



ecosure
improving ecosystems

Comparative analysis of genetic diversity in wild and restored subtropical rainforest trees

Sally Cooper

Acknowledgement

Ecosure acknowledge the Traditional Custodians of the lands and waters where we work. We pay deep respect to Elders past and present who hold the Songlines and Dreaming of this Country. We honour and support the continuation of educational, cultural and spiritual customs of First Nations peoples.





TWEED
SHIRE COUNCIL



**Big Scrub
Rainforest
Conservancy**

The Voice of the Rainforest



**Southern Cross
University**



ecosure
improving ecosystems

Background

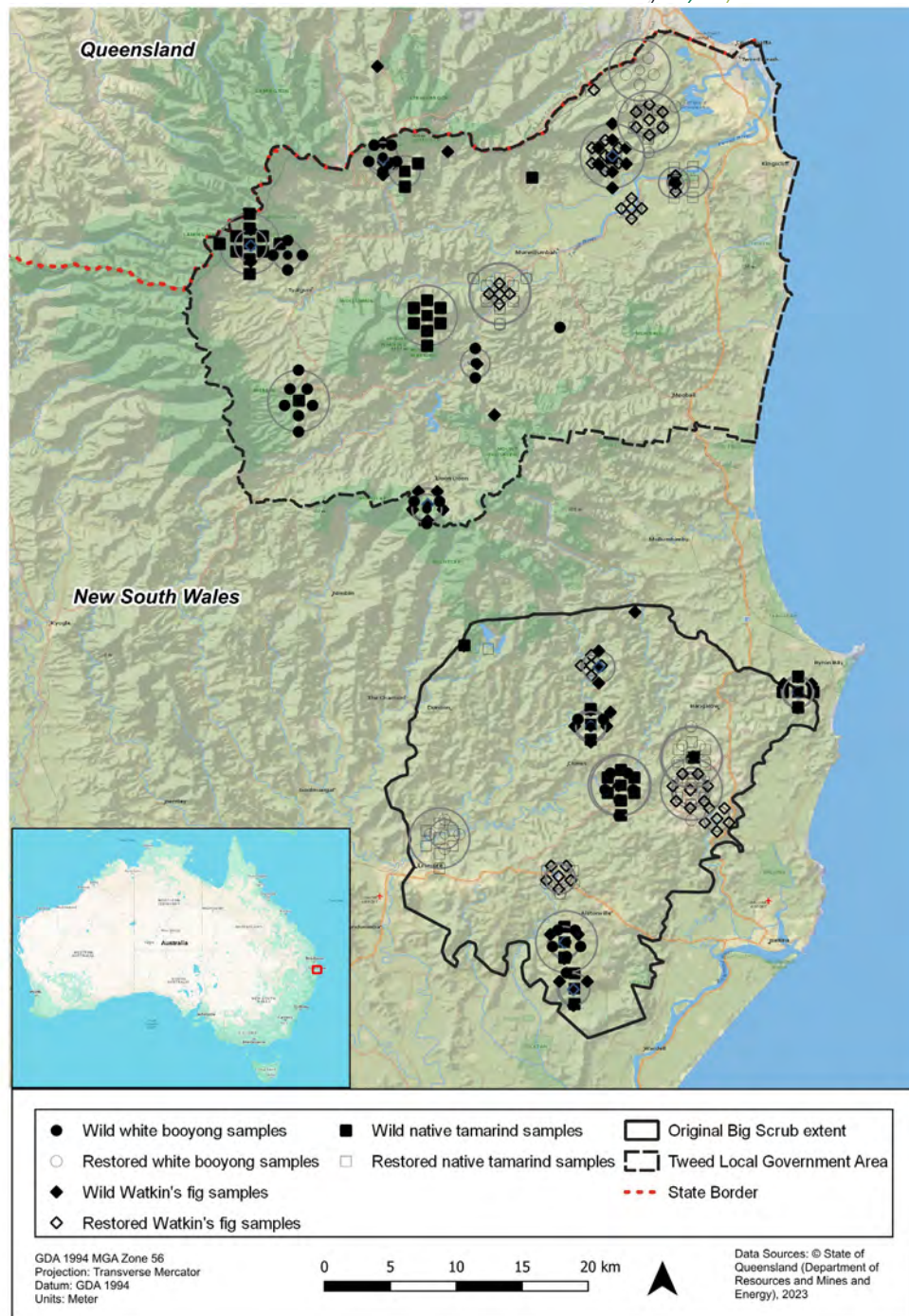
- Genetic diversity is a measure of fitness for a variety of ecosystem functions
- Revegetation (planting) represents a human-driven selection and translocation of genotypes to a restoration site
- Are our restoration efforts capturing enough of the genetic diversity available in wild populations?



