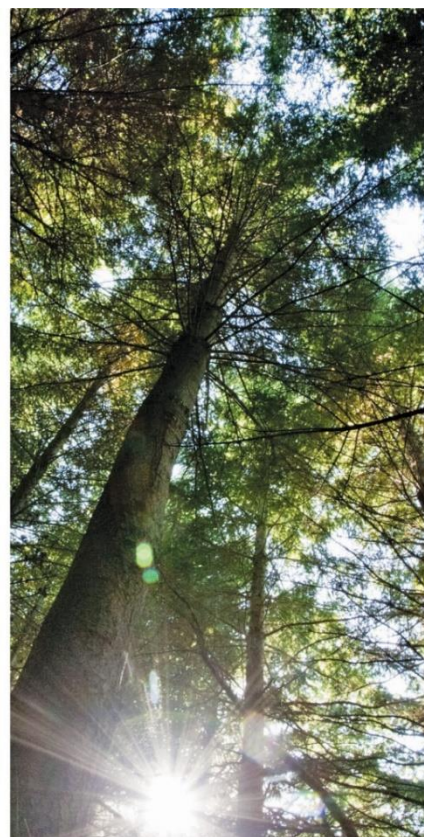
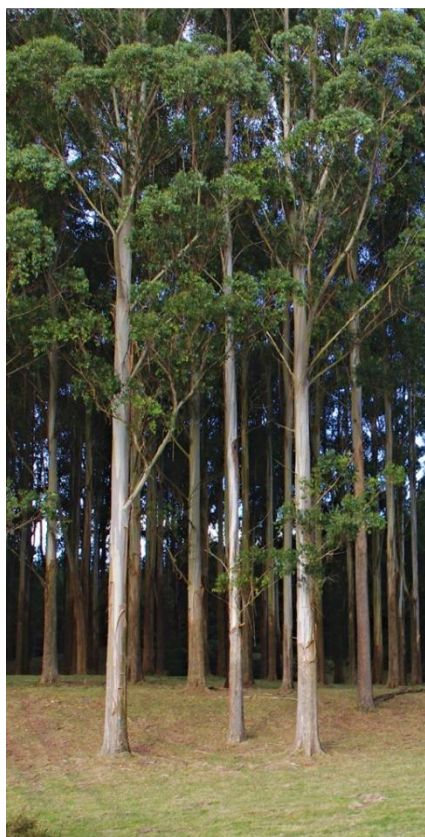


## *Eucalyptus nitens* breeding plan update 2020 (SSIF - Scion aligned funding)

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**Date:** June 2020

**Publication No:** SWP-T104

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# TABLE OF CONTENTS

<i>Eucalyptus nitens</i> breeding plan update 2020.....	1
(SSIF - Scion aligned funding) .....	1
EXECUTIVE SUMMARY .....	1
INTRODUCTION .....	2
<b>EUCALYPTUS NITENS BREEDING</b> .....	3
Genetics research overview .....	3
Genetic variation in selection traits.....	3
New selection methods; Genomic selection (GS).....	3
Genotype by environment interaction (G x E) in selection .....	5
Genetic basis of palatability to <i>Paropsis charybdis</i> .....	5
Screening for Checking and collapse .....	6
Breeding objectives and selection criteria .....	6
Breeding strategy.....	7
Solid wood and pulp production seed-orchards established for South Wood Export .....	7
Selection strategy.....	7
Genomic selection.....	9
Operational actions including genetic research 2020 onwards .....	12
2020-2021.....	12
Research on developing non-destructive methods to assess wood properties .....	12
New infusions of phenotypic and genotypic data for genomic selection.....	12
Aspirational goals for 2021-2026 (subject to funding).....	12
Graft to establish breeding archive .....	12
4th generation progeny trials .....	12
Genetic material exchange with Australia/Genetic gain trials.....	12
Timeline for <i>E. nitens</i> breeding until 2026 .....	13
2020.....	13
2021.....	13
2022.....	13
2023.....	13
2026.....	13
CONCLUSIONS.....	13
REFERENCES .....	14

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# EXECUTIVE SUMMARY

*Eucalyptus nitens* breeding has a long tradition in commercial forestry in New Zealand. It is nowadays the most important *Eucalyptus* species in the country, and as a fast-growing species of good form, it has the potential to offer even greater opportunities to tree growers than currently is the case. The latest breeding plan update following the update in 2016 (Suontama et al. 2016) addressed the importance of developing this species towards solid wood production and consequently, proposed genetic research to gauge possibilities to improve these traits by breeding.

