

SIMULATION TO DETERMINE OPTIMAL WOOD QUALITY SAMPLING STRATEGIES

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INTRODUCTION

The Southern Tree Breeding Association manages a *Eucalyptus globulus* breeding program throughout southern Australia. The program's primary breeding objective is to maximise profits (\$NPV per hectare) from plantations grown for Kraft pulp production. The genetic worth of trees is compared using an economic index (\$Index) that combines three rotation-age breeding objective traits, Volume, Basic Density (BD) and Kraft Pulp Yield (KPY) into a profit function, by weighting each trait by its economic importance.

Direct assessment of KPY is destructive and prohibitively expensive. Near-infrared reflectance analysis can be used to predict KPY (Schimleck and Mitchell 1998). However, NIRA predicted pulp yield (PPY) is still expensive and previous simulation work by Dutkowski and Raymond (2001) suggests that assessment funds would be better spent on core basic density (coreBD) and predicting KPY based on its reported correlation with BD. There are few estimates of this correlation for *E. globulus* reported in the literature and these vary between -0.5 and 0.99 (Raymond *et al* 2001). The STBA currently assumes a value of 0.5 for breeding value estimation.

The aim of this study is to determine, for a wide range of correlations between BD and KPY, whether the STBA should assess PPY in its progeny trials and, if so, what assessment strategy should be adopted.

METHOD

The breeding simulation tool, gSIM (Dutkowski, this proceedings) generates a simulated population with known additive, family and clonal genetic values for the traits that are defined. These values are a random sample from a multi-variate normal population with the trait means, variances and correlations set by the user. gSIM also generates simulated data for all defined traits for every individual using the error variances specified. gSIM uses ASReml (Gilmore *et al* 2002) to analyse the data and produce breeding values.

The "measured" traits Growth<5 years, Growth 5-8 years, coreBD, PPY and the breeding objective traits harvest age Volume, Basic Density and Kraft Pulp Yield were defined. The additive, family and error variances and correlations between traits were specified. Family variances were defined as a quarter of the additive variance for growth and one tenth of the additive variance for density and pulp yield traits (Li, *pers. comm.*). To study the affect of the correlation between BD and KPY, six levels (-0.5, -0.25, 0, 0.25, 0.5 and 0.9) of the correlation between coreBD and PPY were used. The correlations between BD and PPY and that between coreBD and KPY were both set at 0.9 of the coreBD – PPY correlation. The BD - KPY correlation was set at 0.81 of the coreBD – PPY correlation.

For the simulation, gSIM created a base population and two subsequent generations. The base population was generated with 300 open-pollinated families with 25 trees per family. These families were drawn from 19 races with the number of families per race and race means for growth, coreBD and PPY intended to reflect the STBA base population. The best 200 trees on \$Index in each generation, were selected for crossing. The next generation consists of 7,500 trees from three hundred new families, each with 25 trees. No parent could be used in more than 5 crosses. All trees were assessed for Growth<5 years and Growth 5-8 years. For each generation, a fixed budget of \$20,000 for wood quality assessment was assumed. Costs of assessing coreBD and PPY were assumed to be \$3 and \$21 per tree respectively. Six different sampling strategies were tested where the proportion of the budget spent on NIRA assessment of a random sample of trees was increased from 0 to 75%. The proportion of trees samples for coreBD and PPY ranged from 0 to 88.9% across the strategies. These were compared to sampling all trees for all traits. gSIM was run for 1000 iterations for every combination of correlation and sampling strategy.

RESULTS

Genetic gain, expressed as \$Index, increased with the correlation between BD and KPY for all sampling strategies (Figure 1). At all correlation levels, assessing all trees for all traits gave the best gains. At all but the highest correlation (0.9), spending some money on PPY assessment significantly increased

\$Index. Spending the majority of the budget on PPY assessment (75%) was the best strategy only if the correlation was very low (-0.5). At all other correlations this strategy gave the lowest or second lowest gain. When the correlation was between 0 and 0.5 there was no significant difference between strategies spending 50%, 20% or 10% on PPY assessment. Where the correlation was equal to or greater than -0.25, spending 25% of the budget on PPY assessment was as good or better than the other strategies (other than assessing all trees).

