

Breeding Douglas-fir for high-value wood products in the genomic selection era

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Abstract

The Specialty Wood Products Research Partnership (SWP), which is in its third year, has a strong focus on the genetic improvement of Douglas-fir. The background of Douglas-fir in New Zealand and elsewhere, and achievements of the current genetic research programme targeting high-value wood production, with an initiation of genomic selection into the breeding programme is discussed.

Introduction

Douglas-fir is one of the most highly-regarded sawn timbers in the world. New Zealand Douglas-fir is the coastal variety, *Pseudotsuga menziesii* var. *menziesii*, native to the Pacific Northwest of Canada and the US. This species has beautifully coloured wood of great strength, and is one of the few tree species that is able to achieve full sawn timber lengths without knots. Widely used in construction, Douglas-fir is also a common timber in sailing boat masts, demonstrating the excellent wood properties of this species.

In its countries of origin, the economic importance of Douglas-fir is huge, where it forms a multi-billion dollar forest production business and has one of the largest tree breeding programmes in the world (Howe et al., 2013). In the US breeding programme, thousands of parents have been tested. The number of parents in the Northwest Tree Improvement Cooperative breeding programme alone is 20,159; and when parents from all breeding zones are added, the total number is over 33,000 (Howe, 2017).

Douglas-fir in New Zealand

In 150 years, Douglas-fir has established itself in New Zealand as the second most popular planted tree species, the main plantation area being in the South Island. The current total area of planted Douglas-fir is 104,173 ha (Facts and Figures 2016/2017, NZFOA). The outstanding wood properties of Douglas-fir could help map New Zealand into the list of top-ranking wood producers in the world. Douglas-fir is second only to radiata pine in plantation area, but longer rotation times across the country and Swiss needle cast (SNC) (*Phaeocryptopus gaeumannii*) are holding the species back from becoming a more competitive forestry option. SNC has a significant effect on growth, both on the observable and genetic levels (Kimberley et al., 2011; Klápště et al., 2017a). Productivity and growth rates can be improved by breeding. The current targets at a rotation age of 35 years is a total yield of 600 m³ TRV/ha (total recoverable volume), set in the latest breeding plan update (Suontama et al., 2016).

Since the first introduction of Douglas-fir seed to New Zealand from an English nursery by J.B.A. Acland of Canterbury in 1859 (Miller & Knowles, 1994), several



Measuring wood stiffness on 52-year-old Douglas-fir of Fort Bragg provenance

importations of seed have been recorded. These include seed from natural stands or selected material from the Pacific Northwest of the US (Miller & Knowles, 1994; Shelbourne et al., 2007; Low et al., 2009). The first steps of breeding can be considered to have taken place in the 1950s by planting trials to test different provenances from Washington, Oregon and California (Shelbourne et al., 2007). Further provenance tests were planted in the 1970s.

The latest significant seed introduction into the breeding programme was in the early 1990s, with a collection of seed from an impressive 240 open-pollinated families from 21 coastal Oregon and Californian provenances (Shelbourne et al., 2007; Low et al., 2009). This material from the Douglas-fir Research Co-operative was planted out in 1996 at four different sites – one in the North Island and the other trials in the northern and southern parts of the South Island (Dungey et al., 2012). The breeding programme has progressed slowly since then, with the first generation seed orchards currently in production and first attempts to evaluate second generation progeny trials having recently been undertaken.

New research through the SWP Research Partnership

The Specialty Wood Products Research Partnership (SWP) is in its third year (<https://fgr.nz/programmes/alternative-species/swp-programme/>) and has a strong focus on the genetic improvement of Douglas-fir. A comprehensive reassessment of the 1996 progeny trials in Kaingaroa and Gowan Hill at age 21 has recently taken place and the genetic evaluation of the trials provides future direction about how to proceed in breeding. An emphasis on breeding objectives has been put on productivity and vigour since the beginning of the breeding programme.

Additionally, an overall tree form (more specifically stem form), absence of forking, ramicorn branching and density of crown have been critical traits to improve (Shelbourne et al., 2007). When the breeding objectives for Douglas-fir were recently reviewed, one of the major attributes for genetic improvement was stem form, which in some cases has been considered to be below acceptable quality for any sawn timber production in the current breeding programme material. Fortunately, stem straightness in Douglas-fir can be improved by selection since up to 45% of the trait variation is controlled by genetic effects (Klápště et al., 2017a).

