

Effect of selection method on genetic correlation and gain in a two trait selection scheme

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ABSTRACT

Adverse genetic correlations between wood volume and quality traits are one of the main constraints in advancing radiata and other pine breeding programs. To overcome or deal with adverse genetic correlation in radiata pine and other conifer breeding program, a Mont Carlo simulation study for adversely correlated traits DBH and wood density was conducted using allele-based model. Two allelic models were generated for the study: a mixed loci model using independent and pleiotropic loci for adversely correlated traits and an all antagonistic pleiotropic loci model. Initial allele model was assumed additive genetic effect only. Progressive complexity was studied by adding dominance effect, linkage disequilibrium (LD), and optimal selection by coancestry constraint and unequal contribution of parent. Selection was conducted for three scenarios: based on a single trait, based on index selection for two adversely correlated traits (DBH and wood density) with equal or unequal economic weights.

Results indicate:

1. Genetic correlation tends to increase under pleiotropic models and tends to decrease under linkage models with selection.
2. Negative genetic correlation due to linkage disequilibrium is not a big concern in long-term breeding.
3. Dominance genetic variance increases or decreases overall genotypic correlation, but does not affect the trend of genetic correlation under selection
4. Genetic gains for adversely correlated traits (such as DBH and wood density) could be made for many generations with selective breeding if there were independent loci for individual traits.
5. New alleles (from infusion or mutation) with less antagonistic effect are required for further genetic gain of two adversely correlated traits simultaneously if all alleles are fixed except for loci with antagonistic effects.
6. For short term genetic gain of adversely correlated traits, selection based on two traits simultaneously is more effective than selection based on a single trait. Developing economic weight by breeding objective is a sound approach for short term breeding program. Economic weights will influence genetic gain for individual trait as well as genetic correlation.
7. For long term genetic gain, dissecting genetic bases with large association population is recommended. When the genetic mechanism for adversely correlated traits was understood, allele model could be developed to study optimal strategy under different gene actions.
8. Balancing co-ancestry with unequal contribution of parent is probably one of optimal approach to maximize short-term and long-term genetic gain under adverse genetic correlation.

Prediction of breeding values across different cross types, selection histories and clonal replication in *Picea abies* L. (Karst).

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ABSTRACT

Breeding programs often have trials with genetic material of different pedigree type, parents with different selection histories, and sometimes clonal replication. Integrated analysis to select superior genotypes within such diverse genetic material is possible if the additive relationship matrix is used to link genotypes by their pedigree, selection history is taken into account, different ages of measurement are accounted for, and repeated measures for cloned genotypes are used. A seed orchard established in southern Sweden with phenotypic plus tree selections of Norway Spruce (*Picea abies* L. (Karst)) from stands of western European origin was used for ten test experiments. Initial tests used seedlings from open-pollinated (OP) families from the orchard and random control-pollinated (CP) crosses between the parents. Based on early age growth and form measurements new crosses were made between elite parents and the resulting offspring cloned. Early growth data from the clonal trials was combined with the early data and later growth measurements from the seedling trials. The data were adjusted using spatial analysis and standardised by an estimate of the additive standard deviation for each trait on each site, but the combined model allowed for different heritabilities on each site. The selection index combined predicted volume and straightness at harvest on a unit additive standard deviation scale, with three times the weight on volume. Predictions of harvest age traits were based on an age:age correlation model for growth based on the Lambeth equation and a slight adverse correlation between growth and straightness. Of the best 100 genotypes on the index, two thirds came from the cloned genotypes, reflecting their selected parentage and higher breeding value accuracy, despite the lack of form and later age growth data. Only one selection came from the open-pollinated material, and the rest came from the control-pollinated, uncloned material. The accuracy of the breeding values was highest for the parents, closely followed by the cloned CP offspring. The uncloned CP genotypes were less accurate, but still well ahead of the uncloned OP offspring. Within each group, the selected genotypes always had a higher accuracy. This reflects the increased variance of the predicted genetic values of genotypes with higher accuracy due to replication (through offspring or cloning) and thus their increased chance of selection.

