Invasion genomics and adaptation in Australian fireweed

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AUSTRALIAN CENTRE FOR EVOLUTIONARY BIOLOGY AND BIODIVERSITY

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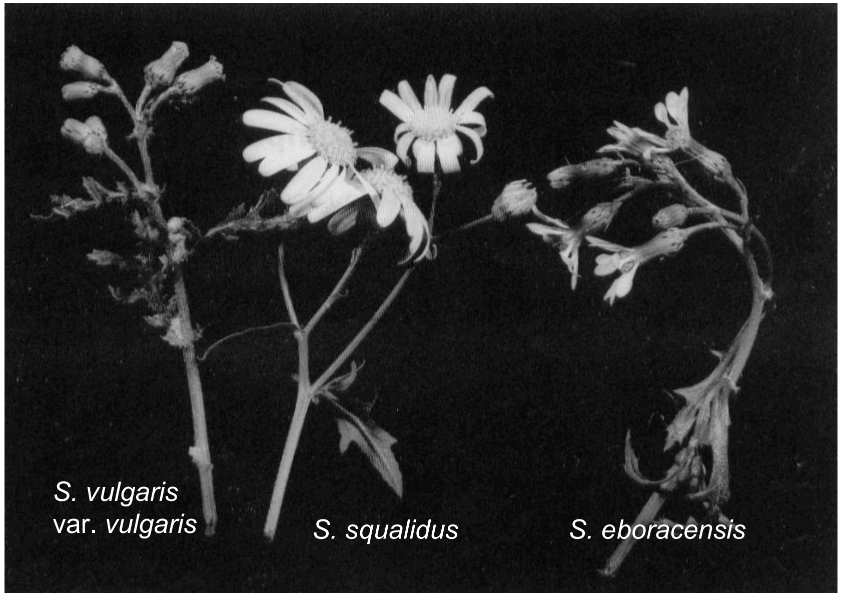

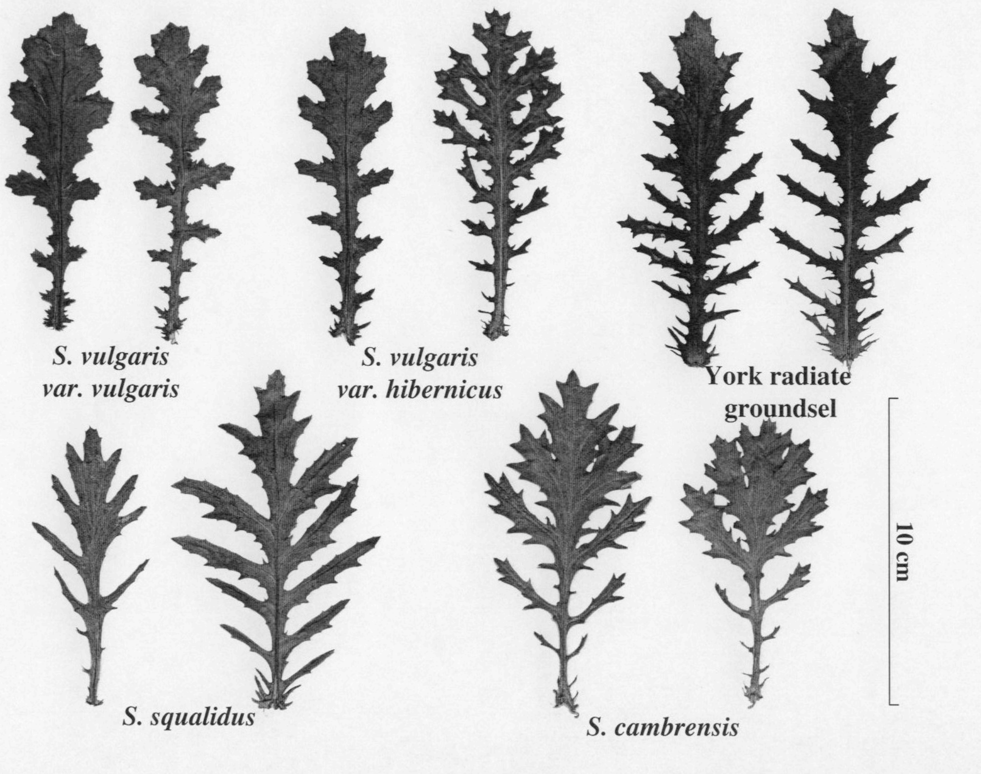

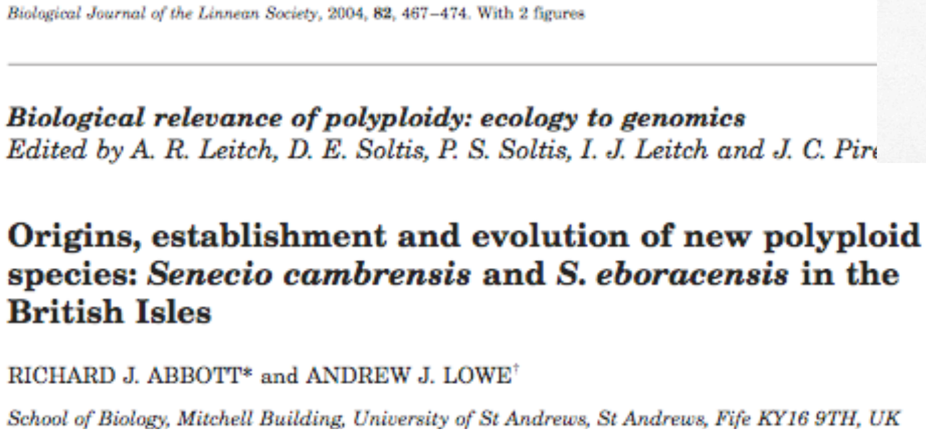
Biological Journal of the Linnean Society, 2004, 82, 467–474. With 2 figures

