Department of Biodiversity, Conservation and Attractions

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# Measuring and managing genetic erosion in plant reintroductions:

## Lessons from 20 years of genetic monitoring of the recovery of *Grevillea scapigera* (Proteaceae)


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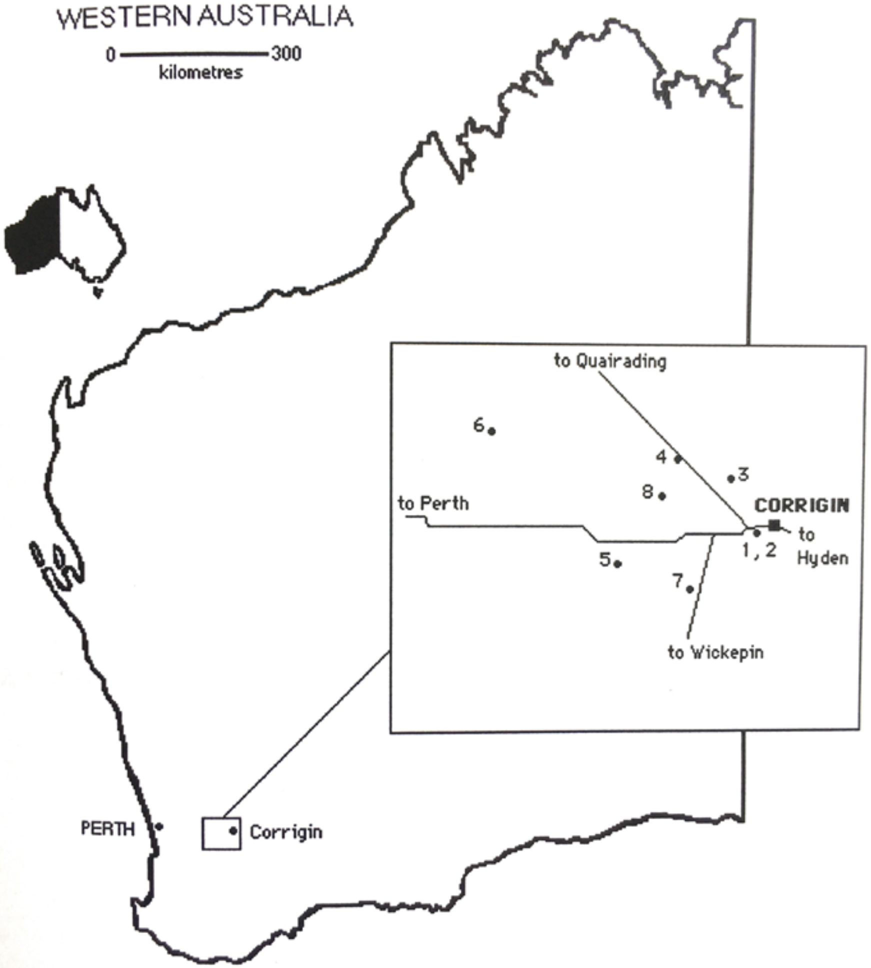
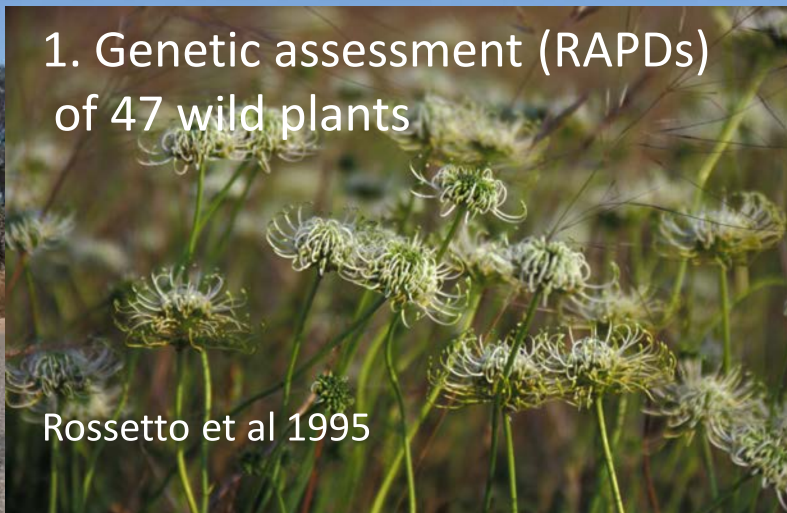
First Collected: 1954
Presumed Extinct: 1984
Rediscovered in Wild: 1990

