

**Seed quality of *Allocasuarina verticillata*
(Allocasuarinaceae) populations in the
Corangamite CMA**



**Report to:
Department of Primary Industries, Victoria**

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CSIRO

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INTRODUCTION

The Corangamite catchment covers some 13,340 square km in southwest Victoria (Fig 1) and is comprised of 6 sub-regions encompassing a wide range of geological and hydrological features as well as climatic zones (CMA 2003). Vegetation clearing has reduced natural vegetation cover in the region to approx. 25% and there is an increasing emphasis on revegetation to address land degradation associated with vegetation loss (CMA 2003). The collection and deployment of seed across the catchment is, at present, guided by general precautionary principles that place an emphasis on local seed sources. However, this approach can be detrimental to revegetation efforts if 'local' populations are small and isolated. These seed sources can have a narrow genetic base and can also suffer from inbreeding effects that can impact on seedling fitness. These issues can seriously impact on restoration efforts by poor initial success in the short term, and through reduced evolutionary potential to meet environmental challenges over much longer time frames. This research sought to enhance and improve best practice currently undertaken by restoration practitioners in the region by providing important data regarding genetic, reproductive and demographic aspects of a key revegetation species, *Allocasuarina verticillata*.



Figure 1: Map of Victorian CMAs.

DROOPING SHEOKE

Allocasuarina verticillata is a medium sized tree (5-9 m) that is widely distributed across southeast Australia, occupying a broad range of environments from coastal and inland regions, including those at higher altitudes. It exists on a variety of soil types and is reported to be more drought resistant than many eucalypts as well as being salt tolerant, particularly in coastal regions. Like other *Allocasuarina* species it has important symbiotic associations with nitrogen-fixing organisms, namely *Frankia*. Apart from revegetation efforts to replace lost communities, *A. verticillata* has several other uses including soil stabilisation and rehabilitation, fuel wood, timber, shelterbelts, and animal fodder. It is also a key foraging species for black-cockatoos and there is evidence that birds feed selectively on highly fecund trees (Crowley and Garnett 2001; Pepper, Male *et al.* 2000). *Allocasuarina verticillata* also harbours a variety of insects and is often visited by small insectivorous birds. This species is dioecious (plants are either male or female), wind pollinated and can resprout from the base.

PROJECT OUTLINE

This project sought to address several key genetic and demographic issues relating to *A. verticillata* within the Corangamite catchment. *Allocasuarina verticillata* populations within the catchment are generally fragmented and it is unclear whether any spatial genetic structure exists to preclude the movement of seed across broad geographic scales to augment restoration in more denuded areas. It is also unclear whether fragmentation is affecting landscape-level interactions between these populations. For example, if pollen movement is more restricted than that occurring prior to land clearing there is the potential to generate strong family structure within remnants which may eventually lead to poor seed viability through inbreeding. In contrast, the movement of pollen across much larger distances may disrupt locally adapted populations and homogenise any genetic structure resident within the catchment. The information generated from this study will help to guide management decisions regarding seed collection protocols, spatial scales of distribution and management of seed sources.

The project set out to specifically address five broad questions to help improve restoration of this species:

1. What levels of genetic diversity are present in *A. verticillata* populations across the Corangamite CMA?
2. Is there any evidence of spatial genetic structure in *A. verticillata* populations within the Corangamite CMA?
3. Does remnant configuration influence the genetic composition of *A. verticillata* seed crops?
4. Does remnant configuration influence the fitness of *A. verticillata* seedlings?
5. Do previously revegetated sites represent an appropriate seed source for future restoration efforts?

SITE SELECTION AND COLLECTION OF MATERIAL

Sites were selected from across the catchment to represent both the spatial scale of *A. verticillata* (Figure 2) and the types of remnants commonly sourced for restoration (Figure 3). A total of 22 sites were selected from within the CMA and one site from a neighbouring catchment to assess whether any spatial genetic structure could be detected. Twelve of these sites were also examined more intensively ('intensive') to assess mating system and seed fitness parameters to determine whether these are appropriate seed sources for restoration. These sites were partitioned according to remnant type:

- Isolated - small, isolated sites often considered to be of high conservation value,
- Linear - road verges sites comprised of long, narrow strips of vegetation,
- Patch - more regularly and often large remnants.

In addition, three revegetated sites were chosen to assess whether these were also suitable seed sources for restoration projects in the catchment (Figure 3).

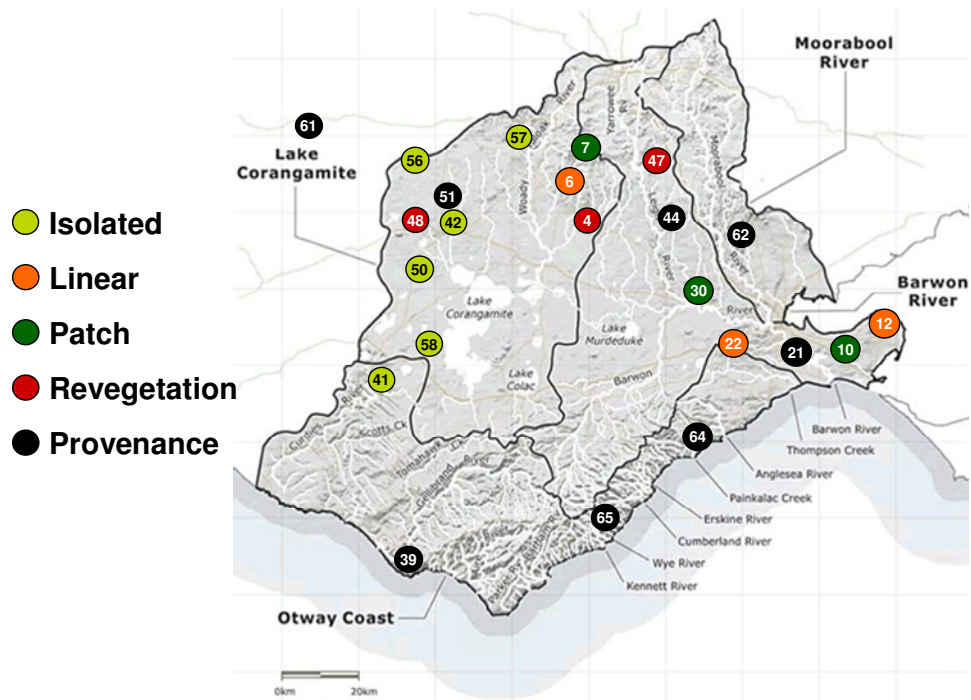


Figure 2: Collection sites for *Allocasuarina verticillata*. Numbers correspond to Site No. in Table 1.

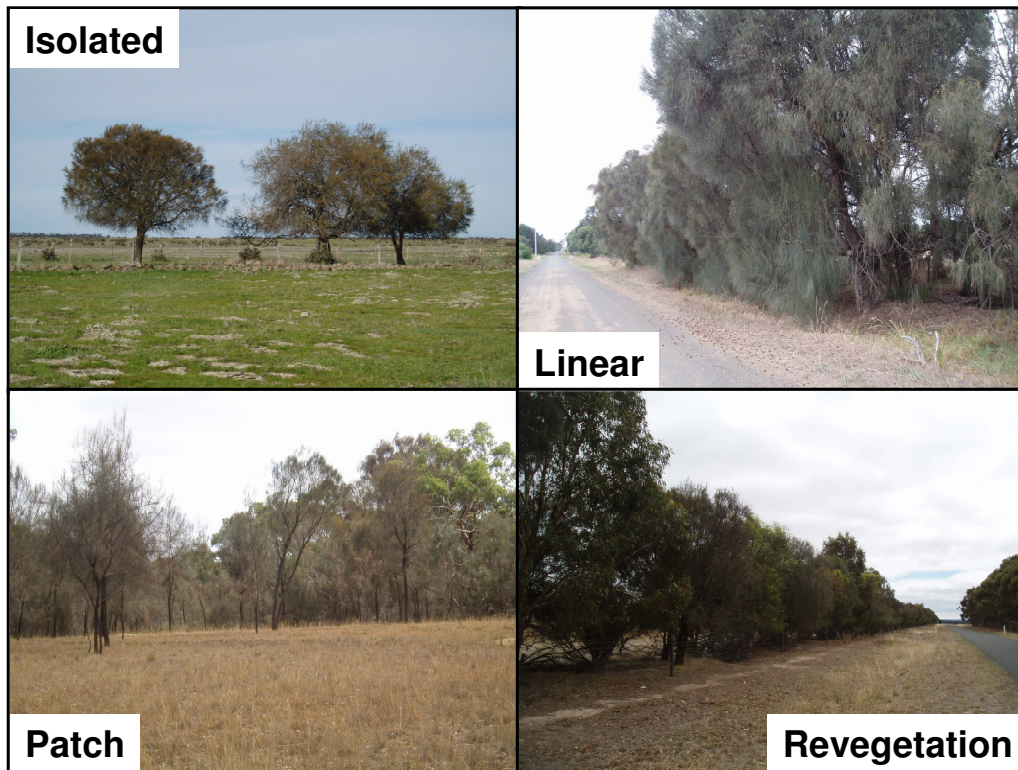


Figure 3: Examples of the remnant types of *A. verticillata* used in this study. (Photographs courtesy of Chris Gartlan).

Table 1 outlines each site selected, its remnant category and the different studies undertaken. At each of the sites assessed for spatial genetic structure only ('provenance'), 2-3 cones were collected from around the canopies of up to 30 plants, air dried and the seed extracted stored for later genetic analysis. At intensive sites, female trees were randomly selected, their GPS co-ordinates mapped and phyllode samples taken for genetic analysis. Cones (2-4) were sampled from each canopy direction (N, S, E, W) where possible, air dried and the seed also extracted and stored for genetic analysis. Two male trees closest to each of the sampled females were similarly mapped and phyllodes sampled. A further 15-20 trees from each of these sites were randomly sampled where possible to augment the spatial genetic structure study.

Table 1: Details of *Allocasuarina verticillata* sites including remnant type and study undertaken.

Remnant type	Site No.	Site Name	Provenance	Genetic diversity	Mating system	Growth Trial
Isolated	41	Bostock Creek	✓	✓	✓	✓
	42	Lismore Cemetery	✓	✓	✓	✓
	50	Kinlock	✓	✓	✓	✓
	56	Ascott Downs	✓	✓	✓	✓
	57	Banongill	✓	✓	✓	✓
	58	Pomborneit North	✓	✓	✓	✓
Linear	6	Skipton-Rokewood Rd	✓	✓	✓	✓
	12	Grassy Point Rd	✓	✓	✓	✓
	22	Buckley School Rd	✓	✓	✓	✓
Patch	7	Cape Clear	✓	✓	✓	✓
	10	Blairwood	✓	✓	✓	✓
	30	Don Wallace Reserve	✓	✓	✓	✓
Revegetation	4	Andy Stevens		✓	✓	✓
	47	Nolan		✓	✓	✓
	48	Titanga		✓	✓	✓
Provenance	21	Williams Rd	✓	✓		
	44	Henderson Rd	✓	✓		
	51	Gala	✓	✓		
	61	Tileys Lane	✓	✓		
	62	Lumbs Rd	✓	✓		
	39	Moonlight Head	✓	✓		
	64	Urquhart Bluff	✓	✓		
	65	Carlisle Falls	✓	✓		

Genetic marker development

New genetic markers called microsatellites were developed specifically for this species. These types of markers provide a means of determining the maternal and paternal contribution to seed crops. Figure 4 is an example of how these markers are used to determine the genetic contributions of mothers and fathers to seed crops. The phyllodes sampled from female and male trees at each site were 'fingerprinted' to provide a unique genetic profile. The seed was then germinated and similar genetic profiles established. In this example, the female contribution to each seed is highlighted by the red arrow. For Seed 1 the male contribution, indicated by the blue arrow, is the same as the sampled male but a different male has sired Seed 2 as highlighted by the green arrow. Six unique microsatellites were developed and used as the basis for determining genetic diversity, spatial genetic structure and mating system patterns for this study.



Figure 4: Diagram showing how the genetic contribution by females and males in seed crops is determined using genetic markers.

RESEARCH FINDINGS

Levels of genetic diversity

Where possible 30-50 seed (3-5 from each tree collected) were germinated for each site and the genetic markers developed used to determine levels of genetic diversity. Seed from Banongill failed to germinate despite several attempts and no genetic assessments could be undertaken which immediately suggests that this site is not an appropriate seed source for restoration projects. For the remaining sites the levels of genetic diversity varied considerably (Table 2). Isolated sites had considerably lower genetic diversity than the other sites with the exception of the Cape Clear patch site which exhibited similarly low levels. Linear sites produced the highest levels of genetic diversity although this was not that different to patch sites when Cape Clear was removed. Revegetation sites produced higher levels of genetic diversity than isolated sites but were lower than linear and patch sites. Genetic diversity in the sites collected for the provenance study also indicate that most of these have reasonable to good levels of diversity.