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Biological relevance of polyploidy: ecology to genomics
Edited by A. R. Leitch, D. E. Soltis, P. S. Soltis, I. J. Leitch and J. C. Pire

Origins, establishment and evolution of new polyploid species: *Senecio cambrensis* and *S. eboracensis* in the British Isles

RICHARD J. ABBOTT* and ANDREW J. LOWE†

School of Biology, Mitchell Building, University of St Andrews, St Andrews, Fife KY16 9TH, UK


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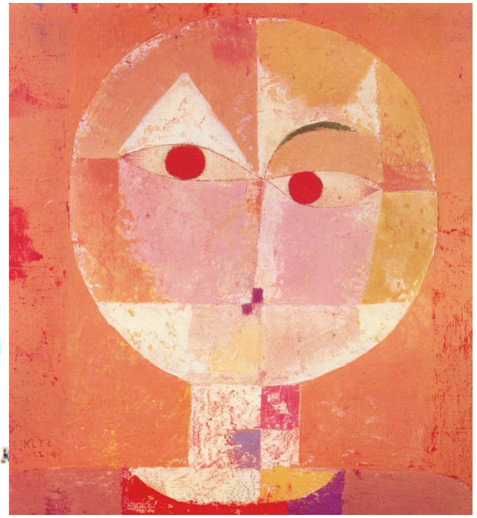
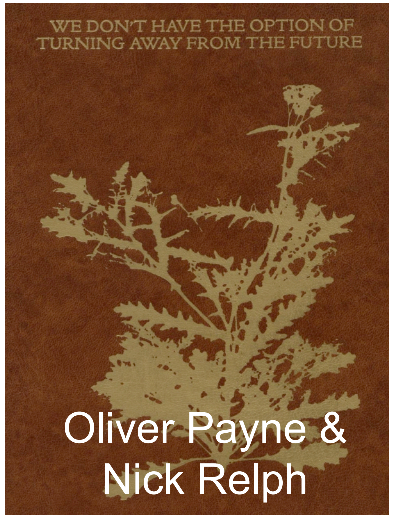
Reproductive isolation of a new hybrid species, *Senecio eboracensis* Abbott & Lowe (Asteraceae)

AJ Lowe[1,2,3] and RJ Abbott[1]
[1]*Division of Environmental and Evolutionary Biology, School of Biology, Mitchell Building, University of St Andrews, Fife, K*
UK; [2]School of Life Sciences, University of Queensland, Brisbane QLD 4072, Australia





Oliver Payne &
Nick Relph

Sleeper weeds

- Lag phase between introduction and population explosion, may last generations
- Range of ecological explanations
  - Demographic population increase
  - Enemy Release from native predators/herbivores
  - Change in climate – more suitable

Sleeper weeds

- Lag phase between introduction and population explosion, may last generations
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  - Change in climate – more suitable
  - Genetic explanations for post introduction adaptation – well known in evolutionary biology but only relatively recently considered for weeds
  - Prentis et al (2008) TIPS; Wilson et al (2008) TREE

Genetic mechanisms of adaptation

1. Admixture
   – source of introduction
2. Hybridisation
   – introgression and demographic swamping
3. Gene expression and genome selection
   – Dynamics and rapid evolution of species

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ARC Discovery funded project fireweed

Elly Dormontt – PhD, Peter Prentis & Skye Thomas Hall - Postdocs

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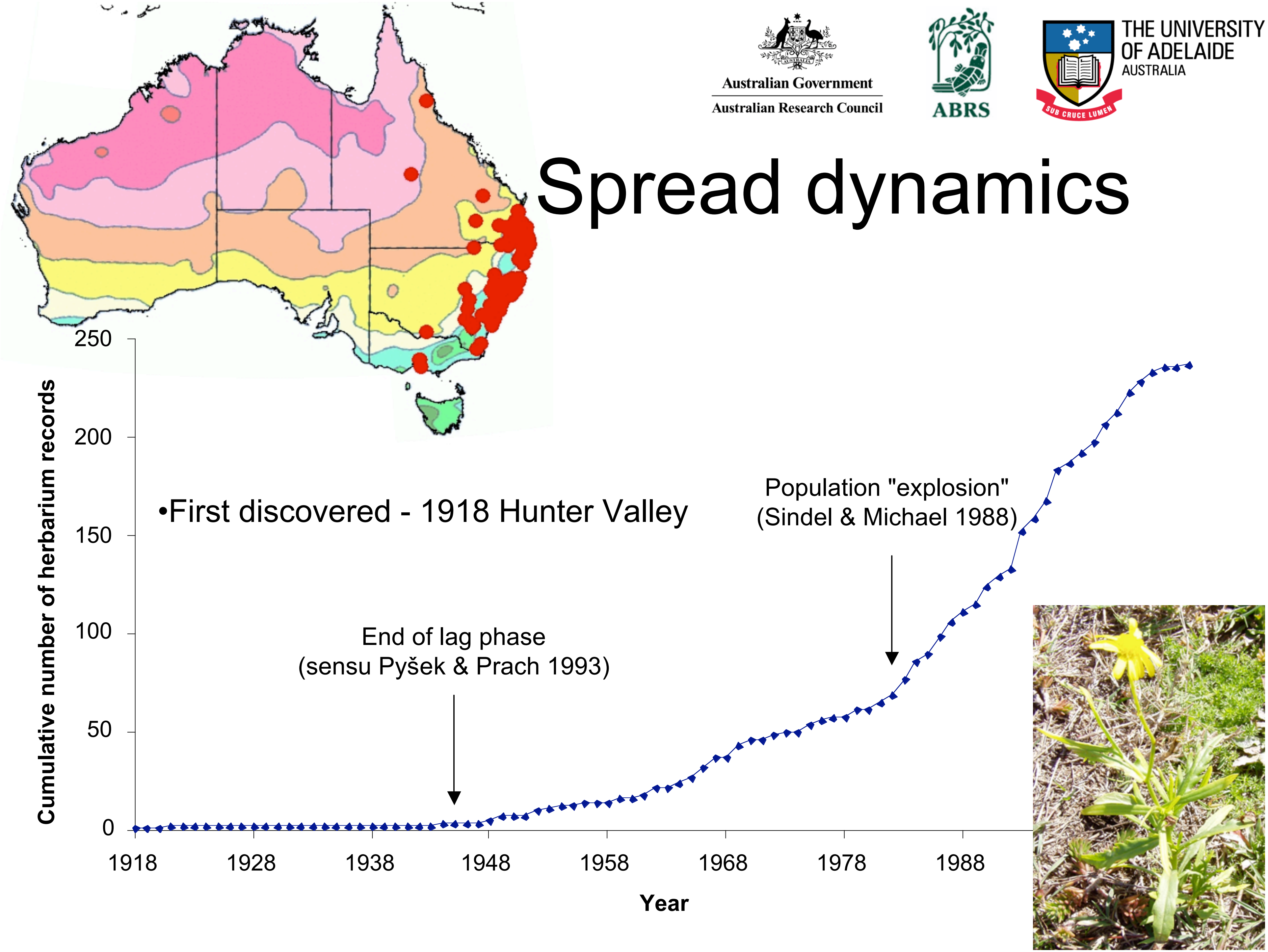
Spread dynamics