Recent genetics research showed good prospects for the genetic improvement of solid wood traits. Selections based on these studies have been made to the Specialty Wood Products (SWP) members' production seed-orchards. Additional selections will form a breeding archive and the basis for a new breeding population. These selections are proposed to be undertaken across three progeny trials in Southland (Keens Block, Fortification Road and Howdens Block) in this update to the breeding plan. Volume, wood quality, form and adaptability are all proposed as breeding objectives in this updated breeding plan. Selections at Keens Block will especially focus on improvement of wood quality whilst selections at Howdens Block (a subset of families) will be used to identify genotypes which have a better resistance to defoliating leaf beetles (*Paropsis charybdis*). Genetic diversity will be maintained by selecting at least 100 families, preferably 150 families based on estimated BLUP breeding values. Progeny from these selections will be planted for testing across two to three sites, if possible two in the South Island and one in the North Island.

The proof-of-concept genomic selection study undertaken in 2015 indicated that using markers gave considerably improved breeding value accuracies than pedigree-only based models. In addition, a business case developed to compare three different breeding scenarios, showed that forest growers will benefit of genomic selections through a predicted \$7 million increase in the net present value compared with traditional breeding. It is therefore strongly recommended that the breeding of *E. nitens* take advantage of this opportunity through the application of genomic technologies in breeding in the future. Expansion of the measurements and genotyping to ensure more robust prediction models will be done by sampling additional genotypes at a second site, including phenotyping more for solid wood properties, effectively doubling the amount of genotyped individuals in the current population.

Essential operational actions in the breeding programme to target the breeding objectives and for implementation of this breeding strategy, as well as supporting genetic research are listed in this report.

# INTRODUCTION

*Eucalyptus nitens* (Deane et Maiden) Maiden is the second most popular commercially planted eucalypt in its native country, Australia, and the most important commercially planted eucalypt in New Zealand. *Eucalyptus nitens* is described as a tall to very tall tree, usually reaching heights of 40 to 70 m and even as tall as 90 m with diameter at breast height 1 to 2 m and above (Boland et al. 1984). This forest tree species is recommended as the best species at sites of 500 to 700 metres in the Central North Island and is the eucalypt species most likely to be successful on most plantation sites in the South Island (Cannon and Shelbourne 1991). *Eucalyptus nitens* is presently distributed across the country, the major planting sites being located in the Southland and in the Central North Island (Meason et al. 2016).

*Eucalyptus nitens* was introduced to New Zealand in the 1920s and a breeding programme was initiated in the mid-1970s. The first cycle of a breeding programme targeted better growth, form and tolerance to environmental stresses. *Eucalyptus nitens* is a fast-growing species which with qualities for pulp-wood production and a great potential for solid wood production. In recent years there has been an increased interest around the world in breeding this species for solid wood products (e.g. Raymond 2002, Kube 2005, Kube and Raymond 2005, Biechele et al. 2009, Hamilton et al. 2009). *Eucalyptus nitens* has been mainly planted for pulp-production in New Zealand, however, developing this species for solid wood products, would ultimately provide scope for larger forest industry revenue via higher value timber products. The main challenge of *E. nitens*, as any other *Eucalyptus*, is in the efficient production of solid-wood products due to growth stresses that cause cracking and shrinkage of wood at drying, as well as timber movement on drying. Targeted breeding against these defects for better wood quality and improved conversion rates from log to lumber would permanently change wood property traits in the population. Significant breeding results will likely, however, require a long period of time (a rotation) to be observed in the harvest of the production population. In the meantime, and complementary to breeding, new wood processing methods may also offer efficient solutions for wood-drying problems by improving drying results for different solid wood products.

*Eucalyptus nitens* is recognised not only for its fast growth but also for good form and cold-hardiness. The first genetic studies for *E. nitens* in New Zealand focussed on testing the suitability of provenances across a range of sites (Franklin 1980, King and Wilcox 1988). Both these studies concluded that Central Victorian families had the best growth rates. King and Wilcox (1981) recommended that breeding should be based on the material originating from Central Victorian provenances which does, to a large extent comprise the current breeding population. As many as 96% of families in the 1990 open-pollinated population came from Central Victorian provenances which showed the greatest growth potential at the early breeding trials (Franklin 1980, King and Wilcox 1988).

