *E. bosistoana* tree-breeding programme.

2 Methodology

2.1 NZDFI's 2009-2012 *E. bosistoana* breeding population

Progeny testing is the fundamental activity in tree improvement. It is required to calculate the breeding values of individual families and therefore identify the best genetics for further development and deployment.

A network of progeny trials was planted between 2009 and 2012 to establish a 1st generation broad-based breeding population. The *E. bosistoana* family seedlots deployed in these progeny trials were sourced from mother trees growing across the natural range of the species from the central coast of New South Wales south to coastal southeastern Victoria.

Table 1 and Figure 2 show the six sites where the nine progeny trials were established and details of the varying environments. These include:

- 2009 progeny trials planted with 66 native forest families and replicated at 3 sites: Marlborough District Council (MDC) Cravens, Lawson, and Martin
- 2010 progeny trials planted with 38 native forest families and replicated at 3 sites: MDC Cravens, Avery, and Martin. Population genomics in 2023 identified that 30 of these families are *E. melliodora*. This is explained in section 2.2.
- 2012 progeny trials planted with 87 native forest families replicated at 3 sites: Juken NZ Ngaumu, Dillon, and McNeill

Table 1. NZDFI's *E. bosistoana* breeding population/progeny trials.

Site ID and name	Year planted	July Min (ºC)	Feb Max (ºC)	Annual Rainfall (mm)	Base Geology
51 – Lawson	2009	2	22	673	Conglomerate
52 – MDC Cravens Road	2009 & 2010	2	22	895	Alluvial Gravel
53 – Avery	2010	4	21	634	Mudstone
54 – Dillon	2012	0	23	692	Alluvial Gravel
56 – Martin	2009 & 2010	2	22	699	Alluvial Gravel
69 – Juken NZ Ngaumu	2012	2	22	1161	Mudstone
70 – McNeill	2012	2	22	1061	Limestone

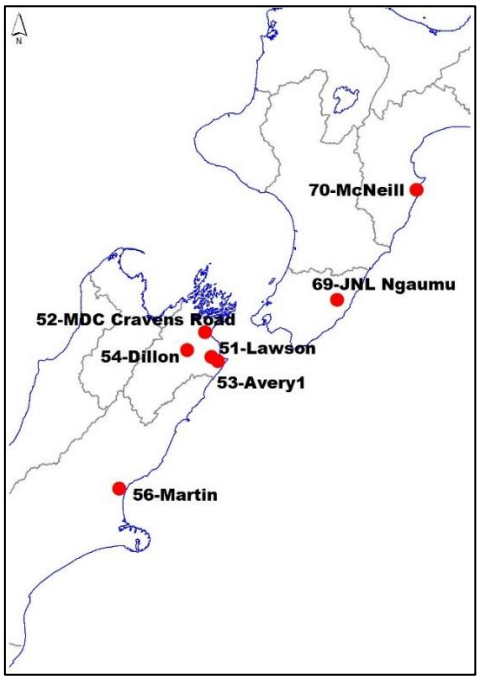

Figure 2: Location of *E. bosistoana* breeding population/progeny trial sites.

In summary, between 2009 and 2012 more than 70,000 trees were planted in 9 progeny trials to test a total of 191 open-pollinated unimproved family seedlots.

All progeny trials were planted in a single-tree-plot alpha-lattice incomplete block design. Trial spacing was 1.8m within the row and 2.4 m between rows which equates to 2312 stems per hectare (sph). This trial design was to allow for substantial within family selection and within-trial redundancy. With up to 80 trees planted of genetic entries, this has permitted the overlaying of other experiments (e.g. wood properties, forest health, permanent sample plots).

Trial records for each site are held in the 'Katmandoo' data system (https://katmandoo.au/) and NZDFI Dropbox files. These include:

- Trial Description Form – site information (location, landowner, experimental design)
- Location Map – including GPS coordinates
- Trial layout map

The 2009, 2010 and 2012 progeny trials have been measured to generate genetic parameters for growth and form, and wood properties such as heartwood diameter and natural durability[5]. There is a strong genetic correlation, >0.9, in the ranking of family performance for growth and heartwood content between progeny trial sites.

Progeny trials of a subset of 171 family seedlots of *E. bosistoana* were also established in a nursery environment at Woodville between 2016 and 2018. In total 11,000 trees were planted at 1.0 m spacing in family replicate blocks of 8 trees and felled at age 1-2 years to produce small stem samples that were used to:

1) screen at young age for growth and wood properties including growth-strain.
2) establish clonal propagation protocols from cuttings.
3) identify families for future breeding population and propagation stock of superior trees/families.

These results[6,7] were combined with data from NZDFI seedling progeny trials planted with the same family seedlots between 2009 and 2012. Twenty-two top-performing families were selected and 33 elite clones were identified from among the 619 clones propagated. These clones were multiplied as rooted cuttings with variable success at the Proseed Amberley propagation facility.

In 2021, these clones along with individual pedigreed collections of 13 first-generation improved seedlots from Proseed's clonal seed orchard; from 16 elite trees producing seed in the 2009/10 *E. bosistoana* progeny trial

located in MDC Cravens Road; and an additional 62 unimproved family seedlots collected in Australia, were established in new *E. bosistoana* progeny trials in three regions; Northland, Hawkes Bay and north Canterbury.

2.2 Genetic structure of families in the *E. bosistoana* breeding populations

In the NZDFI breeding trials planted in 2010, trees grown from 30 family seedlots collected in the northern region of *E. bosistoana's* natural distribution, exhibited inconsistent morphological features for the species. These plants have lanceolate leaves during their juvenile stage, whereas young leaves of *E. bosistoana* are typically known to be oblong to elliptical to ovate in shape[8]. An analysis of the genetic structure of the families in the NZDFI breeding populations by Kim, 2024[9] identified these individuals as *E. melliodora*.

Furthermore, the other 8 family seedlots established in 2010 progeny trials were recorded as having been collected near Waterloo, approximately 9 km north of the town of Beaufort, Victoria. This location is not recorded as an area where *E. bosistoana* naturally occurs[8]. The recent DNA analysis has confirmed these were *E. bosistoana* and a review of the GPS coordinates of the mother trees recorded by the seed collector revealed an error in the original latitudes. The corrected locations placed these trees in the coastal region of eastern Victoria, well within the species' natural distribution.

Figure 3A shows the original locations recorded of the *E. bosistoana* mother trees collected from and deployed in NZDFI's breeding populations[9]. Figure 3B shows the corrected location of the group of west Victorian mother trees and the misidentified *E. melliodora* mother trees in northern NSW. As a result of these errors the 30 families now identified as *E. melliodora* have been excluded from any further analysis of the 2010 progeny trials. The breeding values of the 8 families that were incorrectly located in western Victoria have been reassessed and 9 trees have been selected from 6 of these families to graft in 2025 and will be planted in the Proseed clonal seed orchard.

Knowing the taxonomic identity of a species is essential for ensuring genetic purity in breeding programmes. If a species is misidentified, there is a risk of unintentionally introducing genetic variability from another species or hybridization, which can compromise the integrity of the breeding programme.