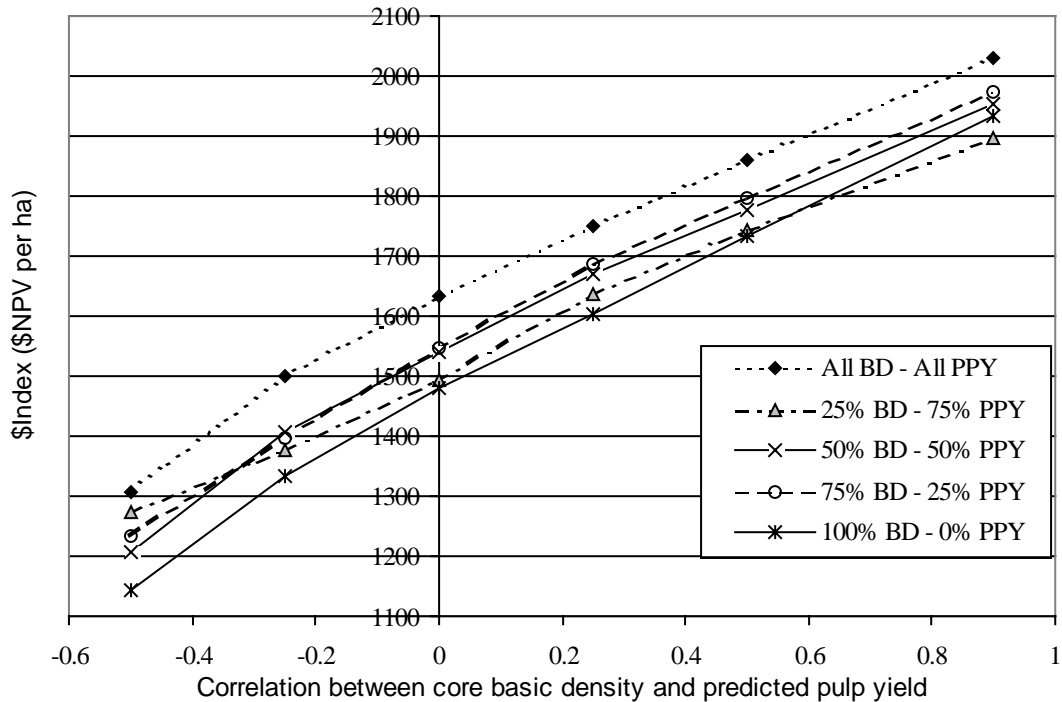


Figure 1: Average \$Index after three generations at different correlations between core basic density and predicted pulp yield for various assessment strategies

DISCUSSION

As in all breeding programs, the gains that can be made are limited by the budget available. The best gains may be made by assessing all trees for all traits; however, the cost of doing this would be nine times the proposed budget.

These results suggest that the STBA will make more gain in its *E. globulus* breeding program if some level of PPY assessment is undertaken. The best strategy appears to be to spend 25% of the wood quality assessment budget on PPY. However, little gain will be foregone if between 10% and 50% of this budget is spent on PPY assessment. The results to a degree contradict the earlier work by Dutkowski and Raymond (2001) for the base population, however in that analysis PPY was only undertaken once core BD had been done as opposed to a random sample.

In this simulation sampling PPY was assumed to be seven times more expensive as sampling BD. This is based on taking a 12mm core, chipping and grinding this before running it through NIRA. It may be possible to reduce the chipping and grinding cost by collecting wood shavings instead of a whole core. By reducing the cost of sampling PPY, is likely that spending a greater proportion on PPY sampling may increase gains.

REFERENCES

- Dutkowski, G.W. and Raymond, C.A., (2001). Proc. Developing the Eucalypt of the Future, 72. Valdivia, Chile.
- Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J. and Thompson, R. (2002). << ASReml User Guide Release 1.0 >> VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.
- Raymond, C.A., Schimleck, L.R., Muneri, A. and Mitchell, A.J. (2001). Forest Genetics. 8(3): 213-224.
- Schimleck, L.R. and Mitchell, A.J (1998). Tappi J. 81: 229-236.