- First discovered - 1918 Hunter Valley

End of lag phase
(sensu Pyšek & Prach 1993)

Population "explosion"
(Sindel & Michael 1988)

Genetic mechanisms of adaptation

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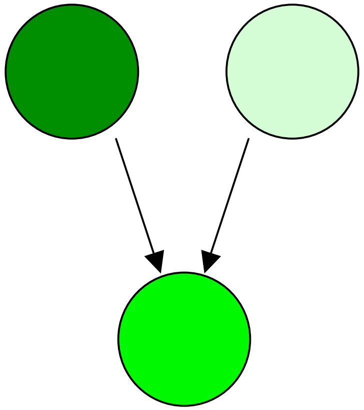
Admixture



Novel gene combinations

Dormontt et al 2010
In 20 of 37 species studied, genetic variation in the introduced range >= native range
Of 24 studies where source number deducible, 22 multiple sources.

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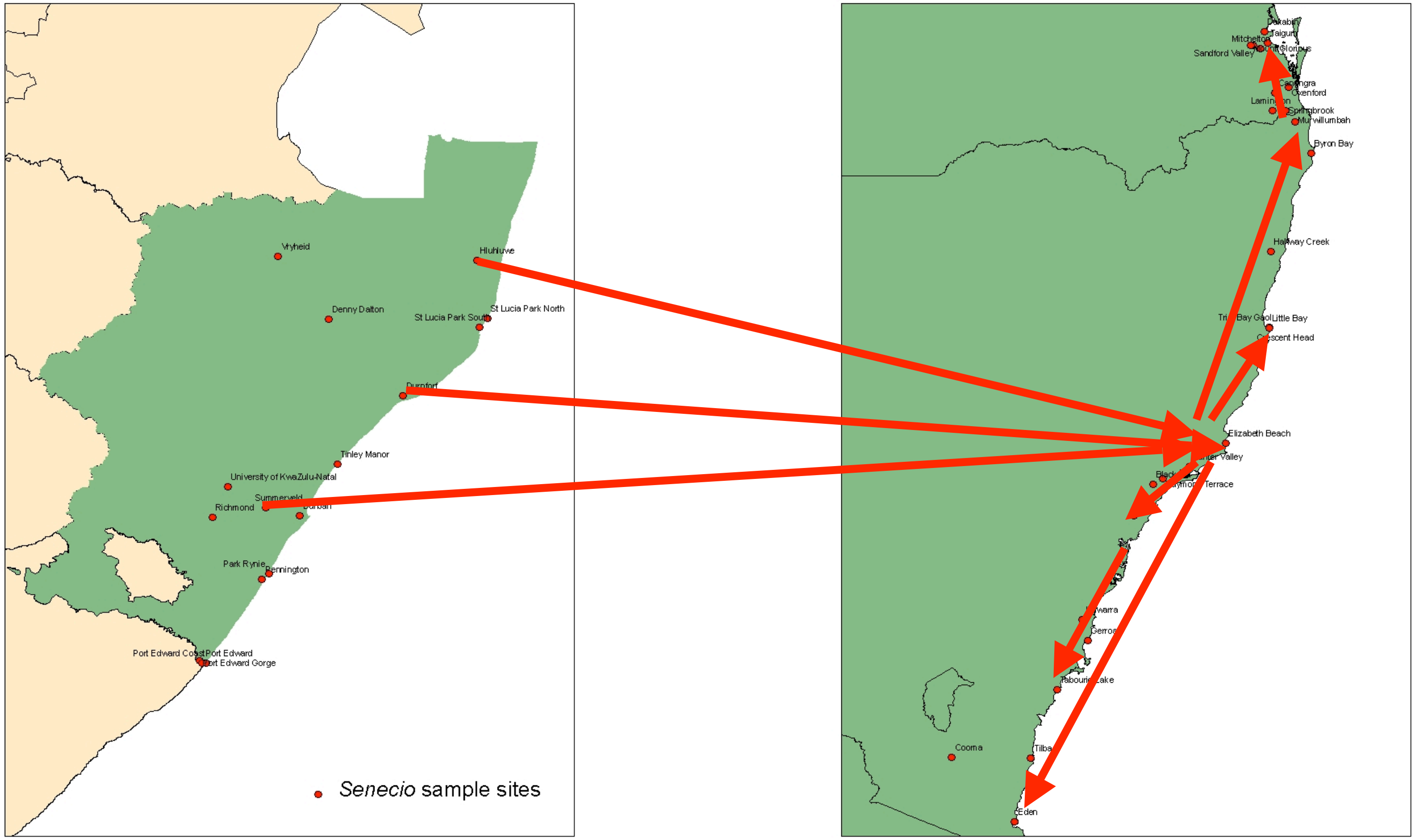
Admixture?