Our recent analysis of the 1996 progeny trials showed that selection for faster growth does not support selection of good stem form (Klápště et al., 2017a). Consequently, selection for multiple breeding objective traits must compromise between productivity and stem form. Other form traits such as branching habit show low genetic variation (both additive genetic variation and provenance level variation), which suggests that other contributors (i.e. silviculture) may have greater



Latest progeny trial planted at Gowan Hill in Southland at young age

influence on this trait. It is interesting that productivity is again unfavourably correlated with branching (Klápště et al., 2017a).

Magalska and Howe (2014) reported similar unfavourable associations between productivity and stem defects in the species natural habitat in western Oregon and Washington, where stem defects were explicitly forks and ramicorn branching. Interestingly, more productive sites expressed more stem defects. Previous studies did not identify any clear associations between abiotic sites' attributes (soil, topographic, climatic) and stem defects (Magalska & Howe, 2014).

Swiss needle cast

The effects of SNC on tree growth since its first identification in New Zealand in 1959 are not trivial and have been well studied. Scion's permanent sample plot (PSP) measurements have shown that over a period of 30 years the average growth loss due to SNC across the

whole country was 30%, and was greater in the North (35%) than in the South Island (23%) (Kimberley et al., 2011). However, the decline in growth rate stabilised to a lower level in later years. The breeding goal is to select against SNC and find resistant genotypes by culling susceptible individuals.

In the recent breeding plan review, the breeding target for needle retention was set to needles being retained for three years of growth (Suontama et al., 2016). Our current knowledge is that the average needle retention in Kaingaroa Forest is the full retention of one-year-old needles and the partial retention of two-year-old needles, estimated from a single progeny trial assessment. Some years ago, Watt et al. (2010) predicted that the average needle retention measured from 34 variable sites across the country was 78% (range from 40% to 100%), where needle retention had a significant negative linear relationship with pathogen abundance. A colonisation of the pathogen was positively associated with early winter temperature and late spring rainfall (Watt et al., 2010), while the disease itself affects growth less on cooler sites (Kimberley et al. 2011).

Early provenance testing identified that Californian provenances were generally more productive than tree material originating from Oregon and Washington (Shelbourne et al., 2007). The Douglas-fir breeding programme is at very early stages compared to a few other New Zealand tree breeding programmes; the most advanced is *E. nitens* moving towards its fourth generation and radiata pine in its third generation. Due to the early phase of breeding, it is obvious that provenance differences play a significant role in selection in Douglas-fir.

When it comes to productivity, we recently estimated based on 21-year-old material (1996 progeny trials) from North and South Island sites, that the tree

material coming from Californian provenances is more productive than those from Oregon, but had poorer tree form (Klápště et al., 2017a). On the other hand, Californian provenances in the North Island are more prone to SNC than Oregon provenances. This leads to the outcome that the growth potential of Californian seed-lots in the North Island is masked by the presence of SNC, and conversely in the South Island, Californian seed-lots seem to grow faster due to the absence of SNC.

Overall, Oregon provenances stood out as having a better genetic potential for the breeding objective than Californian provenances. Selection for resistance to SNC on the basis of needle retention at an early age is a useful direct indicator of a healthy tree since 36% of the trait variation at age 7 was due to genetics (Dungey et al., 2012) and 18% at age 21 (Klápště et al., 2017a). Red needle cast (RNC) is a new threat for Douglas-fir. Monitoring and research are at the early stage for RNC, and genetic studies are required to determine the resistance of different seed sources if the disease turns out to be a large-scale problem for this species.

Research in genomic selection using Scion's Strategic Science Investment Fund

Research on the implementation of genomic selection was initiated during the first year of the SWP programme following the review of the Douglas-fir breeding programme. To support the value proposition of genomic selection in the breeding programme, an economic comparison of traditional and genomic selection breeding was undertaken (Corbett et al., 2017). Genomic selection was projected to deliver \$2.8 million net present value (NPV) for forest growers alone, compared with traditional breeding, which expected a negative NPV of \$4.5 million (assuming a 6% rate of return). Figures for wood processors were \$45 NPV million with genomic



Left to right: Douglas-fir trial in Southland; New Zealand-grown Douglas-fir at age 77; permanent sample plot in Rotorua



Douglas-fir stand in Southland

selection and \$41 million NPV with traditional breeding (Corbett et al., 2017).

