

Borzak, C. L., O'Reilly-Wapstra, J. M. and Potts, B. M. 2014. Direct and indirect effects of marsupial browsing on a foundation tree species. – Oikos doi: 10.1111/oik.01538

Appendix 1

Genetic and non-genetic effects within the diallel

Statistical analysis

Using data from trees in the diallel from the full trial, the significance of genetic and non-genetic effects on early-age traits (e.g. marsupial browsing damage, tree mortality, tree height, and the presence/absence of autumn gum moth damage) were determined by fitting an individual tree mixed model (Dutkowski et al. 2002) with ASReml (ver. 3) (Gilmour et al. 2009). The model fitted was:

$$Y = \mu + \text{rep} + \text{race GCA} + \text{race SCA} + \text{race maternal} + \text{race reciprocal} + \text{row} + \text{col} + \text{additive} + \text{SCA} \\ + \text{maternal} + \text{reciprocal} + \varepsilon$$

where Y is the observation for the response traits, μ is the trait mean, rep is the fixed replicate effect, race GCA is the fixed race general combining ability and represents the race effect averaged across males and females, race SCA is the fixed race specific combining ability and is the deviation of the inter-race crosses from their mid-parent value, race maternal is the fixed race maternal effect and thus whether races generally perform differently as a male or female, race reciprocal is the fixed race reciprocal effect and represents differences between the specific reciprocal crosses between races, row is the random row within *replicate* effect, col is the random column within replicate effect, *additive* is the random within-race additive genetic effect, *SCA* is the random within-race specific combining ability effect, *maternal* is the random within race maternal effect, *reciprocal* is the random within-race reciprocal effect and ε is the residual. The race GCA and race maternal terms were fitted by amalgamating three variables describing the relative contribution of each race to 1) the pedigree of each plant and 2) the pedigree of mother of each plant, respectively, using the grouping option (!G) in ASReml. The additive genetic effects were estimated using a numerator relationship matrix defined using a two-generation pedigree file to determine the genetic covariance between relatives. For presence/absence traits (mortality and AGM damage), a binary model with a logit link function was fitted. The significance of the fixed effects was tested using the incremental Walds F-statistic with the denominator degrees of freedom calculated using the default algebraic derivatives algorithm. The significance of the variance components was tested by using

the Z-test (Zar 1984). To determine the proportion of observed variation within race due to additive genetic variation after accounting for spatial effects, within race narrow-sense heritability (h^2) and its standard error for each parameter were calculated with ASReml by dividing the additive genetic variance component by the total phenotypic variance (estimated as the sum of the *additive*, *SCA*, *maternal*, *reciprocal* and residual variance components). To avoid biased estimation, random terms were not constrained to be greater than zero.

Results

Across the diallel in the full trial, there was no effect of plant genotype on marsupial browsing (Table A1). Marsupial browsing patterns were therefore not related to plant genetics, allowing the investigation of the direct and indirect consequence of browsing without the confounding effects of genetics. For the presence of autumn gum moth the race SCA effect (describing the deviation of inter-race crosses from their mid-parent value) was statistically significant, the effect was small compared with spatial factors such as replicate (Table A1). There was a significant effect of race (race GCA) on tree mortality, and this was due to a relatively higher survival rate and slower growth of plants originating from the Strzelecki race (data not shown). For one-year height there was a significant effect of race SCA and within race additive genetic and reciprocal variation. Such differential genetic patterns in these traits have been previously shown in these populations (Dutkowski and Potts 1999, Stackpole et al. 2010), however, the early non-maternal reciprocal effect on tree height may be a product of a residual nursery effect that often disappears with age (Lopez et al. 2003), and is no longer evident in basal area at 2 and 4 years post browsing (data not shown). Based on the standard error estimates, the heritability values for organism damage and mortality at year 1 were all effectively zero and that for year 1 height marginally greater than zero.

Table A1. Genetic and non-genetic effects on damage by marsupials, mortality, height (1 year post browsing) and the proportion of trees with damage by autumn gum moth (AGM; 9 months post browsing) across the entire trial (diallel only; n = 4040 to 4427 depending on trait). The random additive, specific combining ability, maternal effects refer to within race effects. Walds F-values are presented for fixed effects and Z-values are presented for the random effects. Significant effects are in bold: *, p < 0.05; **, p < 0.01; and ***, p < 0.001. The model was fitted with random effects unconstrained, meaning some variance component estimates were less than zero.

Source of variation	NDF	DDF	Marsupial			
			browse F/Z	Mortality ^a F/Z	Height F/Z	AGM ^a F/Z
<u>Fixed effects</u>						
Replicate	14	238–299	24.2***	3.9***	26.7***	18.4***
Race general combining ability	2	21–26	1.4	6.1**	3.2	0.7
Race specific combining ability	3	128–321	0.0	0.4	6.3***	2.7*
Race maternal	2	30–63	2.6	1.3	1.3	1.4
Race reciprocal	1	225–273	0.0	0.2	0.1	0.2
<u>Random effects</u>						
Row X			7.7***	3.5***	9.1***	6.2***
Column Y			4.5***	1.3	8.1***	2.9**
Additive			1.3	0.5	2.5**	0.4
Specific combining ability			0.0	1.8*	<0	<0
Maternal			<0	0.2	<0	0.7
Reciprocal			1.1	<0	2.1*	<0
h ²			0.011	0.039	0.064	0.010
h ² standard error			0.008	0.070	0.025	0.034

NDF = numerator degrees of freedom for fixed terms

DDF = denominator degrees of freedom associated with the random error terms used to test the fixed effects

h² = within-race narrow sense heritability estimate

^a Presence/absence trait fitted using a binary model with a logit link function

References

Dutkowski, G. W. and Potts, B. M. 1999. Geographic patterns of genetic variation in *Eucalyptus globulus* ssp. *globulus* and a revised racial classification. – Aust. J. Bot. 47: 237–263.

Gilmour, A. R. et al. 2009. ASReml user guide release 3.0. – VSN Int., Hemel Hempstead, UK.

Lopez, G. A. et al. 2003. Maternal and carryover effects on early growth of *Eucalyptus globulus*. – Can. J. For. Res. 33: 2108–2115.

Stackpole, D. J. et al. 2010. Age trends in genetic parameters for growth and wood density in *Eucalyptus globulus*. – Tree Genet. Genomes 6: 179–193.

Zar, J. 1984. Biostatistical analysis. – Prentice Hall.