Hypothesis

- *Hypothesis*: there is a reduction in genetic diversity for restored rainforest tree populations relative to wild populations
- *Null hypothesis*: there is no difference in the genetic diversity of restored populations relative to wild populations
- “*Are trees in restored communities more inbred than those in the wild reference communities?*”

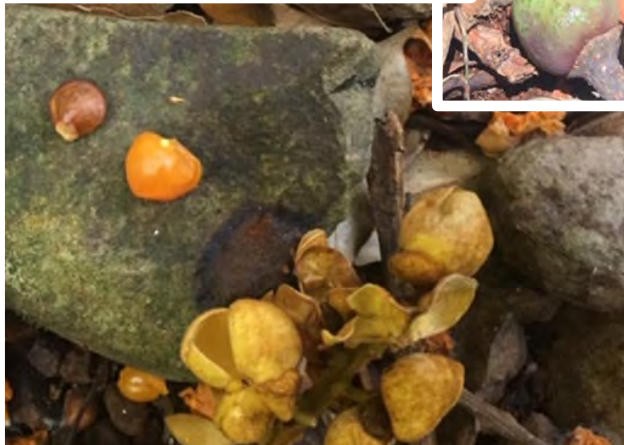




- Wild and restored populations of these species were compared in two neighbouring regions in Northeast New South Wales:
 - the Tweed Caldera
 - the 'Big Scrub'

Methods

- Measured genetic diversity
 - allelic richness (R_s)
 - expected heterozygosity (H_e)
 - inbreeding using Wright's coefficient (F_{IS})
- Three Australian subtropical rainforest trees tested
 - white booyong (*Argyrodendron trifoliolatum*)
 - Watkin's fig (*Ficus watkinsiana*)
 - native tamarind (*Diploglottis australis*)



Results – average allelic richness

Species	Region	Rs		
		Wild	Rest.	P value
A. <i>trifoliolatum</i>	Big Scrub	11.65	10.35	0.079
	Tweed	11.52	10.26	0.289
F. <i>watkinsiana</i>	Big Scrub	12.45	11.78	0.505
	Tweed	12.23	13.34	0.377
D. australis	Big Scrub	15.62	15.13	0.737
	Tweed	14.67	13.51	0.378

- Average allelic richness across all loci was higher in the wild populations compared with restored populations in 5/6 comparisons.
- The Tweed restored *F. watkinsiana* population had higher allelic richness than the wild population.
- No statistically significant differences in any of these comparisons

Results – expected heterozygosity

Species	Region	He		
		Wild	Rest.	P value
A. <i>trifoliolatum</i>	Big	0.81	0.78	0.068
	Scrub			
	Tweed	0.79	0.79	0.882
F. <i>watkinsiana</i>	Big	0.84	0.85	0.707
	Scrub			
	Tweed	0.84	0.87	0.282
D. australis	Big	0.87	0.87	0.826
	Scrub			
	Tweed	0.85	0.77	0.533

- Expected heterozygosity was higher in the wild populations compared to the restored populations in two of the six comparisons, two were the same, two were higher in restored
- No statistically significant differences in any of these comparisons



Results – inbreeding

Species	Region	F		
		Wild	Rest.	P value
<i>A. trifoliolatum</i>	Big	0.09	0.03	0.203
	Scrub			
	Tweed	-0.01	0.06	0.210
<i>F. watkinsiana</i>	Big	-0.05	-0.01	0.239
	Scrub			
	Tweed	-0.02	0.20	0.010
<i>D. australis</i>	Big	0.03	0.04	0.934
	Scrub			
	Tweed	-0.11	0.00	0.571

- Inbreeding was significantly higher in the Tweed restored *F. watkinsiana* population in the Tweed
- Associated with a significant difference in observed heterozygosity (H_o , $p = 0.037$) due to three highly homozygous individuals (probably selfs, $s = 0.26$)
- No detectable differences in inbreeding levels in any of the other comparisons

Results – summary

- Genetic diversity results for all restored populations achieved at least 80% (R_s) and 90% (H_e) of that detected in the wild populations.
- This study suggests that the restored subtropical tree populations substantially match the genetic diversity of their wild source populations.
- Large and significant reductions in genetic diversity in the restored populations were not observed in this study, but there was one incidence of increased inbreeding.



ecosure
improving ecosystems

Discussion – why hasn't data shown a loss of GD in restored populations?

- Intrinsically high within-population genetic diversity of the studied species' source populations
- The lack of strong genetic differentiation throughout the study regions
- Restored population typically created from numerous small restoration projects spread over many years



An adult rose-crowned fruit-dove photographed in Cairns.
Photo by Sonja Ross, NZ Birds Online

Implications for practice

- Restoration activities can influence the genetic composition of plant populations, sometimes contributing to more inbred populations.
- Consider susceptibility of individual populations to losses in genetic diversity
- Obtaining stock from large populations and multiple sources is a sensible safeguard
- Staged restoration (multiple planting events) is likely to mitigate against losses in genetic diversity in restored populations



Question time