The major goal of genomic selection in New Zealand Douglas-fir is to utilise the realised relationships determined from DNA markers for breeding value estimation. Without a doubt, this will enhance Douglas-fir breeding, especially when most of the current tree material in the programme is from open-pollinated seed orchards. Not only will this deliver a greater certainty for the selection of seed orchard and breeding population material, but it is possible that much more rapid delivery of improved seed will be available through shorter generation intervals by skipping the progeny testing phase.

The SWP programme will test genomic predicted breeding values for the first time in the 1996 progeny tests. This work will show us what the potential is for the technology to deliver greater gains to forest growers in New Zealand. We will develop the first genomic prediction models that will allow breeding value estimation on the basis of genomic data only. Genomic data is derived from living tree tissues (needles or cambium) by extracting DNA and genotyping individual DNA samples by comparing them in a collection of genetic markers – Single Nucleotide Polymorphisms (SNPs) – which have been tested to accurately differentiate individual genotypes in a population.

Scion initiated contact with Oregon State University (OSU) during 2016 with the intent to build collaboration around the SNPs that they developed in Douglas-fir. Since then, Glenn Howe has been involved in the SWP programme. The OSU research team led by him have developed a more robust SNP resource for Douglas-fir for genotype population candidates using 60K SNP markers (Howe et al., 2013; Howe, 2017). We are fortunate to be collaborating with this group with access to the SNPs for genotyping.

Many breeding population-specific parameters affect the success of the implementation of genomic



Bark windows for DNA

breeding values in tree breeding programmes. One is the genetic variability of the breeding population that can be measured as effective population size, which calculates parental individuals not related to each other. Therefore, a large genetic diversity in the training population is important. At the beginning of the research project, we revised the breeding population structure by monitoring different breeding trial materials that would cover as much of the genetic diversity as possible (Klápště et al. 2017b).

In addition, robust pedigrees are required in order to compare genomic estimated breeding values with pedigree-based breeding values. Equally important, the availability of sound phenotypic data is necessary and it must describe breeding objective traits well. Based on these key criteria, the two 1996 planted progeny trials in Kaingaroa and Gowan Hill were selected to be the first training population for genomic selection proof-of-concept in Douglas-fir.

In a compromise between the available research funds, field sampling, DNA extraction and genotyping costs, we have sampled 1,000 individuals at Kaingaroa and 1,000 individuals at Gowan Hill for DNA. Due to the reason that these trees were already over 20 years old, needles could not be safely collected, so DNA was extracted from the cambium by cutting bark windows from trees. Timing of the cambium collection is critical since it must be carried out when the cambium is actively developing to ensure enough good quality DNA for extraction (Klápště et al., 2017b).

Seasonal cambium collection at the Kaingaroa site was carried out in February-March and in the Gowan Hill site in early April. Nevertheless, the use of cambium as a source of genomic DNA required testing and modification of our existing standard DNA protocol. Scion has contracted genotyping with the USA service provider GeneSeek/Neogen, where DNA samples have been recently shipped for genotyping. By June 2018, we expect to have the first set of data

to train genomic prediction models for growth, stem form, needle retention and wood stiffness. Inevitably, implementation of genomic selection in operational breeding will be a huge and exciting step forward in coming years for the breeding programme.

Concluding remarks

Douglas-fir is one of the finest structural timbers in the world and forms a multi-billion forest production business in the Pacific Northwest. This species could help New Zealand to rank among the world's top wood-producing countries because of its excellent wood qualities. Long rotation times and the effects of SNC can be targeted for improvement by effective breeding. The current goals for productivity are 35 years at rotation with 600 m³ TRV/ha and 20 m³/ha MAI, for a wood stiffness minimum of 8 GPa, and for tree health needle retention of three years in areas affected by SNC. Implementation of genomic selection initiated in the programme will be a huge step forward enabling much more rapid deployment of improved tree material into forests.

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