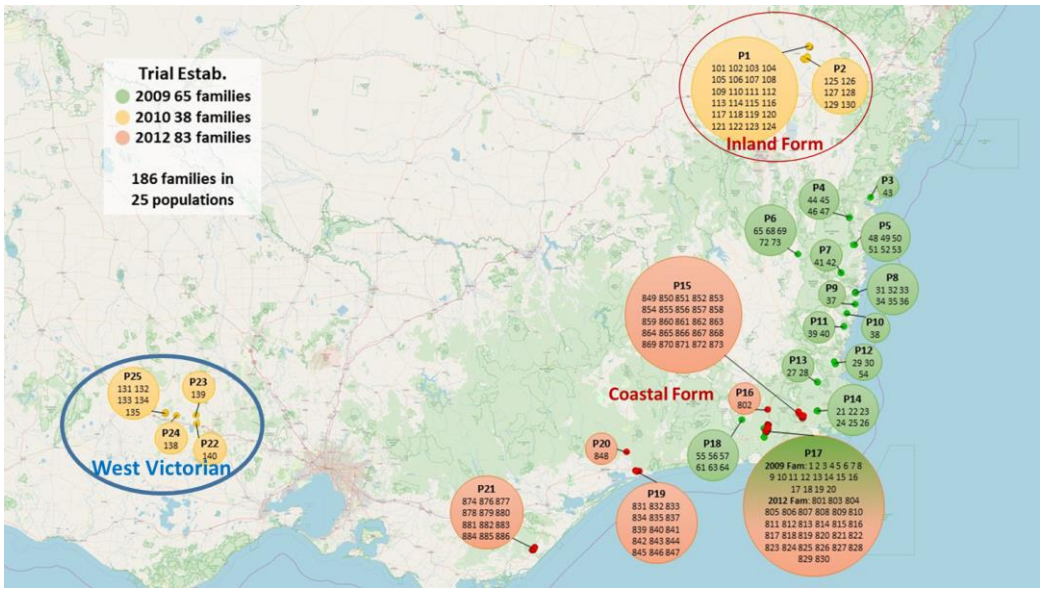

Figure 3A: Original locations recorded of *E. bosistoana* mother trees collected from and deployed in NZDFI's breeding population

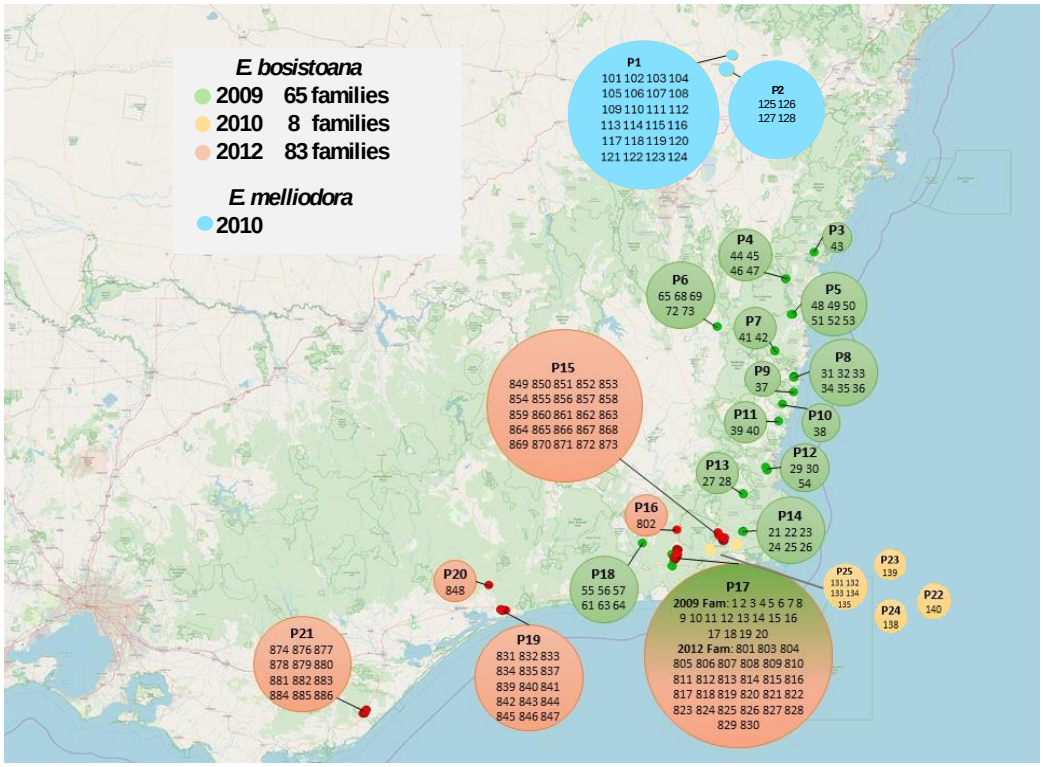

Figure 3B: Corrected location of 2010 *E. bosistoana* mother trees and identification of *E. melliodora* in northern New South Wales.

2.3 Selection criteria and traits for selection

A significant focus of NZDFI's breeding programme is to improve durable eucalypts suitable for plantations that produce small sawlogs, poles, posts and veneers on 15-to-20-year rotations. Some stem criteria are common across these products for example, straightness and heartwood. These criteria have been used to identify the primary traits to target and rank for selecting genotypes to maximise genetic gain.

The more traits included in a breeding programme the smaller will be the gain from selection in each one of them.

Optimal trees for forest growers are defined as:

- Well-adapted to target planting environments
- Vigorous growth – resistance or tolerance to attack by pests and diseases
- High utilisable stem volume – straightness, absence of forking, light branching
- Requisite wood properties – traits and quality aligned with product use.

To effectively deliver genetic gain through selection these traits need to be variable and under genetic control (i.e. be heritable). Data analysis for each trait quantifies genetic parameters which guide genetic improvement within the species. The actual magnitude of any gain depends on the heritabilities and genetic variances of the selection traits as well as selection intensity.

NZDFI progeny trials are designed to allow high selection intensity between and within families. Selection of outstanding individual trees based on some of the key traits has already commenced. Breeding values were calculated for nominated traits at the family level, and a ranking of families was produced (best to worst). These rankings enable selection of families to advance the breeding programme and seed orchard deployment.

In any breeding programme, the objective is typically to improve multiple traits, either by selecting the best or culling the worst families. As traits are typically not independent of each other, selection for one trait has consequences on the genetic gain of others. Therefore, selection for multiple traits requires clearly defined breeding objectives, ideally supported by economic weights.

At present, however, NZDFI has not been able to calculate economic weights as sufficient screening of all traits within its *E. bosistoana* breeding population is incomplete and a sawmill/processing study in a commercial setting has not been undertaken. A simple way of identifying superior genetics is weighing all traits equally and selecting families which have above average breeding values in several traits.

The traits of importance in the NZDFI breeding programme for *E. bosistoana* can be broadly placed in two categories:

1. Growth and form

Growth is recorded as a height (cm) measurement at between 2-3 years old with diameter at breast height (DBH in mm) and heartwood content (mm), measured at later ages. Form is a subjective score generated from an assessment of the stem's suitability for processing based on stem straightness, branching habit and multi-stem habit. Growth and form assessments in NZDFI's older progeny trials have revealed that *E. bosistoana*'s stem form is highly variable and heritable, so significant gains have been made in the 1st generation.

2. Wood properties and by-products

Extractive content (%), growth-strain (με), acoustic velocity (km/s) and stiffness (GPa) are the key traits that have been assessed[5,6,10]. Grain angle[7] and essential oils of the foliage[11] have also been analysed. Heritabilities and variation for these traits already reported from NZDFI's earlier progeny trials and the Woodville trial imply potential for genetic improvement.

2.4 Proseed's *E. bosistoana* clonal seed orchard (CSO)

Commercial seed production is a critical step in realising genetic gains from the tree improvement programme. Increasing improved seed production is best achieved through establishing clonal seed orchards (CSOs). CSOs are established with the top ranked progeny-tested individuals (ortets) by collecting scions from these trees and grafting these onto root stock. This cloning process preserves the more mature physiological state of the scion and thereby promotes faster flowering in the orchard.

A three-hectare CSO has been progressively established from 2016 by Proseed NZ at their Amberley site with the best individuals from the 12 top ranked families identified in the 2009 Cravens Road progeny trial at age 5 years and the 2012 breeding population aged 8 years located in the Wairarapa. The first crop of seed was collected from this clonal seed orchard in 2020.

There was a strong correlation, 0.96, in the ranking of family performance for growth and heartwood content between the progeny trial sites planted with the same families. The selection of the best families for the CSO is robust and therefore only marginally influenced by site.