Implications – Most of the larger sites sampled have high levels of genetic diversity indicating their suitability as seed sources providing they are appropriately sampled (see Research Recommendations). Basing restoration efforts solely on seed from isolated sites is not appropriate given the poor genetic diversity present in these sites and doing so is likely to generate similarly depauperate stands in the future. Given the low levels of diversity in these isolated sites consideration should also be given to introducing new germplasm to improve genetic diversity levels and to alleviate potential inbreeding effects. The levels of genetic diversity in seed from the Andy Stephens and Nolan revegetation sites is as high or higher than many of the other sites, suggesting that these would be suitable seed sources for restoration. However, consideration needs to be given to the genetic maps and implications for male bias if these sites are inappropriately sampled. In contrast, genetic diversity in the Titanga revegetation site is similar to that of isolated sites and at this point in time this seed should not form the sole basis for restoration projects. However, as these revegetation stands age and more trees become reproductive, there is the potential for these to be future seed

sources. At present, it is recommended that seed be collected from these sites and used to augment other collections intended for restoration.

Table 2 – Genetic diversity for the sampled *Allocasuarina verticillata* sites. Sites ordered from lowest to highest within each remnant type.

Type	Site	Average sample size	Genetic diversity
Isolated	Banongill	No germination	
	Bostock Creek	16	0.529
	Lismore Cemetery	133	0.637
	Pomborneit North	89	0.639
	Ascott Downs	44	0.677
	Kinlock	64	0.699
	Mean		0.636
Linear	Lumbs Rd	23	0.718
	Williams Rd	11	0.720
	Henderson Rd	31	0.758
	Tileys Lane	19	0.763
	Buckley School Rd	40	0.765
	Skipton-Rokewood Rd	33	0.789
	Grassy Point Rd	29	0.792
	Mean		0.758
Patch	Cape Clear	27	0.671
	Gala	28	0.705
	Carlisle Falls	31	0.713
	Urquhart Bluff	27	0.724
	Moonlight Head	29	0.751
	Don Wallace Reserve	36	0.751
	Blairwood	34	0.781
Mean		0.728	
Revegetation	Titanga	12	0.685
	Nolan	45	0.749
	Andy Stephens	45	0.795
	Mean		0.743
Overall		857	0.773

Spatial genetic structure

Data generated from the genetic diversity assessment was also used to determine whether any spatial genetic structure could be detected among *A. verticillata* sites across the catchment. No clear spatial genetic structure was found in this study (Figure 5), highlighting the unpredictability of using spatial structure as a guide to seed deployment. There is some evidence to suggest that populations in the east of the catchment form a cohesive group as indicated by the red lines in Figure 4.

However, Moonlight Head is included in this group despite being spatially disjunct. Similarly unusual associations were also evident between other disjunct sites such as Tileys Lane (61) and Urquhart Bluff (64) and between Gala (51) and Carlisle Falls (65). One possible explanation for these unusual results may be that the number of markers used to assess genetic associations is too small to detect appreciable differences in spatial genetic structure. Unfortunately, development of the genetic markers used in this study is extremely difficult and further development is not possible at this point in time. It is also possible that these data indicate that *A. verticillata* is an extremely mobile species with high levels of gene flow through both pollen and seed. Movement across large distances between populations may serve to homogenise gene pools making it difficult to clearly differentiate populations. Although not originally part of this assessment a further analysis was undertaken that included the revegetation sites (Figure 6). This analysis indicates that Andy Stephens and Nolan show similarities with sites sampled nearby, whereas Titanga shows affinity with the distant Ascott Downs site suggesting a much more distant seed collection was used for this site.

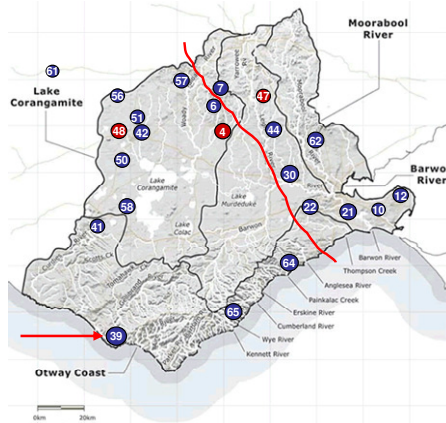
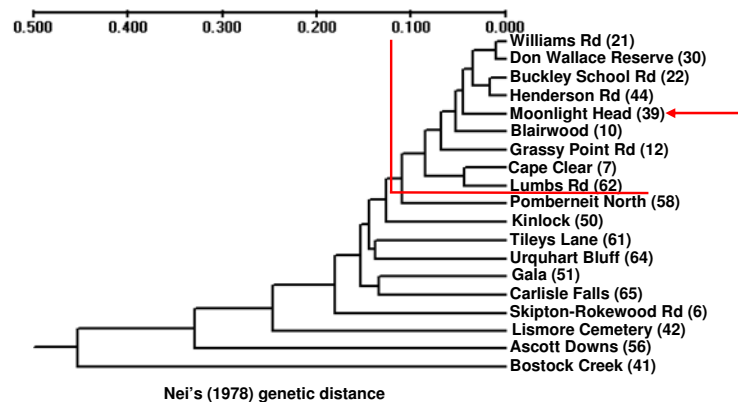


Figure 5: Genetic associations among the *Allocasuarina verticillata* sites.

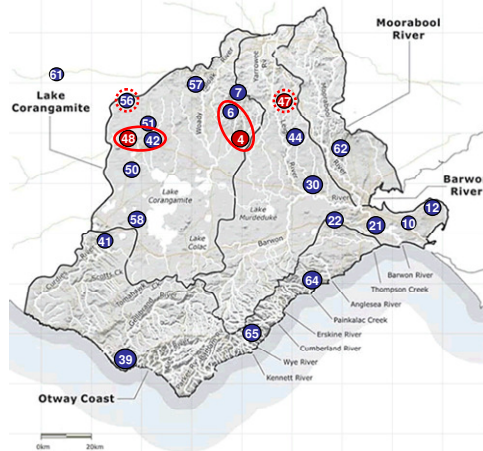
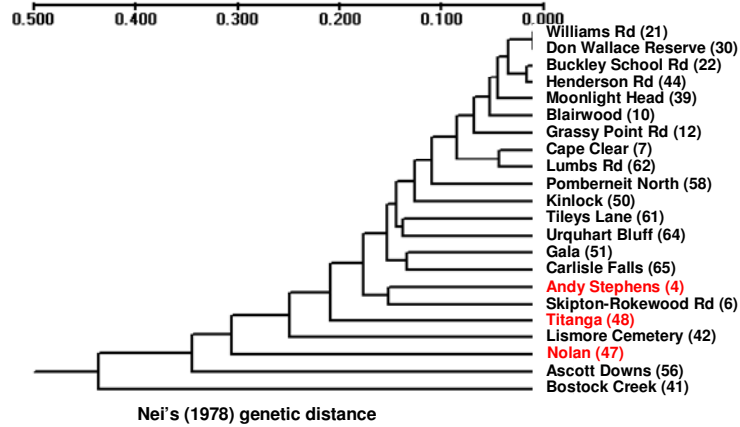


Figure 6: genetic associations among the *Allocasuarina verticillata* sites including revegetation sites.

Implications – These data indicate that seed could probably be deployed more widely across the catchment. However, spatial genetic structure based on neutral markers such as those used in this study do not provide any indicative information regarding local adaptation. While 'local' seed sources are expected to be locally adapted and should be considered as a primary seed source, when populations are small, inbred and genetically depauperate, these do not represent appropriate seed sources for restoration. In addition, *A. verticillata* is a wind-pollinated species with light seed that is probably capable of relatively long distance dispersal. Under these circumstances, an appropriate collection strategy is to place considerably more emphasis on collecting from larger, more genetically diverse populations and to augment these with seed from smaller more 'local' sites where possible. Where possible, further consideration should be given to matching habitats, rather than using distance as a guideline for moving seed.

Mating system

Seed from each mapped female tree within intensive sites were germinated and the genetic markers used to determine mating system patterns. Where possible, these were partitioned according to canopy direction to determine whether this influence which father sired the seed produced. In general, mating system patterns varied considerably among female trees within sites as well as among the sites and the remnant types. Mating system 'maps' for each site are provided in Appendix 1. In general, seed is produced at the larger sites by a range of fathers with no single male dominating. There is evidence, however, that placement within a site and canopy direction influence the contribution of males to the seed crops of each mother (see genetic map for Grassy point Rd in Appendix 1). In smaller sites, some fathers made no contribution to seed crops (see genetic map for Bostock Creek) while in others dominated seed crops from individual mothers (see genetic map for Lismore Cemetery). As might be expected in larger sites where more males exist to sire the seed, up to 25% of the seed crops were produced by males other than the 20 trees sampled. The Cape Clear patch site was unusual in that almost half of the seed produced was not from one of the sampled males. This site also performed poorly in terms of germination and growth and has low genetic diversity. It is possible that changing wind patterns associated with the surrounding pine plantation is disrupting mating system patterns at this site.

Implications – it is important that appropriate sampling strategies be undertaken for this species. Sampling widely from across a site is important to ensure that the genetic diversity collected is representative of each site. In addition, sampling around the canopy is required to reduce the effects of localised male-bias in seed crops.

Seed quality

The quality of seed from the intensively studied sites was assessed in two experiments. The first experiment examined differences in seed production and weight within and among the remnant types while the second experiment assessed seedling germination, growth and survival in a replicated fitness trial.

Seed production and weight

Seed collected from each cone around tree canopies was counted and weighed and is part of an ongoing Honours thesis by Chris Gartlan (University of Ballarat). While preliminary data only are available at this time, initial indications clearly suggest that both the isolated and revegetation sites produce fewer, lighter seed than that from linear and patch sites (Table 3). Within each of the remnant types, seed quality in terms of production and weight were very similar among the linear and patch remnants but considerably more variation was observed among the isolated and revegetation sites.

Table 3: Seed counts and weights for the *Allocasuarina verticillata* remnant types.

Remnant type	Site Name	Mean seed count	Mean seed weight (g)
Isolated	Bostock Creek	79.42	0.362
	Lismore Cemetery	81.87	0.308
	Kinloch	54.87	0.233
	Ascott Downs	50.50	0.311
	Banongill	98.38	0.341
	Pomborneit North	70.14	0.187
	Mean	72.53	0.290
Linear	Skipton-Rokewood Rd	103.34	0.486
	Grassy Point Rd	97.23	0.286
	Buckley School Rd	100.34	0.347
	Mean	100.30	0.373
Patch	Cape Clear	98.09	0.350
	Blairwood	109.21	0.424
	Don Wallace Reserve	101.72	0.449
	Mean	103.00	0.408
Revegetation	Andy Stephens	77.11	0.259
	Nolan	84.12	0.379
	Titanga	59.60	0.233
	Mean	73.61	0.290

Plant growth

The replicated growth trial was conducted over 18 weeks to assess the germination, growth and survival of seed collected from the different remnant types. Germination was assessed daily for the first three weeks and then weekly until the trial was finalised. Plant growth was assessed at weeks 7 and 18 by

measuring plant height and counting the number of phyllodes. At the end of the trial the shoot component of each plant was harvested, dried and weighed.

The final percentage germination ranged widely across the different remnant types from 24.7% in isolated sites to 37.2% in patch remnants (Table 4). Linear sites produced a similar value (31.9%) to that of patch remnants while revegetation sites were slightly higher (27.7%) than isolated sites. The time taken by seed to germinate also varied among the remnants types with isolated and linear remnants germinating 7-9 days quicker than patch and revegetation remnants. Germination responses for each site with the remnant types also varied (Figure 7). For example, germination failed completely in the isolated Banongill site and was very poor at Bostock Creek. Seed from the remaining isolated sites performed slightly lower than from most other sites with the exception of Lismore Cemetery. The Blairwood patch site produced the best overall germination response of any of the sites assessed while the Andy Stephens revegetation site performed worst of this remnant type.

Table 4: Final mean germination responses for each *Allocasuarina verticillata* remnant type.