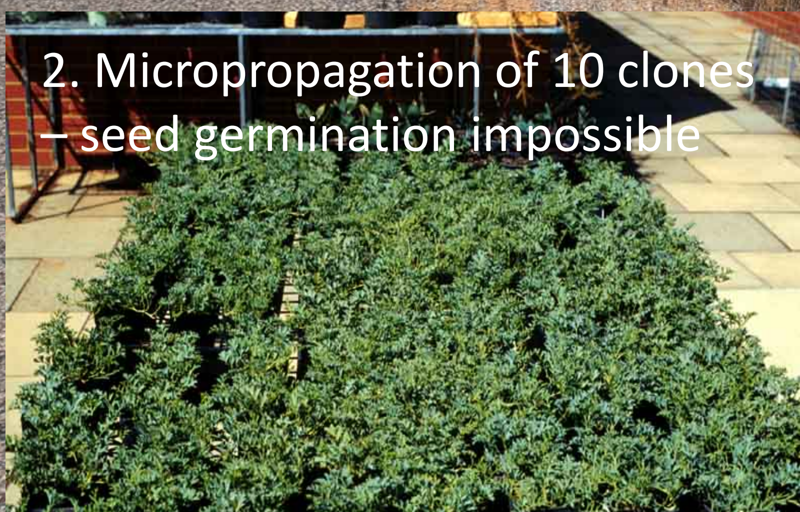


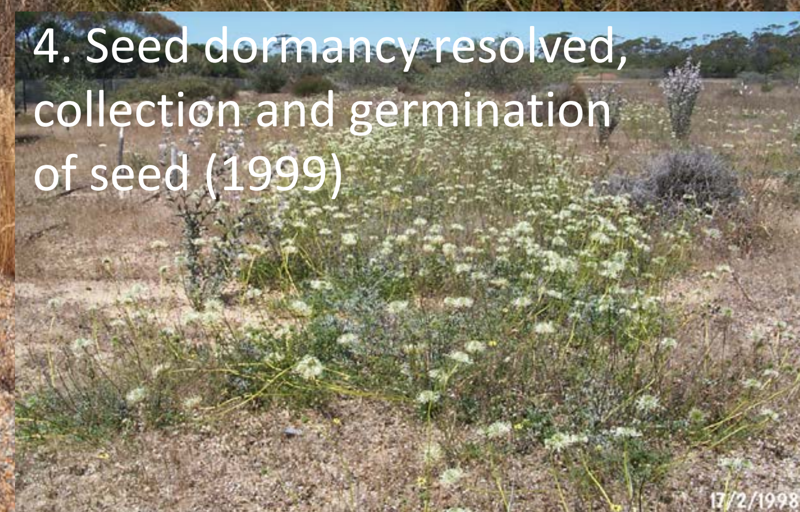

Rossetto et al. (1995) Mol. Ecol
Rossetto et al. (1995) PhD

# Translocation of *Grevillea scapigera*







# Initial Genetic Assessment of Founders and their F1 offspring (in 1999)

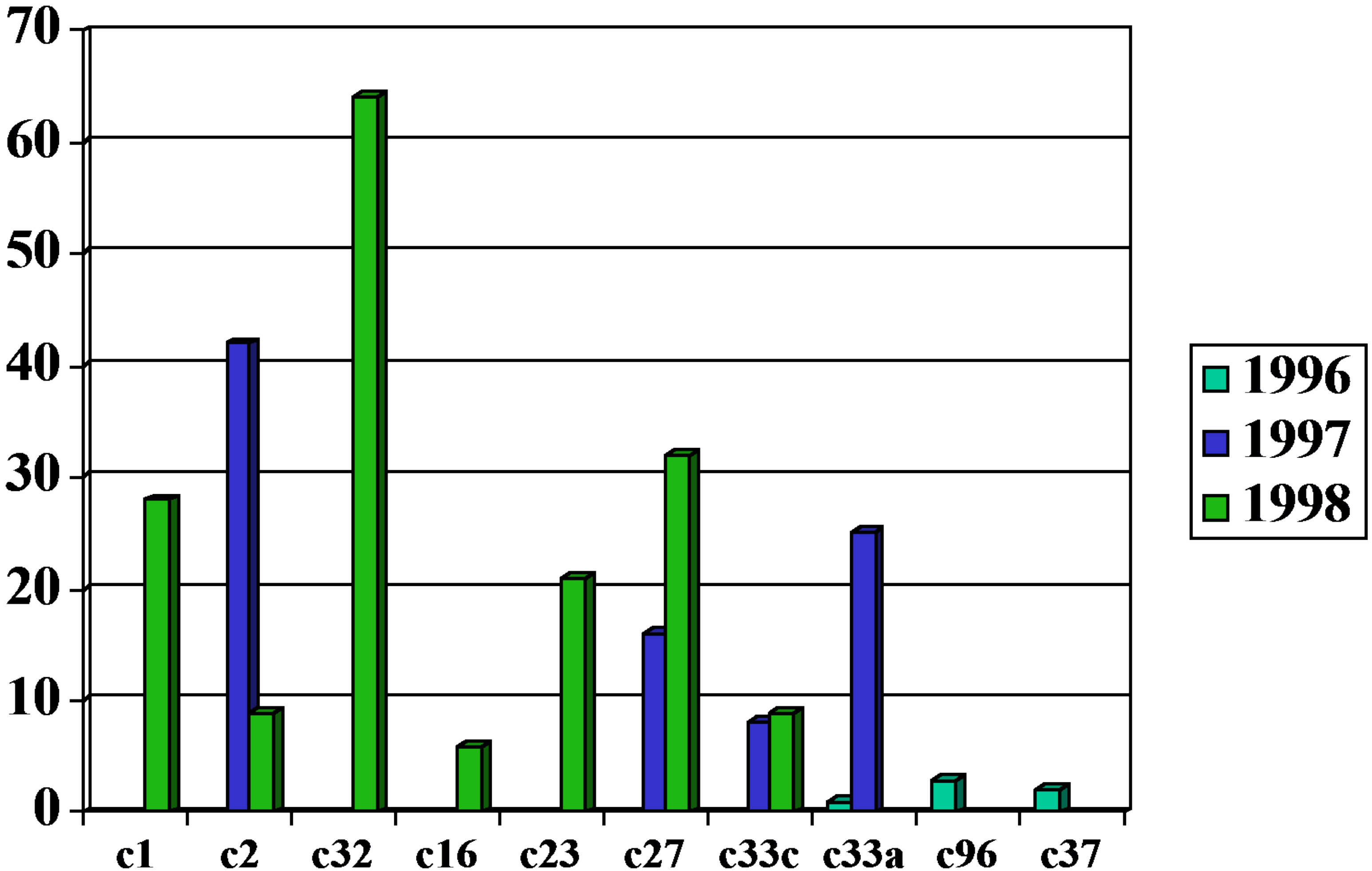
1. Assess genetic fidelity of the founding clones (n = 10) through *ex-situ* propagation
2. Assess genetic erosion by comparing genetic variation between founders and offspring (n = 103)
3. Assign paternity to progeny to assess reproductive success of each clone

143 AFLP markers

Krauss et al (2002) *Conservation Biology* 16:986-994.

