Economics of genetics in tree breeding and deployment

Field tour visit to the National Genetic Resource Centre
13 May 2014

Dr Richard Kerr

PlantPlan Genetics Pty Ltd/
Southern Tree Breeding Association Inc.
Australia
National Genetic Resource Centre

- Funded by STBA, SA Govt. and FWPA
- Established 2005
- Facilitates efficient breeding
- Manages risk
- Conservation plantings
Australian landraces

Consolidation of historic state, company and federal programs

ROLLING FRONT TREE IMPROVEMENT

Current elite genetic material (most of which is in NGRC)

Year 1
Assess TREE PLAN Select

Year 2
Assess TREE PLAN Select

Year 3
Assess TREE PLAN Select

Plant trial

Year 4
Assess TREE PLAN Select

Year 5
Assess TREE PLAN Select

Plant trial

Year 6
Assess TREE PLAN Select

Year 7
Assess TREE PLAN Select

Year 8
Assess TREE PLAN Select

Year 9
Assess TREE PLAN Select

Year 10
Assess TREE PLAN Select

Year 11
Assess TREE PLAN Select

Plant trial

Most activities in the tree improvement program are undertaken each year

Continuous flow of information into DATAPLAN

TREPLAN is run each time new assessment data comes on line

SEEDPLAN

MATE
Optimise crossing

SELECT
Selections for breeding and deployment

INDEX
Customised objectives

DESIGN
Optimal placement in an OP orchard

OP clonal orchards
CP families
stool beds
Seedlings
Cuttings
Improved trees targeted for operational forests

Current elite genetic material (most of which is in NGRC)
The Breeding Train

• Discrete Generation

  Base
  ↓
  Resources Grow
  ↓
  Measure
  ↓
  Analyse
  ↓
  Select
  ↓
  Cross
  ↓
  Genetic Resources

• Every activity happens to the whole population once per generation.

• A bit slow as have to wait for everyone to be ready.
More or less rolling

- Joint trials now with far less resources
- Kick up as NGRC is used
- Waves due to resources and echoes of first waves

Not all pre STBA trials in database
The Deployment Taxis

- New material available every year

Stream A
- Genetic Resources
- Grow
- Measure
- Analyse
- Select
- Cross
- Genetic Resources
- Grow
- Measure
- Analyse
- Select

Stream B
- Genetic Resources
- Grow
- Measure
- Analyse
- Select
- Cross
- Genetic Resources
- Grow
- Measure
- Analyse
- Select

Stream C
- Genetic Resources
- Grow
- Measure
- Analyse
- Select
- Cross
- Genetic Resources
- Grow
- Measure
- Analyse
- Select

→ Graft into OPSO
→ Graft into OPSO
→ Graft into OPSO

CP cuttings
CP cuttings
CP cuttings
Pinus radiata Pedigree
Selection
“Getting the balance right” kind of problem

Choosing the best, but these are often related

The upside
  • High genetic gain
  • Better profit margins

The downside
  • Reduced genetic diversity
  • Potential losses due to inbreeding depression
The SELECT tool is used to optimise selection

Can be used to select
- genotypes for a seed orchard (deployment)
- additions to the breeding arboretum (breeding)

SELECT will maximise genetic gain subject to
- a lower limit on status number (if deploying)
- a lower limit on effective population size (if breeding)
- limits defined for each candidate on how many scions can be taken
Candidates can come from

- Orchards
- Field Trials
- Arboreta
- Other programs
- Overseas (California)

If predictions of genetic value for all candidates are expressed relative to a common base, direct comparisons can be made across trials, generations, companies, countries (as long as they are linked genetically).
What is an appropriate status number when selecting genotypes for an orchard?

<table>
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<th>Status number</th>
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<th>Mean genetic gain of seed in radiata clonal OP orchard (marginal $NPV/ha)</th>
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Status number - how many unrelated founder trees the genotypes in the orchard would be equivalent to

**Low status number**
- increased gain
- increased risk of inbred progeny

**High status number**
- reduced gain
- reduced risk of inbred progeny

Status number is the inverse of average relatedness
- low relatedness = high status number
- high relatedness = low status number
The DESIGN tool is used to place the ramets in the orchard when status number is 20 no problems occur spacing apart the ramets for a particular genotype.