The major limiting factor for the productivity of *E. nitens* is susceptibility to *Paropsis charybdis*, which is a defoliating *Eucalyptus* tortoise beetle (Wilcox 1980, King and Wilcox 1988). A preliminary assessment of *Paropsis* chewing using a scoring technique developed in 2018, in a progeny trial at Howdens Block in Southland resulted in a narrow sense heritability estimate of 0.15 (Klapste 2019). The results also indicated differences between seed sources, with those of New South Wales origin doing best. This difference between provenances had been previously seen in a provenance trial planted on a warm site in Rotoehu forest in 1993 (Low 2000). Selection of trees showing improved resistance to browsing by *Paropsis* in the next generation would offer an effective tool to enhance forest health and forest productivity.

A successful implementation of biocontrol using a natural enemy of *Paropsis*, called *Eadya paropsidis*, would offer an environmentally friendly method to target to more resilient *Eucalyptus* forests in the short-term (Withers et al. 2015). In 2019 a population of *Eadya* was collected in Australia and imported to New Zealand, unfortunately the collection was contaminated with a previously unknown microsporidian or a sporozoan species and was unable to be released

(Withers et al. 2020). Further collections from uninfected populations are planned if funding can be found.

Another pathogen observed on warm sites is *Mycosphaerella*, a fungus that attacks *E. nitens* leaves in their juvenile state (up to five years of age). However, *Mycosphaerella* is not found on the majority of sites currently planted in *E. nitens*. The occurrence of the disease, however, may rise along the warming climate and therefore would be important to monitor whenever inspecting breeding trials.

The selection of the fourth generation is underway in the current breeding programme. Third generation progeny trials in Southland have been assessed for growth, form and wood density (Baltunis et al. 2013a, Baltunis et al. 2013b) and one of these was also assessed for solid wood properties (Stovold and Suontama 2015, Suontama et al. 2016). Selections for pulp and solid wood populations were made for South Wood Export's production seed-orchards in 2015 (Low et al. 2015). Research on new traits for solid wood production goals estimated good possibilities to improve trees by breeding based on considerable genetic variation between individuals. The objective of this paper is to update breeding objectives, selection criteria and strategy as well as outline the next operational actions and contents of genetic research for *E. nitens*.

## **EUCALYPTUS NITENS BREEDING**

### **Genetics research overview**

#### **Genetic variation in selection traits**

One of the main points of interest in genetics research for this species is in the selection of solid wood traits in order to improve wood processing and drying. New drying and processing methods offer additional, more rapid solutions for end-product users to mitigate effects of wood shrinkage and internal checking. Nevertheless, growth stress effects in wood are a combination of genetics and environmental factors such as silviculture practises (Kubler 1987) that can have a large effect on the development of growth stresses and related wood properties.

We estimated moderate heritabilities for traits important to solid wood production (growth strain, wood shrinkage and collapse, internal checking), showing good prospects for selection in this breeding population (Suontama et al. 2016). Since the wood properties are expensive to measure and development of non-destructive methods require a considerable amount resources, indirect selection by using surrogate traits such as volume or wood density can offer an option to expensive phenotyping. A correlated genetic response of wood properties would depend on the heritability of a trait and its genetic correlation with a surrogate trait. Due to a relatively small amount of data for quantitative genetic analysis, we were not able to conclude if indirect selection for expensive to measure wood property traits would be effective. However, estimated genetic correlations indicated that selection for some of the 'easily' measured traits should also result in an improvement in other traits of interest. Selection for wood density and stiffness should result in improvement of the quality of sapwood and heartwood (decrease in internal checking) (Suontama et al. 2016). Simultaneous selection against growth strain (split after sawing) and wood shrinkage would be possible due to favourable genetic correlations. It also implies that genetic gains would be achievable in both traits. The same study showed that ill-effects due to growth stresses and drying at different log lengths (at 3 and 6 metres) are likely to be determined by the same genetic pathways, based genetic correlations approaching unity. Consequently, selection could be carried out irrespective of log length.