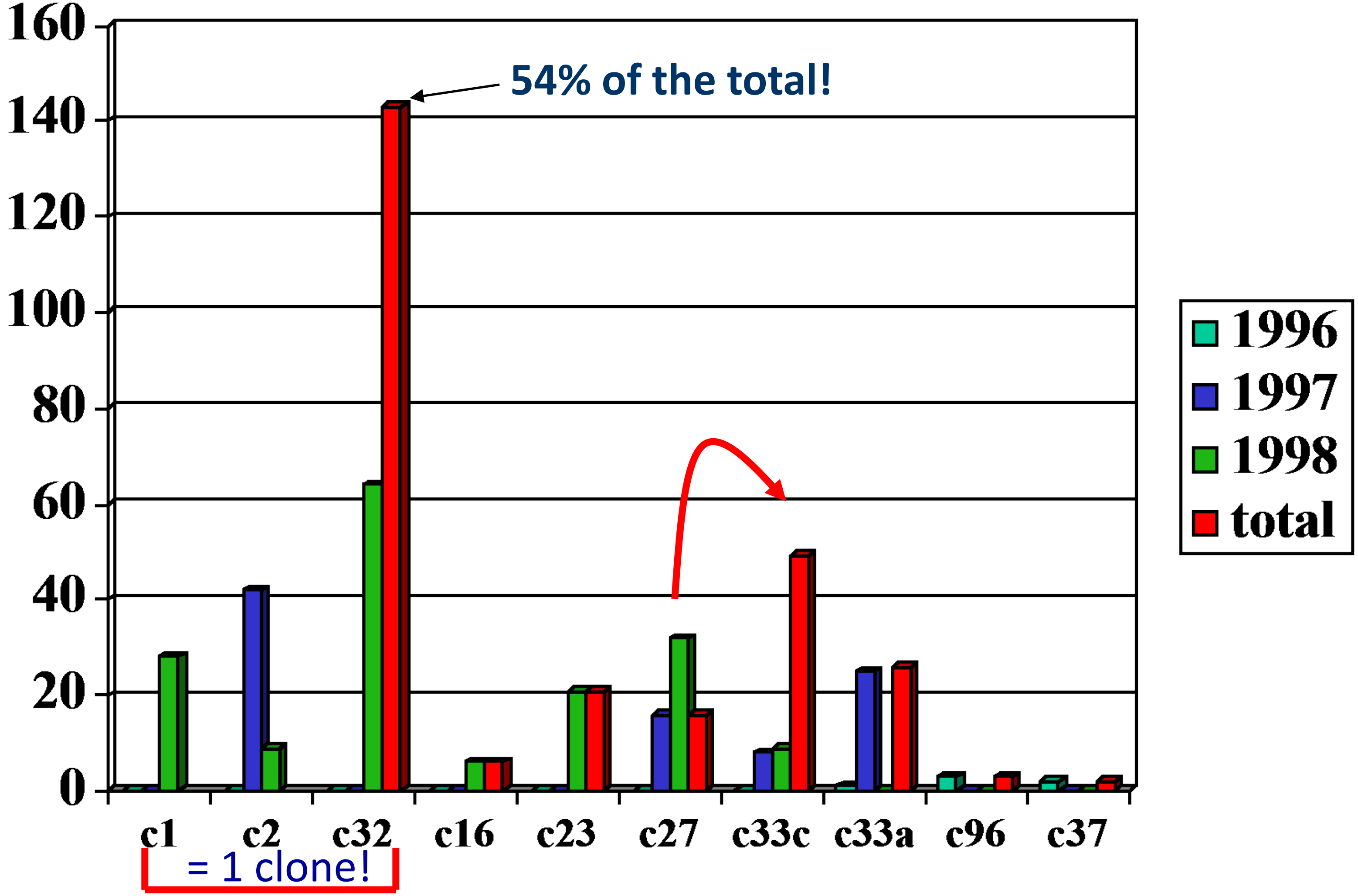
# 1. Genetic fidelity

# of plants of each clone surviving in the Corrigin translocation site in Jan 1999, by year of planting
Total = 260



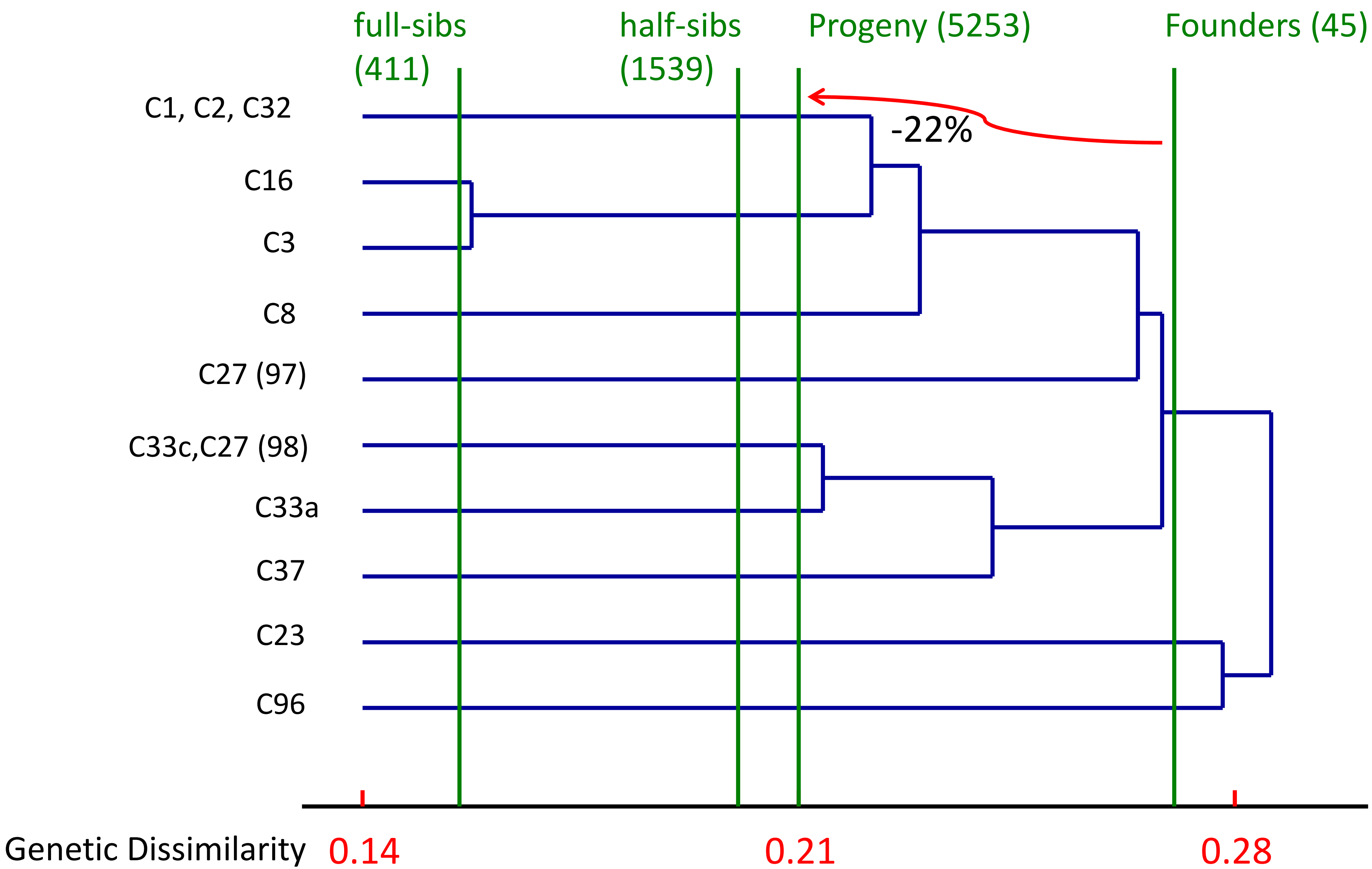
