

## Optimal use of genetics in deployment using SEEDPLAN tools

McRae<sup>1</sup> T A, Kerr<sup>2</sup> R J, Dutkowski<sup>2</sup> G W, Buxton<sup>1</sup> P A, Cunningham<sup>1</sup> P D and Pilbeam<sup>1</sup> D J

<sup>1</sup>Southern Tree Breeding Association Inc. PO Box 1811, Mount Gambier, SA 5290, Australia

<sup>2</sup>PlantPlan Genetics, PO Box 1811, Mount Gambier, SA 5290, Australia

Email: tmcrae@stba.com.au

**Keywords:** tree breeding, deployment, genetic improvement, economic worth

The objective of a tree improvement program is to breed, select and deploy genetic material with improved biological characteristics for traits of commercial importance.

The Southern Tree Breeding Association (STBA) and its partners work with various tree species grown for different production environments and processing systems. A large amount of biological data has been collected on trees over decades of breeding in Australia for the main commercial species of *Pinus radiata*, *Eucalyptus globulus* and *E. nitens*. The national cooperative (STBA) uses its web based DATAPLAN system to manage the data and information, as well as facilitate access by breeders, researchers and industry personnel. The TREEPLAN system is used for the genetic analysis of tree breeding data on a program, species wide or global basis. All performance data collected in hundreds of trials over time is combined as part of national genetic evaluations using full pedigree. The resultant genetic values for selection criteria (measured traits) and commercially important breeding objective traits allows for the objective comparison of trees and genetic material for breeding and deployment. Results are reported on a regional basis, to ensure genotype by environment interactions are accounted for and the best genetics is identified for each situation.

Making optimal use of genetics in deployment systems can be problematic given the large amounts of information (genetic, economic and inventory) to consider and the range of genetic material (seed and plants) available at any given time. As part of the SEEDPLAN project, we are developing a suite of software tools that will assist the breeder and forest grower in the optimal use of genetics when developing orchards and seed lots for specific combinations of environments and processing systems.

A selection tool, SELECT, is designed for selecting genotypes for grafting into breeding arboreta or deployment orchards for seed production. Placing limits on group co-ancestry and determining the optimal contributions from individual genotypes are major considerations, while monitoring trends in reproductive and fitness traits is also considered. The MATE allocation module is used to determine what crosses are best for maximising gain for a particular objective, subject to constraints associated with potential inbreeding. Design of seed orchards and the optimal placement of ramets to avoid mating among close relatives are done using the DESIGN module. Determining the genetic composition of seed harvested from trees in an open pollinated orchard with the COMPOSE module needs to account for census information and dynamics of pollen dispersion. Companies can use the INDEX module to refine their economic weights for important traits in their deployment objectives, depending on the particular target environment and production system under consideration. The MATCH module allocates seed and plant lots to stand types in an optimal manner to maximise enterprise profitability.

In developing software tools to aid decision making, it is important they be flexible to cater for the different needs of the many users dealing with various species and business environments. It is also important the modules are integrated within the overall framework of tools for managing data and information flows.