— POSTER —

The Genetic Control of Flowering Time in *Eucalyptus globulus*, *E. nitens* and their F_1 hybrid

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Abstract

Flowering time in a base population trial of *Eucalyptus globulus* ssp. *globulus* was highly variable and under strong genetic control. Races from the east coast of Tasmania and the Furneaux Group flowered approximately 1 month earlier than races from Victoria and King Island. These racial differences in flowering time were inherited in an additive manner in interprovenance F_1 hybrids, whereas the flowering time of interspecific F_1 hybrids between *E. nitens* and *E. globulus* was more similar to the late-flowering *E. nitens*.

Introduction

Genetically based asynchrony in flowering has important implications for the incorporation of selections into seed orchards and open-pollinated (OP) breeding populations. This paper examines the genetic control of flowering time within an OP base population of *Eucalyptus globulus* ssp. *globulus*, and controlled crosses of ssp. *globulus*, *E. nitens* and their F_1 hybrid.

Methods

Flowering was monitored in a base population trial of ssp. *globulus* established at Shale Oil by North Forest Products (Jordan *et al.*, 1994). The trial comprised families from OP seed collected from throughout the geographical range of ssp. *globulus* (and populations intergrading with mainland subspecies) by the CSIRO Australian Tree Seed Centre in 1987-88. The families were planted in two-tree line plots, in an incomplete block design of 5 replicates with 25 incomplete blocks per replicate (Jordan *et al.*, 1994). As only 456 of the 6000 trees in the trial were assessed, a new incomplete blocking structure (n=11) was superimposed upon the data to best account for the distribution of flowering trees within the trial. Trees with flower buds were assessed at two-weekly intervals, from 2/11/93 to 24/2/94, for the percentage of the total season's bud crop which was flowering. This data were used to derive estimates of start (first flowering date), peak (highest % flowering), end (10 days after the last flowering date) and range (end minus start) of flowering for each tree, expressed as the number of days after the 1/7/93. A bud was considered to have commenced flowering if the operculum had been shed and to have finished flowering when stamens had withered. Variance components associated with incomplete block, geographical race (Jordan *et al.*, 1994), localities within race, families within localities, plots within families and within plot effects were estimated with the REML procedure of SAS using a random model. Individual narrow-sense heritabilities were calculated from these OP families, assuming a coefficient of relatedness of 0.4 (Potts *et al.*, 1995) as:

$$h^2_{op} = \frac{2.5^* \sigma^2_{fam(loc)}}{(\sigma^2_{fam(loc)} + \sigma^2_{plot} + \sigma^2_{residual})}$$

The flowering of controlled crosses of *E. nitens* (as a half-diallel), *E. globulus* (as an intra- and interprovenance factorial) and their F_1 hybrids was monitored in a trial established in July 1990 at West Ridgley, Tasmania (Volker, 1995). The *E. nitens* parents were from the Toorongo provenance and the *E. globulus* parents were from King Island (K), Taranna (T) and Flinders Island (F, one female only). Trees with more than 10 inflorescences were assessed at two-weekly intervals, from 4/11/93 to 7/3/94, as previously described. Cross types were compared using a one-way GLM analysis (SAS) based on family means.

Results and discussion

The average flowering period of individual trees in the base population trial at Shale Oil was 37 days. However, the time of flowering of individuals was extremely variable. Flowering in the trial extended over more than 8 months (assessment period and flowering observations in July 1993). Most of the variation in the start, peak and end of flowering was attributed to racial differences within ssp. *globulus* (36 to 47%), with the variation between localities within races (16 to 20%) and between families within localities (9 to 15%) accounting for less, but significant, portions of the variation (Table 1). The individual narrow-sense heritabilities for