Kwa-Zulu Natal

Multiple sources

East coast Australia



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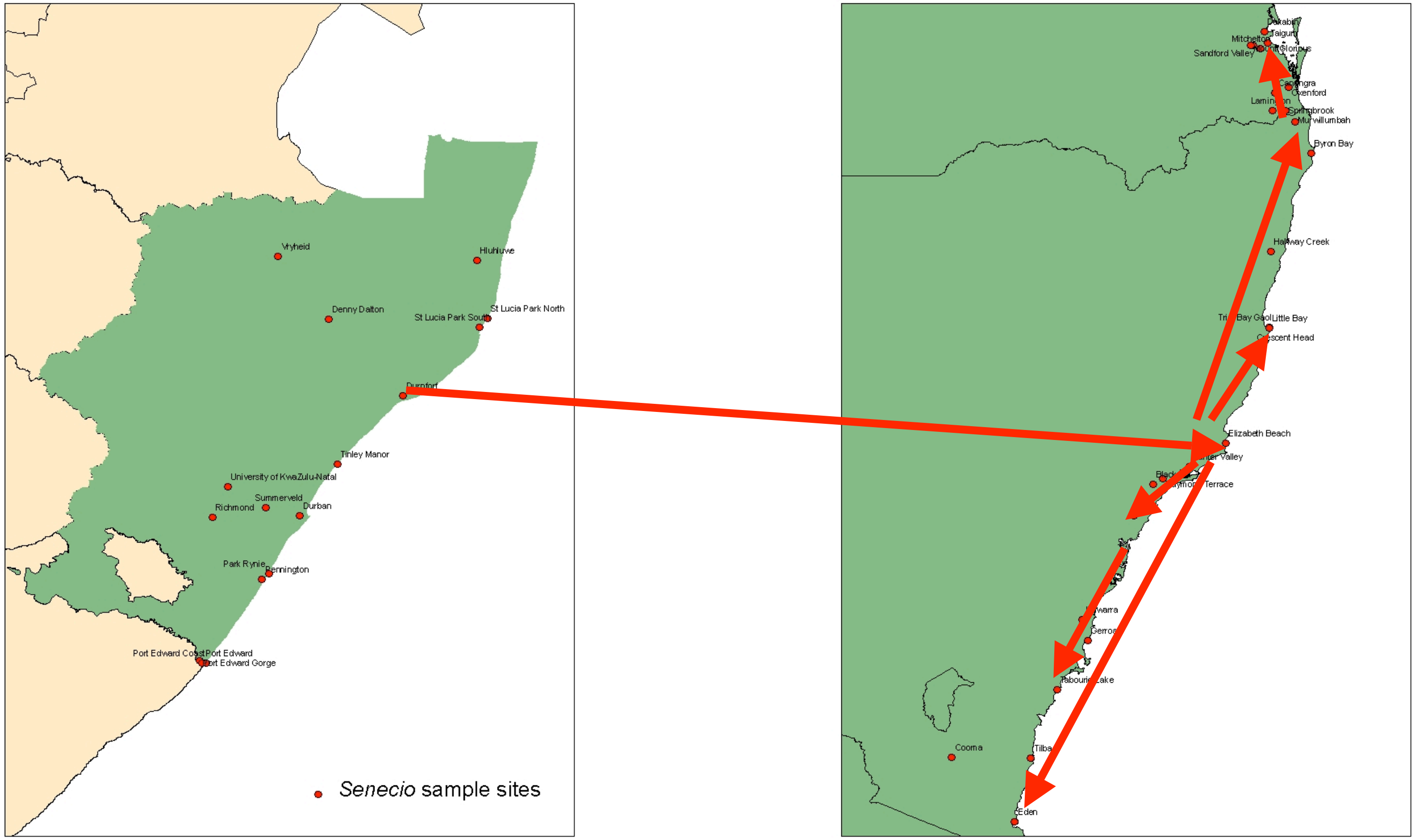
Admixture?

Kwa-Zulu Natal

Single source

East coast Australia



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Genetic mechanisms of adaptation

