

## Last word

John Hay

How many times have we heard the tired expression ‘this industry is at the crossroads’? I have tried to think of a better expression, perhaps ‘decisions made now will decide the future of this industry’. Whatever the phrase, it certainly does apply to New Zealand’s forestry industry.

The papers preceding this commentary outline the chronological and technical progress which has been made in improving New Zealand’s most economically important tree species, *Pinus radiata*. Phenotypic selection of this species began in the early 1950s (see John Butcher paper), and with the rapid development of quantitative genetics (see Heidi Dungey et al paper) an estimate, which is becoming increasingly more accurate, can be made of the heritability of the phenotypic trait being measured. This could be growth rate, wood density, disease resistance, wood stiffness etc, and is a result of the interaction of the genotype with the environment. Armed with this information, collected over many years on three to four generations of slowing improving tree populations, plant breeders moved to put this genetic information to best use for the industry through the development in the 1980s of the GF Scheme.

To obtain accurate phenotypic information to feed into a quantitative genetics programme in pine trees, the timeframe is much extended compared with annual crops such as cereals and perennial pasture species. This is due to the trees having to be 8–10 years old before accurate commercial traits can be measured. Inevitably, this timeframe means a very slow turn-around of improved generations. Speeding up the delivery of genetic gain is vital for return-on-investment in breeding, and rotation-end productivity, health and wood quality.

The relatively recent development of genomic selection (GS) has provided an important pathway for a huge reduction in the time to select elite plants for controlled crossing to produce the next generation of improved populations. This accelerated breeding process is based on variations in DNA sequences (markers) that have been found to be associated with traits, which are the specific characteristics or properties of an organism (see Yongjun Li et al paper). The most common marker used in GS consists of a single base change in the DNA sequence, known as single nucleotide polymorphism (SNP). SNP markers are used widely in studies that link DNA and gene expression to physical traits. Human medicine has been the driving force in this science area, but more recently GS is the established technology for driving improvement in poultry, dairy, sheep, wheat and many other horticultural and agricultural crops.

The broader area of genomics is the study of the complete genome of an organism, including the determination of the entire DNA sequence and the construction of fine-scale genetic maps (see Phillip Wilcox & Lucy Macdonald paper). Scion, with assistance from other organisations, is sequencing the huge megagenome of radiata pine, and with this is assembling the whole genome of radiata pine using the recently released loblolly pine genome as a template. The first working draft assembly will be completed next year. This, of course, will be just the beginning. Scion-led efforts and ongoing international contributions will improve the genome by increasing the genome coverage and creating a more accurate assembly over time. Having this genomic resource in Scion will improve research efficiency, speed up the development of DNA-based tools (such as genetic transformation and metabolomics), and most importantly can lead to the development of new germplasm with novel features (see Yongjun Li et al and Phillip Wilcox & Lucy Macdonald papers).

New Zealand has a comprehensive and robust biosecurity policy that includes proven methods of coping with uncontained incursions of pests and diseases. However, these policy documents have a notable gap with regard to conserving, managing and preparing to utilise back-up forest genetic material for combating a possible biotic crisis (see Rowland Burdon & Heidi Dungey paper). Radiata pine originates from a winter rainfall area of the world, a climate not matched in New Zealand, and although it relishes the summer rainfall it makes it more prone to fungal diseases. The prospective impacts of global warming will most likely elevate the pest and disease risks for New Zealand, rather than improve growth conditions.

The main mechanism to fight these risks is to introduce genetic diversity and identify broad-scale resistance genes in our target species. While the application of GS will speed up this solution, the importation of tree stock with known resistance to common pests and diseases, through our tight border security system, is a political and financial nightmare. I go back to my opening statement – that there are issues and new technologies which the New Zealand forestry industry will have to grapple with, and invest in, to keep competitive. The industry is at an important crossroads.

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