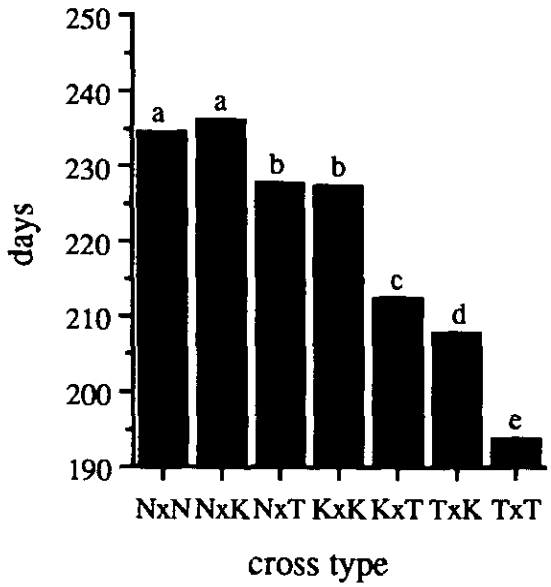
Table 1. Percentage of the variation in flowering traits in *E. globulus* ssp. *globulus* attributed to the effects of incomplete blocks in the Shale Oil trial, race of origin (as defined by Jordan *et al.*, 1994), localities (parent trees within approx. 10km of each other) within race, open-pollinated families within localities, plots within families and within plots. The individual heritability (h^2_{op}) was calculated assuming a coefficient of relatedness amongst OP sibs of 0.4 (n = 424-456). The degrees of freedom relevant to peak flowering are indicated.

Effect	df	Flowering			
		Start	Peak	End	Range
Blocks	10	2%	1%	1%	4%
Races	10	36%	42%	47%	2%
Localities	23	16%	20%	18%	3%
Families	188	15%	9%	9%	13%
Plots	144	8%	11%	0%	0%
Within plots	54	23%	16%	25%	79%
h^2_{op}		0.81	0.65	0.64	0.35

the start, peak and finish of flowering were extremely high (Table 1) and may be inflated (see Potts *et al.*, 1995).

Racial differences were mainly due to populations on the east coast of Tasmania and the Furneaux Group flowering approximately 1 month earlier than populations from Victoria and King Island. These racial differences in flowering time were maintained in the West Ridgley trial established from control-pollinated progenies of east coast (Taranna) and King Island provenances of ssp. *globulus*, and were inherited in an additive manner in interprovenance F_1 hybrids (Fig. 1). In contrast, interspecific F_1 hybrids between *E. nitens* and *E. globulus* showed a strong bias toward the later flowering *E. nitens*.

Figure 1. Mean days (from 1/7/93) to peak flowering of *E. nitens* (NxN; n=272), *E. globulus* ssp. *globulus* and their interspecific F_1 hybrids (King Island males, NxK, n= 31; Taranna males, NxT, n= 68). The crosses involving ssp. *globulus* have been partitioned into those amongst parents from Taranna (TxT, n=336), King Island (KxK, n=255) and the interprovenance F_1 hybrid (KxT, n=390 and TxK; n=129).



The large, genetically based differences in flowering time within ssp. *globulus* and intergrade populations has important implications for randomised mating in breeding or deployment (e.g. seed orchards) populations which rely on open-pollination. A key result is the demonstration of large differences in flowering time of populations on islands in Bass Strait (i.e. King Island versus Furneaux Group), yet this material has been grouped together in the same subline in several breeding programs. Grouping material on the basis of geographical race as defined by Jordan *et al.* (1994) would contribute significantly to synchronisation of flowering. However, even then, genetic differences between localities and families within races would still hinder random mating under open-pollination.

References

Jordan, G. J., Borralho, N. M. G., Tilyard, P. and Potts, B. M., 1994. Identification of races in *Eucalyptus globulus* ssp. *globulus* Labill. based on growth characteristics in Tasmania. Silvae Genetica, (in press).

Potts, B. M., Volker, P.W., Hodge, G. R., Borralho, N. M. G., Hardner, C. H. and Owen, J. V., 1995. Genetic limitations to the exploitation of base populations of *Eucalyptus globulus* ssp. *globulus*. This volume.

Volker, P.W., 1995. Evaluation of *Eucalyptus nitens* x *globulus* for commercial forestry, (this volume).