# 1. Genetic fidelity

actual #’s of each clone surviving



# 2. Genetic erosion

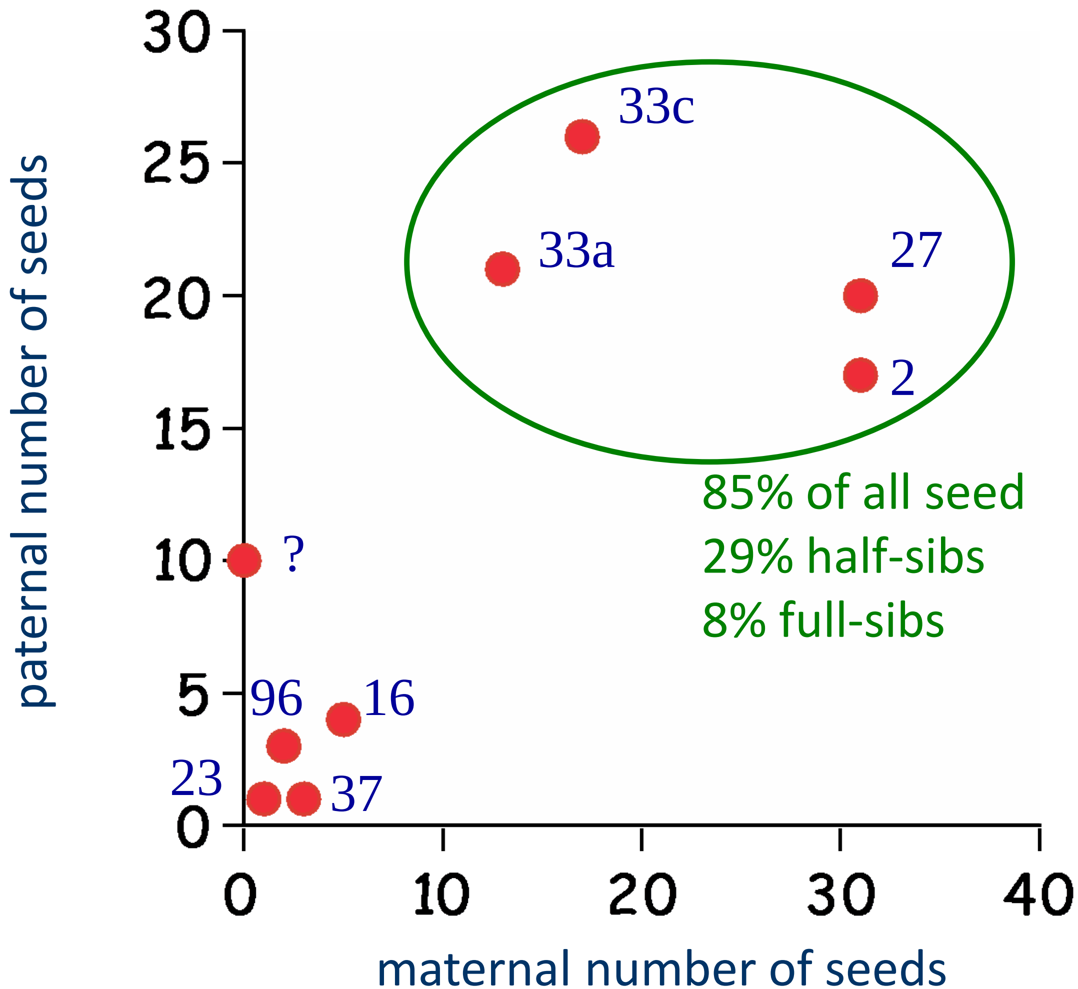
Average pairwise genetic dissimilarity at 143 AFLP markers – 1998 founders (n=10) and their F1 progeny (n=103) in 2000



