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Short Note: The Genetic Correlation Between Air-dried Density and Basic Density in *Eucalyptus Nitens* Wood Cores

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Abstract

Cores extracted from trees to assess wood chemistry are generally not used to assess basic density in eucalypt pulpwood breeding programmes, as the measurement of basic density requires high temperature drying. However, both wood chemistry and air-dried density can be assessed on the same core. This study found that the inter-trait genetic correlation between core air-dried and basic density to be effectively equal to one in two Tasmanian *Eucalyptus nitens* progeny trials. This implies

that selection for basic density could be undertaken using air-dried density with little or no reduction in genetic gain, thus negating the need to extract a separate core to assess basic density and wood chemistry. The adoption of this practice could considerably reduce the cost of assessing these traits in eucalypt breeding programmes.

Key words: *Eucalyptus nitens*, selection trait, non-destructive assessment, air-dried density, basic density, wood chemistry, pulp yield, cellulose content, near infrared spectroscopy (NIR), genetic correlation.

Introduction

Eucalypt pulpwood breeders routinely select trees according to diameter at breast height and wood core basic density (i.e. oven-dry weight divided by green volume; TAPPI, 1989). Furthermore, near infrared

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reflectance spectroscopy (NIR) is increasingly utilised as a cheap and non-destructive means of selecting trees according to wood chemistry (e.g. cellulose content, pulp yield, lignin content and/or extractive content; RAYMOND *et al.*, 2001; POKE and RAYMOND, 2006).

Assessment of basic density requires cores to be oven-dried at approximately 105 °C (TAPPI, 1989). Conversely, cores extracted for chemical analysis are dried at low temperature to prevent significant alteration of wood chemistry (e.g. below 35 °C; AS/NZS 1301.002s 2004). Accordingly, the measurement of both core basic density and wood chemistry has historically required the extraction of multiple cores from each tree (e.g. RAYMOND and SCHIMLECK, 2002). However, if trees from breeding populations could be efficiently selected for high basic density on the basis of the air-dried density (i.e. air-dried weight divided by green volume) of cores extracted for the assessment of wood chemistry, the total cost of assessing these traits in eucalypt breeding programmes could be substantially reduced. The principal aim of this study was to investigate the feasibility of this approach by examining the strength of the genetic correlation between air-dried and basic density in *E. nitens*.

Materials and Methods

This study was undertaken on a sub-sample of trees growing in two first-generation open-pollinated *E. nitens* progeny trials located near Meunna (41°06' S, 145°28' E) and Tarraleah (42°20' S, 146°27' E) in Tasmania, Australia (for details see DUTKOWSKI *et al.*, 2001). The trials were incomplete block designs comprising five replicates of 21 incomplete blocks, each containing 20 five-tree row-plots of open-pollinated families. The trials included families from all three of the races proposed by DUTKOWSKI *et al.* (2001). These races were defined based on geographic patterns of quantitative genetic variation in the central Victorian population of *E. nitens*. The Meunna trial was pruned and thinned to two large trees per plot six years after planting.

Nine years after planting, 12-mm bark-to-bark wood cores were extracted 0.9 m from the base of trees from 12, 36 and 56 selected families in the Connor's Plain, Northern and Southern races respectively. Where possible, four families were randomly selected for coring from each locality from which seed was collected (refer to DUTKOWSKI *et al.*, 2001) so as to include families from a broad geographic range within each race. The majority (102) of the sampled families were common to both trials. Within each family, three to six (usually four)

healthy unforked trees were selected for coring so as to include stems from multiple replicates and a broad range of diameters (all greater than 9.5 cm at 1.3 m).

Green volumes were measured (TAPPI, 1989) before cores were loosely stacked in trays and air-dried in a laboratory to equilibrium moisture content (mean 8.78%, std. dev. 0.68%). The cores were then weighed and their air-dried densities determined. Finally, cores were oven-dried at 105 °C for 24 hours, weighed and their basic densities calculated.