#### **New selection methods; Genomic selection (GS)**

The *Eucalyptus nitens* breeding strategy is based on an open-pollinated population that uses forwards selection with a rolling-front strategy. A proof-of-concept study indicated that utilization of genomic selection (GS) in the estimation of breeding values would be useful for a new breeding strategy (Klapste et al. 2016). The proof-of-concept study was carried out on the Keens Block

progeny trial for growth, form and solid wood properties. The genotyping platform was a high-density single-nucleotide polymorphism (SNP) chip (EUChip) 60k developed for 12 different *Eucalyptus* species including *E. nitens* (Silva-Junior et al. 2015). The improved efficiency in breeding is established through two pathways in genomic selection. First, a possibility to decrease the time from selection to deployment by skipping a progeny trial assessment phase and selecting at the seedling stage will enhance genetic improvement (Resende et al. 2012). Second, genomic estimated breeding values would improve breeding value accuracies and the genetic gain available for selection, this is primarily due to the fact that genetic gain predictions based on open-pollinated tree populations lack the genetic information coming from a male parent. Ultimately, the aim is to obtain sufficient data so that later-age wood properties may be predicted using the markers from the EUChip (or equivalent), which would in turn improve the rate of genetic improvement in wood properties, and providing there is continuing support for the breeding programme, a more rapid turnover in generations.

Around 12,000 genomic markers were useful for the prediction of genomic breeding values in the *E. nitens* population after filtering which, based on statistical significance of a SNP marker in the study by Klapste et al. (2016). The accuracy of genomic predicted breeding values significantly surpassed the accuracies of BLUP breeding values in the proof-of-concept study for most of the traits (Klapste et al. 2016). Resende et al. (2012) reported that proportion of the accuracy of phenotypic BLUP selection recovered by GS in *Eucalyptus* varied from 0.75 to 1.20 depending on the trait and population in question.



**Figure 1.** Keens Block progeny trial in Southland where the tree material in the breeding population was evaluated for solid wood properties.

Economic analysis also supported the use of genomic selection, which was demonstrated in a business case for *E. nitens* based on parameters derived from this population (Corbett 2016). The business case analysis was built up for three breeding scenarios including traditional, genomics and genomics with clonal options for selection. Results indicated that using genomic selection, the net present value (NPV) results in \$7 million increase for forest growers compared with traditional

breeding. Further, the same study found that the NPV increases were even larger for end product processors, with an estimated gain of \$34 million obtained for laminated veneer lumber (LVL) (Corbett 2016).

### Genotype by environment interaction (G x E) in selection

The breeding strategy for *E. nitens* should be based on cost-effective methods due to a relatively small amount of planted area of this species in New Zealand, currently at around 12,000 hectares. Possible effects of genotype by environment interaction (G x E) on selections must, however, be considered. This means that new tree material must be tested across different environments if economically possible. Eucalypts are generally rather site-specific in their performance which can result in rank changes in breeding values estimation. This interaction between genotypes and environment impairs selection accuracy and consequently, results in decreased realized genetic gains. We estimated genetic correlations across the two progeny trials at Keens Block and at Fortification Road which indicated significant G x E for volume (a genetic correlation of 0.29) (Table 1). Whilst other traits important to breeding objectives (DBH, wood density) did not express biologically important (genetic correlations were higher than 0.60) or statistically significant G x E. The two sites are located in a small distance apart in Southland, and these sites are likely to be characterised by similar site features. This may explain to some extent high/non-significant genetic correlations across two sites. On the other hand, the progeny trials shared only 29 families of the same origin and this is likely to have affected the magnitude or significance of these genetic correlations.

The South Island has been traditionally considered as best suited region for planting *E. nitens* due to cold, wet conditions limiting the population numbers and thus damage from defoliating insects (King and Wilcox 1988), although the current knowledge declares that *E. nitens* plantations from Southland to the Central North Island can be heavily defoliated by *Paropsis* (Withers et al. 2015). There has been a recent interest in planting this species in the Central North Island (Withers et al. 2013) and some observations on young *E. nitens* have shown that it thrives at colder parts of the Kaingaroa Forest. It is therefore important to address, through genetics research, if there is a difference between genotypes in deployment at North and South Island sites. This should be done by testing the tree material of the similar backgrounds at least two or three more distant sites using the most common regions for the current commercial plantations of this species.

**Table 1.** Estimated genetic correlations ( $R_g$ ) with their standard errors (std. error) between two progeny trials in Southland.