Remnant type	Mean final % germination	Mean days to germination
Isolated	24.7	25.4
Linear	31.9	28.6
Patch	37.2	33.5
Revegetation	27.7	34.7

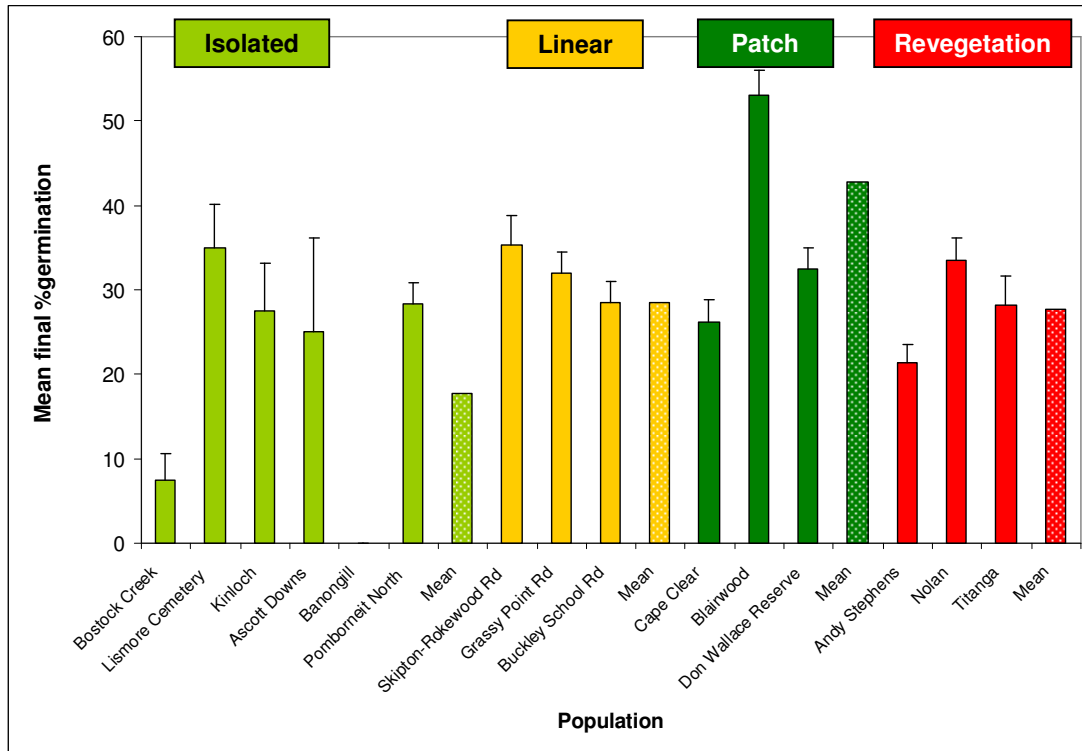


Figure 7: Mean final percentage germination for individual *Allocasuarina verticillata* sites (solid bars) and mean for each remnant type (speckled bars).

Plant growth also varied among the different remnant types (Table 5). The mean number of stems produced by the end of the trial and plant dry weights were lower in isolated and revegetation sites than in linear and patch remnants. Interestingly, this trend was not evident in plant height where isolated and linear remnants grew taller than patch and revegetation remnants.

Table 5: Mean plant growth for each *Allocasuarina verticillata* remnant type at week 18 of the plant growth trial.

Remnant type	Mean no. of stems	Mean height (mm)	Plant weight (g)
Isolated	4.33	110.87	53.24
Linear	5.50	118.21	61.57
Patch	5.11	105.19	54.99
Revegetation	4.61	101.55	50.71

Differences in plant growth were also evident among sites within each remnant type (Figures 8-10). In some cases, poor response in one growth variable signalled poor response in the others. For example, Cape Clear and Titanga seedlings produced fewer stems, were smaller and weighed less. In contrast,

Bostock Creek seedlings produced fewer stems but grew taller than any other isolated site and produced moderate plant weights.

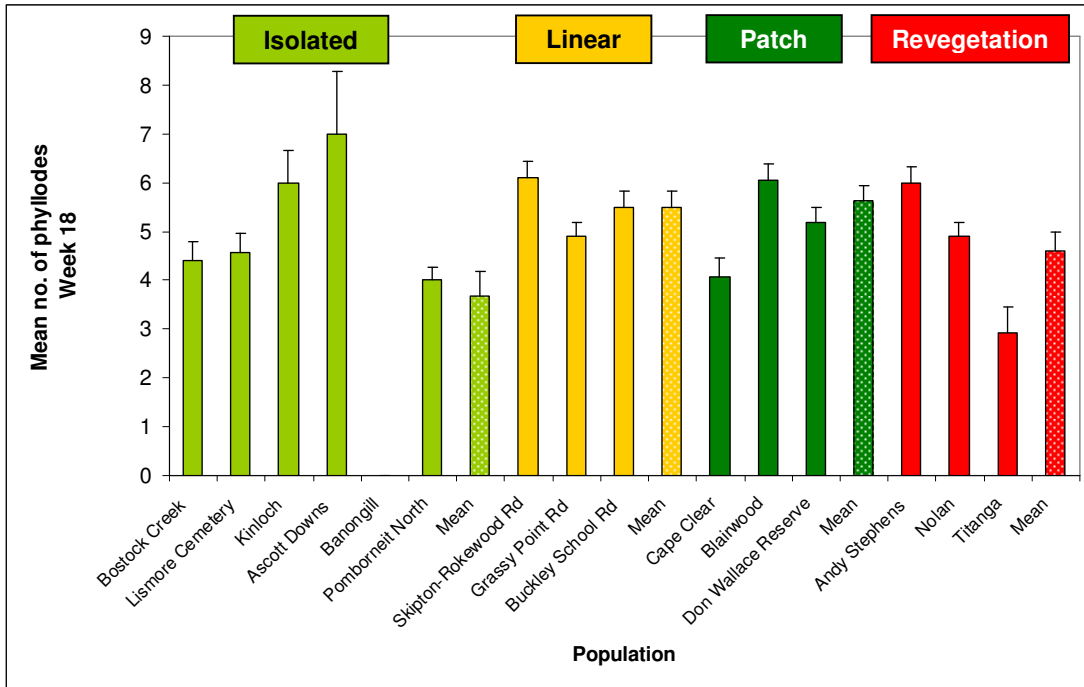


Figure 8: Mean final percentage germination for individual *Allocasuarina verticillata* sites (solid bars) and mean for each remnant type (speckled bars).

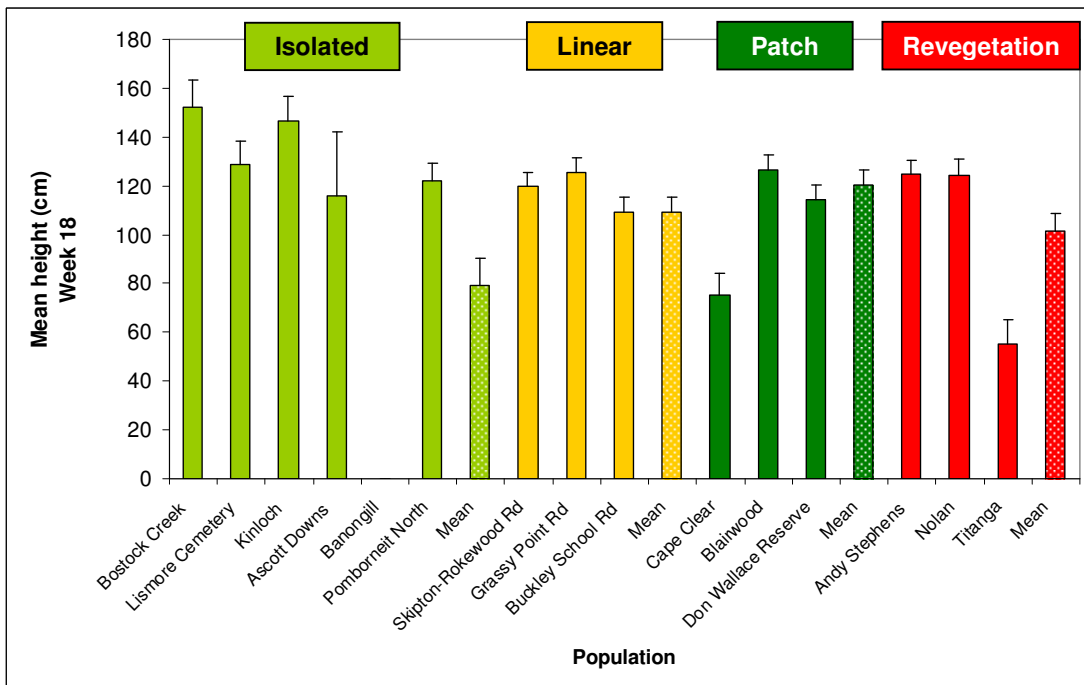


Figure 9: Mean plant height for individual *Allocasuarina verticillata* sites (solid bars) and mean for each remnant type (speckled bars).

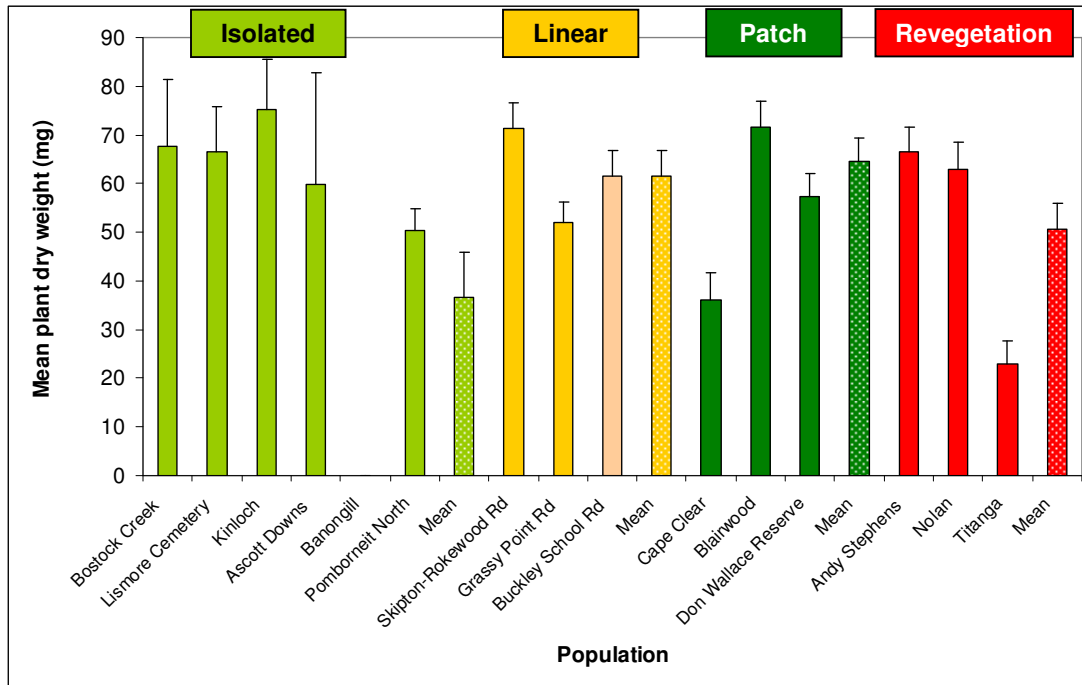


Figure 10: Mean plant weight for individual *Allocasuarina verticillata* sites (solid bars) and mean for each remnant type (speckled bars).

Implications – In general, isolated and revegetation sites did not germinate or grow as well as linear or patch sites suggesting that this seed is less fit. The low genetic diversity at isolated sites in particular further supports this suggestion. As such, it should not form the basis of large restoration projects but can be used to augment other collections. Poor seedling fitness and low diversity in seed from Cape Clear also indicates that this seed be used cautiously and augmented with other collections. It may also be necessary to use larger volumes of poorly performing seed to compensate for poor germination and seedling failure when augmenting other collections for restoration.

Research recommendations

1. Small isolated sites do not represent a viable source of seed for large scale restoration projects. These sites often exhibit poor seed production, germination, growth and survival, low diversity and biased contribution of some fathers to the seed crop. It is recommended that seed from these sites be used to augment other collections to ensure the genetic diversity

present is included. This strategy may also serve to spread the extinction risk for these sites.

2. Consideration should be given to augmenting these small isolated sites with new germplasm to boost low levels of genetic diversity and to alleviate potential inbreeding effects.
3. Linear and patch remnants often exhibit similar levels of seed production, germination, growth and survival and genetic diversity and as such represent excellent sources of seed for revegetation.
4. Seed collection from all sites should ensure that many (20-30) trees are sampled broadly from across each site and that samples are taken from around each tree canopy. This will ensure that the genetic diversity sampled is representative of the site and should preclude localised male bias in seed crops.
5. At this point in time the revegetation sites do not represent seed sources on which restoration should be solely based. Seed from these sites, however, may be used to supplement other collections intended for revegetation. It may be appropriate at this stage to cautiously utilise Titanga seed given its poor performance and that it appears to have been sourced from a non-local source unlike Andy Stephens and Nolan. It is possible that as these latter sites mature and more trees become reproductive, they may become valuable seed sources that can help to reduce the collection burden on remnant vegetation but this would need to be assessed at a future date.
6. There is no strong evidence of spatial genetic structure in the sites sampled suggesting that seed may be more widely deployed than is currently being undertaken. It is recommended that where possible the closest large 'local' seed source be used as the primary seed source and to augment this with smaller sites if possible. This sampling should also consider habitat matching where possible.

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Appendix 1: Genetic maps of *A. verticillata* sites

The following diagrams indicate the most probable father of seed sampled for mothers at each of the study sites.