Bivariate mixed model analyses were conducted separately for each trial using ASREML (GILMOUR *et al.*, 2002) by fitting the following model, in matrix notation:

$$y = X_1b + X_2r + Z_1f + e$$

where y is a vector of phenotypic observations for air-dried and basic density, b is a vector of the fixed replicate effects, r is a vector of the fixed race effects, f is a vector of the random family within race effects, e is a vector of residuals for both traits, and X_1 , X_2 and Z_1 are incident matrices relating the phenotypic observations to the effects in the model. Incomplete block effects were not fitted in the model, as incomplete block variance estimates were found to be very low and not significantly different to zero in preliminary analyses. For each trial, an estimate of the inter-trait family correlation (i.e. the additive genetic correlation) between air-dried and basic density was derived from family (co)variance components estimated using a restricted maximum likelihood (REML) procedure (GILMOUR *et al.*, 2002). Within-race narrow-sense heritabilities (h_{op}^2) for each trait and site were calculated from variance components estimated using equivalent univariate models and assuming a coefficient of relationship within open-pollinated families of 0.4 to account for an assumed selfing rate of 30% (GRIFFIN and COTTERILL, 1988). Within-site inter-trait Pearson's phenotypic correlation coefficients were estimated using the CORR procedure in SASTM (SAS INSTITUTE INC., 2002).

Results and Discussion

Estimates of the inter-trait genetic correlation between air-dried and basic density were effectively equal to one at both sites (*Table 1*). This implies that selection for whole-tree basic density could be undertaken using core air-dried density instead of core basic density with little or no reduction in genetic gain. Furthermore, given that air-dried density and wood chemistry can be measured on the same core and assuming that

Table 1. – Means, heritabilities and intertrait correlation coefficients for core air-dried and basic density by trial site. Standard errors are in parentheses.

Trial	Measure of density	Least squares mean (kg m ⁻³)	Narrow-sense heritability	Intertrait genetic correlation	Intertrait phenotypic correlation
Tarraleah	Basic	449 (2)	0.423 (0.117)	1.001 (0.001)	0.997 (0.003)
	Air-dried	488 (2)	0.420 (0.117)		
Meunna	Basic	404 (2)	0.378 (0.113)	1.000 (0.001)	0.996 (0.004)
	Air-dried	440 (2)	0.381 (0.113)		

both of these core traits exhibit a strong genetic correlation with relevant whole-tree traits (i.e. objective traits; refer to RAYMOND et al., 2001), these findings suggest that only one core needs to be extracted from trees to assess both density and wood chemistry in eucalypt breeding programmes. The adoption of this practice, combined with the use of solid wood rather than ground samples to measure NIR spectra (POKE and RAYMOND, 2006), could considerably reduce the cost of assessing wood properties in eucalypt pulpwood breeding programmes.

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Heterogeneity and Spatial Autocorrelation for Chloroplast Haplotypes in Three Old Growth Populations of Northern Red Oak

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Abstract

In eastern North America, evidence for cryptic northern refugia could contribute to resolving Reid's Paradox, the disparity between the rate of oak recolonization indicated by pollen deposition and the rate indicated by contemporary seed dispersal studies. Severe anthropogenic disturbance of oak-dominated forests throughout eastern North America followed by regeneration from isolated patches and deliberate planting in some regions could obscure the signal of discontinuity expected from small, cryptic refugia. In this study of northern red oak, *Quercus rubra* L., the dominant representative

of *Quercus* section Lobatae in the eastern United States, we address the question of appropriate sample size for accurate detection of the biogeographical distribution of chloroplast haplotype diversity in *Q. rubra*. We examined chloroplast DNA (cpDNA) variation in all *Q. rubra* over 17 cm in diameter (310 trees) in three forest fragments with documented histories of minimal disturbance for the last 100–190 years. cpDNA polymorphisms in three intergenic regions revealed different haplotype frequencies between the two local fragments located within 1 km of each other and complete discontinuity for the predominant haplotype between these two sites and a site 207 km distant. Haplotypes displayed positive spatial autocorrelation over 10–40 meter distances. Sample sizes of 10 or fewer taken at 50 meter intervals along a linear transect yielded poor estimates of haplotype frequencies and did not accurately detect haplotype richness.

Key words: cpDNA, *Quercus rubra*, chloroplast, genetic diversity, patch size, postglacial migration.

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