An equal weighting for stem diameter and heartwood diameter has been applied in the selection index to identify the top families that have been grafted and planted in the Proseed CSO. Following that first selection of ortets from among the families planted in 2009, over 4,000 cores were collected from all families in the 2009 and 2010 breeding populations. These were used to measure heartwood percent and to assess extractive content using near infra-red spectrometry (NIR). During this same 2016-2017 period the University of Canterbury established a trial at Woodville Nursery and evaluated growth-strain from two-year old tree stem samples[6,10].

A third assessment in 2018 of the 2009 and 2010 progeny tests produced data to recalculate family breeding values for growth and form. Based on analysis of this data, along with wood quality data, Proseed rogued the CSO to remove five families that were no longer in the top ranking and 15 new trees from the top ranked families were grafted and planted to supplement the clonal orchard.

The breeding population established in 2012 in Juken NZ's Ngaumu Forest, Wairarapa was assessed in 2019 for growth and form and the breeding values calculated. These families were included in the Woodville nursery trials and the breeding values for growth-strain and stiffness were included as selection traits. In 2019, an additional 9 selections from 6 families in this 2012 breeding population were grafted and planted in the Proseed clonal seed orchard. The current composition of families and number of grafted clones (called ramets) of each is shown in Table 2.

Table 2. Table of clones in Proseed *E. bosistoana* seed orchard.

Clone	Family	Rank	No. Ramets in Orchard 2024	Clone	Family	Rank	No. Ramets in Orchard 2024
214001	12	25	8	219014	24	1	5
214002	54	5	14	219015	20	2	13
214003	72	3	18	219016	24	1	13
214004	10	24	7	220001	804	14	4
214005*	16		1	220002	855	19	6
214007	11	6	14	220003	870	8	6
214009	10	24	9	220005	824	18	6
214014	18	16	7	220006	837	3	5
214015	54	5	11	220007	804	14	9
214016	12	25	5	220008	822	9	6
219013	20	2	8	220009	837	3	10
* No longer in the top ranking, to be removed from the CSO						Total	185

While selecting a small number of elite trees of a few top performing families for seed production maximises genetic gain for deployment, it reduces genetic diversity. Genetic diversity is important as inbreeding or self-pollination is known to cause a reduction in the germination and growth potential of resultant seed. Clonal seed orchards of eucalypt species are generally open-pollinated and flowering needs to be widespread across all clones and occurring at the same time to ensure outcrossing is possible. To enable this, Proseed have successfully artificially stimulated the early onset and the timing of anthesis (flowering) by application of paclobutrazol, an inhibitor of the gibberellin plant hormones, that acts to stunt vegetative growth while enhancing flowering and seed production.

Assuming an equal proportion of seed from each family, the estimated gains from the top-ranked families in this clonal seed orchard compared to the unimproved breeding population is 11.4% for DBH and 22.6% for

heartwood content. Stem form was included as a selection trait and an improvement is expected but the level of gain has not been quantified. The introduction of additional clones of elite trees will further advance genetic gain and supply of *E. bosistoana* seed marketed under the XyloGene® brand.

2.5 Growth and form assessment of 2012 *E. bosistoana* progeny trials at Juken NZ Ngaumu, Dillon and McNeill

The *E. bosistoana* breeding population planted in 2012 was replicated at 3 sites, Dillon (Marlborough), Juken NZ Ngaumu (Wairarapa) and McNeill (Hawkes Bay).

The Juken NZ Ngaumu site was measured in November 2019 when DBH and stem form were recorded. This data was used to select individual trees in each family to take core samples for evaluating wood properties. Up to 20 trees with a DBH greater than 40 mm from across the diameter range in each family were cored. The results showed very little heartwood was present at this age[12].

In March 2022, a growth and form assessment of the McNeill trial was planned but only 12 blocks were assessed as growth was poor across three-quarters of the trial. Also at that time, 10 trees were felled within the trial surround and tested with methyl orange to show heartwood development. From the results of these trees, it was considered unlikely that there would be 15 trees per family with a suitable DBH to core and obtain robust genetic parameters for this trait at that time[13].

Further progress was delayed until December 2024 when the Dillon site was assessed followed by the McNeill site in January 2025. These trials were assessed for DBH, height and stem form. An acceptability score, 1 acceptable and 0 unacceptable, was recorded for stem straightness, tree form and crop acceptability.

An analysis to rank and select elite families was undertaken using the recent growth and form data collected from the Dillon and McNeill sites and combined with the 2019 data from the Juken NZ Ngaumu site. The growth rates at each site are variable as shown in Table 3.

Table 3. Diameter at Breast Height (DBH) for NZDFI 2012 *E. bosistoana* breeding population at three sites.

Trait	Site	Assessment age (years)	Mean (mm)	Mean annual increment (mm)
DBH (mm)	Dillons	12	69.9	**5.8**
	McNeil	12	91.9	**7.7**
	Ngaumu	7	61.0	**8.7**

There was notable variation in growth across the Dillon site due to the upper slopes of the trial area being affected by drought and wind exposure whereas the lower slopes have greater soil moisture and are sheltered aiding tree growth. Some distinct areas at the McNeill site had poor tree survival and growth due to poor soil fertility and being south facing.

Stability of family performance across sites is important as then the selection of the best families for the clonal seed orchard will not be influenced by site and it is likely that the seed produced will perform above average on deployment sites. A high correlation between two different sites of 0.96 was obtained for the ranking of family performance for growth and heartwood content between the *E. bosistoana* progeny trial sites planted in 2009 in Marlborough[5].

2.6 Selection of candidate trees in 2010 progeny trials for wood properties assessment

To effectively deliver genetic gain and progress genetic improvement within the species, traits must be heritable. Calculating heritabilities of wood properties requires sampling several individuals from a larger number of families across a broad range of tree sizes to characterise the population. Previous work has

indicated that sampling 10 individuals per family per site is sufficient to conduct robust genetic analysis for heartwood traits[14].

The assessments within the Dillon and McNeill progeny trials also showed that there was enough additional growth since the last assessment for selection of candidate trees of suitable size in each family at both sites to take core samples for heartwood content and extractive content measurement. Therefore, a sample of 10 trees from each family was selected for taking cores. The trees encompass the diameter range, with a minimum DBH set at 50 mm and a preference given to individuals with an acceptable crop stem score but not exclusively. Wood quality assessments by coring requires more resources than growth and form assessments. By excluding individuals with poor form and growth, which will not meet criteria for selection into the seed orchard, resources can be used more effectively.

Full stem diameter cores were extracted from a sample of the trees present at the two sites. Growth (tree height; DBH) and form assessments (acceptable; unacceptable), tree selection and coring have been described in reports for Milestones 2 and 3 under this project.

A total of 751 trees from 80 families were sampled at the Dillon site and a total of 826 trees from 80 families were sampled at the McNeill site.

2.7 Heartwood assessments of cores sampled in 2010 progeny trials

Core length, i.e. stem diameter under bark at coring height (~0.5 m), and heartwood diameter were measured on the cores in the green state with a ruler to the nearest 1 mm after highlighting heartwood with aqueous 0.1% methyl orange solution. The core samples were then dried in an oven at 60°C. The dry cores were then flattened on transverse face (end-grain) by sanding with 120 grit paper before acquiring NIR spectra. NIR spectra were taken every 5 mm along the heartwood with a fibreoptic probe attached to a Bruker Tensor 37 spectrometer. Sapwood depth was defined as half of the difference between core length and heartwood diameter. Extractive content was predicted from each spectrum by a previously developed multivariate model[15]. Predicted extractive contents were averaged for each core.