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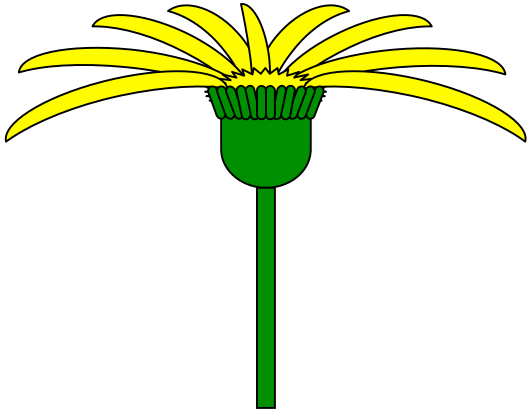
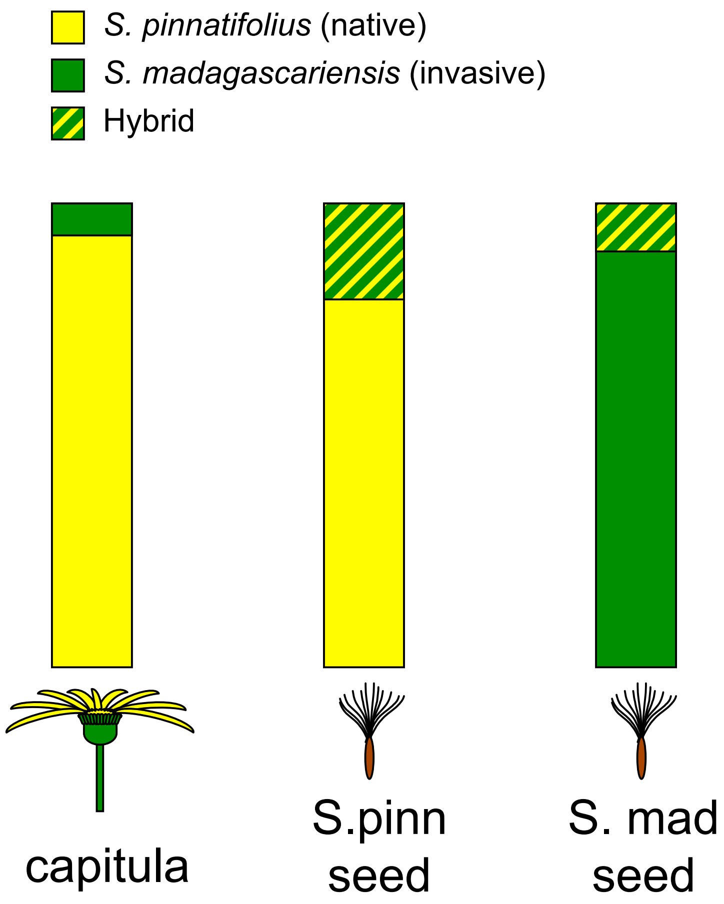
Hybridisation

- Hybridisation
  - Sample collections from hybrid zones with *S. pinnatifolius*



Hybridisation

- *S. pinnatifolius* Springbrook tableland variant (Prentis et al, *New Phytol.* 2007)



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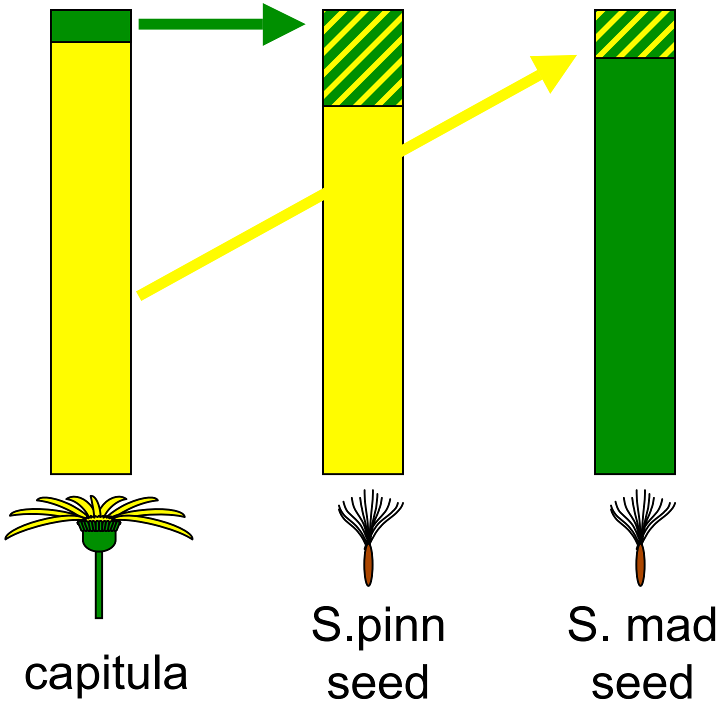
Hybridisation

- *S. pinnatifolius* Springbrook tableland variant (Prentis et al, *New Phytol.* 2007)

🟨 *S. pinnatifolius* (native)
🟩 *S. madagascariensis* (invasive)
▨ Hybrid



capitula

S.pinn seed

S. mad seed

Undue influence by fireweed on level of hybridisation in native
-asymmetric hybridisation

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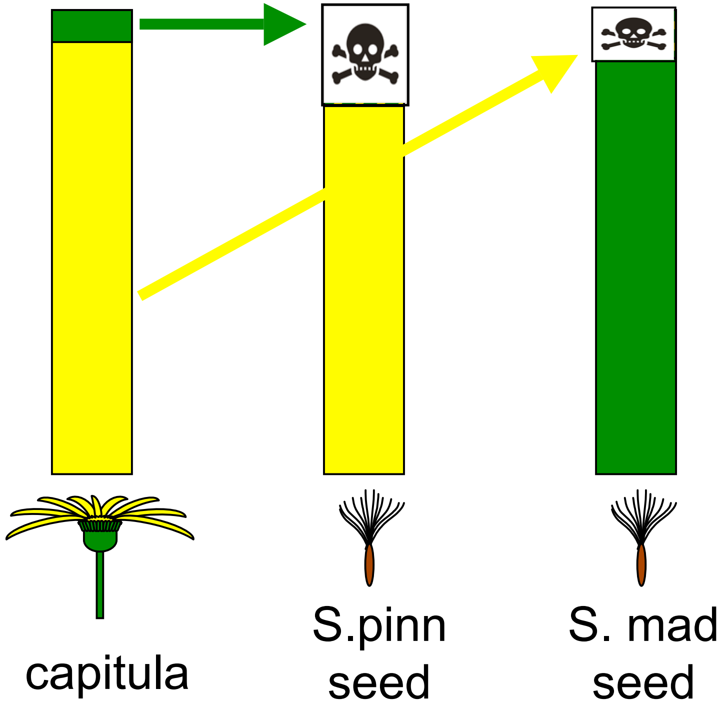
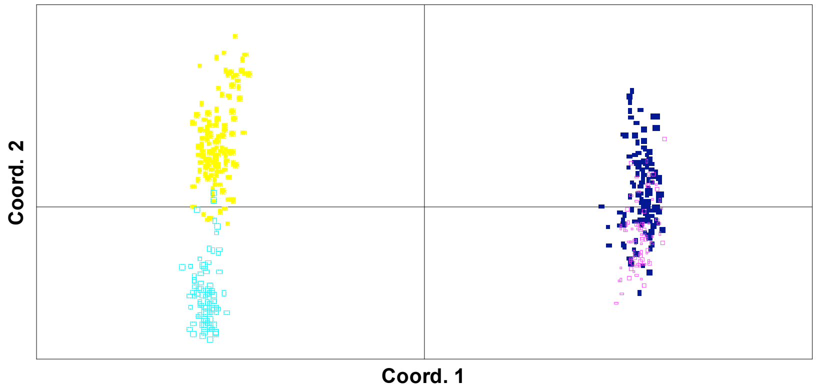