1. Mothers are indicated by numbered circles.



2. Fathers are indicated by coloured circles.



3. Contribution of each father to overall seed are indicated by pie charts where each father's contribution is coloured coded:

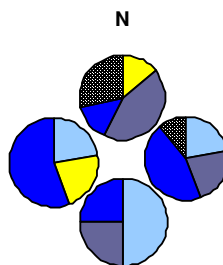
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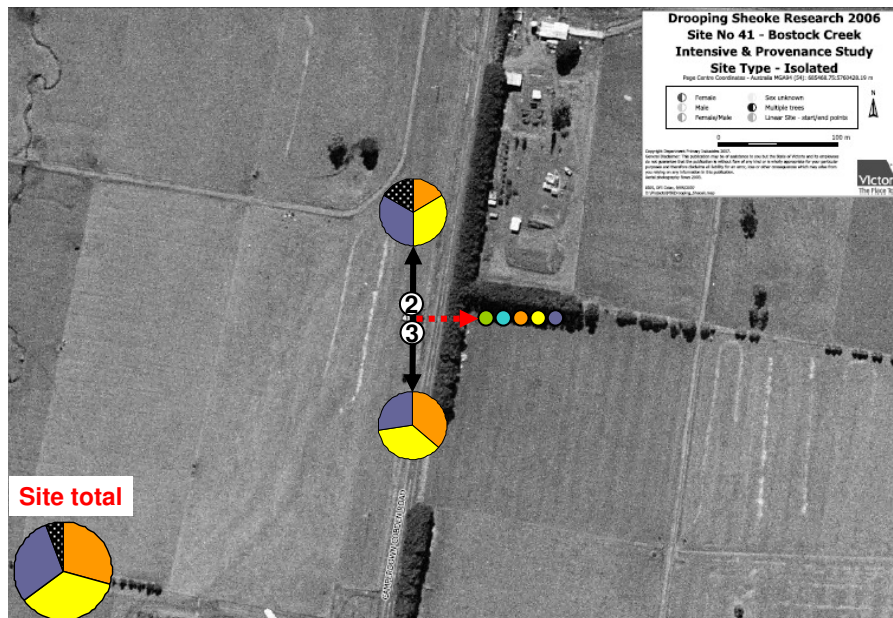
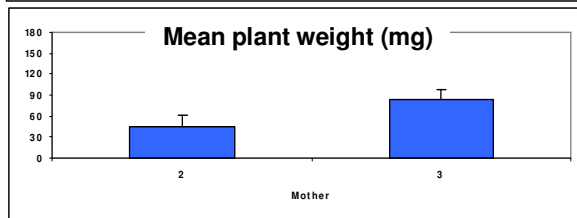
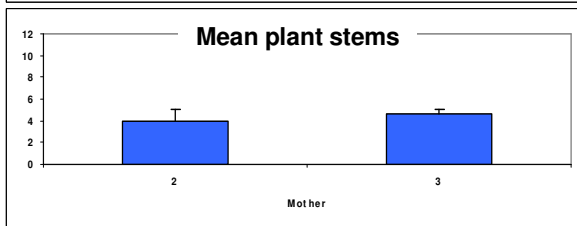
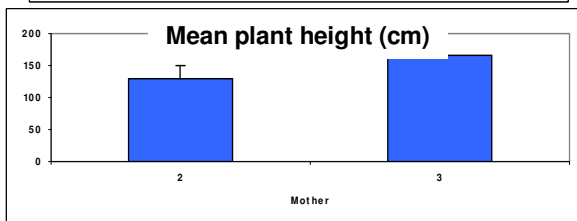
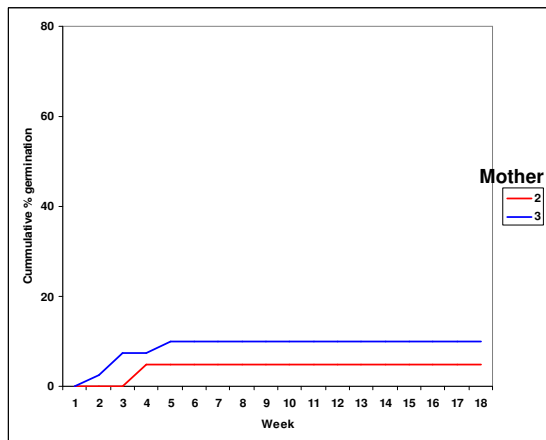
4. Seed from unsampled fathers is represented by speckling on the pie chart.



5. When available, the contribution of fathers to seed collected from each canopy direction is represented as separate pie charts.



6. If too few seed are available for analysis, data is provided but qualified by an asterisk.



Site Summary

Seed production – poor seed production and low seed weight.

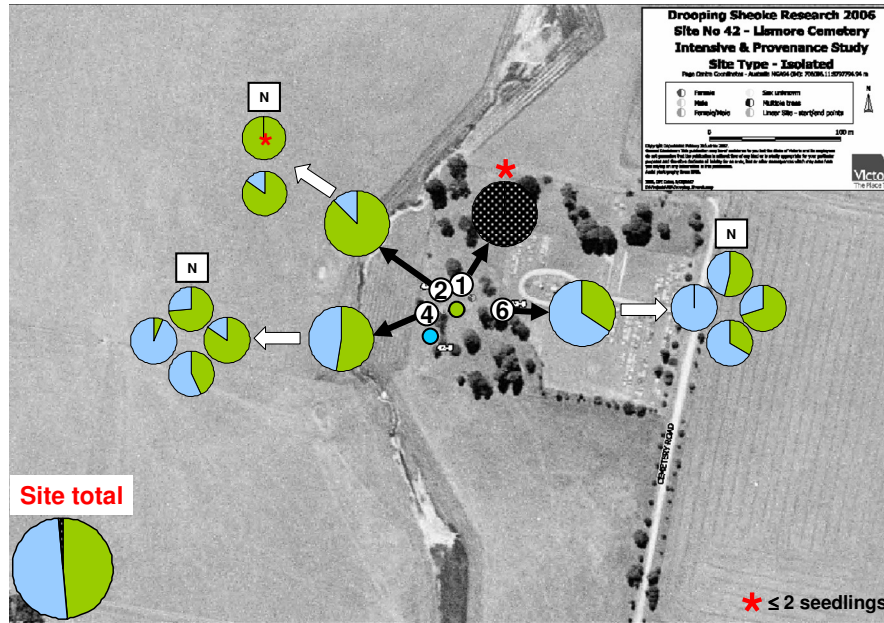
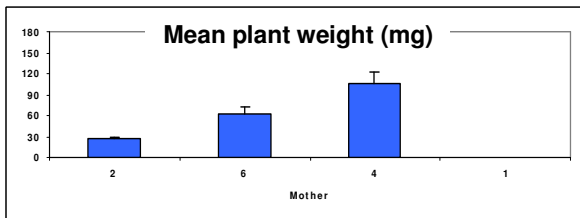
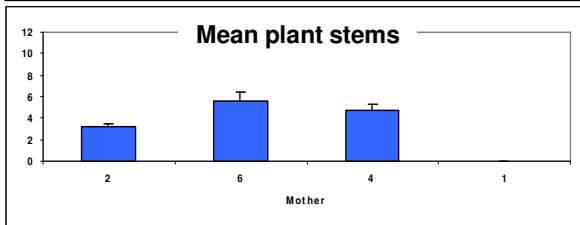
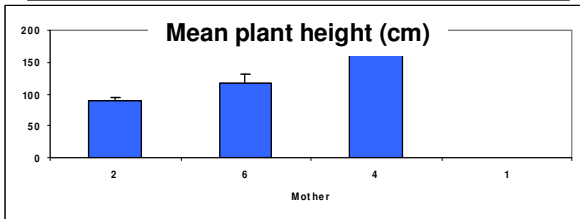
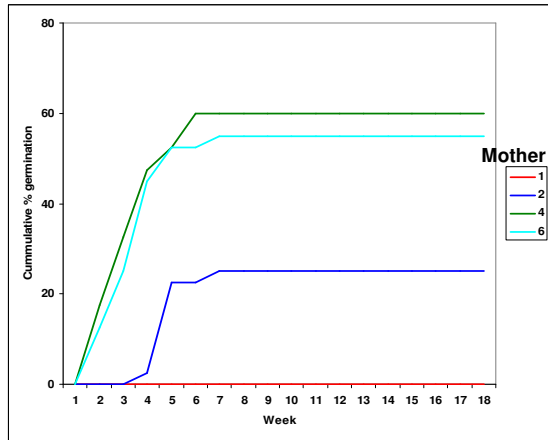
Germination and growth – very poor final germination rates (5-10%) that were moderately fast with poor survivorship (88%).

Genetics – genetic diversity lowest of all sampled sites.

Mating system – two fathers made no contribution to pollen pool while the remaining three contributed equally.

Recommendation: collect from all trees and especially collect around each canopy. Not recommended for use as a seed source for revegetation but a small sample could be added to other collections.

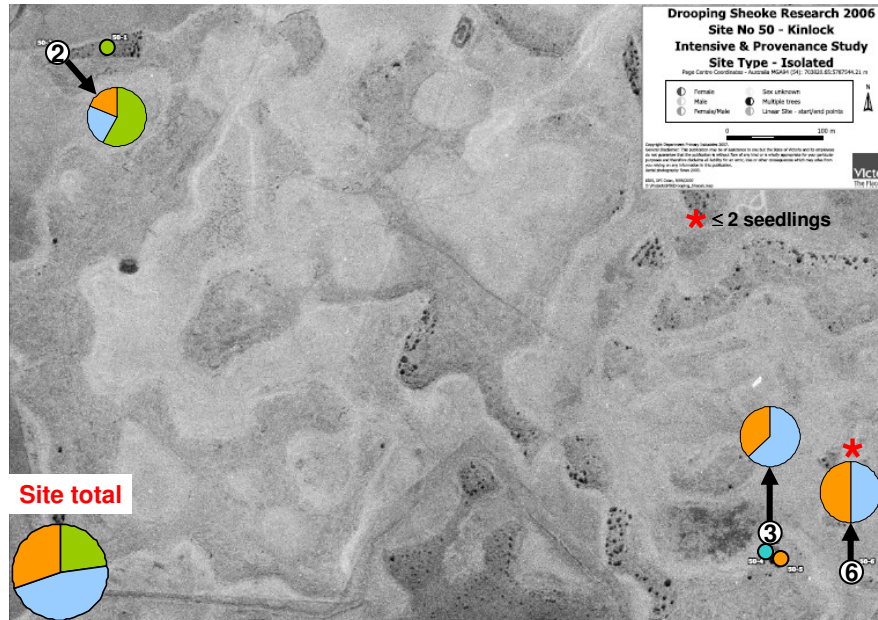
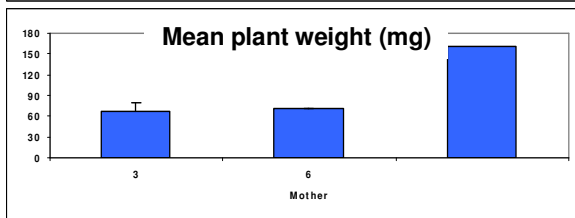
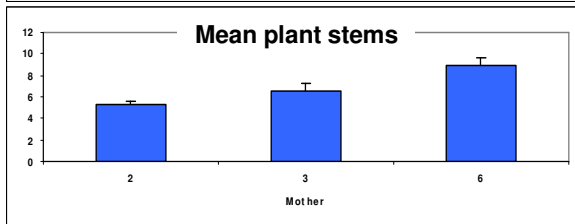
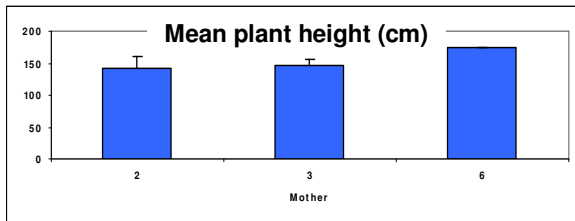
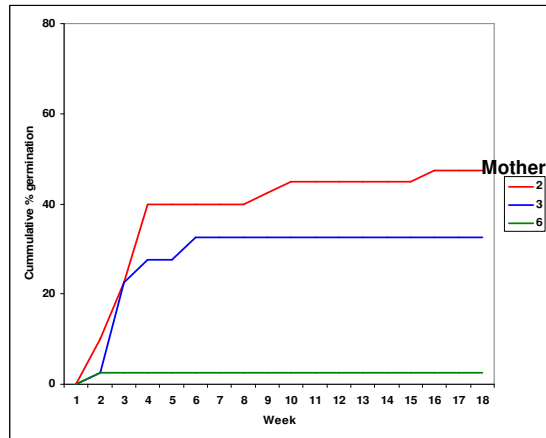
Bostock Creek (Isolated)



Site Summary

Seed production – reasonable seed production with moderate seed weight.
Germination and growth - moderate final germination rates (0-60%) that were moderately fast with very high survivorship (99%).
Genetics – genetic diversity low.
Mating system – both fathers equally contributing to pollen pool but this contribution varies according to the mother and canopy direction sampled.
Recommendation: collect from all trees and especially collect around each canopy. Not recommended for use as a seed source for revegetation but can be used to contribute to other collections.