2.8 Data analysis

Data was analysed with the R software[16]. Univariate analyses were simplified from a general model including a fixed overall mean and random replicate, plot and additive effects. The model was fitted with the ASReml package[17] to generate the correlation between the traits' phenotypic and genotypic variation. The phenotypic and genotypic variation was estimated to compute the narrow sense half-sib heritability (h^2) of each trait according to

$$h^2 = \frac{Var(A)}{Var(Y)} = \frac{4\sigma_f^2}{\sigma_f^2+\sigma_b^2+\sigma_r^2}$$

Where σ_f^2 is the additive genetic variance for the family; σ_b^2 is the variance for the block and σ_r^2 is the residual variance. The heritability estimated in this study assumed a relationship coefficient among families of one quarter, i.e. true half-sibling progeny.

3 Results

3.1 Selection of trees for grafting

Error! Reference source not found. Table 4 shows summary statistics for measured traits in the 2012 Dillon and McNeill *E. bosistoana* progeny trials. Trees of the same families at Dillon and McNeill expressed the same average form. However, on average, the trees of all families grew larger at McNeill compared to Dillon. The larger stem diameter at McNeill was reflected in a larger average heartwood diameter as the trees at both sites maintained a similarly wide sapwood band of ~30 mm. The faster growing trees at McNeill also had more extractives in their heartwood. However, predicted extractive contents at the two sites (~3%) were lower than those reported earlier (~8%) for the species at age 7-years-old at two sites with twice as fast growth[5].

The breeding values for the families planted in 2012 at Dillon and McNeill have been calculated and are listed in Appendix 1. These breeding values have been plotted in Figure 4 and the families with above average breeding values for combined form, heartwood diameter and extractive content are marked in blue and located in the top right quadrant of the plot.

An equal weighting was applied to the breeding values (BVs) for DBH, combined straightness and form (CSF), heartwood diameter and extractive content across the two sites to rank the families. The top 24 families were identified and 1 to 3 trees in each of these families have been selected in both, the Dillon and McNeill trials (Appendix 2). Scion material will be collected from at least one selection per family and grafted onto rootstock for planting in the Proseed clonal seed orchard in 2026 (Milestone 5 of this contract).

Table 4: Summary statistics for breeding traits for 13-year-old *E. bosistoana* trees at two sites. SD: standard deviation; combined form and straightness score (CFS).

Trait	Site	Mean	SD	Min	Max
DBH (mm)	Dillon	69.88	29.92	4	268
	McNeill	91.87	41.5	11	304
Tree height (m)	Dillon	5.61	1.57	0.4	13.4
	McNeill	7.34	2.35	2.4	15.6
Straightness	Dillon	0.58	0.49	0	1
	McNeill	0.58	0.49	0	1
Form	Dillon	0.27	0.44	0	1
	McNeill	0.3	0.46	0	1
CFS	Dillon	0.32	0.47	0	1
	McNeill	0.36	0.48	0	1
Corelength (mm)*	Dillon	75.39	18.6	30	168
	McNeill	100.17	27.95	30	202
Heartwood diameter (mm)*	Dillon	11.23	16.2	0	90
	McNeill	37.85	30.72	0	130
Sapwood depth (mm)*	Dillon	32.08	7.13	0***	55
	McNeill	31.16	9.16	6.5	85
Predicted extractive content (%)**	Dillon	2.79	1.25	0.96	8.4
	McNeill	3.27	1.63	0.55	13.64

* only trees larger than 50 mm DBH were selected for coring inducing bias

** trees without heartwood are not included

*** some cores broke and were incomplete, i.e. missing sapwood

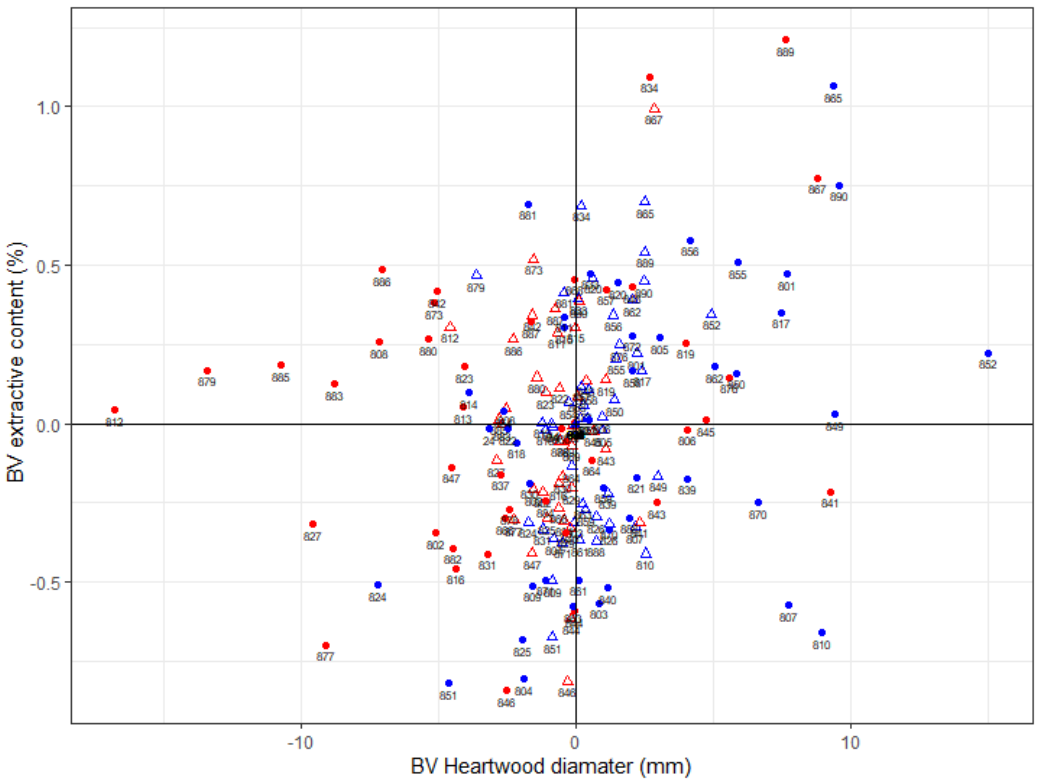

Figure 4: Breeding values for 13-year-old *E. bosistoana* at Dillon (open triangle) and McNeill (filled circle) for heartwood diameter and extractive content. Families with above average combined form and straightness score (CSF) are marked blue and families with below average CSF are marked in red.

3.2 Genetic gain estimates

Genetic gain is not fixed and the ongoing improvement of seed sources can be achieved in several ways:

- The precision of the genetic parameters and selections increases with tree age and the response of genotypes to changing health risks and environmental factors over time. The evaluations of progeny trials targeting the key traits of interest - growth, form, and heartwood and extractive content - are used to calculate breeding values and estimated gain.
- The levels of gain can be improved through more intense within- and between-family selection while also maintaining acceptable levels of genetic diversity.

The breeding values for all the 87 families were computed and ranked based on their performance from the highest to the lowest. The genetic gain was estimated using the equation:

$$Genetic\ gain\ (\%) = \frac{Gs}{Population\ mean} \times 100,$$

with Gs being the average of the breeding values of the top 10 or to 24 selected families.

Comparing the top 10 and top 24 selections in Table 5 shows small differences in gain for DBH, extractives and stem acceptability but more gain for heartwood among the top 10. However, we do not know much about the synchronism of flowering among the families so selecting a broader number of families to begin with will maintain genetic diversity in the seed orchard and allow opportunity to rogue later.

Table 5: Percentage genetic gains for individual traits of *E. bosistoana* compared to the population mean.

Trait	Site	Top 10 families	Top 24 families
DBH	Dillon	14%	17%
	McNeill	19%	19%
CFS	Dillon	43%	43%
	McNeill	53%	43%
Heartwood diameter	Dillon	21%	13%
	McNeill	20%	14%
Predicted extractive content	Dillon	12%	11%
	McNeill	16%	14%

The realised gain from a stand planted with an improved seedlot can be influenced by the percentage representation of the families. Calculations of genetic gain assume equal contribution from each parent. The performance of individual families through the nursery should be monitored and variation in germination success recorded. Adjustments may need to be made to the ratio of seed per family that is included in a seedlot to compensate for this.