Trait	$R_g$ (std. error)
Height	0.40 (0.36)
DBH	0.38 (0.37)
Volume	0.29 (0.39)
Wood density	0.68 (0.28)
Malformation	1.00 (0.39)
Straightness	0.82 (0.18)

### Genetic basis of palatability to *Paropsis charybdis*

A trial of 180 families from the New Zealand breeding program was established in 2011 at Howdens block (FR507) in the Southwood Exports estate in Southland. With the support of SouthWood export, no chemical control was undertaken, in anticipation of the *Paropsis* population building up and attacking the trial at a level that each family could be scored in some way and breeding values for palatability estimated. In early 2018, a scoring technique to assess chewing damage by *Paropsis* was developed and tested at a site in Kaingaroa forest. Monitoring at the Howdens site each year showed low levels of damage, not enough to attempt scoring. A decision was taken to seed the trial with adult beetles collected from Poronui station in the central North Island. Around 2800 beetles were caught and translocated to the site and released on the 31<sup>st</sup> of



October. Release was carried out across the site in a regular pattern as four females and four males at each release location. The site was then monitored monthly to see if suitable levels of chewing was occurring and around April of 2019 a decision was made that there was enough damage and an assessment of each tree was carried out in May 2019.

Results from analysing the chewing data (Klapste 2019) showed a narrow sense heritability of 0.15 indicating some potential for genetic improvement through breeding. The distribution of parental breeding values also showed some differences between different origins, with Tinkers seed orchard material most sensitive to chewing, and the least sensitive material coming from New South Wales provenance material.

### **Screening for Checking and collapse**

*Eucalyptus nitens* frequently develops within ring checks and collapse (washboarding) during drying, making the wood unsuitable for use as sawn timber. Numerous studies have tried altering drying conditions to reduce levels and checking and collapse, but this has not been completely successful, and low recovery due to drying defects is a major barrier to its use for sawn timber. A study was undertaken Sargent (2017) to pre-screen 200 trees from a known seed source (Tinkers seed orchard) using a variety of non-destructive measures (core shrinkage, density and acoustic velocity), and from these 100 trees were destructively sampled to confirm predicted checking, and from these 30 trees with a range of properties were sawn and the boards used in a drying study. Good correlations were found between the non-destructive measures and the average level of degrade for each log, suggesting potential to pre-screen to identify logs which should have reduced degrade. A second study was undertaken to verify these results, sampling trees and logs from the same stand, however in this study correlations were lower than the original study, inferring less confidence in using pre -screening with the tools available at the time, and further work on identifying other possible techniques/new technologies for non-destructive screening would be undertaken in the future.

### **Breeding objectives and selection criteria**

There are two main objectives of the breeding programme, one is to breed for pulp-wood to produce high-value paper products. The second is to breed for solid-wood to produce sawn timber and appearance products. Maintenance of tree form and ability to resist defoliation is also important. Current breeding goals are:

- 1) **Wood quality** which is defined by high wood density, low growth strain (growth stress), low shrinkage, a small number of or absence of internal checking and collapse (recovery after drying).
- 2) **Volume** defined as a function of diameter at breast height (1.3 m) and height.
- 3) **Form** defined as stem straightness and acceptability.
- 4) **Adaptability** defined as improved resistance to defoliation by insects.

A breeding index is used for selection. The index is derived from an aggregate of and individual tree's breeding values from measured traits 1) to 4). The overall aim is to deliver the tree material for the NZ forest industry that has a satisfactory wood quality for both high-quality solid wood and paper products, good growth and form and improved resistance to pests and insects (*Paropsis charybdis*).

**Table 2.** Breeding objectives and selection criteria.

<b>Trait</b>	<b>Target</b>	<b>Impact</b>
Wood density	Increase by 5 per cent Target population threshold 500 kg/ m <sup>3</sup>	Increased yield of higher value pulp and solid wood
Wood shrinkage	Culling of genotypes above average rates of shrinkage	Better utilization of timber for specialty wood products and reduced processing costs
Internal checking	Culling of genotypes above average rates of checking	Better utilization of timber for specialty wood products
Volume yield	Increase by 5 per cent	More efficient production and lower costs to harvesting
Stem straightness	Maintain overall good form, cull all individuals below population avg. score 7	Better utilization of log at saw mill
Foliar health	Improved resistance to pests	Better growth rates and increased survival in different environments

The average values for growth and form and wood properties were described in Suontama et al. (2016) based on the assessments at Keens Block progeny trial at age six (growth, form, wood density) and age seven (wood density, shrinkage and internal checking). The average values for selection traits will be, however, were re-estimated at the next phase of selections when all historical and new data have been merged for the latest analysis and selection purposes.