# 3. Paternity assignment to assess reproductive success

103 Offspring: 102 outcross, 1 self

Maternal and paternal success of each founding clone




# Effective population size ($N_e$) of translocated population in 1999

While n = 260:

1. $N_e = H_0 / 2 ( H_0 - H_1 )$

= **2.5**

2. $N_e = ( Nv_k - 1 ) / [ V_k - 1 + var(k) / V_k ]$

= **1.5**

where Vk = ave # of progeny per individual with variance var (k)

# Strategies to reverse/prevent genetic erosion in translocations

- equalize founder numbers

- avoid population genetic structure in translocations

To avoid selfing, maximise multiple siring and minimise mean kinship of offspring

- increase population size

Add new wild clones as discovered (only source of new alleles)

Use seed, but this creates a size/kinship conflict.

- restore historical processes

Naturally small, ephemeral populations, so restore metapopulation dynamics with multiple pops and genetic connectivity through seed.

- Promote large seed banks and natural recruitment

Natural selection against inbred seed from large, long-lived seed bank

(*Ex-situ* propagation reduces selection against inbred seed).

# *Grevillea scapigera* recovery time-line: a brief history

| | |
|---|---|
| 1954 | • First collection |
| 1986 | • Presumed extinct when only known plant dies. |
| 1987-1992 | • *Ex situ* collection (TC & cryo) established as new wild plants discovered |
| 1994 | • 47 plants from 7 wild populations genotyped with RAPD (Rossetto *et al*. 1995) |
| 1996-1998 | • First transplantation sites established, n = 260 in 1998, from tissue cultured plants of 10 representative clones, as deep seed dormancy prevents germination. All plants irrigated. |
| 1999 | • Seed dormancy broken, germination possible. |
| | • Prolific flowering and seed set, >30,000 seed collected |
| 2000 | • Founders and their offspring genotyped (AFLP), $N_e$ = 2 (Krauss *et al*. 2002) |
| 2000-2007 | • Seedlings propagated at Kings Park from wild pollinated seed sourced from, and planted back into, 3 translocation sites. |
| | • Supplemented with under-represented clones from *ex-situ* collection. |
| 2004-2006 | • Experimental *in-situ* seed germination promoted. |
| 2003- | • Estimated seed production > 1,000,000, into soil-stored seed bank p/a. |
| 2011- | • Natural recruitment in translocation sites: e.g. Corrigin 145 (2011), 147 (2014) |
| 2012 | • 9 new wild collections incorporated into *ex situ* collection, n = 19. |
| 2013/2018 | • Genetic assessment with microsatellites. |

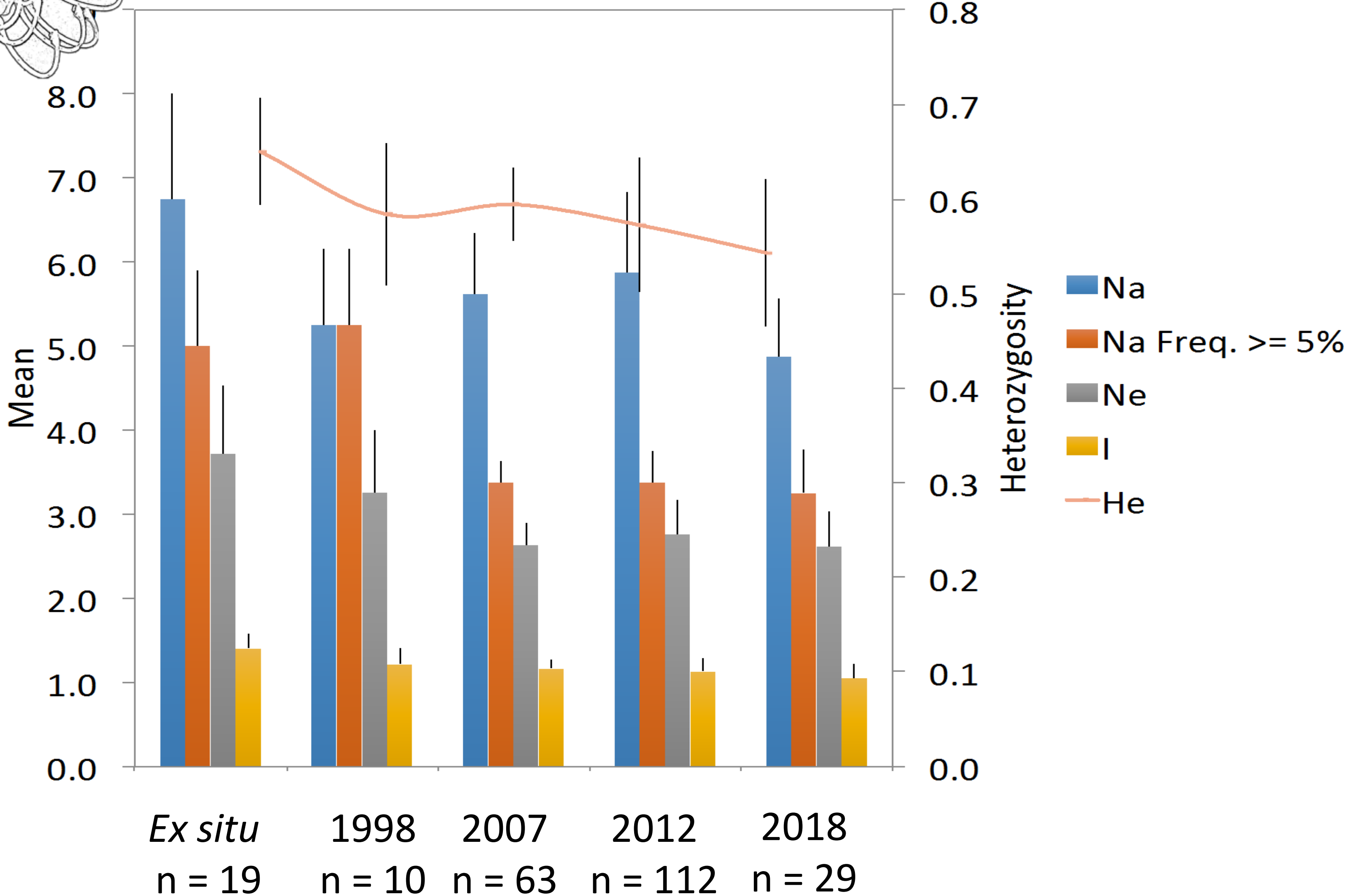
# Genetic assessment of *G. scapigera* translocation F2 and F3 offspring