3.3 Site correlations

Correlations of breeding values between sites were strong Table 6. This gives confidence that selected genotypes from these sites will also perform better when deployed on other sites. The smaller number of assessed trees for heartwood diameter and extractive content contributed to their larger standard errors.

Table 6: Correlation of breeding values for 2012 *E. bosistoana* trials at the Dillon and McNeill sites

Trait	Site correlation	Standard error
DBH	0.74	0.07
Tree height	0.74	0.08
Straightness	0.81	0.09
Form	0.93	0.17
CFS	0.7	0.11
Heartwood length	0.82	0.92
Extractive content	0.66	0.43
Core length	1	NA
Sapwood depth	1	NA

3.4 Correlations between traits

Estimated heritabilities of the individual traits were comparable between the two sites (Table 7 - diagonal). Restricting core sampling to trees with a DBH greater than 50 mm contributed to the lower heritabilities for core length and heartwood diameter compared to DBH. Stem straightness was more heritable than form. The characteristics assessed for form are ramicorns, multi-leaders, and stem shift. These features can be influenced more by environment than genetics.

Table 7 also lists the phenotypic and genotypic correlations between traits for the 2012 *E. bosistoana* trials at the Dillon and McNeill sites. The growth traits DBH, tree height, core length and heartwood diameter showed strong positive phenotypic correlations. The positive correlation between heartwood diameter and extractive content was favourable as trees with higher quality heartwood also produced more heartwood.

Table 7: Heritabilities (diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations between traits for 13-year-old *E. bosistoana* at two sites (Dillon above McNeill). 95% Confidence interval in parenthesis)

Dillon McNeill	DBH	Height	Core-length	Heartwood Diameter	Sapwood Depth	Extractive Content	Form	Straight-ness	Combined Form Score
DBH	0.44	0.86	0.83	0.71	0.28	0.15	0.02	0.36	0.39
	(0.31, 0.57)	(0.85, 0.87)	(0.80, 0.85)	(0.67, 0.74)	(0.21, 0.34)	(0.04, 0.26)	(-0.01, 0.05)	(0.33, 0.38)	(0.36, 0.41)
	0.42	0.87	0.89	0.81	-0.01	0.21	0.15	0.38	0.4
	(0.27, 0.56)	(0.87, 0.88)	(0.87, 0.90)	(0.79, 0.83)	(-0.07, 0.06)	(0.14, 0.29)	(0.12, 0.19)	(0.35, 0.41)	(0.37, 0.43)
Height	0.82	0.31	0.66	0.55	0.24	0.02	0.15	0.41	0.48
	(0.74, 0.89)	(0.2, 0.41)	(0.62, 0.70)	(0.50, 0.60)	(0.17, 0.3)	(-0.09, 0.13)	(0.12, 0.18)	(0.39, 0.44)	(0.46, 0.5)
	0.84	0.2	0.7	0.61	0.04	0	0.33	0.45	0.5
	(0.76, 0.92)	(0.12, 0.29)	(0.67, 0.73)	(0.57 ,0.66)	(-0.03, 0.11)	(-0.08, 0.08)	(0.30, 0.36)	(0.42, 0.48)	(0.47, 0.52)
Core-length	0.99	1	0.11	0.67	0.54	-0.01	-0.22	-0.02	0.03
	(0.96, 1.00)	(0.80, 1.22)	(-0.02, 0.25)	(0.63, 0.71)	(0.49, 0.59)	(-0.12, 0.1)	(-0.28, -0.15)	(-0.09, 0.05)	(-0.04, 0.1)
	0.97	0.9	0.22	0.81	0.17	0.2	-0.11	0.06	0.15
	(0.94, 0.98)	(0.80, 1.00)	(0.05, 0.38)	(0.78, 0.83)	(0.10, 0.23)	(0.13, 0.28)	(-0.17, -0.04)	(-0.01, 0.13)	(0.08, 0.21)
Heartwood Diameter	0.91	0.79	0.02	0.04	-0.26	0.26	-0.23	-0.06	0.03
	(0.76, 1.05)	(0.30, 1.25)	(-2.08, 2.25)	(-0.11, 0.19)	(-0.33, -0.19)	(0.16, 0.36)	(-0.30, -0.16)	(-0.13, 0.01)	(-0.04, 0.1)
	0.92	0.75	0.7	0.11	-0.44	0.39	-0.11	0.06	0.07
	(0.84, 0.98)	(0.57, 0.93)	(0.39, 1.00)	(-0.02, 0.24)	(-0.5, -0.39)	(0.32, 0.45)	(-0.18, -0.04)	(-0.01, 0.12)	(0.00, 0.14)
Sapwood Depth	0.83	0.59	0.84	-0.5	0.2	-0.26	-0.02	0.04	0.01
	(0.60, 1.07)	(0.21, 0.95)	(0.17, 1.48)	(-1.68, 0.63)	(0.01, 0.36)	(-0.36, -0.15)	(-0.09, 0.05)	(-0.03, 0.11)	(-0.06, 0.08)
	0.28	0.35	0.62	-0.1	0.29	-0.28	0.02	0	0.1
	(-0.06, 0.63)	(0.00, 0.71)	(0.22, 1.05)	(-0.74, 0.53)	(0.1, 0.47)	(-0.35, -0.2)	(-0.05,0.09)	(-0.07, 0.07)	(0.03, 0.17)
Extractive Content	-0.11	-0.38	-0.91	0.27	-0.91	0.24	-0.09	-0.05	0.01
	(-0.65, 0.48)	(-0.88, 0.12)	(-2.35, 0.48)	(-1.22, 1.80)	(-1.89, -0.07)	(-0.15, 0.57)	(-0.19, 0.03)	(-0.16, 0.06)	(-0.1, 0.12)
	0.1	-0.11	-0.17	0.51	-0.72	0.2	-0.07	-0.04	-0.07
	(-0.31, 0.50)	(-0.52, 0.32)	(-0.77, 0.44)	(-0.02, 1.05)	(-1.18, -0.29)	(0.02, 0.38)	(-0.15, 0.01)	(-0.11, 0.04)	(-0.15, 0.01)
Form	0.18	0.52	0.85	0.74	0.44	0.06	0.09	0.26	0.43
	(-0.12, 0.49)	(0.24, 0.77)	(0.37, 1.35)	(0.12, 1.43)	(-0.11, 0.95)	(-0.58, 0.69)	(0.04, 0.13)	(0.23, 0.28)	(0.4, 0.45)
	0.3	0.58	0.7	0.8	0.1	0.27	0.07	0.32	0.55
	(-0.04, 0.65)	(0.28, 0.86)	(0.23, 1.17)	(0.23, 1.37)	(-0.36, 0.59)	(-0.27, 0.83)	(0.02, 0.11)	(0.29, 0.35)	(0.53, 0.58)
Straightness	0.39	0.49	0.35	0.22	0.13	-0.19	0.59	0.2	0.53
	(0.16, 0.62)	(0.28, 0.71)	(-0.37, 1.09)	(-0.69, 1.17)	(-0.37, 0.60)	(-0.69, 0.34)	(0.34, 0.85)	(0.12, 0.28)	(0.51, 0.55)
	0.52	0.73	0.79	0.94	0.01	-0.04	0.76	0.22	0.59
	(0.32, 0.74)	(0.58, 0.88)	(0.49, 1.07)	(0.58, 1.32)	(-0.40, 0.41)	(-0.51, 0.43)	(0.53, 1.01)	(0.13, 0.31)	(0.57, 0.61)
Combined Form Score	0.52	0.71	0.89	0.82	0.29	0.17	0.85	0.82	0.16
	(0.31, 0.71)	(0.56, 0.86)	(0.08, 1.69)	(-0.58, 2.22)	(-0.23, 0.79)	(-0.42, 0.72)	(0.67, 1.01)	(0.69, 0.94)	(0.09, 0.23)
	0.56	0.79	0.78	0.83	0.18	0.05	0.97	0.93	0.18
	(0.35, 0.77)	(0.66, 0.92)	(0.46, 1.11)	(0.35, 1.30)	(-0.25, 0.57)	(-0.42, 0.51)	(0.83, 1.12)	(0.84, 1.02)	(0.1, 0.26)

4 Discussion

Genomic technologies have been applied to understand the genetic diversity and relationships in the *E. bosistoana* population[9]. This helps to quantify and manage levels of inbreeding and genetic diversity within the breeding and production populations. It also enables calculation of more precise breeding values and genetic gain delivered from the breeding programme.

