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# Genetic gain optimisation in tree breeding (MATEPLAN) and deployment (SEEDPLAN)

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# **Genetic gain optimisation in tree breeding (MATEPLAN) and deployment (SEEDPLAN)**

Prepared for

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by

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# Genetic gain optimisation in tree breeding (MATEPLAN) and deployment (SEEDPLAN)

## The objectives of the Research Project

During the last decade the Southern Tree Breeding Association (STBA) has generated and developed strategically important intellectual property and tools for tree improvement in *Pinus radiata*, *Eucalyptus globulus* and other species. These include: the economic weights and profit indices for ranking genetic material for use in breeding and selection; a web based data management system (DATAPLAN®) and national databases that include pedigree information and data on a range of traits measured on several hundred thousand trees for each species; and TREEPLAN® genetic evaluation, which provides breeding values for commercially important traits, using a multi-variate analysis across generations, years, sites and traits.

This significant intellectual property can be more fully exploited by developing an even more advanced toolset. Tools are needed which can guide decision making in the national breeding and deployment programs for plantation species, ensuring genetic gain is maximised, while managing inbreeding and genetic diversity across generations.

While the STBA is primarily a breeding organisation, it must ensure that important value creating intellectual property such as accurate genetic values are utilised at the commercial end of the industry. To facilitate this, a tool is needed that can package the genetic and economic knowledge in order to strategically match genetic material to particular production environments and production systems. Another tool is needed that can guide decision making in seed orchards and nurseries, better matching trees to industry requirements. Biological and genetic constraints need to be simultaneously considered, while maximising gain for defined deployment objectives.

In keeping with the "PLAN" nomenclature used by the STBA, this advanced toolset will contain components known as MATEPLAN™ and SEEDPLAN™. MATEPLAN™ is the tool that will guide and optimise selection and crossing in the breeding program. SEEDPLAN™ will stand for a collection of tools that can be used in various deployment tasks, such as selection of genotypes for a seed orchard, the creation of deployment values for seedlots, and the optimal matching of seedlots to plantation stands.

Specific objectives were as follows

- Develop software (MATEPLAN) to optimise selection and mate allocation in the national breeding programs, while managing inbreeding, genetic diversity and risk across generations.
- Develop software (SEEDPLAN) to assist with orchard management and the matching of seed and plants to specific production systems.
- Optimise the use of improved genetics in plantations grown for a variety of products, under a range of production environments.
- Improve the efficiency, delivery and rate of adoption of improved genetics to industry.
- Determine and manage the biological and genetic constraints influencing the uptake of improved genetics.
- Develop a framework for integrating economic and genetic information, given multiple objectives, different production environments and processing systems.

## **The extent to which the Research Project objectives were achieved**

Develop software (MATEPLAN) to optimise selection and mate allocation in the national breeding programs, while managing inbreeding, genetic diversity and risk across generations.

The project has been successful achieving this objective. MATEPLAN™ has been used in both the *P. radiata* and *E. globulus* national breeding programs in 2007 and 2008. Grafting selections and mate allocations have been determined using the software program. These selections and mate allocations comply with defined constraints on increase in overall relatedness in the populations for both species. MATEPLAN™ has greatly facilitated the computation of co-ancestry, a task which becomes increasingly difficult for breeders as generations advance. A detailed description of the theory and results is contained in the confidential "Detailed Research Report" by Kerr *et al.* (2008).

## **Develop software (SEEDPLAN) to assist with orchard management and the matching of seed and plants to specific production systems.**

The project has been successful in achieving this objective. A pilot implementation of the software program demonstrated that the matching of individual tree seedlots to specific plantation compartments adds a further \$250 net present value per hectare in harvested product on average, relative to a strategy of evenly allocating seedlots to stands. The software program assists the orchard manager with all aspects of the allocation, including the computation of seedlot expected genetic values, and the integration of economic characteristics of each stand to be planted. The seedlot genetic values reflected the modeled contributions of pollen within the seed orchard and genetic groups outside the orchard, and any specific interactions between genotypes that are naturally or artificially crossed. The economic characteristics of each stand will vary because of differences in bio-economic characteristics such as productivity, haulage distance, establishment, maintenance and harvesting costs. These differences, as well as differences in expression of genes due to differences in scale and genotype by environment interaction, make each stand unique in the combinations of traits that give the highest economic gain.

As planting horizons move further away in time, there exists the potential to optimise creation of seedlots for anticipated planting through orchard culling and infusion and ramet placement. Additional modules of SEEDPLAN™ assist orchard managers in these areas. The computation of co-ancestry and predicted loss through inbreeding is an important component of these modules.