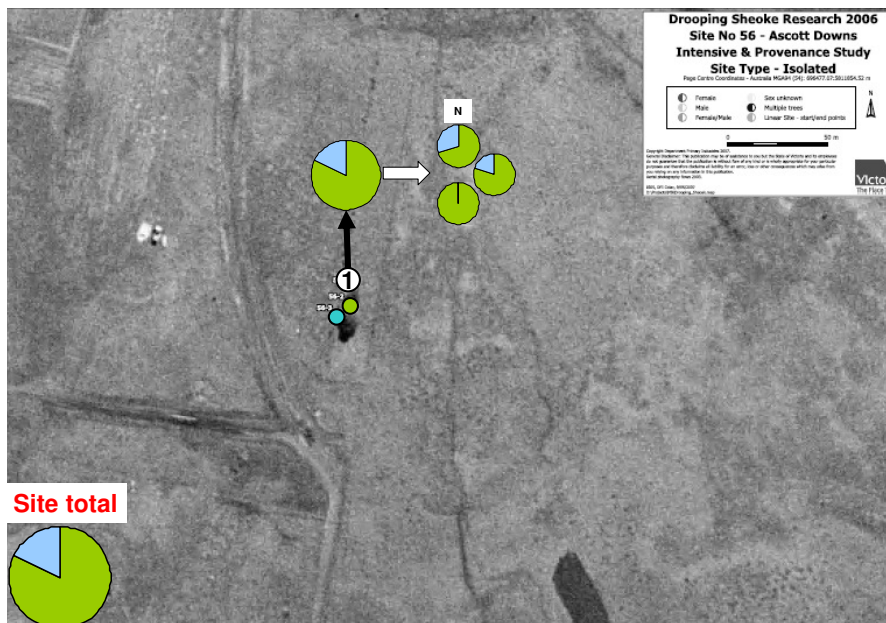
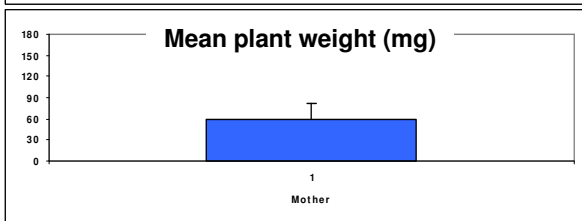
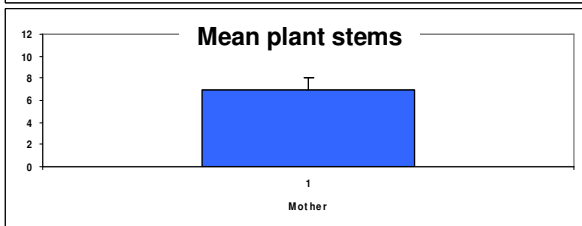
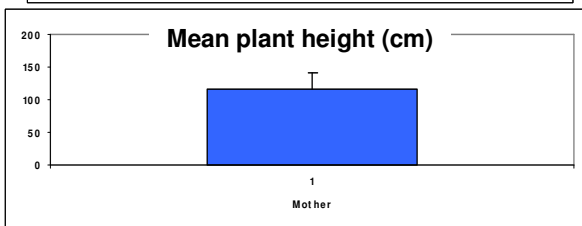
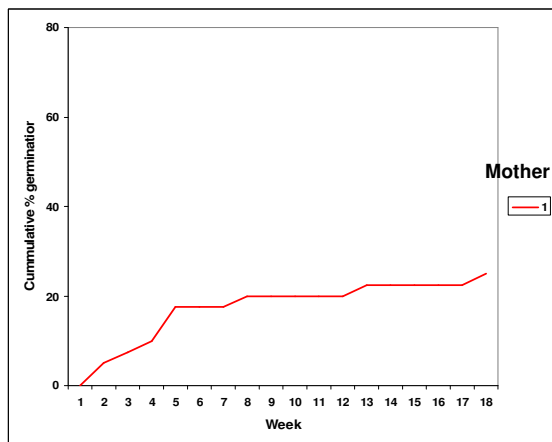
Lismore Cemetery (Isolated)



Site Summary

Seed production – very poor seed production and very low seed weight.
Germination and growth – reasonable final germination rates (3-48%) that were moderately fast with high survivorship (97%).
Genetics – genetic diversity moderate.
Mating system – all fathers contributing to the pollen pool but one makes the largest contribution. Pollen flowing across relatively large distances.
Recommendation: collect from all trees and especially collect around each canopy. Not recommended for use as a seed source for revegetation but a small sample could be added to other collections.

Kinloch (Isolated)



Site Summary

Seed production – lowest seed production and seed weight of all sites sampled.

Germination and growth – reasonable final germination rate (25%) that was very slow but excellent survivorship (100%).

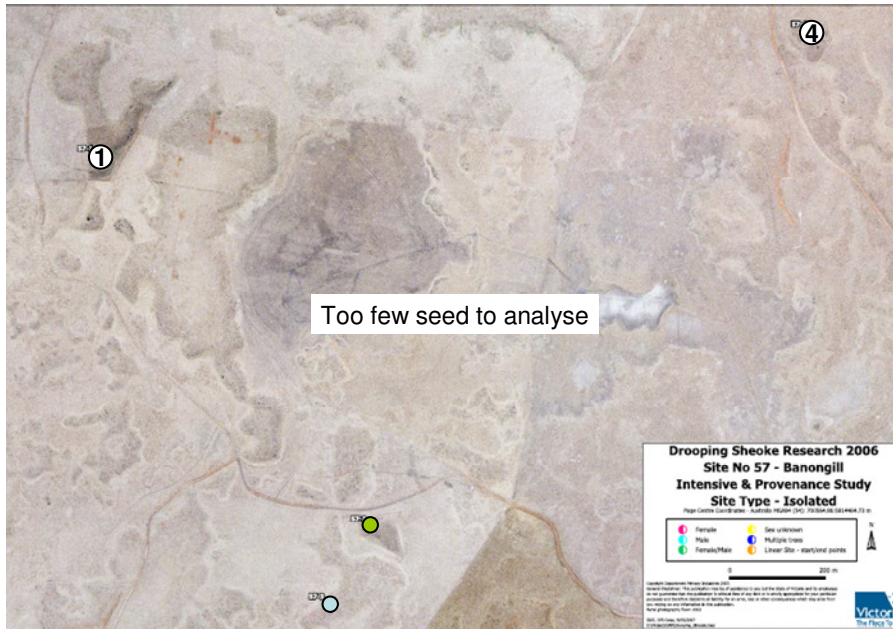
Genetics – genetic diversity low.

Mating system – both fathers contributing to the pollen pool but one makes the largest contribution. Canopy direction very important for fathers contribution.

Recommendation: collect from around the canopy. Not recommended for use as a seed source for revegetation but a small sample could be added to other collections.

Ascott Downs (Isolated)

Banongill (Isolated)



Site Summary

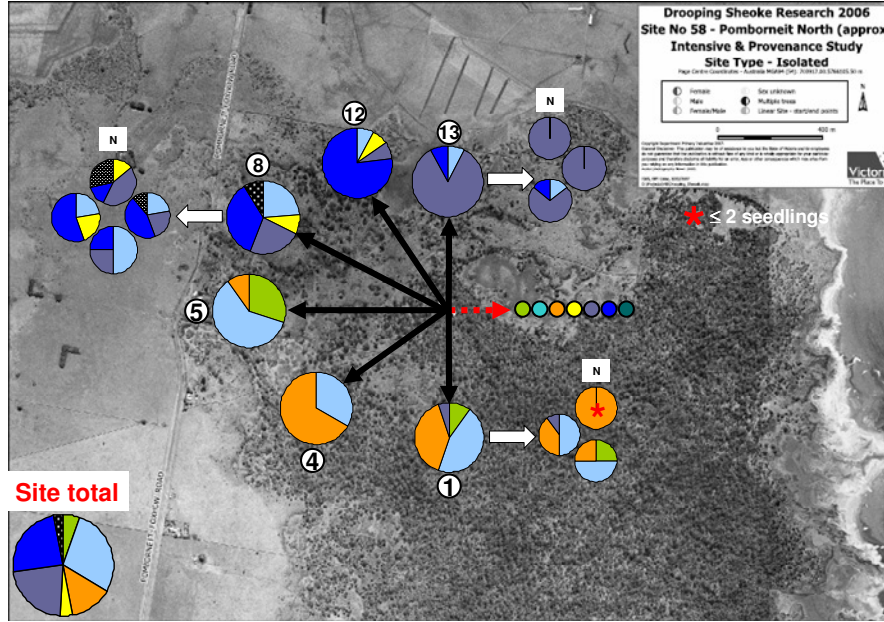
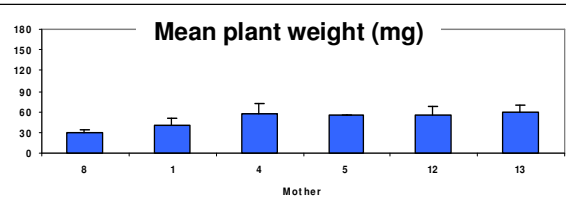
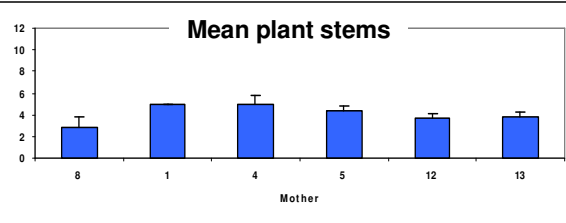
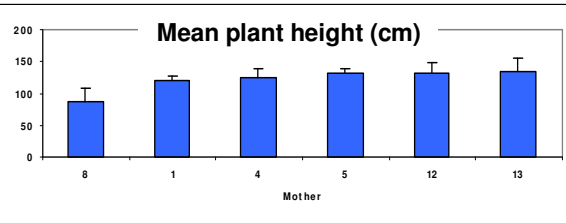
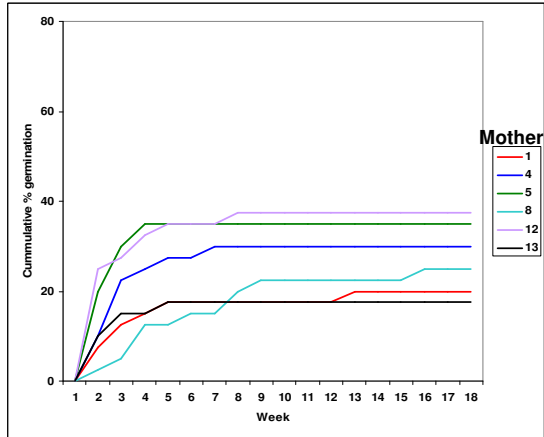
Seed production – good seed production with moderate seed weight.

Germination and growth – germination failed.

Genetics – unable to assess due to poor germination.

Mating system – unable to assess due to poor germination.

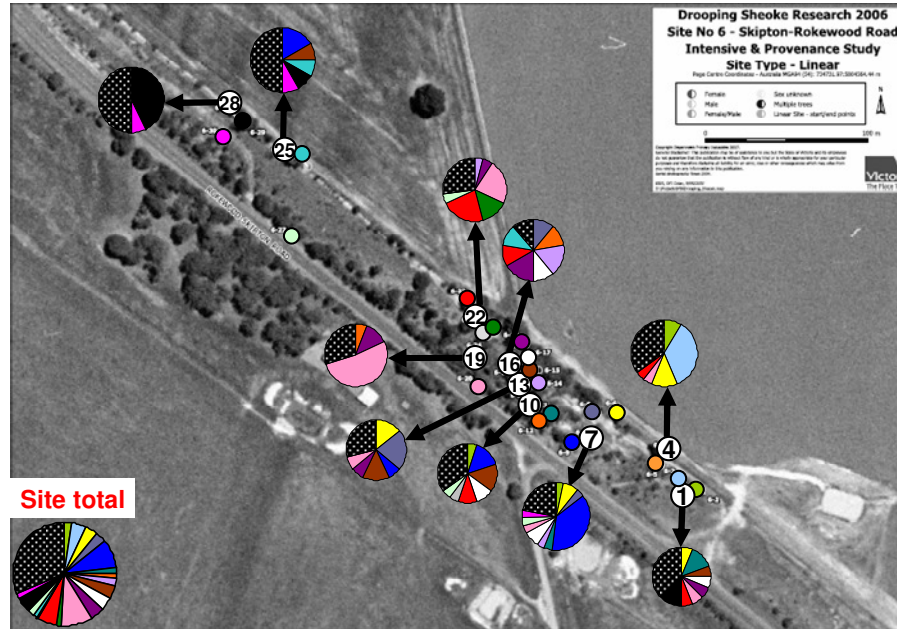
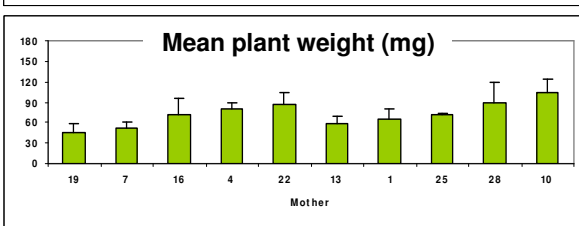
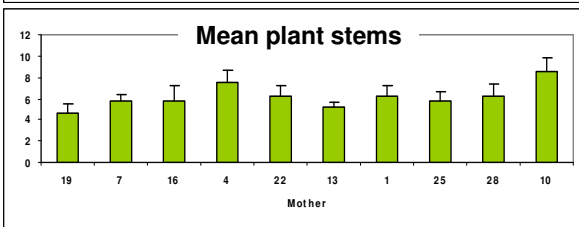
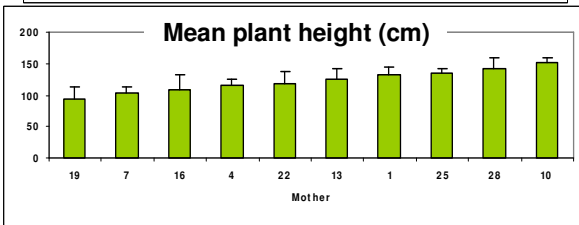
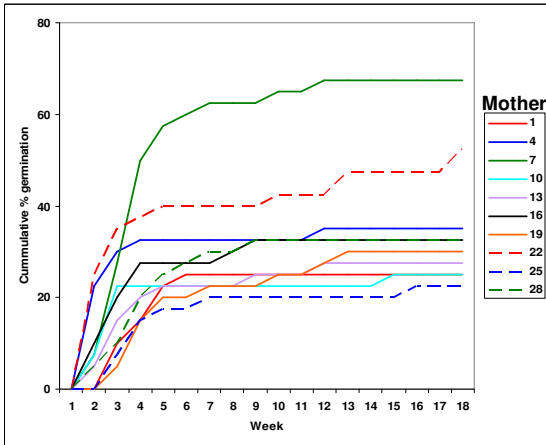
Recommendation: could collect from around the canopy but not recommended for use as a seed source for revegetation. A very small sample could be added to other collections.