Understanding the flowering phenology of *E. bosistoana* is relevant to both the open-pollination breeding programme and seed production. Flowering needs to be widespread across families and occurring at the same time to ensure outcrossing is occurring. Inbreeding or self-pollination is known to cause a reduction in the germination and growth potential of resultant seed. Seed production trees should be monitored to record the flowering window of each genotype, and seed from trees that flower without synchronously can be removed or not included in the seed harvest.

Control-pollination in the seed orchard and clonal propagation of tree stocks will deliver the best genetic gain. This is the deployment system routinely used for radiata pine, however the flower phenology of *E. bosistoana* is not suited to this and would be costly and unreliable. Open-pollinated seed is the best option to produce genetically improved tree stocks of *E. bosistoana* for establishing commercial plantations.

In addition to the Proseed CSO, the 2009 Cravens Road progeny trial has proved to be a good flowering site and many trees are producing flowers and setting capsules. The trial has been progressively thinned to remove the poor performing families and small seed collections have been made from this trial. The selection of individual trees seed collection in the Cravens Road stand was made based on a selection index including diameter, form, and heartwood content and offers a readily available improved seed resource. An increase in genetic gain can be assumed however, the stand must be managed on a silvicultural basis and retain an even distribution of trees across the site. Selection intensity is restricted because some genetically lower-ranked trees must remain in the stand.

There is always a trade-off between seed quantity and genetic quality. Seed can be selectively collected from only the best parents to increase the genetic quality of a seedlot. However, this reduces the quantity of that seedlot compared to a collection from all the trees in the orchard or stand. Seed collected from the remaining lower-ranked parents into another seedlot will express less genetic gain.

NZDFI is committed to providing the best genetically improved seed and therefore collections made in progeny trials that have been converted to seed stands are exclusively from the top-ranked families. These trials have been thinned to remove most poor performing families and individuals. Seed produced from these stands of mixed family origin will express outcrossing vigour.

5 Conclusion

The benefits of planting the best genetics are realised as increased productivity, log grade and wood quality gains at the end of rotation.

Future production of improved *E. bosistoana* seed from Proseed's clonal seed orchard will increase as flowering on the ramets in the orchard is enhanced by chemical application and from the addition of new selections from the 2010 and 2012 breeding populations.

The evaluation of the 2012 progeny trials for growth, form and wood quality traits has identified the top ranked 24 families among the 87 families established in the trial. These families will be grafted by Proseed to expand NZDFI's clonal seed orchard and ensure a high quality XyloGene® seed supply to nurseries and forest growers. Proseed will collect scion material in December 2025 and graft new individual trees for planting in their Amberley clonal seed orchard in spring 2026.

The family ranking has also been used to selectively thin the trial and remove the poor performing families. Seed collected from these trials in the future will yield some genetic gain.

The surviving trees of the 30 families in the 2010 progeny trial located at Cravens Road that have been identified as *E. melliodora* can be removed to avoid hybridisation with the remaining *E. bosistoana*. A further 9

trees have been selected from 6 of these families to graft in 2025 for inclusion in Proseed's CSO. This trial has been converted to the seed stand and is a source of improved seed.

NZDFI commenced a second cycle of breeding and improvement with the establishment of three replicated *E. bosistoana* progeny trials in 2021. These trials have extended NZDFI's breeding population with the infusion of 62 new families collected in Australia, seed from the best families in the 2009/10 progeny trial at MDC Cravens Road and early clonal seed orchard collections of 1st generation improved seed. Future assessments of these trials should identify additional elite selections to add to or replace the early selections already deployed in the clonal seed orchard.

Acknowledgements

Funding: Forest Growers Levy Trust; Te Uru Rākau – New Zealand Forest Service; University of Canterbury and NZ Dryland Forests IP Ltd.
Landowners: Susan Dillon, The Throne, Marlborough and Ben McNeill, Waimarama, Hawkes Bay. Thanks also to Juken NZ Ltd, Wairarapa.

Appendices

Appendix 1: Breeding values for *E. bosistoana* families aged 13 years-old for the Dillon and McNeill sites. Note: Families 24, 823 ,880 and 882 were only planted at McNeill whereas families 853, 869, 884 and 888 were planted only at Dillon.