No viable hybrids found at field site, hybrids are not developing and are therefore gamete sink



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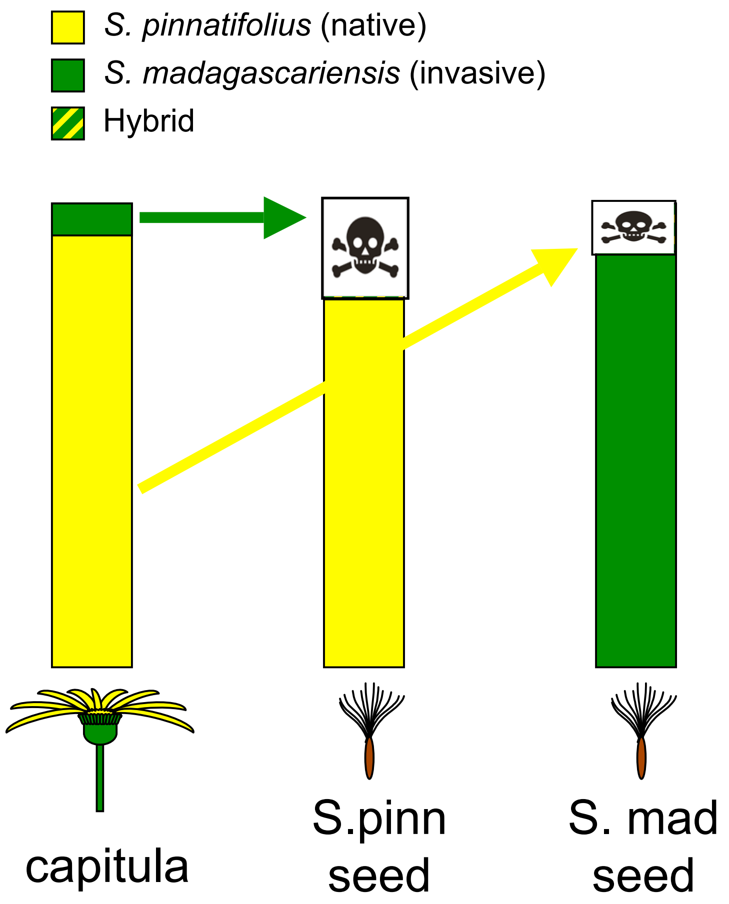