Genetic parameters for *Eucalyptus globulus* kraft pulp yield

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ABSTRACT

Genetic parameters were estimated for predicted kraft pulp yield (pulp yield), core basic density (density), and diameter at breast height (DBH), from a harvest-age open-pollinated, base population trial of *Eucalyptus globulus* in Tasmania. Wood cores were obtained from 2170 trees from 467 families from 17 races. Large scale assessment of pulp yield was possible through the application and validation of a global pulp yield model based on near infrared technology. Significant race and family within race variation was detected for all traits.

Heritabilities were 0.40 ± 0.05 for pulp yield, 0.51 ± 0.06 for basic density, and 0.25 ± 0.03 for DBH. Within subraces, the genetic correlation between pulp yield and DBH was positive and highly significant $r_G = 0.53 \pm 0.12$, whereas between pulp yield and density the correlation was not significantly different to zero $r_G = 0.18 \pm 0.10$. Both of these results differ from previous reports in the literature.

In contrast to the absence of a genetic correlation between pulp yield and density within races, the between race correlation was significantly negative $r_R = -0.58 \pm 0.19$. Race means for pulp yield increased with increasing latitude whereas those for density decreased. This result is contrary to previous assumptions and suggests that the genetic merit of southern Tasmanian races for pulpwood production has been underestimated.

Genotyping of young trees for kraft pulp yield can shorten generation interval in *Eucalyptus globulus*.

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ABSTRACT

Prediction of genetic values from molecular information is rapidly becoming a potential new tool for breeding. Strategies for its optimal use need to be defined. Stochastic simulation of strategies based on an early generation breeding program for *Eucalyptus globulus* were evaluated to see how such a tool may best be used. The breeding objective aimed to maximise the discounted per hectare profit of growing and producing kraft pulp by increasing harvest volume, basic density and kraft pulp yield. Breeding values for these traits were predicted from phenotypic measurements of early (age 4 years) growth, core basic density and NIRA predicted pulp yield (NIRAPPY), and later (age 8) growth. Growth was assumed to have a low heritability and relatively low age:age and between site correlations but was measured for all trees, whereas the wood quality traits were assumed to be measured only on a limited sample (5-10%), but have a higher heritability and be more stable across ages and site types. An auxiliary trait of NIRAPPY predicted using molecular information was also used, assuming it to have a high heritability (low measurement error) but only predicting a proportion (e.g. 30%) of the additive variation of the trait. The breeding population was assumed to comprise both first and second generation trials, all of which had already been measured for the phenotypic traits, and a new generation of trials with no measurements. Gain was assessed for both the breeding population and for seed orchard establishment.

We found that extra measurement of NIRAPPY either on a phenotypic or molecular basis in existing trials gave very little extra gain. Measurement of the growth and wood quality traits on the new generation of trials yielded similar gains irrespective of the form of NIRAPPY measurement. Very early (age 1 or less) assessment or molecular NIRAPPY did however boost gain in advance of phenotypic data collection. This strategy could be used to make early selections for seed orchards, or to reduce generation interval by grafting preliminary selections into clone banks to encourage flowering so that crosses could be made as soon as phenotypic growth and other wood quality information was collected.

Modeling aggregates of different genotypes in genetic evaluation of forest species

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ABSTRACT

Individual tree models are finding wider use in the genetic evaluation of forestry breeding populations. These models use information from all of an individual's relatives when estimating its breeding value. However, in forestry often the exact identity of the male parent is unknown, such as in the case of open-pollination or in the use of polymixes. Treating the male parent as unknown ignores prior knowledge on the identity, and hence genetic characteristics, of the pollinator. In open-pollinated field trials there will be knowledge that a proportion of the progeny from a female parent will be selfed and that males producing outcrossed progeny derive from a sub-population with a different genetic mean to males in another trial. In polymix crosses the identity of the male can be restricted to a finite set of individuals. This paper examines three approaches to modelling individual trees with unknown pollinators. The simplest method treats pollinator as unknown, the second assigns all individuals from a group of pollinators to a single genetic group and the third method shares the paternal ancestry among potential candidates, where candidates can be either individual genotypes and/or genetic groups. The results of the three methods are compared and their implications discussed.