Site Summary
Seed production – poor seed production and very low seed weight.
Germination and growth - poorer final germination rates (18-38%) that were moderately fast with moderate survivorship (84%).
Genetics – genetic diversity low.
Mating system – some fathers making very little contribution to pollen pool while contribution of fathers varies around each canopy.
Recommendation: collect from all trees and especially collect around each canopy. Not recommended for use as a seed source for revegetation but can be used to contribute to other collections.

Pomborneit North (Isolated)

Skipton-Rokewood Rd (Linear)



Site Summary

Seed production – excellent seed production and high seed weight.

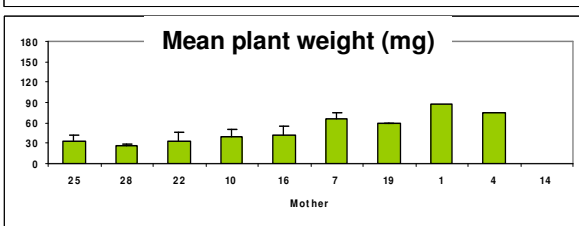
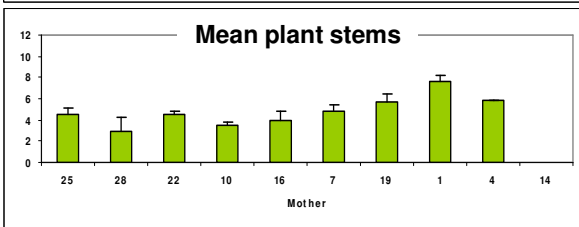
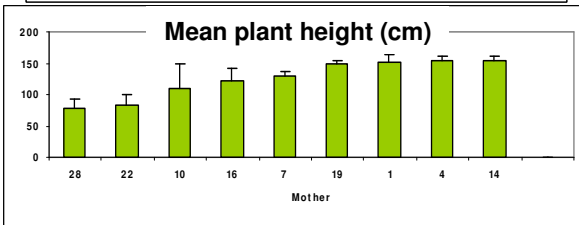
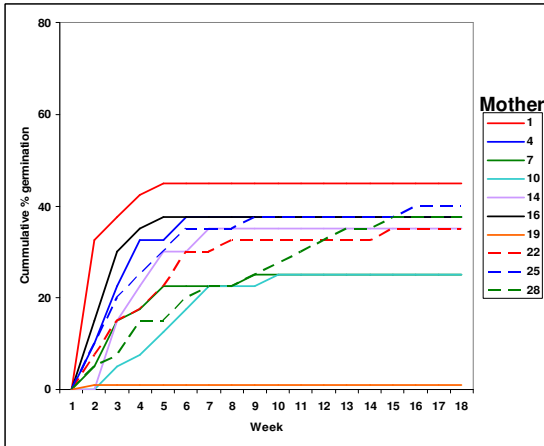
Germination and growth - good final germination rates (25-68%) that were moderately fast with high survivorship (93%).

Genetics – genetic diversity high.

Mating system – Many fathers contributing to the pollen pool with some localised effects associated with placement in the linear strip. More than 25% of the seed not from one of the sampled fathers.

Recommendation: collect from as many trees as possible and sample around the canopies to capture contributions from as many father as possible. A good site for revegetation seed provided collected appropriately.

Grassy Point Rd (Linear)



See over for details

Site Summary

Seed production –good seed production but low seed weight.

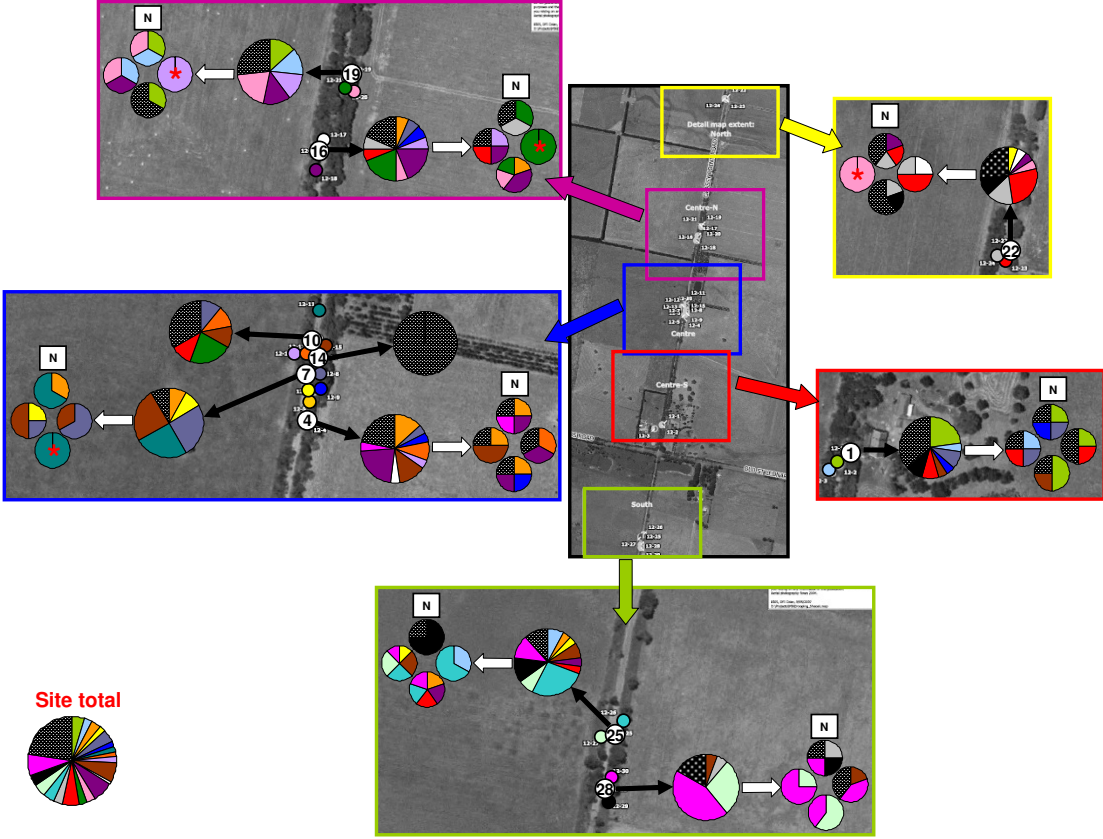
Germination and growth - moderate final germination rates (3-45%) that were moderately fast with lower survivorship than most sites (82%).

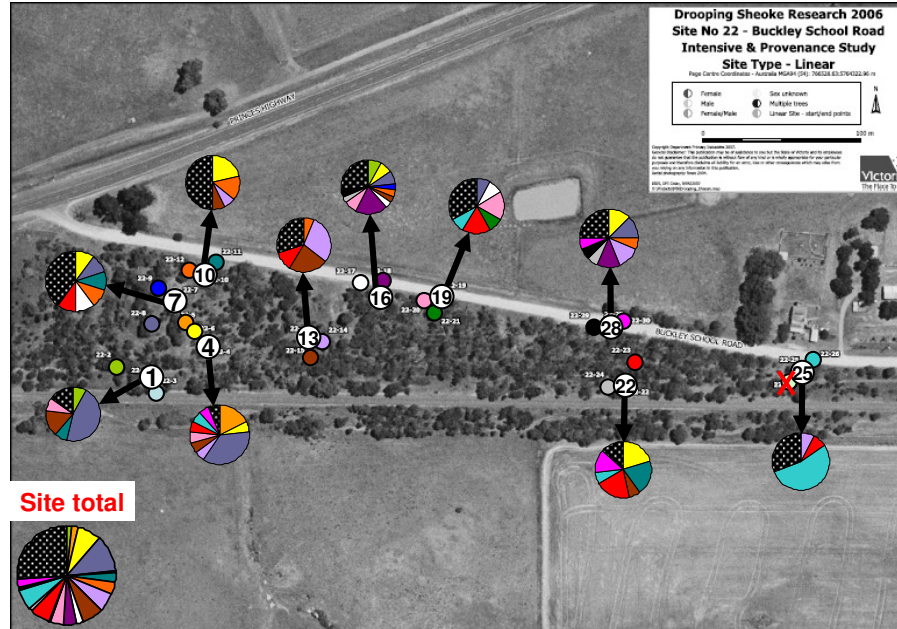
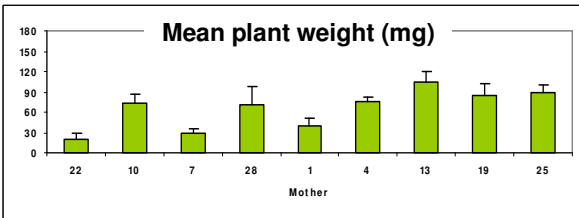
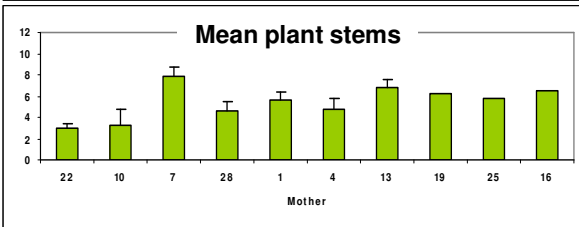
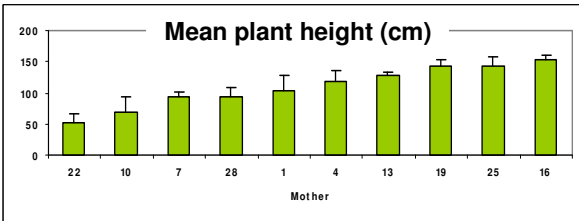
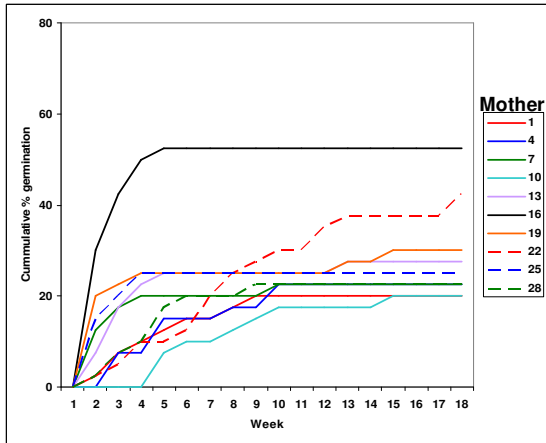
Genetics – genetic diversity high.

Mating system –Many fathers contributing to the pollen pool with some localised effects associated with placement in the linear strip. Clear effects associated with where seed are collected from around the canopy. Some 25% of the seed not from one of the sampled fathers.

Recommendation: collect from as many trees as possible and sample around the canopies to capture contributions from as many fathers as possible. A good site for revegetation seed provided collected appropriately.

Grassy Point Rd (Linear)





Site Summary

Seed production – excellent seed production and moderate seed weight.