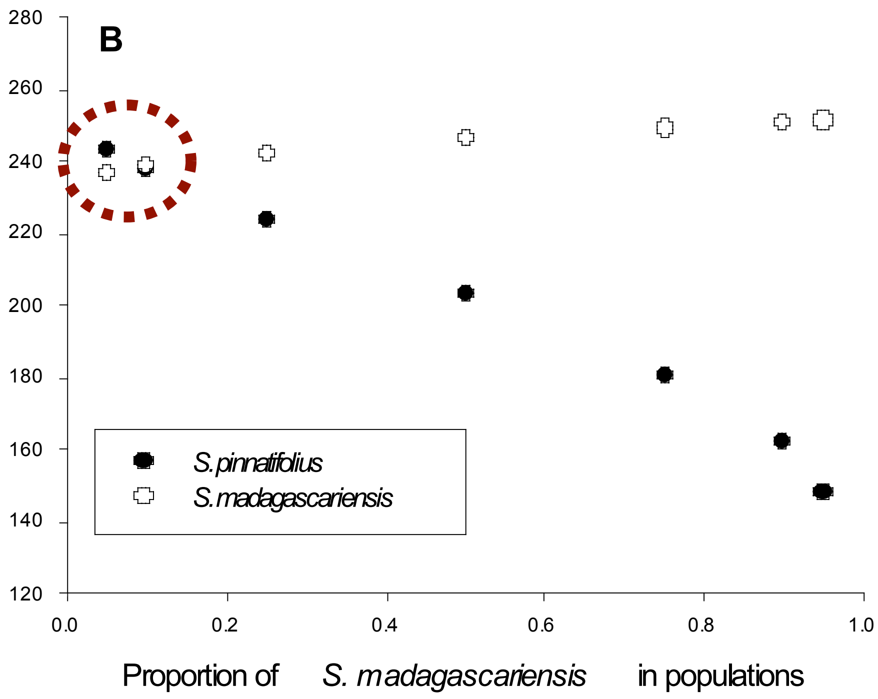

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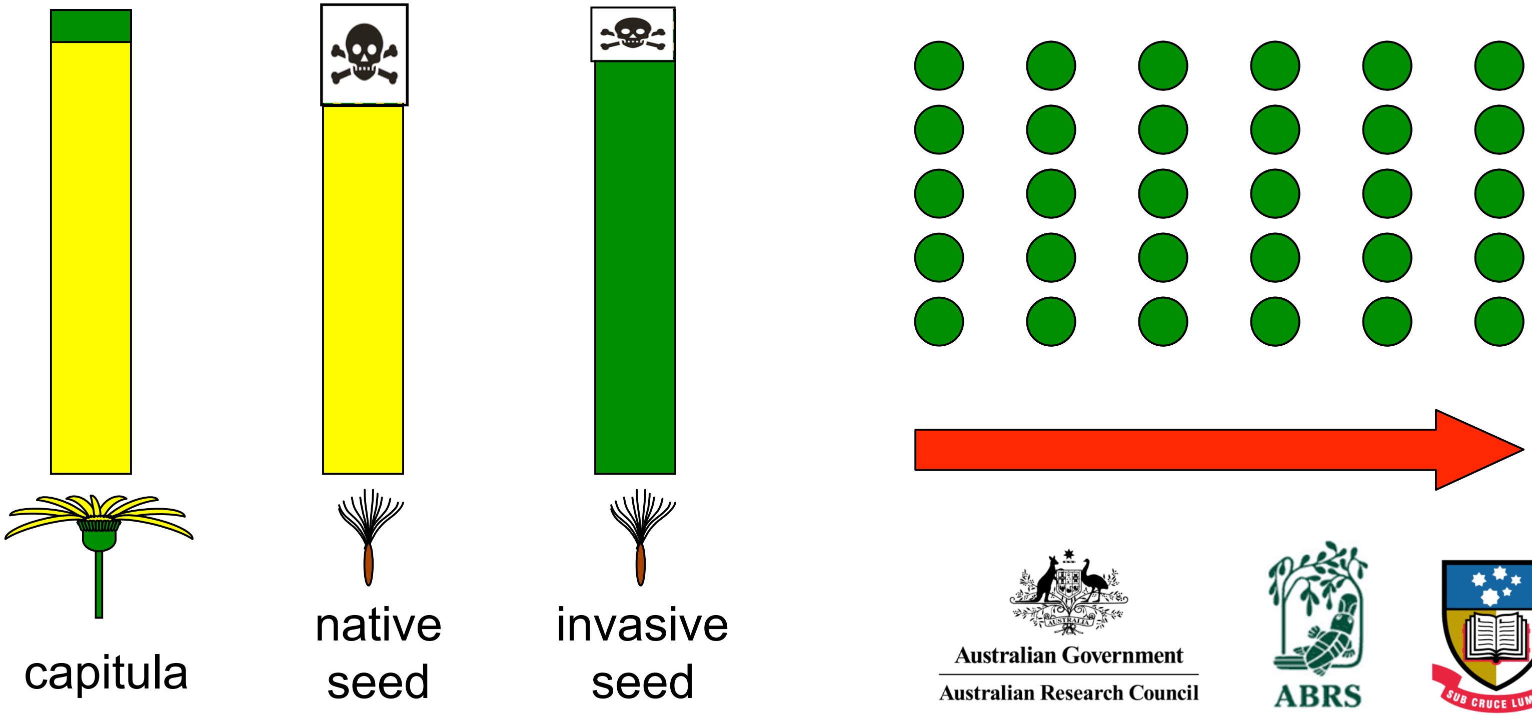

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Hybridisation

- Testing hybridisation outcome with dune variant
- Track species markers in herbarium record

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Studying invasion at the gene level:
454 sequencing provides large scale EST resources

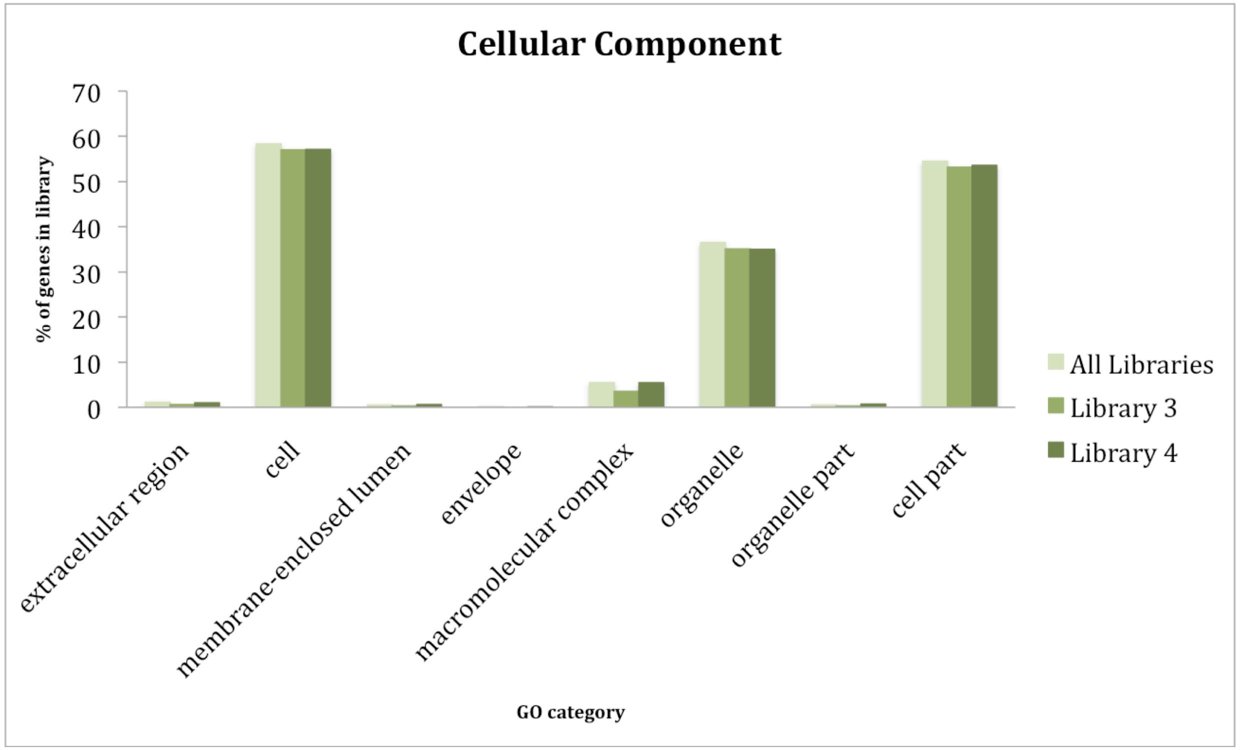
- Plants of fireweed from South African and Australian sources raised under range of conditions to max expression
  - abiotic: drought, ABA, salt, heat, cold, frost, low/high nutrient/light,
  - hormone treatments (MJ, SA, ethylene, auxin, cytokinins)
  - control or no treatment
- Tissue harvested from:
  - leaf and stem, flowers and roots
  - young plants, young flowering plants and old flowering plants (6)
  - seedlings sampled at germination (1 day), 7 days and 14 days