Key words: Numerator relationship matrix, aggregate, genetic evaluation

Breeding Radiata Pine to Maximise Profits by Mitigating Climatic and Biotic Risks

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ABSTRACT

Risk can be defined as the product of probability of occurrence of an adverse event and severity of its effect. In this study we evaluated probability of known and potential climatic and biotic risks, and estimated effects of those risks on plantation profitability. We developed a selection index using the relative economic importance and genetic parameters for drought, *Essigella* aphid, *Dothistroma* needle blight, and *Fusarium* pitch canker. The relative importance of these risks over the entire plantation estate of radiata pine was estimated in order to determine optimal allocation of resources into breeding against the risks.

Planting on drought-prone sites with low productivity (15 m³/ha/y) could achieve an IRR of >7.0% only if the land rental was sufficiently low (i.e. <\$ 25/ha/y). Among the three pests, the effect of *Essigella* was the most widespread and presented the most significant risk for Australian radiata pine plantations. With the 13.5 % defoliation level, the impact of the aphid on profitability through deployment of resistant trees was similar between the production systems in Green Triangle (2.3% NPV) and in NE Victoria (3.9%). However, economic importance of resistance relative to MAI over the entire radiata pine plantation estate was relatively low: 1.9%, 0.6%, and 0.3% for pine aphid, needle blight, and pitch canker resistance, respectively.

Narrow-sense heritability for survival on drought-prone sites was low to moderate (median $h^2 = 0.12$), with a significant proportion of non-additive variance ($d^2 = 0.18$). In contrast, heritability for *Essigella* defoliation was quite high (mean $h^2 = 0.50$) with a significant maternal effect. For *Dothistroma* defoliation, estimated heritability ranged from non-significant to high, with a median of $h^2 = 0.29$. Genetic correlations with other selection-criteria and breeding -objective traits were also calculated, and selection indices were formulated. Implications of these results for assessment, breeding and deployment strategy against risks were discussed.

Optimal deployment of genetic gains in wood quality across Southern Australian radiata pine plantations

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ABSTRACT

Wood quality surveys in radiata pine revealed that genetics and site were the two most important factors influencing variation in wood density. Understanding of the genetic and site variation of wood quality traits in Australian radiata pine can optimise utilization of the existing stock and deployment of new stock. The availability of the Australia-Wide Diallel (AWD) tests provided a good opportunity to benchmark wood density and stiffness in Australia radiata pine families across the southern Australian pine plantations. We measured density, time-of-flight (surrogate for stiffness or modulus of elasticity (MoE)) and diameter at breast height in eight Australia-Wide-Diallel (AWD) trials at age 20/21 years.

Faster growth rates in radiata pine at 20/21 years of age were observed in Western Australia, South Australia and Victoria than in New South Wales, confirming trends observed at age 10/11 years. Density was higher in New South Wales trials than in non-New South Wales trials. As expected, there was a general tendency towards a negative genetic correlation between DBH and density at all sites. There was significant genotype x environment interaction (GEI) for DBH growth in this series of experiments but we could not conclusively confirm any significant GEI for wood density. We investigate for evidence of GEI for a selection index combining growth and density. Selection of appropriate genotypes for deployment to different sites would bring large economic benefits for both sawmill and forestry enterprises.

Association genetics reveal candidate gene SNPs affecting wood properties in *Pinus radiata* (D. Don)

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ABSTRACT

Association, or linkage disequilibrium (LD) mapping, is an emerging approach for identification of molecular markers linked to phenotypic variation. Forest trees are ideally suited to association mapping due to their low genomic LD which permits high resolution mapping of marker associations. Using this approach several single nucleotide polymorphisms (SNPs) potentially influencing economically important wood traits (density, cellulose microfibril angle and modulus of elasticity) were identified in a *P. radiata* provenance trial. 149 SNP markers from 44 cell wall candidate genes were examined. After accounting for population structure and multiple testing 16 SNPs demonstrated significant associations at $P < 0.05$. We have demonstrated that linkage disequilibrium in the native populations of *P. radiata* decays within the length of a gene. Therefore, the identified associations may result from the SNP under examination, or a linked SNP within the same gene. Despite a moderate population size, Bayesian post-hoc estimation, incorporating priors for allele frequency, p-value and population size indicated good strength of evidence for the observed associations. Without accounting for multi-collinearity between markers, the proportion of trait variance attributed to individual SNPs ranged from 1.5 to 7.9 %. SNP associations are presently undergoing validation in a 2nd generation STBA progeny trial. The small proportion of total quantitative variation contributed by individual SNPs, indicate molecular breeding strategies would achieve greatest gains utilising combinations of SNPs. Establishing methods for efficient transfer of validated SNPs into breeding selection models is essential for the uptake of the marker technology identified here, which is the focus of ongoing research.