1. Assess genetic variation and fidelity of the 2012 *ex situ* collection
   ($N$ = 19 MLGs from 24 accessions)

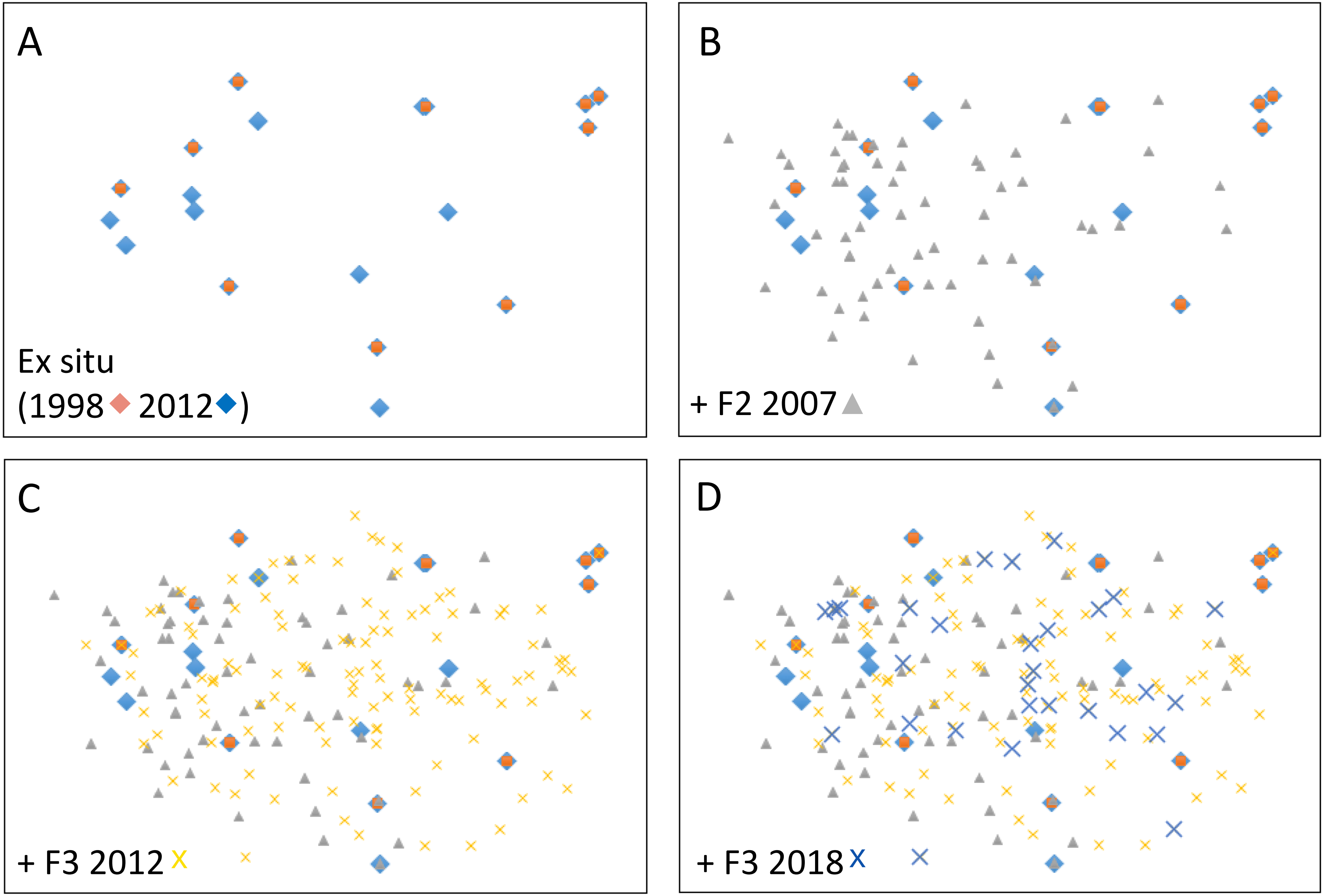
2. Assess genetic erosion by comparing genetic variation between
   F0 (1998; n = 10), F2 (2007; n = 63), and F3 (2012/2018; n = 112/29)