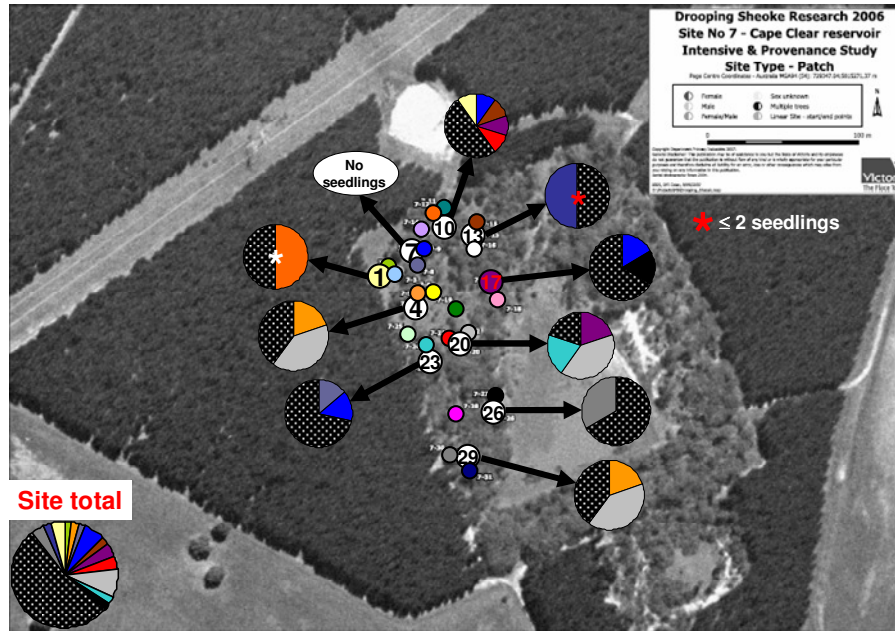
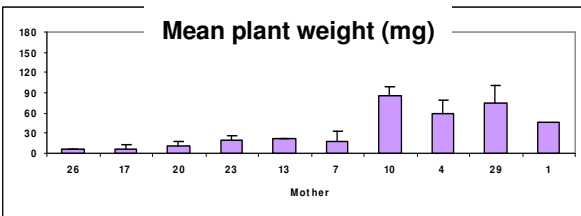
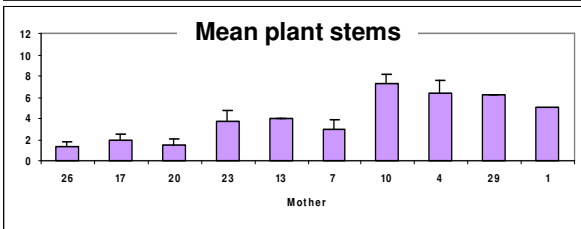
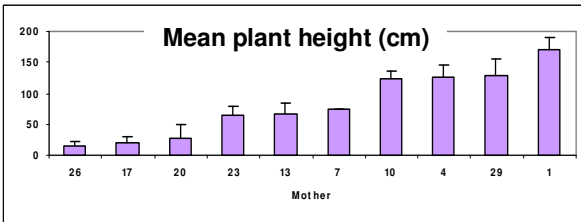
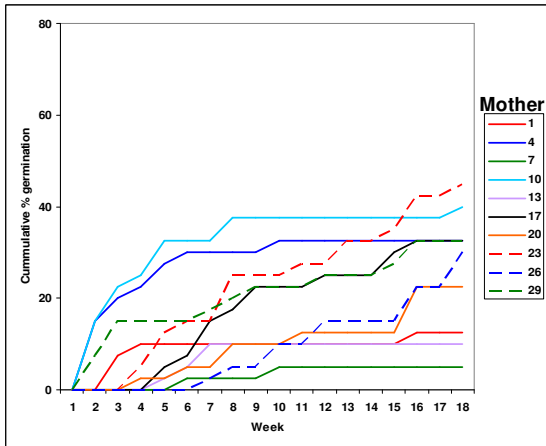
Germination and growth - poorer final germination rates (20-53%) than other linear remnants. Slower germination with good survivorship (90%).

Genetics – genetic diversity high.

Mating system – Many fathers contributing to the pollen pool with some localised effects associated with placement in the linear strip. Approx. 25% of the seed not from one of the sampled fathers.

Recommendation: collect from as many trees as possible and sample around the canopies to capture contributions from as many fathers as possible. A good site for revegetation seed provided collected appropriately.

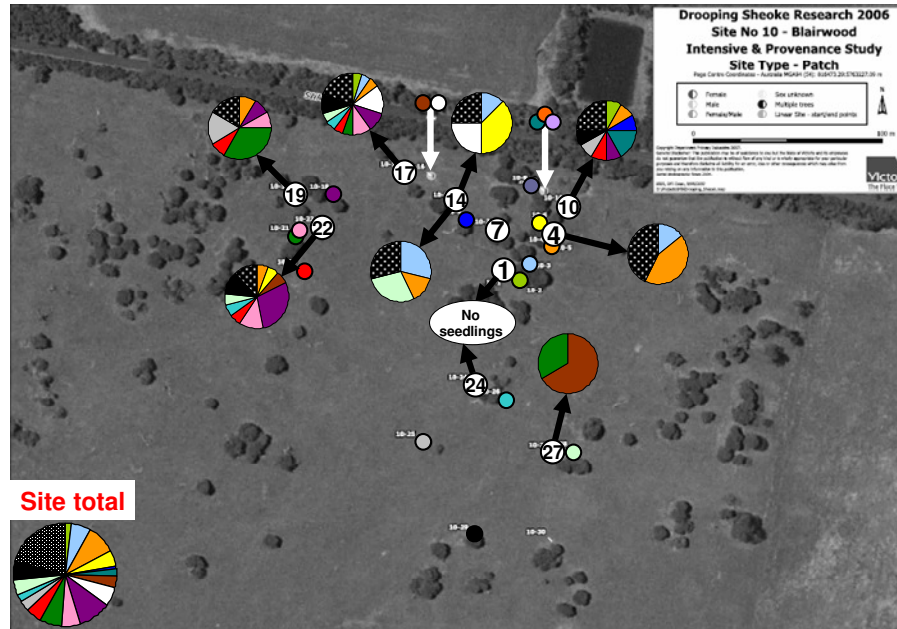
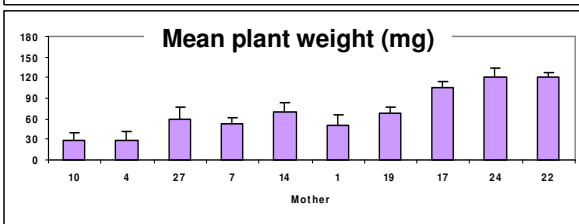
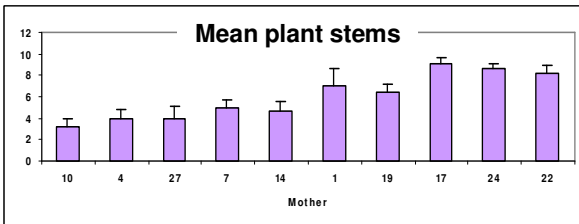
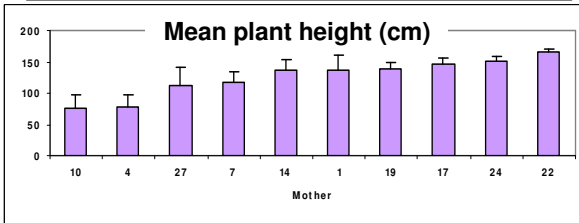
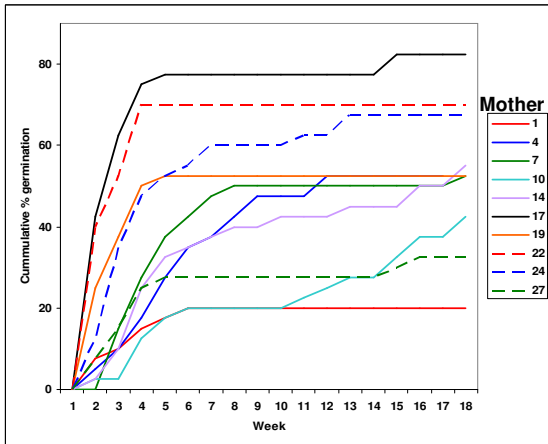
Buckley School Rd (Linear)



Site Summary

Seed production – good seed production with moderate seed weight.
Germination and growth - poorest final germination rates (5-45%) of all patch sites with similar germination rates but lower survivorship (87%).
Genetics – genetic diversity similar to that observed in small isolated sites.
Mating system – evaluation impossible for one tree. Some sampled fathers not contributing to the pollen pool. Both hermaphroditic trees (1 and 17) produced seed in nearby mothers. Many unsampled fathers contributing to the pollen pool.
Recommendation: collect from 20-30 trees and sample around the canopies to capture as much genetic diversity as possible. A reasonable site for revegetation seed, however, may be prudent to supplement with seed from other collections.

Cape Clear (Patch)



Site Summary

Seed production – very good seed production and seed weight.

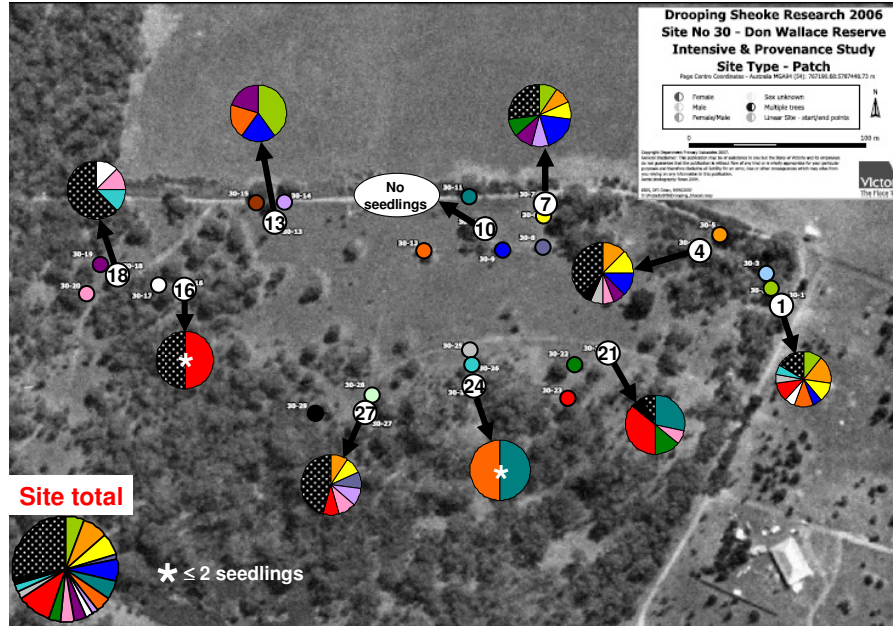
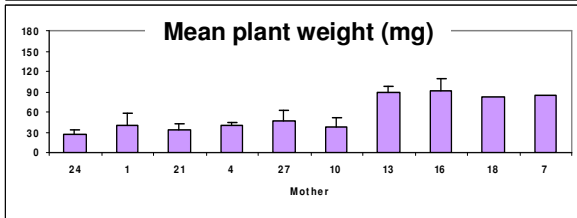
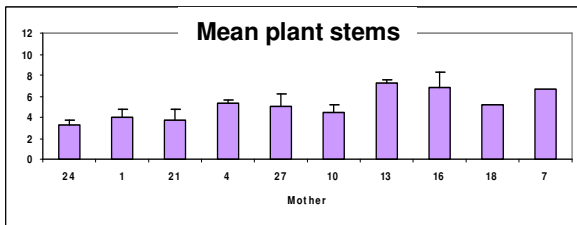
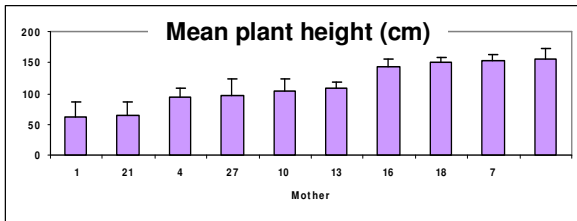
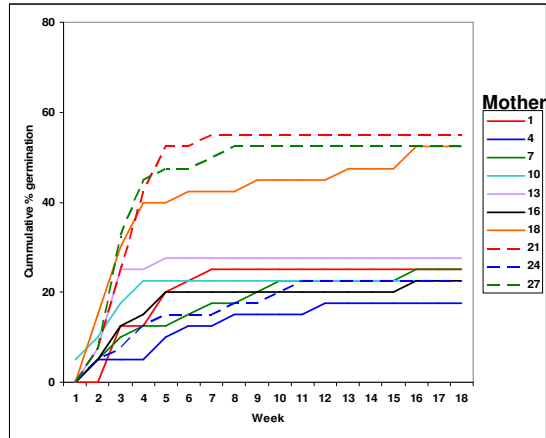
Germination and growth - excellent final germination rates (20-83%) that were moderately fast with high survivorship (93%).

Genetics – genetic diversity high.

Mating system – evaluation impossible for one tree. Many fathers contributing to the pollen pool with no single tree dominating seed production across the site although some fathers dominate 'locally'. Almost 25% of the seed not from a sampled father.

Recommendation: collect from 20-30 trees and sample around the canopies to capture as much genetic diversity as possible. A very good site for revegetation seed.

Blairwood (Patch)



Site Summary

Seed production – very good seed production and seed weight.