Is there a need for a national genetic certification scheme in forestry?

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Seeds (and other genetic material) of forestry tree species are being marketed to forest growers (nationally and internationally) with various claims of source, quality and level of genetic improvement. This trade is usually being done without any form of independent certification, and in the absence of agreed guidelines. In the past, activities associated with the collection, production and sale of forest and orchard seed in Australia and New Zealand was largely overseen by government agencies, which provided a level of implied quality assurance. Increasingly government utilities are tending to divest themselves of commercially related activities in agriculture and forestry, including aspects relating to seed and plant trade, particularly in commercially important species.

Tree improvement programs for commercially important species (such as *Pinus radiata*, *Eucalyptus globulus*, *E. nitens*, *P. pinaster*, *P. elliotii*, *P. caribaea* and hybrids) have entered advanced generations of genetic improvement. It is important the performance of improved genetics which is deployed in plantations matches the claims made about it. If not, this will jeopardize ongoing investment as well as damage the reputation of tree breeders, geneticists, seed and plant producers. More importantly, it will reduce the international competitiveness of forestry based industries.

This paper discusses if there is a need and the likely ingredients for a National Forest Genetic Certification Scheme (NFGCS). Such a scheme could be based on voluntary participation, with participating bodies accredited and expected to comply with recommended protocols and procedures. A NFGCS should establish and publish guidelines to cover seed and other genetic material sourced from native forests, seed orchards and other propagation systems. An efficient system for endorsing and monitoring compliance is essential, but also a basic requirement is to ensure industry engagement and consumer confidence. Some of the technical challenges in implementing a scheme will be discussed.

Optimal allocation of seedlots to stands improves forest profitability

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ABSTRACT

Allocation of seedlots to stands requires knowledge of family expected values (EGV), how families are put together into seedlots and the bio-economic characteristics of each stand to be planted. EGV were computed for three harvest age traits, for 156 families that represent seed collected from individual trees in a clonal, open-pollinated seed orchard. The EGV were computed taking into account the modelled contributions of pollen within and outside the orchard. The seedlots were assumed to have remained segregated. Bio-economic characteristics, including site-type, productivity, haulage distance and harvesting costs, were obtained on 20 stands and used to derive selection indices customised for each stand. For each of the 20 stands, each seedlot has a selection index value, which expresses its net present value (NPV) per hectare. Linear programming was used to optimally allocate seedlots to each stand, subject to maximising profit.

When seedlots were evenly allocated to stands the projected NPV of the total area harvested across all 20 stands (1576 ha) was \$2,129,132, relative to planting baseline genetic material. Optimally allocating seedlots to stands yielded a projected NPV of total area harvested of \$2,527,485, an increase of approximately \$400,000, or an increase of \$253 per hectare.

The study demonstrates that 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 will give the highest economic gain.

Site classification to account for genotype by environment interaction in *E. globulus*

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ABSTRACT

Eucalyptus globulus is grown in a range of environments spread across temperate Australia. The national cooperative tree improvement program uses over 120 progeny trials established on site types representative of the areas growing commercial plantations. Previous research suggests that genotype by environment interaction may be important across this environmental range, and is driven by factors that affect water stress during summer.

Pre-dawn water potentials for all progeny trials sites were predicted using the CABALA growth model and climatic data was obtained from Data Drill. Sites were then classified into three types based on the number of days that age four pre-dawn water potential was predicted to be less than -3.0MPa. A fourth site type is also used where trees are likely to be severely affected by *Mycosphaerella spp.*

GxE for growth traits is accounted for in the national genetic analysis by treating growth in each site type as separate but correlated traits. Future work will refine these correlations.