

# New Zealand forestry enters the genomics era – applications of genomics in tree breeding

Yongjun Li, Emily Telfer and Phillip L. Wilcox

## Abstract

Genomics is a word you have probably been hearing a lot about in recent years. Lately, new techniques for capturing genomic information have exploded across the science landscape, making it cheaper and easier to create huge amounts of information about how genes work and how they interact with the environment.

In humans and in many important agricultural and forestry species, variations in DNA sequences have been found that are associated with traits, which are the specific characteristics or properties of an organism. This is the basis for genomic selection – an accelerated breeding process currently being used by the sheep and dairy industries in New Zealand and in other countries, and increasingly being introduced into agricultural and horticultural plants and tree species. At a time when forestry is competing with other primary industries for land use, we need to make the most of every opportunity to increase the quality and competitiveness of the forests we grow in New Zealand by fully using genomic tools.

## Genome and genomics

The genome is the sum of all the genetic information contained in a living organism. It is encoded as DNA, a double helical molecule with a sugar-phosphate backbone and four bases – adenine, thymine, guanine and cytosine – that are connected in pairs down the middle. The order of the base pairs describes the genetic information stored in DNA. The genes are discrete sequences of base pairs in DNA. Genomics is the study of the genome of an organism, including the determination of the entire DNA sequence and the construction of fine-scale genetic maps. Comparative genomics looks at the differences between individuals from the same species, or even different species.

## DNA markers – variations of genome

A DNA marker is a gene or DNA sequence with a known location on a chromosome that, as a result of mutation in the DNA base pairs, can be observed as a variation in the genome. A DNA marker could be a small repeating sequence called a simple sequence repeat (SSR), or microsatellite marker, that varies in the number of repeats between individuals. These markers are useful for many studies, particularly in kinship and parentage identification or DNA fingerprinting, and population genetics. Another type of DNA marker

consists of a single base change in the DNA sequence, known as a single nucleotide polymorphism (SNP). SNP markers have been widely used in studies that link DNA to the physical traits, particularly in human medicine and health studies. More recently, SNP markers have been used to select for better performance in plant and livestock breeding programmes.

The most useful DNA markers are located in genes and are therefore directly related with specific biological functions of an organism. This is called an association, which is of immense interest to scientists studying inheritance of traits such as growth and wood quality, tolerance to diseases and drought, and lignin content in cell walls. Some DNA markers are genes themselves, but others are small pieces of DNA that do not have any functions but are still associated with specific traits.

## Genomic resources for forest breeding

Thanks to large research programmes both overseas and in this country, and advances in genomic science and computing power, massive genomic resources are now available to New Zealand forestry. Scion has developed a large SNP marker resource derived from sequencing 17 transcriptomes, which are the parts of the genome being actively used to react to an environmental or developmental cue. They can tell us which genes are important for which traits, and are a very good place to look for DNA markers that may be associated with these traits. The transcriptomes were isolated from 10 different tissue types and eight different trees. Scion is also assembling a whole genome sequence of radiata pine using the recently released loblolly pine genome as a template. Having these genomic resources in Scion will improve research efficiency, speed up the development of DNA-based tools, and can lead to the development of new germplasm with novel features.

Several categories of marker panels are under development by Scion and its collaborators using these SNP marker resources. They range from marker panels that cover the whole genome to various small panels with very specific purposes. Genome-wide approaches are extensively used in human medical genetics research to develop diagnostic tools. An example application in forestry could be to accelerate the development of tolerant trees to new pests and pathogens and the development of trees with high growth rate and improved wood properties. The smaller marker panels may consist of hundreds of DNA markers and are

substantially cheaper than the genome-wide panels. Examples of its applications include parentage testing, fingerprinting and differentiation of species.

## Possible applications of genomics in NZ forestry

### Genomic selection

In genomic selection, individuals in a breeding population are ranked and selected based on patterns of DNA markers. When the genetic effects of a marker pattern are known through its relationship with phenotypic information, the breeding value (BV) of the individual based on these markers can be calculated and used for selection. The use of genomic selection has brought about a revolutionary change in plant and livestock selection. Genomic selection increases the accuracy of genetic evaluation by the use of dense genomic markers associated with most of the genes controlling a trait.

Importantly, in forestry breeding genomic selection can be implemented well before trees are mature enough to be measured to assess improvements in traits of interest, and even at the stage of seedlings in plants. For example, percentage heartwood in radiata pine is a trait that seldom gets measured before trees are 14 years old. Genomic estimates of heartwood in seedlings would shorten the generation interval (the average age of parents when their offspring are born) and so increases genetic gain per year. Genomic selection is especially effective for species like forest trees with long generation intervals and for traits with low heritability (e.g. growth traits), that are expensive to measure (disease resistance) or that are expressed late in life (e.g. wood quality traits).

The Radiata Pine Breeding Company (RPBC) and Scion are starting a genomic selection programme with the aim of accelerating genetic improvement in radiata pine. The importance of genomic selection to radiata pine breeding is in eliminating the need for progeny testing, together with related improvements in bulking up technologies, in shortening the breeding and deployment cycle, and in increasing genetic gain per unit time. If this selection methodology is successfully applied in radiata pine breeding, we would expect the first tranche of germplasm selected using this new methodology to be available to nurseries by 2022.

