The extended phenotype of *Eucalyptus globulus*

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The extended phenotype

“The effects of genes at levels higher than the population” (Dawkins 1982; Whitham et al. 2003)

Foundation species
Dominant or keystone species that have a disproportionate influence on the ecosystem in which they occur

from Whitham et al. 2006
Trees as foundation species

*Populus* in USA

- Conservation and management of biodiversity
- Restoration ecology
- Predict the broader impacts of anthropogenic changes (e.g. GMOs)
- Community structure & evolution

Whitham *et al* 2003, 2006
The case of *Eucalyptus globulus*

- Dominant of lowland forest in SE Australia and Tasmania
- A major plantation species in temperate regions of world
- Extensive genetic resources available
- Extensive quantitative and molecular studies of gene pool
Significant spatially structured genetic variation in numerous traits

Partition of variation within Gunns Ltd trials (46 traits, 13 races, 46 localities, 450+ families)

- Residual: 74%
- Race: 9%
- Locality: 3%
- Family: 9%
- Block: 5%

Localities from the 1987/88 CSIRO range-wide collection of 600+ OP seedlots and racial classification

Potts et al. 2004

Dutkowski & Potts 1999
Dependent herbivores respond to genetic variation in tree traits

**Sawfly (Perga affinis)**
Foliage damage greater on thick barked trees ($r_g = 0.44$ ***)

Dutkowski & Potts 1999
Jordan *et al.* 2002
Kelly 1997

**Autumn gum moth (Mnesampela privata)**
Oviposition is affected by genetic variation in the aliphatic ester ($C_{24}$) benzyl n-tetracosanoate

Jones *et al.* 2002
Rapley *et al.* 2004a,b,c

**Brush tail possum**
Foliage intake is affected by genetic variation in formylated phloroglucinol compounds (FPCs) [sideroxylnonal A and macrocarpal G ]

Significant racial differences in defensive chemistry

Adult foliage condensed tannins

O'Reilly-Wapstra et al. submitted
How far does the effect of genetic variation at the race level flow through the ecosystem?
The experiment

Gunns Ltd *E. globulus* base population field trial at West Ridgley, NW Tasmania (CSIRO 1988/89 OP seedlots)

1. 160 felled trees
   - age 15 years
   - 8 races across 2 replicates
   - 20 trees per race (10 families per race, 2 trees/family)

2. 100 standing trees
   - age 16 years
   - 5 races across 2 replicates
   - 20 trees per race (10 families per race, 2 trees/family)
Defining the extended phenotype

Genetic variation

Tree canopy communities (fungi, invertebrates, marsupials, [birds],)

Canopy & leaf decay rates & communities

Chemical and nutrient leaching into soil

Seedling recruitment

Soil nutrients & micro-biota

Bark communities (invertebrates)

Log & disc decay rates & communities (invertebrates, fungi)
Race of decaying canopy can affect soil quality

Linseed bioassay of soil extracts taken from beneath decaying canopies after 7 months

% germination

radical length
Race of decaying canopy affects litter invertebrate community

Pitfall traps beneath decaying canopies of trees from Southern Tasmania and Strzelecki Ranges

Significant (P<0.05) variation in community traits was found

Community NMDS ordination

Species richness
Total invertebrates

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<tr>
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<th>S Tas</th>
<th>Strzelecki</th>
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<td>n species</td>
<td>30</td>
<td>35</td>
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Abundance
Non-collembolan invertebrates

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<tr>
<th></th>
<th>S Tas</th>
<th>Strzelecki</th>
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<td>n individuals</td>
<td>60</td>
<td>120</td>
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Tree race affects soil nutrient availability

NO$_3$ levels in soil at base of standing trees

Resin bags at base of tree
Tree race affects bark community

All loose bark & associated invertebrates removed from the trunk of 100 trees

30-50% of individuals are spiders and other predators

Height of loose bark

Species abundance

Arthropod abundance

Race
Conclusion

There is increasing evidence for extended community and ecosystem effects of genetic variation at the racial level in *E. globulus*, but their stability and extent are as yet unclear.

Community and ecosystem genetics is an emerging field in ecology.

Forest trees are key study organisms and studies will increasingly focus on lower levels of genetic variation with community heritability $H^2_c/h^2_c$ estimates and QTL$_c$ studies appearing.
Thank you

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References