## **Breeding strategy**

### **Solid wood and pulp production seed-orchards established for South Wood Export**

The forty-year-old breeding programme has undergone three rounds of selections. The current breeding archives originate from the second generation progeny trials established during 1990-1992 (Figure 4). The breeding archive material was planted out to test progenies at three different sites in Southland between 2005 and 2011. In addition, a small subset of these seeds-sources was left and sown in Kaingaroa in 2011. All four trials partially share the same family material (Figure 4).

Two progeny trials, Keens Block and Fortification Road, were assessed at age six for growth and form and wood density (Baltunis et al. 2013a, Baltunis et al. 2013b). Age seven measurements for solid wood properties were undertaken at Keens Block (Stovold and Suontama 2015, Suontama et al. 2016). Based on these assessments, selections were carried out to establish new production seed-orchards at South Wood Export LTD and Proseed. In 2015, two orchards were established, the first seed-orchard targeted for solid-wood production, and second seed-orchard targeted for high-yield pulp-wood production. At the first phase, the best genotypes based on BLUP (Best Linear Unbiased Prediction) estimated breeding values for DBH, wood density and growth strain (splitting after sawing) were selected for grafting. At the second phase, selections against wood shrinkage and internal checking were included in the seed-orchards. The grafted seed-orchards involve families which were assessed as the best material for the two production lines (Low et al. 2015).

### **Selection strategy**

This updated breeding strategy continues to follow forest industry's demand to produce high-quality sawn timber and appearance products and high-quality paper (solid wood and pulp-chip). The new breeding population will be managed as a single population with a 'rolling front strategy' using forward selection based on the estimation of individual tree breeding values (BLUP). A new breeding archive should be established by selecting 100 to 150 families to form the next generation's parents. The best families are recommended to be determined by ranking the families based on their estimated breeding values (progenies) and then selecting the best individuals based

on their own estimated tree breeding values. Selecting an adequate number of families will ensure that genetic diversity is maintained and enabling genetic progress continues in the breeding programme.

The next selections should be conducted across the three latest progeny trials at Keens Block, Fortification Road and Howdens Block. Genotype by environment (G x E) interaction was not significant across Keens Block and Fortification Road, except for volume. However, this should be explored, including Howdens Block, for which data was collected in 2019. In the case of no G x E across these sites, among-site selection can be undertaken. Otherwise, consideration should be given to models where tree performances of similar genetic background are considered as genetically different traits when exposed to different environments or site conditions. Selections within sites should also be considered in this latter case. Selections with consistent performance among sites will be preferred.

Selections will be carried out by taking forward the best individuals within the best families and at minimum, involving at least 50% of the families from each origin (seed-orchard). Breeding objectives at the progeny trials will be emphasized as following:

1. Keens Block: **wood quality** (all traits), volume, form,
2. Fortification Road: wood density, volume, form, **predicted wood quality, using cores and NIR based models**
3. Howdens Block: volume, form, **adaptability (increased tolerance to *Paropsis*)**

Forward-selected material from the breeding archives and production seed-orchards will be tested in progeny trials when the seed is available. As stated earlier, two to three progeny trials will be planted to test the stability of tree performance in different environments. Trials should contain a set of the same families, at least 20-30 % but preferably much more, to ensure good genetic connectivity between the sites. This ensures we can test for genotype by environment interaction as well as the future identification of environmentally stable genotypes/families. Testing G x E will be essential for new breeding traits (especially wood properties) since this knowledge is not widely available currently in the breeding programme. However, no significant predicted G x E was found for *E. nitens* wood properties in Australia (Hamilton et al. 2009).

Developing cost-effective options to measure wood quality is necessary to address through research in the future. An NIR (Near Infrared Spectroscopy) model to phenotype trees will be developed in 2020 and may offer a cost-effective and non-destructive option to maintain progressing in breeding for solid wood properties, i.e. shrinkage, collapse and internal checking. If non-destructive methods to measure wood quality do not prove to be reliable for breeding objectives, indirect selection for traits important to solid wood production should be sought after.



**Figure 2.** New production seed-orchards established at Clarkes Forest (South Wood Export) in 2015 targeting for improved solid wood properties.



**Figure 3.** *Eucalyptus nitens* progeny trial at Howdens Block in Southland was established in 2011. The tree material at this trial originates from Alexandra, Tinkers and Waiouru seed-orchards and was established to test a sub-set of the families in the breeding population for resistance to the leaf-eating beetle *Paropsis* data is now available from this site to use in selection next generation parents for testing.