## **Optimise the use of improved genetics in plantations grown for a variety of products, under a range of production environments.**

The project has been partly successful in achieving this objective. The pilot study of SEEDPLAN™ for *E. globulus* used only a single production model for each stand – Wood Chip Export for Kraft Pulp Production. The model calculates profitability as Net Present Value (\$NPV) of growing a hectare of plantation for wood chip export, with mill chipping and debarking at either the chip mill or at the export port (depending on stand location), with the chip price only related to dry matter (no premium for kraft pulp yield), unit haulage cost related to haulage distance, and unit harvesting cost related to stand productivity.

Other production models defined for *E. globulus*, such as the Domestic Kraft Pulp Production and the Saw Log production models, have not been implemented yet in any pilot study. Production models in *P. radiata* have been defined, but are still to be tested in a pilot study.

The software is at a stage where any production model can be defined and used in the allocation problem. The limiting factor in the uptake of the software for improving genetics for a variety of products, under a range of production environments, is the availability of data. It is not a simple matter of merely asking for the data. A process of training is required as assembling the required parameters and inputs is not a simple procedure. A future Stage II project should invest resources into the appropriate education of the relevant people in industry.

## **Improve the efficiency, delivery and rate of adoption of improved genetics to industry**

The project has been successful in achieving this objective. A deficiency in the past has been the inability of orchard managers to associate the latest TREEPLAN® genetic values to genotypes in their seed orchards, and translate these genotype genetic values into mean values for an aggregated seedlot. The SEEDPLAN™ system includes software that determines the composition of a seedlot, viz, the probabilities of pollen contributions from individual ramets, and creates a seedlot genetic value based on these probabilities. Automatic degradation of genetic values due to inbreeding depression also takes place.

## **Determine and manage the biological and genetic constraints influencing the uptake of improved genetics**

The project has been successful in determining these biological and genetic constraints. There are also important economic constraints. The constraints that have been identified include the points discussed above, viz:

- the routine computation of co-ancestry and complex functions based on co-ancestry such as founder genome equivalents and effective population size,
- the building and codification of economic models for different sites and production systems,
- the translation of TREEPLAN® genetic values, which are stored at a genotypic level, to a seedlot level, and
- modeling the pollen dynamics of a seed orchard, and
- the general recovery of information in DATAPLAN® and its integration with each organisation's own data information systems.

These constraints have now been overcome by use of various software models of the MATEPLAN™ and SEEDPLAN™ systems and the changes made to DATAPLAN® to incorporate data and parameters relevant to these systems. In the past these data (i.e. phenological, reproductive and economic data) and parameters (i.e. scaling parameters), have normally resided in each organisation's own data management system. Great progress has been made in standardisation of formats and protocols for storage of this data.

Constraints influencing the uptake of improved genetics have also included incomplete knowledge of a genotype's:

- propensity to produce abnormal seed,
- self-incompatibility,
- incompatibility with other genotypes,
- propensity to be productive, and its
- predicted flowering time and length.

While models in SEEDPLAN™ account for these aspects of the genotype, knowledge about them remains incomplete. Strategies have been put in place that will help in the collation of information that will be used in the recovery of this knowledge from operational deployment and breeding programs. Both DATAPLAN® and TREEPLAN® will have important future roles to play in this area.

Another constraint identified is the fixed budget that is allocated to scion collection for grafting selections. It is likely that the best selections for seed orchards will be obtained from field trials. However, a fixed budget may not extend to covering the differential expense of locating all selections from field trials. It is likely some scions have to be collected from breeding arboreta. The SEEDPLAN™ software takes account of this constraint by defining the cost aspect of scion collection from individual trials, which are spread across the plantation estate of southern Australia.

## **Develop a framework for integrating economic and genetic information, given multiple objectives, different production environments and processing systems.**

The project has been successful in meeting this objective. The module of SEEDPLAN™ which optimally allocates seedlots to stands links in with another module that determines the value for each nominated seedlot. The value determined is in reference to a set of characteristics that are defined either at the organisational level or at the stand level. These characteristics include:

- the type of product that is harvested from the stand,
- a prediction of the productivity of the stand and the reference genotype on which this prediction is based,
- distance to processing plants such as chipping, pulping and saw-log mills,
- post-processing freight charges to ports,
- rotation lengths,
- site types,
- area losses due to fire and other hazards,
- harvest and chipping losses,
- costs associated with
  - loading
  - transport
  - freighting
  - processing,
- prices for the harvested product, and
- assumed interest rate for discounting to present value.