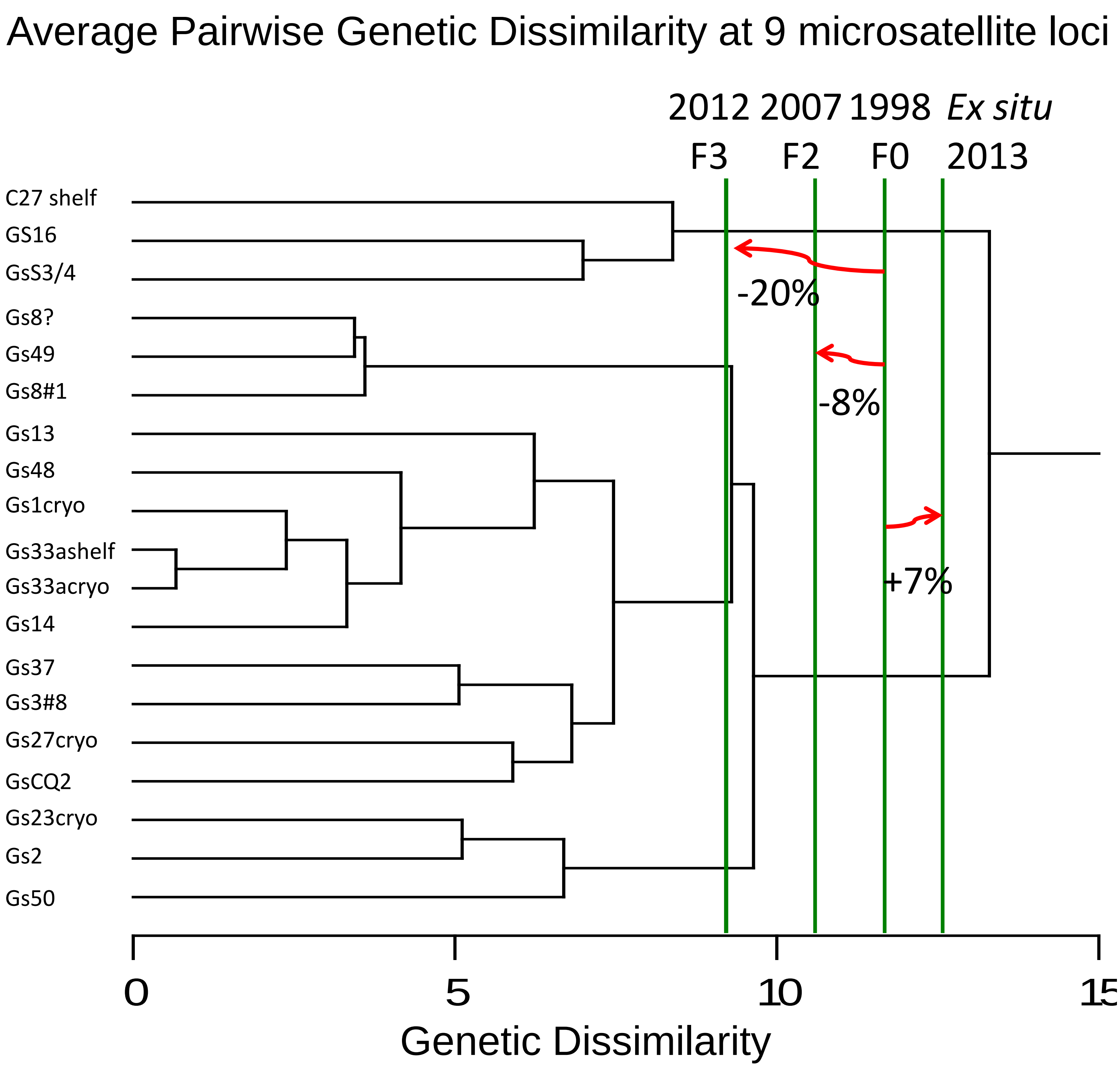
3. Assess inbreeding depression

Microsatellite allelic diversity in *G. scapigera*: 9 loci
*ex situ* collection 2012,
translocation: 1998 (F0), 2007 (F2), 2012 (F3), 2018 (F3)



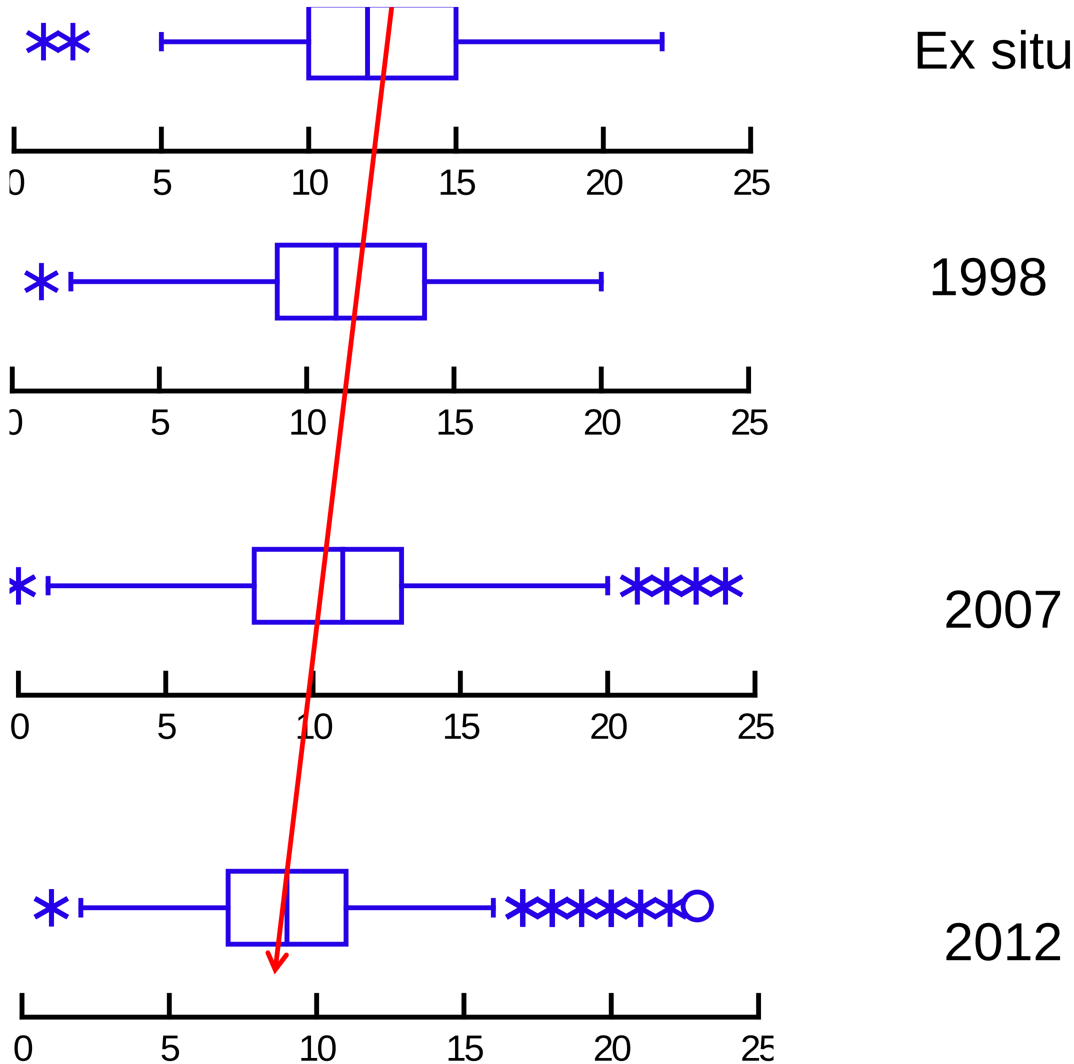
Ordination of genetic variation in *ex situ* collection and translocation site (1998-2018)