### Genomic selection

Implementing genomic selection to predict breeding values of the tree material will be pursued in the breeding programme. Nevertheless, this requires collecting more material to ‘validate’ predictions for a wider range of phenotypes and genotypes to predict genomic breeding values at the seedling stage reliably. Klapste et al. (2016) emphasized the importance of capturing a large

amount of genetic variation in training population to produce robust prediction models and proposed to keep the breeding population as a separate 'arboretum' to achieve genetic gains using genomics as efficiently as possible.

The implementation timeline after 2022 will depend on the priorities and funding from the Specialty Wood Products Partnership (and its successor) and the continued availability of Scion Strategic Investment Funding (Scion Core Funding).

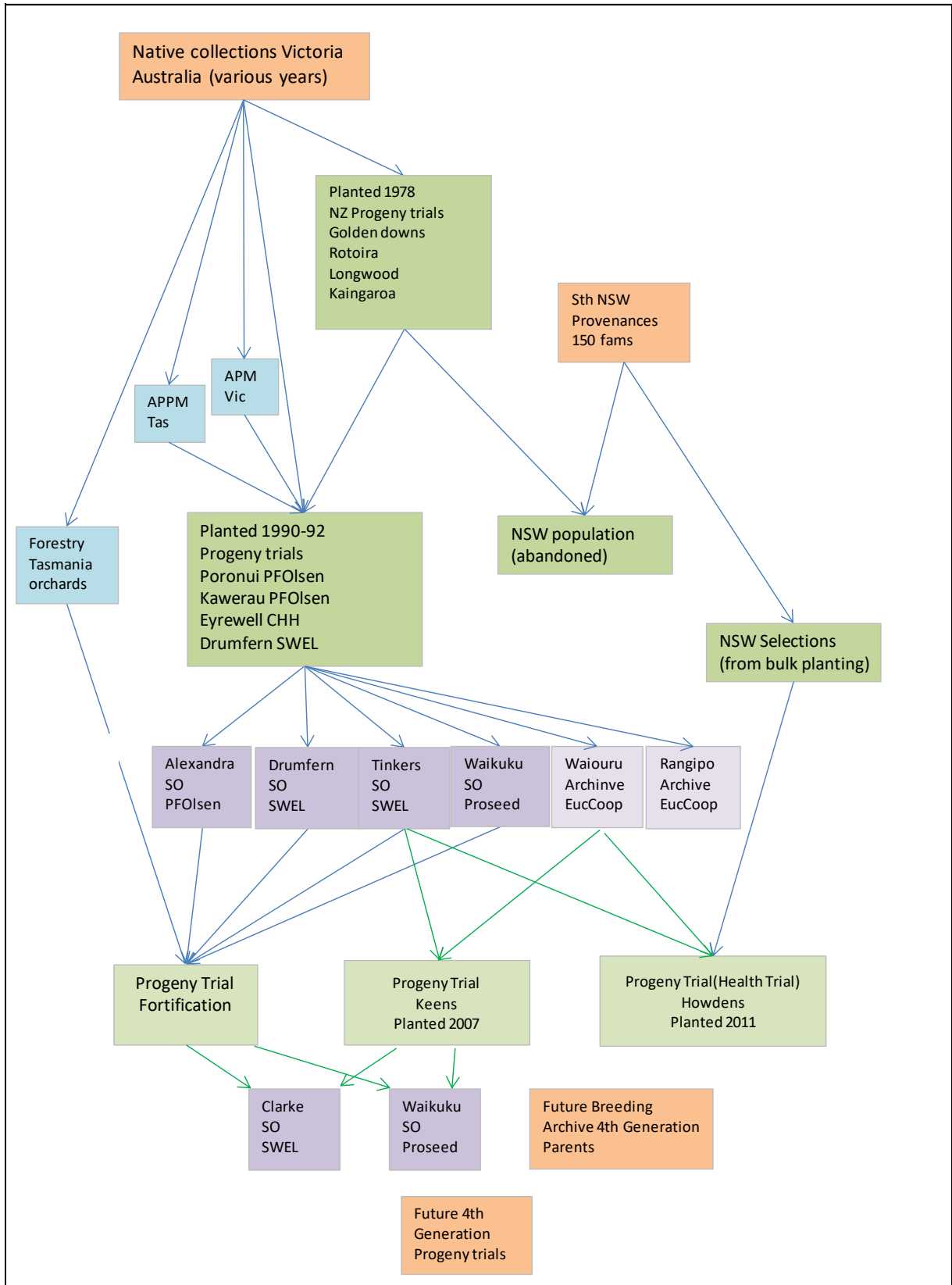


Figure 4. *Eucalyptus nitens* breeding programme. (After Stovold et al. 2010 and Baltunis et al. 2013).