An important part of the determination of seedlot value is the customisation of economic weights that are used to combine the breeding objective traits into a single index value. A dedicated module exists for this to occur.

At play in the optimal allocation of seedlots to stands is the orchestration of data exchanging between separate modules, each with a specific purpose. These purposes are:

- seedlot composition,
- seedlot value creation,
- solving customised economic weight functions, and
- solving the matrix transportation problem (i.e. the optimal allocation of seedlots to stands)

Each of these modules can also work independently. If a breeder or client wishes to obtain values for historical seedlots using a customised economic profit index, the framework also exists to allow them to do so, outside the context of the allocation problem.

## **The Research results and benefits**

The research results are contained in the detailed research report TR08-04IP, which is confidential to the Southern Tree Breeding Association.

The STBA in partnership with FWPRDC (FWPA) and CSIRO has recently developed economic weights for *P. radiata* for a solid wood production system (PN01-1904). The STBA has adopted the industry economic weights, with genetic values produced for growth (MAI), branch size (BRANCH), stem straightness (SWEEP) and timber stiffness (MOE). Given different production systems and economic drivers for different companies, these indices can be customised for particular circumstances.

The STBA in partnership with the Cooperative Research Centre (CRC) for Temperate Hardwood Forestry, and later with the CRC for Sustainable Production Forestry developed economic weights for *E. globulus* for a domestic kraft pulp production system and for a wood chip export for kraft pulp production system. These weights combine volume (VOL), density (DEN) and predicted kraft pulp yield (KPY) into a single NPV value to reflect the economic worth of using particular genotypes. Again, given different

production systems and economic drivers for different companies, these indices can be customised for particular circumstances.

Seed producers, nurseries and forest managers will no longer rely on *ad hoc* approaches to the management of genetics in orchards, propagation systems and plantations. With TREEPLAN® genetic values and indices, improved material can be benchmarked across industry, with SEEDPLAN™ making this operationally straightforward. Complex tasks such as computation of co-ancestry, the prediction of pollen flows and the prediction of loss through inbreeding depression have in the past prevented the accurate prediction of a seedlots value. Inability to achieve these tasks has also impeded the ability of the orchard manager to infuse existing orchards with the latest, advanced genetic material. Orchard managers were prone to rely on old, genetically inferior, but reliable material. Now SEEDPLAN™ can provide them with tools that make such tasks accessible and easy, so they have more confidence in placing the best genetic material available in orchards.

Industry (FWPA, STBA and SA Government) has recently established the National Genetic Resource Centre at Mount Gambier for plantation forestry. Elite selections are introduced into arboreta for breeding purposes, on a dynamic rolling front basis. MATEPLAN™ is essential for the STBA to maximise value from the national genetic resources, while managing relatedness and inbreeding over generations. Gene conservation and genetic diversity are increasingly important for *P. radiata*, as new introductions from overseas are prohibited through AQIS due to pine pitch canker (*Fusarium circinatum*). The infusion of novel genes will be important for maintaining diversity and management of risk against pests, diseases and changes in objectives.

## **Details of all Intellectual Property Rights and Confidential Information**

Data and information contained in the national tree improvement databases (DATAPLAN®) for *P. radiata* and *E. globulus*, including pedigree, TREEPLAN® genetic values, economic weights and profit indices is owned by STBA, and deemed 'Confidential Information'.

Details of breeding and deployment strategies for *P. radiata* and *E. globulus* remain the property of STBA and its Members.

MATEPLAN™ and SEEDPLAN™ software (including source code) and algorithms and processes developed as part of the project are owned by the STBA and PlantPlan Genetics. It is not envisaged the software will be sold as unit sales, but utilised as part of broader services to industry provided by STBA and PlantPlan Genetics in genetic improvement.

Data and information associated with seed orchards and deployment systems, including flowering time, costs, orchard design and marketing information, which was provided as background IP belongs to the organisation which provided the Confidential Information.

Improved Genetic Material for *P. radiata* and *E. globulus* owned by the STBA, is available to industry, subject to restrictions and payment of royalties by non-Members.

Software associated with the web based data management system (DATAPLAN®) is owned by the STBA. DATAPLAN® is available to industry through provision of services in tree improvement by STBA and PlantPlan Genetics.

The results of test runs using MATEPLAN™ belong to the STBA.

The results of test runs using SEEDPLAN™ belong to the organisation which provided the orchard data and information.