- Total RNA ➔ cDNA ➔ normalised library ➔ 454 seq.
- 2 subtractive libraries: Oz - S.Afr, S.Afr – Oz
- Contigs: BLAST, GO (gene ontology)

Prentis et al submitted

Studying invasion at the gene level: 454 sequencing provides large scale EST resources

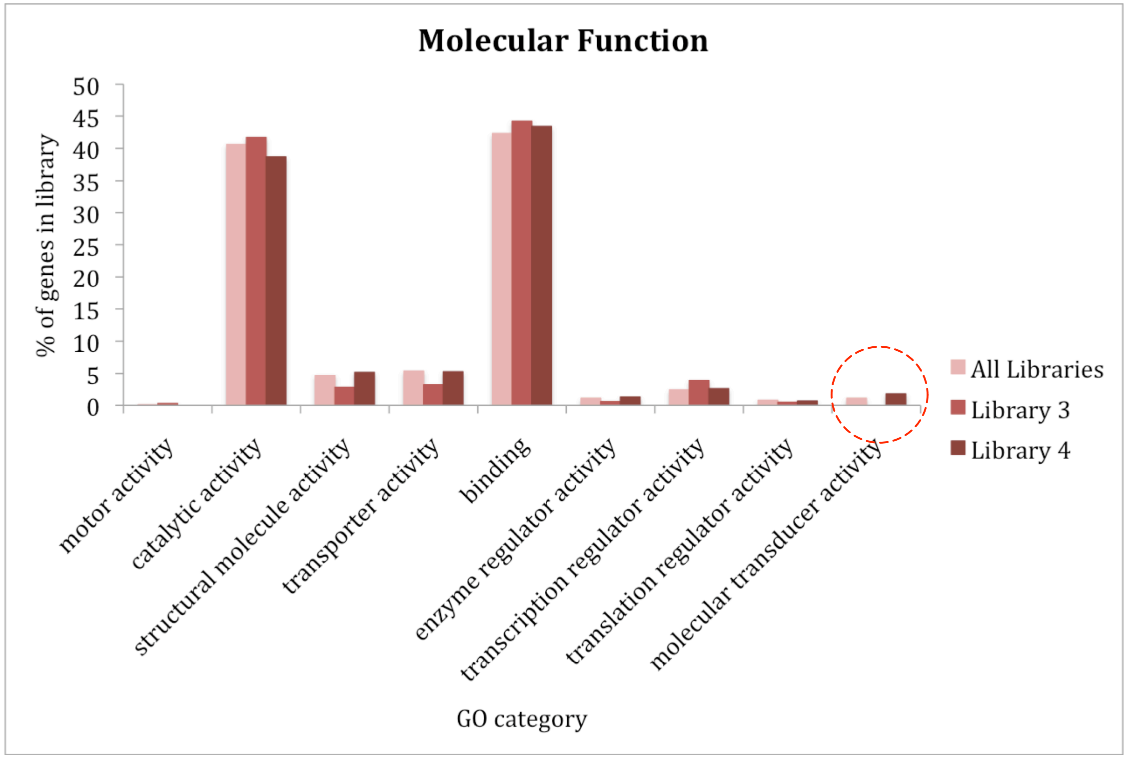
- 221,746 EST sequences (~210 bp)
- 12 442 contig sequences (~264 bp) 5.68 x coverage (per nucl)
- Most common GO category:
  - Cell Function > Molecular Function > Biological Process



Prentis et al submitted

Studying invasion at the gene level:
454 sequencing provides large scale EST resources

- Over representation of gene categories in subtractive libraries
- The molecular transducer activity (external response) GO category significantly enriched in Australian compared to South African material
- 33 genes differentially expressed (20 candidate genes ➔ further testing)



Prentis et al submitted

Using genomics to test ecological explanations

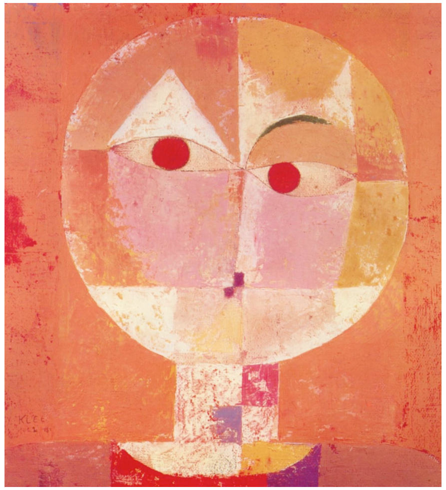
- Ecological explanations for lag phase break
  - Demographic population increase
  - Release from native predators/herbivores
  - Change in climate – more suitable

Genomics futures

- ESTs and Genome scan outlier analysis – Illumina RADs
- Combined with ecology, transplants & QTL mapping
- Allows link between gene loci and ecological traits of interest
- ARC discovery application in, another in development

- TREND - Species and gene turnover along ecological transects
- 4-20 species, including Asteraceae
- 20 population phenomes (BGI)
- Pooled population samples – interogate ‘gene space’
- Connectivity and selection along environmental gradient

- Genome/phenome sequence *S madagascariensis* useful



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- Prof Dave Richardson and Dr John Wilson (Stellenbosch, South Africa)

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