## **Operational actions including genetic research 2020 onwards**

All operational actions are subject to having sufficient funding. Work will be extended into additional financial years if this is the case.

### **2020-2021**

#### **Research on developing non-destructive methods to assess wood properties**

800 disks from the Keens progeny trials site have been scanned using Scions Discbot scanner. A NIR-prediction model will be developed for wood shrinkage based on the data collected. A sample of the 800 discs will be ground and cellulose content measure, to create a second cellulose prediction model. These models will be able to be used to non-destructively predict shrinkage and cellulose content if the Fortification Rd site is sampled using 12mm increment cores. This will significantly reduce the costs of measuring these trials for these traits.

#### **New infusions of phenotypic and genotypic data for genomic selection**

Collection of increment cores for non-destructive measurements for solid wood properties at Fortification Road will be subject to the availability of functional NIR correlation curves (we expect this will be completed in 2020). The selections made from Fortification Road will then contribute additional seed-orchard material that has, as yet, been untested for wood properties (originating from Alexandra, Drumfern, Waikuku).

In addition to the collection of new increment cores, each tree sampled at Fortification will have cambium collected and DNA extracted. Genomic data will be generated from this and added to genomic data already collected from Keens Block, doubling the size of the genomic training population and new genomic breeding values will be calculated. Genomic and traditional breeding values will be used to identify further selections for new orchard and archives.

### **Aspirational goals for 2021-2026 (subject to funding)**

#### **Graft to establish breeding archive**

Existing selections and new selections from Keen's Block, Fortification Road and Howdens Block will be grafted to establish a breeding archive.

The selections will be established in a breeding archive and at two commercial orchards where required (South Wood Export LTD., Proseed).

#### **4th generation progeny trials**

Once the breeding archive and/or the commercial orchards are producing seed, new progeny tests should be established. Two to three sites, preferably one in the North Island and two in the South Island. Some material from the previous generation seed orchards should be included for comparison. Target number of entries/families in the trial should be between 100 to 150.

#### **Genetic material exchange with Australia/Genetic gain trials**

After four generations, the diversity in the breeding population will have reduced. Some consideration should be given to negotiating an exchange of material (seeds) with one of the Australian breeding programmes. This material could be tested alongside the 4<sup>th</sup> generation NZ material, for future infusion and/or used to set up genetic gains trials.

## Timeline for *E. nitens* breeding until 2026

### 2020

Update breeding Plan  
Create NIR-based model for wood quality

### 2021

Take additional DNA samples at the Fortification Rd trial and re calculate genomic breeding values  
Predict wood quality from new cores from Fortification Rd using the NIR model developed in 2020.

### 2022

Identify and graft new selections.

### 2023

Establish breeding archive.

### 2026

Collect seed and establish new progeny trials at 2-3 sites.  
Genetic material exchange with Australia.

## CONCLUSIONS

This breeding plan outlines updated breeding objectives for solid wood and pulp-wood production in *Eucalyptus nitens*. The breeding objective for the two production purposes are to improve wood quality, volume, form and adaptability. In addition to new selection traits for solid wood production, adaptability in terms of resistance to pests is considered as a critical trait to be a part of the breeding objective as well. *Paropsis charybdis* is the major factor impacting productivity and Forest Grower's interest in planting more of this species in New Zealand. The breeding population will be managed as one population, but with selections targeted at the two production purposes; pulp and solid-wood. The breeding strategy uses forwards selection in an open-pollinated breeding population, where the number of families maintained is at least 100 to 150 to ensure continuing genetic diversity and on-going genetic gains.

Genetic evaluation will be conducted using progeny testing and estimation of individual tree breeding values. Genomic selection options will be pursued in the breeding programme by additional phenotyping and genotyping to increase the robustness of prediction models. Progeny tests (trials) will be established at two to three sites which are regarded as commercially important forest growing areas for this species. Testing across multiple sites will elucidate the stability of genotypes across different environments, with specific attention paid to the plasticity of solid wood properties. Non-destructive, cost-effective methods to phenotype solid wood selection traits will be investigated. Investigation of the effectiveness of using indirect selection and prediction of genomic breeding values as an alternative to NIR methodology is also recommended.



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