### Parentage testing and fingerprinting

Accurate pedigree information ensures that trees with the desired pedigrees are selected and crossed for future generations and that accurate BVs are obtained in genetic evaluation. It helps breeders to manage in-breeding levels in open-pollinated seed orchards. In tree breeding, false parentage assignment can happen and parentage recording is a labour-intensive process. SNP or SSR markers can be used to confirm or reconstruct parent-progeny relationships. It can also reduce the labour involved in parentage recording or controlled pollination.

Parentage testing is based on the detection of DNA markers. Each tree inherits two copies of the genome: one copy from the mother and one from the father. If a marker is present in a tree, but absent in both candidate parents, the tree must be excluded as the offspring of the candidate parents. Parentage testing always works by exclusion, i.e. proving a tree is not the offspring of a parent rather than proving that it is.

The overall accuracy of a parentage testing depends on both the degree of variability of each marker and the number of markers used in the test. SSR markers have high variability, but a lower robustness in comparison to SNP markers which have lower variability, but higher transferability across a wide range of genotyping platforms. Current parentage testing or fingerprinting in plants and livestock has 10 to 20 SSR markers or 100 to 200 SNP markers. Scion has been working in parentage testing and fingerprinting for forest purposes. We plan to develop small targeted SNP panels for fingerprinting and parentage testing kits in both pine and *Eucalyptus* over the next few years, using markers from larger genomic resources.

### Disease pathogen detection

Rapid detection and accurate identification of disease pathogens is one of the most important strategies for controlling forest diseases and initiating preventive or curative measures. Pathogens with different host ranges or pathogenicity often differ in only a few base pairs of DNA sequences in target genes that are commonly used for identification. Genomics-based diagnostic assays can be easily designed to discriminate different disease pathogens.

Scion has developed a suite of marker panels to identify known pathogen threats such as *Endocronartium harknessii* (Western gall rust), *Fusarium circinatum*, the causal agent of pine pitch canker, various *Botryosphaeria* species, *Dothistroma pini* and *D. septosorum*, *Phytophthora ramorum* and *P. pseudosyringae*, and several others, even when physical symptoms of the diseases are absent. These marker panels have been used for several years and are being updated with newly developed resources such as whole genome sequencing and gene expression markers.

### Forest species differentiation

This differentiation is important for natural resource management and biodiversity monitoring. Genomic information can be applied to differentiate closely-related tree species. When genome sequences of different species are available, DNA markers that exhibit fixed differences among species can be identified and used in species differentiation. Both the presence and distribution of markers can vary between different species.

Interspecific hybrids are of interest for both tree improvement and the study of natural ecosystems, but they can be difficult to differentiate from parental species, particularly at the seedling stage. Such is the case for hybrids of *P. radiata* and *P. attenuata*, which are

particularly suitable for some South Island sites and for naturally occurring hybrids of totara (*Podocarpus totara*) and Hall's totara (*Podocarpus cunninghamii*), as well as other *Podocarpus*. DNA marker panels are particularly useful for differentiating among parental species, as well as hybrids, even when phenotypic differences are not apparent. This can give nursery managers and tree breeders confidence in the parental origins of seedlots.

## Summary

Genomic technologies have the potential to significantly impact forestry in New Zealand. The tools and breeding populations are ready and waiting for this technology to be applied in the commercial forestry sector. In the short term more targeted marker panels will become important for quality assurance, clone and species identification, biosecurity and parentage reconstruction. Longer term, the introduction of the

larger genome-wide panels will deliver accelerated genetic gain, initially in radiata pine, and later in a whole range of other species and traits of economic and ecological importance. In short, the delivery of genetic gain will be at a pace, and with quality assurance, that the forestry industry has not seen before.

## Acknowledgements

The authors would like to acknowledge the contributions from Heidi Dungey, Natalie Graham and John Butcher in the preparation of this article.

*Yongjun Li is a Scientist and Emily Telfer a Research Leader at Scion based on Rotorua. Phillip Wilcox is a Senior Scientist at Scion and a part-time Senior Research Fellow at the University of Otago.*

NZIF Conference  
NZIF 87th AGM  
NZIF Foundation Awards Dinner



New Zealand Institute of Forestry  
- Te Pūtahi Ngāherehere o Aotearoa Incorporated -

# NZIF 2015 Conference

Developing forest policy for a changing future • Te Papa, Wellington • 10 August 2015



In late 2014, a group of concerned forestry professionals established the "Forest Policy NZ" project. This includes five working parties to draft future strategies and policies covering the full scope of forests and their use. They are looking 100 years ahead to assess the likely effects on the sector of future changes such as climate and the cost of energy.

## PURPOSE

The important task of this conference is to receive the reports of the five working parties, discuss and debate the draft strategies and policies and make recommendations on the further development and implementation of a National Forest Policy. The ultimate aim of the project is to produce a national

policy that will be accepted and used by all parts of the sector and by the Government. There will be opportunity for attendees to debate the issues and recommendations and to influence further work on the policy.

## ATTENDEES

All those involved with New Zealand's forests, their protection, management and use are stakeholders in the National Forest Policy. The members of the "Forest Policy NZ" project fervently hope that as many as possible will come to Wellington to assist with this critical phase.

For more details see NZIF website.