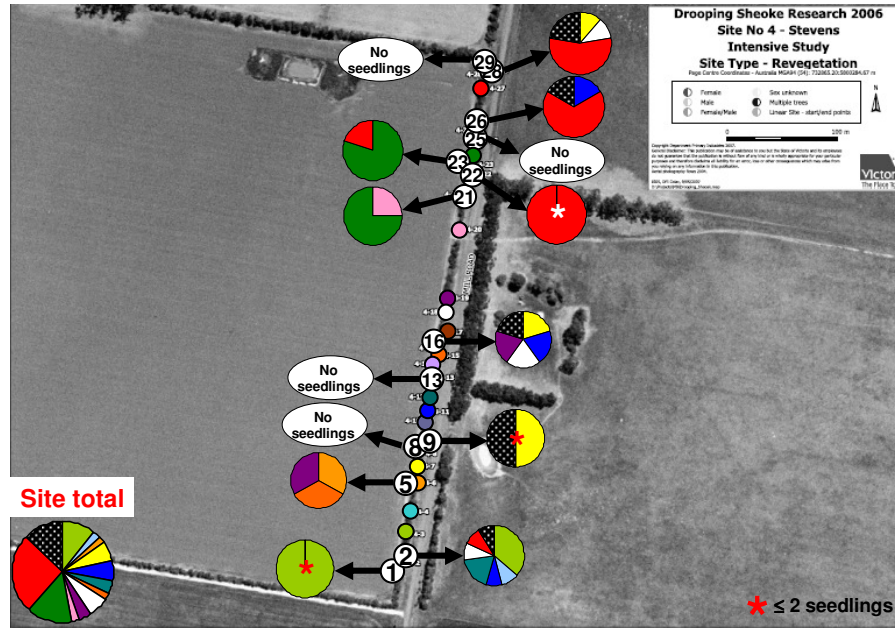
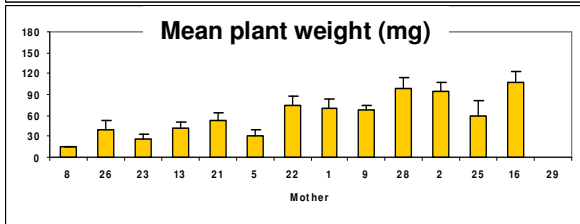
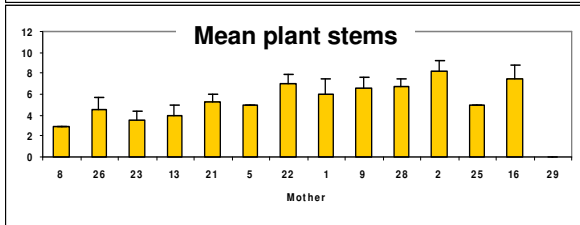
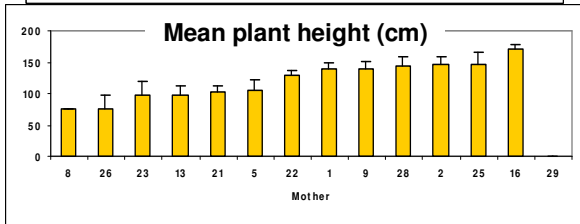
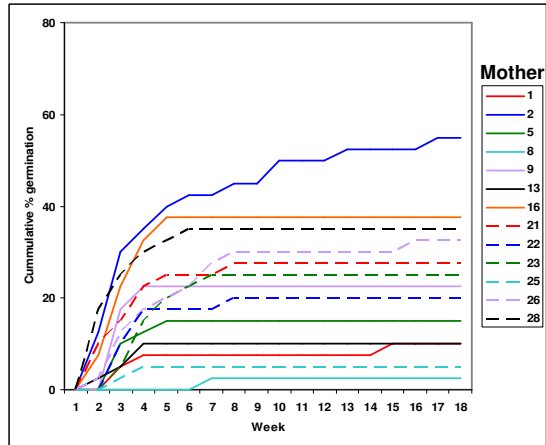
Germination and growth - good final germination rates (18-58%) that were moderately fast with high survivorship (91%).

Genetics – genetic diversity high.

Mating system – evaluation impossible for one tree. Many fathers contributing to the pollen pool with no single tree dominating seed production across the site. Some fathers dominate 'locally' with approx. 25% of the seed not from one of the sampled fathers.

Recommendation: collect from 20-30 trees and sample around the canopies to capture as much genetic diversity as possible. A very good site for revegetation seed.

Don Wallace Reserve (Patch)



Site Summary

Seed production - fewer, lighter seed.

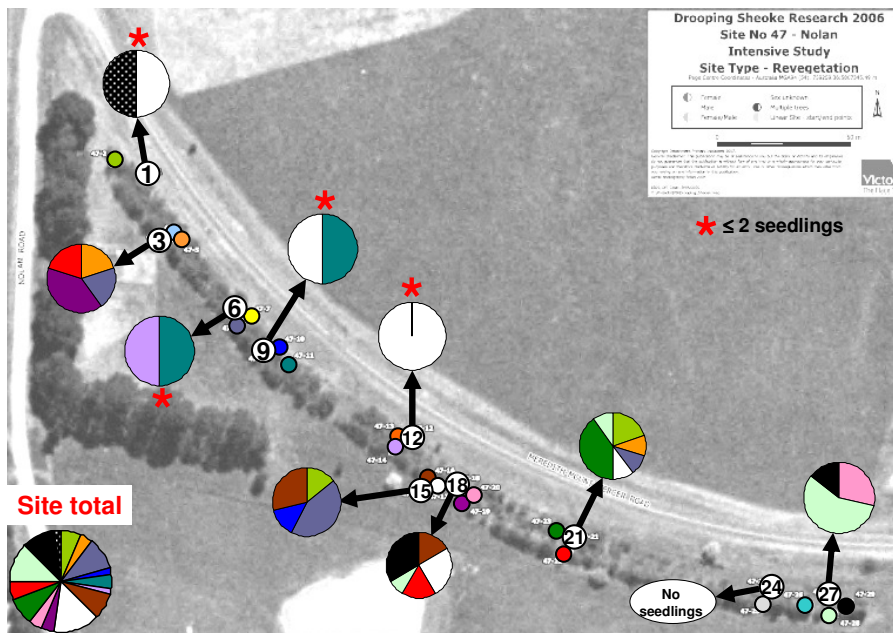
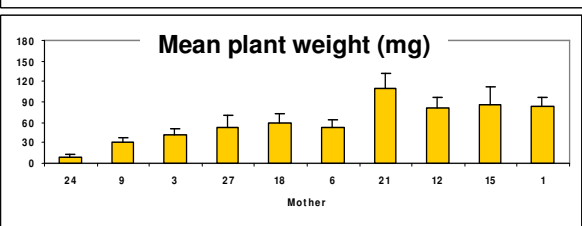
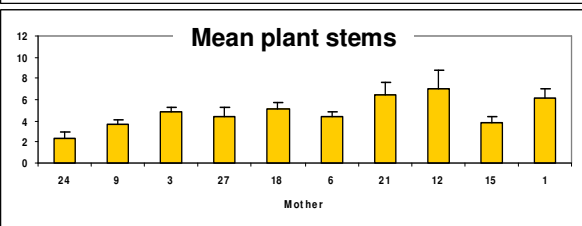
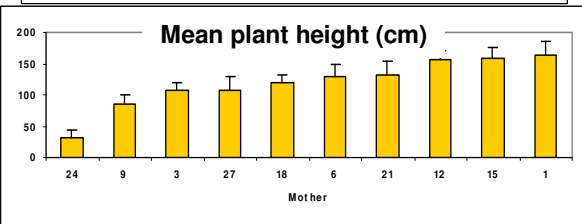
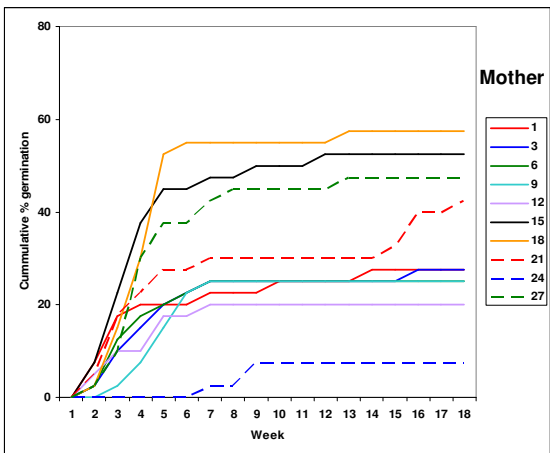
Germination and growth - final germination rates vary widely (0-55%) although germination was generally quick with high survivorship (97.4%).

Genetics - one of the highest sites for genetic diversity.

Mating system - evaluation impossible for several trees. Many fathers contributing to pollen pool but some seed sampled dominated by 1-2 fathers only.

Recommendation: collect from as many trees and ensure sampling from around each canopy. Should be used to supplement other collections for revegetation at this stage.

Andy Stephens (Revegetation)



Site Summary

Seed production – more, heavier seed than other revegetation sites.

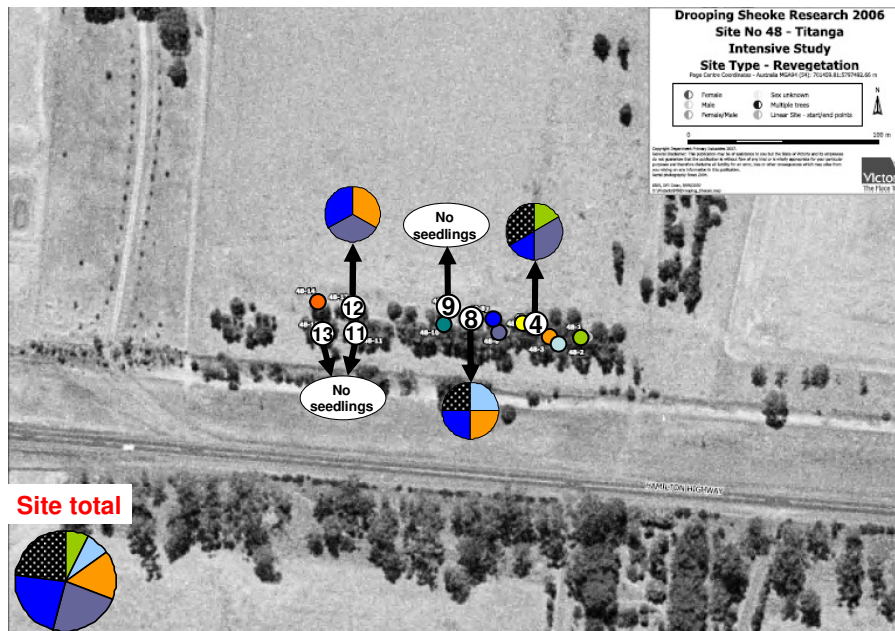
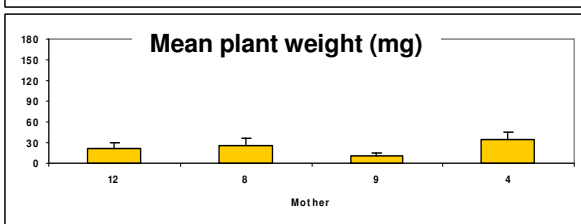
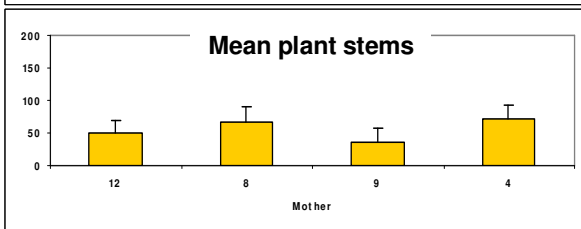
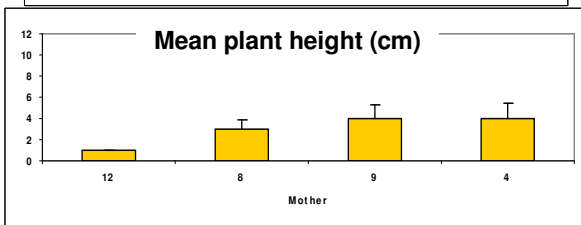
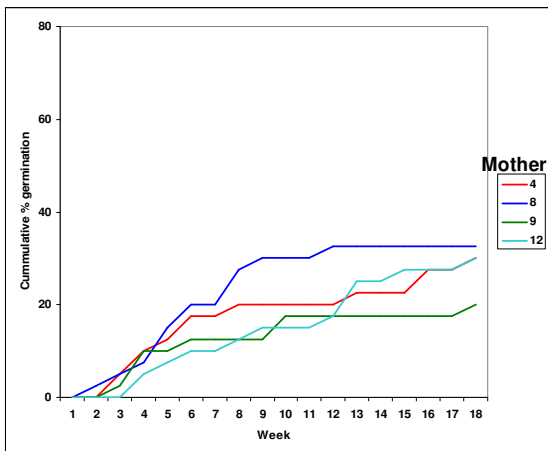
Germination and growth - final germination rates varied widely (10-58%) with <20% germination for two of the 10 plants. Germination generally quick with high survivorship (92.1%).

Genetics – moderate levels of genetic diversity.

Mating system – evaluation impossible for one tree. Many fathers contributing to pollen pool but seed from some mothers often dominated a single father.

Recommendation: collect from as many trees as possible and ensure sampling from around each canopy to capture genetic contributions from many fathers. Could be used for revegetation if sampled appropriately and to supplement other collections.

Nolan (Revegetation)



Site Summary

Seed production – one of the poorest sites sampled.

Germination and growth - final germination rates reasonable (20-33%) but germination was slow. Survivorship was high (95%).

Genetics – genetic diversity low and similar to small isolated sites.

Mating system – evaluation impossible for several trees. Few fathers contributing to the pollen pool with 2-3 dominating. Many fathers contributing to pollen pool but seed from some mothers often dominated a single father.

Provenance – similar to

Recommendation: collect from as many trees as possible and ensure sampling from around each canopy to capture as much genetic diversity as possible. Should not be used for revegetation but could supplement other seed collections if desired.

Titanga (Revegetation)