## Commercial implementation of the results

The STBA manages the national tree improvement programs for *Pinus radiata* and *Eucalyptus globulus* and provides genetic evaluation services for *Eucalyptus nitens*.

The STBA is integrating the SEEDPLAN™ and MATEPLAN™ systems with the national database (DATAPLAN®) and TREEPLAN® genetic evaluation systems. MATEPLAN™ has been used in the STBA operational breeding programs for *P. radiata* and *E. globulus* in 2007 and 2008, and will be used on an annual basis in future for selection and mate allocation purposes.

SEEDPLAN™ has been pilot tested in *E. globulus* (WAPRES) and *P. radiata* (*seedEnergy*). It will also be available for further use, subject to enhancements.

The STBA has scheduled workshops in *E. globulus* (August 2008) and *P. radiata* (September 2008) to promote the benefits of the technologies, and facilitate the uptake of the outcomes by industry.

The research provider and its breeders regularly liaise with Member organisations and licensed seed producers to facilitate the efficient adoption and use of SEEDPLAN™.

Input data (genetic values, economic weights and genetic material) for the project is accessible across the web by authorised users of DATAPLAN®. Seed producers are being encouraged to put data and information on orchards into DATAPLAN® to streamline the utility of SEEDPLAN™. It is envisaged support will be ongoing, as new genetic material and updated genetic values are regularly delivered to industry.

Industry participants will review progress and facilitate interpretation and adoption of results through industry workshops and regular technical meetings of the STBA Technical Advisory Committee. Pilot studies are being done with existing commercial orchards and propagation systems, ensuring specifications are robust and the tools are designed for operations. Non-Members of the national breeding efforts (breeders of other species) can access the products developed under a fee for service model with STBA and/or PlantPlan Genetics.

## The difficulties encountered

The major difficulty has been the sheer scope of the project and the limited time allocated for its completion. The bar was set high in that it was hoped graphic user interfaces (GUI) to all software components could be developed within the 18 month time frame. As the project progressed, it was realised that full utility would not be achieved as the complexity of each task provided challenges and opportunities.

A decision was made early in the project to devote limited resources to all components in order to demonstrate the concepts and value of such comprehensive tools for breeding and deployment. This was preferable to choosing one of the software components in isolation and bringing it to final completion with GUI. This strategy has meant that MATEPLAN™ and SEEDPLAN™ software components have only what could be described as raw, but still serviceable user interfaces. Good progress has been made, and it has allowed the research organisation and industry to more fully understand the constraints facing deployment of improved genetic material.

Designing algorithms was not a difficulty as such, but the principle investigator would benefit from more direct interaction with other practitioners of this area of computer science.

## Project Manager's recommendation

The research has been very successful in largely achieving the objectives of the project. The delivery of improved genetics to plantation growers needs efficient deployment systems supported by effective breeding programs. The SEEDPLAN™ system provides a platform to better inform orchard managers, seed suppliers, nurseries and plantation growers about the benefits and access to improved genetics for *P. radiata*, *E. globulus* and other species. SEEDPLAN™ also provides a tool for the breeder to package genetic and economic information in an easily interpreted format.

The pilot studies have greatly assisted in scoping out the important issues, as well as delivering preliminary results and providing recommendations for future actions.

It is clear more resources are needed to provide graphic user interfaces for each of the MATEPLAN™ and SEEDPLAN™ modules. This is important to ensure the tools have utility beyond the breeder, and are widely adopted by industry to capture benefit in plantations.

More research into the differential evolutionary (DE) or other types of genetic algorithm is required. Further research and resources are needed to improve the response time and efficiency of the algorithms, and to facilitate liaison and access to IP developed by animal breeders (i.e. Professor Brian Kinghorn).

Resources are needed to educate relevant personnel in the industry in the area of customised breeding objectives (especially in *P. radiata*). Though the framework exists to use prices and cost structures and wood flows that are unique to an organisation, and productivity levels and economic drivers that can change from stand to stand, the provision and collation of such material is not easy.

The use of molecular studies to validate the seedlot composition models is desirable. A molecular study using a seedling seed orchard would validate the models we have used in predicting the probability of pollination based on phenological data. We need molecular tools to help us in defining asymmetric distance functions – how does pollination probability change with distance and orientation with respect to dominant wind direction?

A future SEEDPLAN™ project would complement a TREEPLAN® version 3 project that targets the incorporation of flowering and fecundity traits into routine national analyses for *P. radiata* and *E. globulus*.

A Stage II project should be developed to continue this strategic work.

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