Fam_code	DBH (mm)		Height (m)		Form		Straightness		Combined Straightness Form	
	Dillon	McNeill	Dillon	McNeill	Dillon	McNeill	Dillon	McNeill	Dillon	McNeill
24	10.70	19.92	0.49	0.80	0.06	0.06	0.07	0.09	0.11	0.17
801	-2.86	10.44	-0.58	-0.05	-0.02	-0.03	0.06	0.15	0.09	0.10
802	-12.09	-41.09	-0.94	-1.66	-0.07	-0.07	-0.03	-0.14	-0.03	-0.25
803	13.97	19.42	0.67	0.90	0.03	0.02	0.28	0.23	0.29	0.20
804	24.34	31.01	1.38	1.98	0.08	0.09	0.37	0.39	0.20	0.30
805	-5.85	-5.19	-0.28	0.05	0.05	0.06	0.01	0.04	0.00	0.09
806	-1.76	-7.52	-0.28	-0.59	-0.06	-0.06	-0.05	-0.12	0.01	-0.12
807	28.51	16.46	0.92	0.78	-0.08	-0.06	0.23	0.22	0.06	0.18
808	-2.88	2.56	0.13	0.60	0.00	0.01	-0.14	-0.13	-0.05	-0.01
809	8.24	32.28	1.04	1.79	0.14	0.11	-0.01	0.01	0.12	0.09
810	19.76	24.55	1.28	1.35	0.11	0.11	0.14	0.26	0.18	0.19
811	-6.62	11.49	-0.16	0.41	-0.01	0.00	0.07	0.19	-0.04	0.01
812	-15.25	-51.74	-1.22	-2.49	-0.07	-0.06	-0.02	-0.09	-0.09	-0.14
813	0.76	-4.90	0.69	-0.06	-0.02	-0.01	-0.16	-0.22	0.05	-0.06
814	3.51	6.63	1.02	0.98	0.03	0.02	0.16	0.15	0.21	0.17
815	-9.54	-3.95	-0.42	-0.31	0.08	0.10	0.13	0.22	-0.01	0.24
816	-8.51	-21.37	-0.28	-0.63	-0.11	-0.09	0.17	0.12	-0.01	-0.04
817	1.65	0.75	0.60	0.49	0.12	0.11	0.48	0.37	0.18	0.08
818	-10.70	-17.41	-0.49	-0.61	0.13	0.12	0.02	-0.05	0.03	0.04
819	9.31	-2.52	0.04	-0.39	-0.17	-0.15	-0.42	-0.40	-0.36	-0.33
820	-8.08	5.13	-0.13	0.50	0.15	0.14	-0.14	0.04	0.05	0.26
821	19.74	13.34	0.84	0.46	0.13	0.11	0.02	-0.06	0.13	0.10
822	6.21	-1.02	0.26	0.16	0.09	0.08	-0.09	-0.07	0.00	0.06
823	-13.78	-26.37	-0.34	-0.75	0.00	0.01	0.08	0.09	-0.09	-0.20
824	-7.21	-14.23	0.09	0.26	0.22	0.20	0.28	0.27	0.30	0.35
825	3.11	13.00	-0.04	0.06	-0.03	-0.03	0.08	0.12	-0.06	0.01
826	-3.54	5.20	0.62	1.00	0.02	0.01	0.29	0.25	0.14	0.15
827	-5.44	-16.08	0.07	-0.45	-0.09	-0.08	-0.31	-0.35	-0.13	-0.14
829	-1.39	6.06	0.61	0.72	0.08	0.07	0.01	-0.01	-0.03	-0.03
830	-12.20	-16.60	0.25	-0.12	-0.08	-0.07	0.08	0.15	-0.01	0.06
831	2.00	1.68	0.18	0.25	-0.07	-0.06	-0.07	-0.11	0.00	-0.04
832	-27.65	-28.25	-1.11	-1.01	0.05	0.05	-0.13	-0.11	-0.19	-0.15
833	6.51	10.10	0.56	0.69	0.01	-0.01	0.14	0.20	0.14	0.11
834	13.43	-5.08	-0.20	-0.85	0.04	0.03	-0.03	-0.09	0.02	-0.01
835	-17.88	-18.27	-1.28	-1.17	-0.13	-0.11	-0.30	-0.26	-0.20	-0.15
837	-10.86	-10.99	-0.01	0.12	-0.04	-0.03	0.08	0.01	-0.01	-0.06
839	3.54	13.81	1.01	1.20	0.16	0.12	0.25	0.13	0.30	0.18
840	-20.81	3.50	-1.11	-0.09	0.02	0.02	0.17	0.21	-0.01	0.08
841	0.35	11.52	-0.35	-0.01	0.01	0.01	-0.15	-0.14	-0.13	-0.07
842	-19.50	-28.27	-1.70	-1.54	-0.05	-0.03	-0.01	0.08	-0.27	-0.15
843	-2.37	-6.46	-0.54	-0.22	-0.15	-0.14	-0.20	-0.16	-0.18	-0.22
844	1.37	10.23	-0.45	0.06	-0.16	-0.15	0.08	0.15	-0.14	-0.17
845	7.73	56.85	0.30	1.58	-0.14	-0.14	0.14	0.13	0.00	-0.04
846	-2.69	-1.80	0.05	-0.10	-0.08	-0.07	-0.26	-0.11	-0.23	-0.11
847	-6.22	-9.20	-0.74	-0.47	-0.07	-0.06	0.00	0.03	-0.13	-0.10
848	-19.74	-24.97	-1.10	-1.15	-0.14	-0.13	-0.34	-0.42	-0.16	-0.24
849	23.03	43.80	1.58	1.94	0.26	0.25	0.12	0.25	0.31	0.42
850	-14.01	-0.65	-0.52	-0.04	0.08	0.08	0.23	0.20	0.00	0.07
851	23.08	20.27	0.87	0.84	0.04	0.02	0.15	0.02	0.17	0.04
852	0.04	19.04	0.16	0.97	0.01	0.02	-0.26	-0.18	0.08	0.02
853	2.54	2.59	0.00	0.00	0.11	0.09	0.25	0.21	0.16	0.12
854	2.68	2.85	0.52	0.32	0.10	0.10	0.19	0.16	0.07	0.06
855	-3.79	14.85	0.26	1.08	0.11	0.11	0.01	0.14	0.06	0.23
856	6.57	2.17	0.35	0.27	0.04	0.04	-0.01	0.07	0.07	0.17
857	-19.08	-18.11	-1.00	-1.08	0.08	0.07	-0.12	-0.11	0.02	0.00
858	8.03	5.77	0.62	0.43	0.16	0.13	0.24	0.11	0.29	0.17
859	9.16	27.05	0.52	1.18	-0.11	-0.09	-0.05	0.08	0.01	0.05
860	-3.06	3.00	-0.01	0.13	0.00	-0.01	-0.10	-0.09	-0.03	-0.03
861	-2.47	0.19	0.31	0.57	0.13	0.14	0.06	0.21	0.02	0.22
862	15.59	11.37	1.02	0.94	0.08	0.08	0.15	0.16	0.22	0.29
863	11.40	-4.25	0.83	0.08	0.16	0.11	0.26	0.20	0.26	0.14

Fam_code	Corelength (mm)		Heartwood Diamter (mm)		Sapwood Diameter (mm)		EC (%)	
	Dillon	McNeill	Dillon	McNeill	Dillon	McNeill	Dillon	McNeill
24	0.30	0.65	-0.83	-3.14	1.88	2.93	-0.01	-0.02
801	0.33	0.73	2.24	7.68	-3.78	-5.87	0.22	0.47
802	0.65	1.42	-1.52	-5.08	3.30	5.12	-0.21	-0.35
803	8.44	18.38	-0.06	0.86	5.79	8.98	-0.31	-0.57
804	2.21	4.82	-0.78	-1.87	2.37	3.67	-0.36	-0.81
805	1.06	2.30	0.99	3.06	-0.84	-1.31	-0.02	0.27
806	2.79	6.09	0.98	4.06	0.06	0.10	0.02	-0.02
807	5.76	12.54	2.18	7.74	0.47	0.73	-0.33	-0.57
808	-2.15	-4.66	-2.52	-7.14	2.09	3.24	0.05	0.26
809	2.35	5.14	-0.83	-1.59	2.56	3.97	-0.50	-0.51
810	9.37	20.43	2.56	8.97	2.82	4.39	-0.41	-0.66
811	-0.37	-0.78	-0.65	-0.39	0.24	0.38	0.29	0.34
812	-12.45	-27.11	-4.56	-16.75	-1.15	-1.77	0.30	0.04
813	-1.49	-3.25	-1.20	-4.07	0.40	0.62	0.00	0.05
814	0.66	1.43	-0.86	-3.88	2.14	3.33	0.00	0.10
815	1.53	3.34	-0.01	-0.38	1.23	1.93	0.31	0.30
816	-7.69	-16.78	-0.61	-4.34	-3.84	-5.96	-0.19	-0.46
817	2.72	5.91	2.42	7.46	-1.77	-2.76	0.17	0.35
818	-0.77	-1.65	-1.10	-2.15	0.59	0.92	-0.02	-0.06
819	6.56	14.28	1.11	4.04	2.67	4.13	0.14	0.25
820	0.49	1.06	0.63	1.56	-0.42	-0.64	0.46	0.45
821	-1.01	-2.21	0.41	2.23	-1.99	-3.10	0.01	-0.17
822	0.13	0.26	-0.58	-2.48	1.28	1.98	0.11	-0.02
823	-10.75	-23.44	-1.07	-4.05	-6.05	-9.40	0.10	0.18
824	-2.52	-5.48	-1.70	-7.20	1.46	2.29	-0.31	-0.51
825	-1.65	-3.59	-1.02	-1.93	-0.08	-0.14	-0.30	-0.68
826	2.37	5.15	0.76	1.23	0.97	1.52	-0.29	-0.33
827	-4.06	-8.85	-2.87	-9.58	1.82	2.82	-0.12	-0.32
829	1.91	4.16	-0.13	-0.37	1.92	3.00	-0.20	-0.34
830	-3.46	-7.52	-0.48	-1.65	-1.86	-2.89	-0.17	-0.19
831	-3.28	-7.15	-1.17	-3.22	-0.53	-0.83	-0.33	-0.41
832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
833	1.53	3.33	0.10	0.53	0.91	1.41	0.39	0.47
834	-0.15	-0.30	0.21	2.68	-1.29	-2.01	0.69	1.09
835	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
837	-3.13	-6.84	-0.10	-2.71	-1.23	-1.89	-0.01	-0.16
839	9.98	21.73	1.18	4.05	5.48	8.50	-0.22	-0.17
840	-1.03	-2.22	-0.19	1.15	-0.88	-1.37	-0.33	-0.52
841	6.83	14.89	2.33	9.28	0.67	1.03	-0.31	-0.22
842	-5.27	-11.45	-1.58	-5.03	-1.24	-1.92	0.34	0.42
843	2.30	5.01	1.10	2.97	0.22	0.35	-0.08	-0.25
844	1.82	3.96	-0.15	-0.04	1.49	2.32	-0.62	-0.59
845	4.35	9.53	0.65	4.74	1.26	1.97	-0.02	0.01
846	2.72	5.88	-0.30	-2.50	2.82	4.37	-0.81	-0.84
847	-2.37	-5.16	-1.57	-4.50	0.71	1.10	-0.41	-0.14
848	-7.23	-15.70	0.41	2.09	-5.99	-9.28	0.14	0.43
849	6.12	13.29	3.00	9.43	-0.10	-0.17	-0.17	0.03
850	0.91	1.99	1.41	5.84	-1.97	-3.06	0.07	0.16
851	3.88	8.42	-0.85	-4.60	4.64	7.21	-0.67	-0.82
852	5.78	12.57	4.95	15.03	-3.68	-5.72	0.35	0.22
853	1.76	3.83	0.18	0.46	1.06	1.64	0.02	0.01
854	-2.01	-4.37	-0.24	-2.59	-0.67	-1.02	0.07	0.04
855	3.87	8.44	1.47	5.88	0.39	0.61	0.21	0.51
856	-0.32	-0.71	1.38	4.15	-2.37	-3.69	0.34	0.58
857	-3.24	-7.05	0.21	1.11	-2.82	-4.39	0.12	0.42
858	1.23	2.67	0.48	2.08	-0.02	-0.03	0.11	0.17
859	2.06	4.48	0.38	1.01	1.10	1.70	-0.27	-0.20
860	-1.15	-2.52	0.13	-0.54	-0.96	-1.49	0.38	-0.01
861	2.25	4.90	0.15	0.13	1.35	2.10	-0.37	-0.49
862	-3.09	-6.75	2.09	5.07	-4.94	-7.66	0.39	0.18
863	-1.84	-4.02	0.27	-0.10	-2.03	-3.14	-0.25	-0.58

