

A GENETIC BASIS TO THE DESTRUCTION OF *EUCALYPTUS GLOBULUS* SEED BY WASPS FROM THE GENUS *MEGASTIGMUS*

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INTRODUCTION

Megastigmus spp. are tiny wasps (bodies 2.5-6.5mm in length) from the hymenopteran family *Torymidae* that destroy the seed of forest trees (Elliott and deLittle 1984). Many studies have examined their destructive effect on seed production in conifers, such as: *Pseudotsuga*; *Abies*; *Cedrus*; *Cupressus*; *Juniperus*; *Larix* and *Picea* (Roques and Skrzypczyńska 2003). In Australia, they have been reported to feed on the seed of at least seven eucalypt species. However, despite reports of losses both in open-pollinated seed orchard and controlled crossed seed of *Eucalyptus globulus* extending over many years, little is known of the biology and taxonomy of these insect species, nor the extent of the decrease in seed production they cause. The only study available suggests that the female wasps lay their eggs in eucalypt flowers (Drake 1974). After hatching, each small larva tunnel down into the developing seeds and gradually consume the content of a seed. The larva goes through several instars and the pupa develops within the seed coat. Fully-grown adult wasps emerge from the seed coat through a circular exit hole, and then exit through the top or side of the capsule usually before it opens. In this study we quantified the percentage of seed damaged by *Megastigmus* spp. predation in 384 seedlots of *Eucalyptus globulus* and examined whether there was a genetic basis to differences in the levels of seed predation observed.

MATERIAL AND METHODS

Seed lots were obtained by seedEnergy Pty Ltd from an *E. globulus* seed orchard in Mount Gambier, South Australia (Bawdens) containing 156 open-pollinated families from ten sub-races (Strzelecki Ranges, Strzelecki Foothills, King Island, Western Otways, Flinders Island, Inland North-eastern Tasmania, Southern Tasmania, North-eastern Tasmania, South-eastern Tasmania and Western Tasmania; see Dutkowski and Potts [1999] for sub-race locations) from the 1987 CSIRO collection of native stand trees. The orchard contained 4 replicates, within which families were initially fully randomised, but at the time of this study the family representation within replicates was variable due to thinning to 800 trees. In 2000 a sub-sample of 25 open pollinated capsules was

collected from two of the replicates (384 trees) following whole tree capsule harvests from the orchard. These subsamples were weighed; the seed and chaff extracted, a count made of the numbers of seed damaged by *Megastigmus*, as well as the number of larvae and wasps per seedlot. The seedlots were then cleaned and the number of viable seed counted. A mixed model was fitted to the percentage of seed damaged with a fixed sub-race effect and random replicate and family within sub-race effects using ASREML (Gilmour 1999). The narrow-sense heritability (h^2_{op}) was calculated using the family within sub-race variance component divided by a coefficient of relatedness of 0.4 to estimate the additive variance, and dividing by the phenotypic variance estimated from the sum of the family within sub-race and error variance components. Genetic correlations between the percentage of damaged seed, capsule weight, and flowering time were calculated using bivariate models fitted with ASREML (Gilmour 1999). The significance of the difference of each correlation from zero was tested by a likelihood ratio test assuming a χ^2 distribution with one degree of freedom for the difference in $-2 \log$ (likelihood) between a model in which the correlation was constrained to be zero and the unconstrained model (Shaw 1991).

RESULTS AND DISCUSSION

The percentage of seed damaged by *Megastigmus* was shown to be under genetic control, with both significant sub-race ($P < 0.001$) and family within sub-race ($P < 0.01$) effects detected. Although the proportion of seed damaged was on average small (3.3%) it ranged from between 0 and 21% between trees. The within sub-race heritability was 0.38 ± 0.15 . This heritability is moderate in comparison with damage caused by other pests of *E. globulus*, which range from 0.00 for shoot feeding weevils (*Myllobius* sp. - Jones and Potts 2000), 0.11 for infestation of the southern eucalypt leaf beetle on juvenile leaves (*Chrysophtharta agricola* - Rapley *et al.* 2004), 0.13 for browsing damage from two marsupials (*Trichosurus vulpecula* and *Thylogale billardierii* - O'Reilly-Wapstra *et al.* 2002), to 0.43 for leaf damage by sawfly *Perga affinis* ssp *sinsularis* (Jordan *et al.* 2002). Trees from the Strzelecki Ranges had the

highest percentage of damaged seed (least square mean 4.8%) followed by Strzelecki Foothills (4.1%), King Island (3.2%) and Western Otways (1.9%). The Strzelecki Ranges and Western Otways sub-races are among the most valued for pulpwood plantations. The remaining sub-races had very low percentages of damaged seed with least square means ranging between 0.3% and 1.7%.

The genetically based variation in the percentage of seed damaged in this *E. globulus* seed orchard could be due to genetic variation in biological characteristics of the tree such as flower bud size (as reflected by capsule weight) and flowering time. Flower bud size may be a determinant of the level of *Megastigmus* damage, as capsule weight was negatively correlated to percentage *Megastigmus* damaged seed both at the sub-race ($r_{\text{sub}}=-0.99$, $P=0.01$) and the family within sub-race ($r_{\text{g}}=-0.64$, $P=0.000$) levels. This correlation could be due to the small ovipositor of the wasp not being able to efficiently penetrate the larger flower buds of some sub-races to deposit eggs. However, variation in *Megastigmus* damaged seed was also correlated with flowering time at the sub-race level ($r_{\text{sub}}=0.94$, $P=0.02$), with later flowering sub-races having a higher percentage of damaged seed. This correlation did not occur at the family within sub-race level ($r_{\text{g}}=0.25$, $P=0.36$), suggesting that both flowering time and flower size may have independent effects on the susceptibility to *Megastigmus* damage. It is difficult to unravel these effects at the sub-race level as the sub-races with the smaller capsules also flower later ($r_{\text{sub}}= -0.86$, $P=0.054$). Nevertheless, it is noteworthy that while the Strzelecki Ranges sub-race did not differ

significantly in mean flowering time from the Western Otways sub-race, the Western Otways sub-race had significantly larger capsules and significantly less damaged seed.

As this study involves only a single seed orchard and a single season of flowering, it is unclear whether the genetic based differences observed in *Megastigmus* damaged seed would be expressed at other sites and in other seasons. The same ranking would be expected if the *Megastigmus* populations maintain the same oviposition capacity and the same phenological pattern relative to the *E. globulus* flowering. However, too little is known about the life history and ecology of the seed-feeding *Megastigmus* wasps in Australia to assess whether the genetic patterns we observed will be stable.

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