Example 25 row by 40 column clonal seed orchard (1000 stems).

Each ramet is separated by at least 3 planting rows.
When status number is 10 problems do occur!

It becomes impossible to always place ramets at least 3 planting rows apart
Crossing is a “getting the balance right” problem

Higher incidence of better, but related parents in crosses

The upside
- High genetic gain
- Better profit margins

The downside
- Unable to purge deleterious gene variants
- Risk losing gene variants important for fitness
Given what is reproductively available, how do I optimise the mating plan?

Census of reproductive availability is needed before crossing can begin.

**Pollen**
- Full jar = 50 uses as a male parent
- 10 flowers = 1 use as a female parent

**Breeding arboretum**
- Genotype A has 50 flowers
- Genotype B has 10 flowers
- Genotype C has 100 flowers
- Genotype D has 10 flowers

Progeny trial
- Fridge
The MATE tool is used to optimise crossing

Uses a genetic algorithm to maximise genetic gain

subject to
- not mating individuals who are closely related
- limiting the increase in average relatedness (of current and future parents)
- current parents’ number of uses as a male and female parent

The result:
Mate A with D
Mate B with E
etc

MATE results for *E. globulus* breeding population

- Decided on 0.5% as the desired change in co-ancestry
- Expected mean value of progeny resulting from proposed mating (marginal $\text{NPV/ha}$)
- Percent change in population co-ancestry as a result of proposed mating
Crossing in full swing

Male flowers

Drying the seed once harvested

Isolating the female flower

Female flower
### Spreadsheet for managing control pollination

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Progeny trials with embedded gains trials

Block families into groups of similar genetic value for MAI, *so a progeny trial can also serve as a gains trial*

1  lowest MAI
7  highest MAI
M  unknown and  controls

Central low MAI block surrounded by one of each group in order of MAI

Each colour is a minor replicate
Trial Assessment

Time of flight and acoustic velocity

NIRA Kraft Pulp Yield

Chinese visitor measuring DBH

Basic Density Coring
Information management and genetic evaluation are key to a successful tree improvement program

• All data, pedigree and parameters stored and processed in central database (DATAPLAN)
• Facilitates fast processing of data from experiments
  • Impacts decision making immediately
• Genetic evaluation system is supported by livestock industries and international forestry organisations

- Economic weights customised for each organisation
- Statistical models
- Trial data
- Pedigrees
- Genetic & environmental parameters
Measured traits are **Selection Criteria (SC)**

- **SC** trait parameters (correlations and variances) need estimating in order for **TREEPLAN** to predict robust genetic values

  - The proportion of the variance we observe due to genes
  - Inter-trait correlations (how much does one trait tell us about another?)
  - Inter-site correlations (trees can rank differently between sites – what is the extent of that difference?)
  - Inter-age correlations (are the sets of genes that affect the same trait at different ages the same?)
SC trait parameters are assembled into a matrix

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The matrix is a key part of the BLUP methodology

Inter-site, inter-age correlation
Breeding Objective Traits (BOT) are traits that directly affect profit

- Mean Annual Increment (MAI) (m³/ha/yr)
- Mean STIFFNESS of sawn timber from sawlogs over rotation (MPa)
- Mean BRANCH size of sawlogs over rotation (cm)
- Mean SWEEP of sawlogs over rotation (mm/m)

Defining variances for BOT and correlations between SC traits and BOT allows us to predict genetic values for BOT.
The matrix of correlations between SC and BOT

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STRONG CORRELATION

WEAK CORRELATION
Economic weights are derived using a bio-economic model

Management variables
  e.g. rotation length, interest rates, number of thinnings

Costs
  establishment, harvesting, mill

Prices
  chip, pulp, sawlogs

Means for BOT
  MAI, BRANCH, SWEEP
  STIFFNESS

Assumptions
  volume assortment across classes and thinnings; branch limits for premium sawlogs

Profit function describes how they inter-relate to predict discounted profit on a per ha basis
Economic weights indicate the relative importance of each breeding objective trait in the index

The weights are used to combine the genetic values for BOT into an overall merit index which measures the effect the genotype or family has on discounted profit ($NPV)

Weights are customised