Appendix 2: Selections at Dillon and McNeill for grafting.

Site	Family	Ranking	BLOCK_NO	TREE_NO	Comments	
Dillon	801	11	36	29		Cored
Dillon	803	23	41	14		Cored
Dillon	810	16	32	7		Cored
Dillon	810	16	54	14		Cored
Dillon	817	10	95	16	Good tree	Cored
Dillon	820	14	25	32		Cored
Dillon	821	17	137	20	Ramicorn	Cored
Dillon	833	13	41	3	Good tree	Cored
Dillon	833	13	46	34		Cored
Dillon	839	18	61	6	Good tree	Cored
Dillon	849	4	32	27	Good tree, Ramicorn	Cored
Dillon	849	4	51	24		Cored
Dillon	849	4	125	24		Cored
Dillon	853	21	40	36		Cored
Dillon	855	8	54	20		Cored
Dillon	856	9	42	27	Good tree	Cored
Dillon	858	12	14	36		Cored
Dillon	858	12	20	2	Good tree	Cored
Dillon	858	12	53	8		Cored
Dillon	862	3	67	11		Cored
Dillon	870	19	56	28		Cored
Dillon	888	22	125	27		Cored
Dillon	889	5	31	21		Cored
Dillon	890	1	45	5		Cored
McNeill	801	11	8	20		Cored
McNeill	801	11	117	13	Ramicorn	Not cored
McNeill	803	23	106	1	Good tree	Cored
McNeill	803	23	107	32	Ramicorn	Cored
McNeill	807	20	115	1		Cored
McNeill	807	20	119	31		Cored
McNeill	810	16	103	5		Cored
McNeill	810	16	118	25	Good tree	Cored
McNeill	810	16	120	8		Cored
McNeill	817	10	106	24		Cored
McNeill	817	10	119	12		Cored
McNeill	820	14	84	9	Ramicorn	Not cored
McNeill	821	17	118	11	Good tree	Cored
McNeill	833	13	26	8	Butt Sweep	Cored
McNeill	833	13	119	36	Good tree	Cored
McNeill	834	15	109	15		Cored
McNeill	839	18	8	9		Cored
McNeill	839	18	26	19		Cored
McNeill	839	18	81	3		Cored
McNeill	849	4	107	19		Not cored
McNeill	852	6	112	21		Cored
McNeill	855	8	120	15	Good tree	Cored
McNeill	856	9	118	34		Cored
McNeill	858	12	24	16	Good tree	Cored
McNeill	859	24	40	14		Cored
McNeill	862	3	6	33		Cored
McNeill	865	2	21	11	Good tree	Cored
McNeill	865	2	32	3	Good tree	Cored
McNeill	870	19	117	16	Good tree	Cored
McNeill	872	7	64	24	Good tree	Cored
McNeill	872	7	120	11	Good tree	Cored
McNeill	889	5	55	15		Cored
McNeill	889	5	118	6		Cored
McNeill	890	1	112	17	Ramicorn	Cored
McNeill	890	1	116	13	Ramicorn	Cored

6 References

[1] Durable eucalypts: A multi-regional opportunity for New Zealand's drylands. NZDFI Strategy 2020-2030.
[2] Variation in adaptability and productivity between durable eucalypt species in different New Zealand environments - SWP Technical Report T164 (July 2023,
[3] A comparison of the performance of six eucalypt species planted in 2018 NZDFI demonstration trials. - ITP Technical Report T013 (October 2023)
[4] Bootle KR. 2005. Wood in Australia. Types, properties, and uses. 2nd ed. McGraw-Hill Australia.
[5] Li Y, Apiolaza LA, Altaner C. 2018. Genetic variation in heartwood properties and growth traits of *Eucalyptus bosistoana*. Eur J For Res. 137(4):565-572.
[6] Altaner C. 2019. Minimising growth-strain in eucalypts to transform processing. Christchurch, New Zealand: University of Canterbury. ISBN 978-0-473-49233-5
[7] Sharma M, Dijkstra SM, Garrill A, Collings DA, Altaner CM. 2024. Assessing wood grain and twist in a 2-year-old *Eucalyptus bosistoana* breeding population. Trees.
[8] Slee, A., Brooker, M. I. H., Duffy, S., & West, J. (2015). EUCLID. Centre for Australian National Biodiversity Research. https://apps.lucidcentral.org/euclid/text/intro/index.html
[9] Kim S-J. 2024. Population genomic study of a *Eucalyptus bosistoana* breeding programme: a thesis for the degree of Doctor of Philosophy in Forestry, University of Canterbury by Seol-Jong Kim.
[10] Davies NT, Apiolaza LA, Sharma M. 2017. Heritability of growth-strain in *Eucalyptus bosistoana*: a Bayesian approach with left-censored data. New Zealand Journal of Forestry Science. 47.
[11] Rajapaksha C, Apiolaza LA, Squire MA, Altaner CM. Genetic parameters of essential-oil traits for *Eucalyptus bosistoana*. Austral For. 68(2):90-99.
[12] SWP-T108 C. Altaner, M. Sharma (2020) Heartwood in *Eucalyptus bosistoana* (Juken NZ Ngaumu 2012 trial)
[13] SWP-FN137 R. McConnochie (2022) Assessment of 2012 *E. bosistoana* Breeding Population at McNeill property, Hawkes Bay
[14] SWP-T121 C. Altaner (2021) Recommended sampling intensity for phenotyping durable eucalypt breeding trials for heartwood quality.
[15] Li Y. and Altaner C. (2019) Calibration of near infrared spectroscopy (NIRS) data of three Eucalyptus species with extractive contents determined by ASE extraction for rapid identification of species and high extractive contents, Holzforschung 73(6): 537-545.
[16] R Core Team. (2022). R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from http://www.R-project.org/
[17] Butler D., Cullis B., Gilmour A. and Gogel B. (2009). ASReml R package version 3.0. Hemel Hempstead, UK, VSN International Ltd.