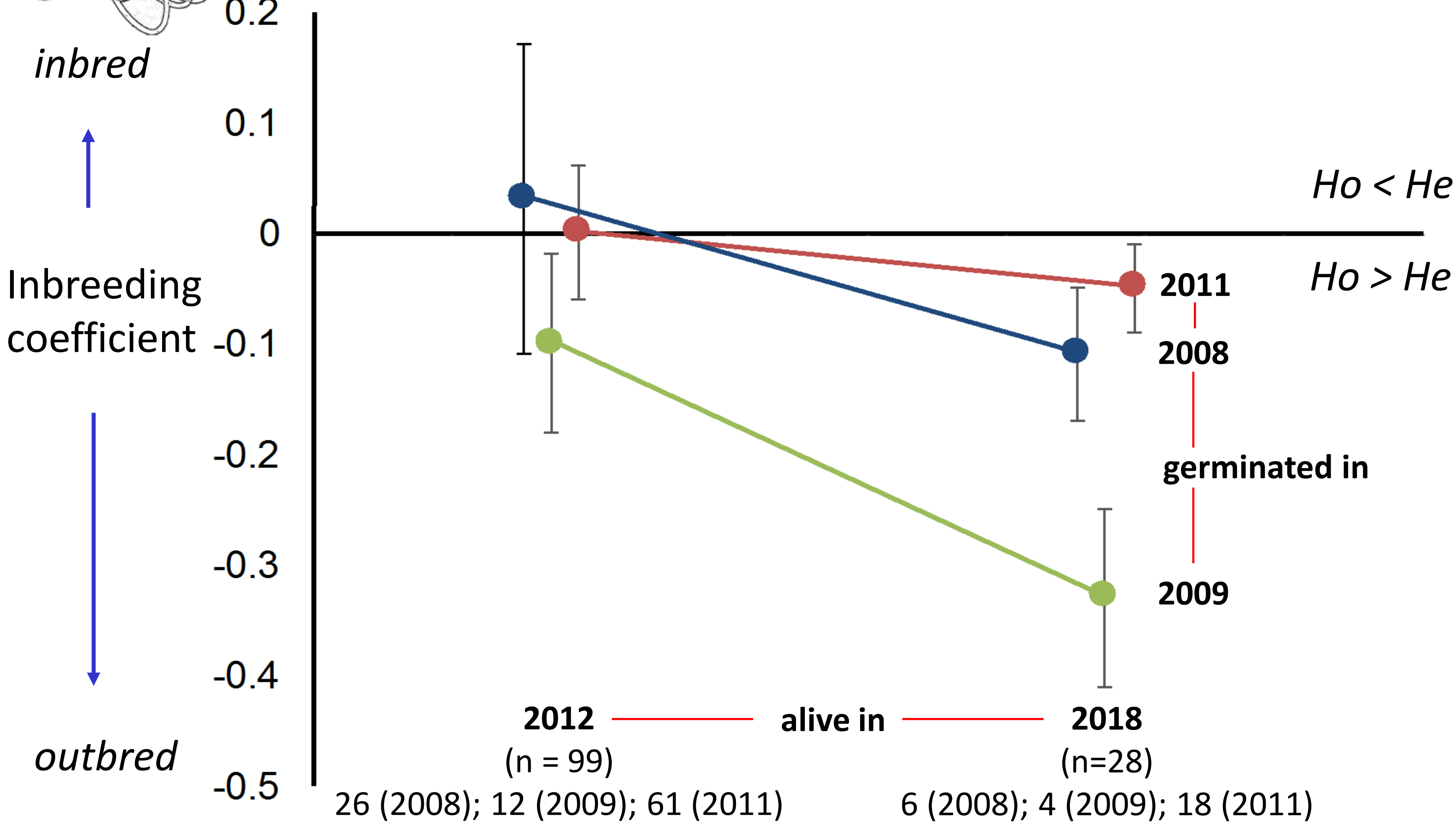


Average Pairwise Genetic Dissimilarity at 9 microsatellite loci
2012 2007 1998 *Ex situ*
F3 F2 F0 2013
C27 shelf
GS16
GsS3/4
Gs8?
Gs49
Gs8#1
Gs13
Gs48
Gs1cryo
Gs33ashelf
Gs33acryo
Gs14
Gs37
Gs3#8
Gs27cryo
GsCQ2
Gs23cryo
Gs2
Gs50
-20%
-8%
+7%
0
5
10
15
Genetic Dissimilarity

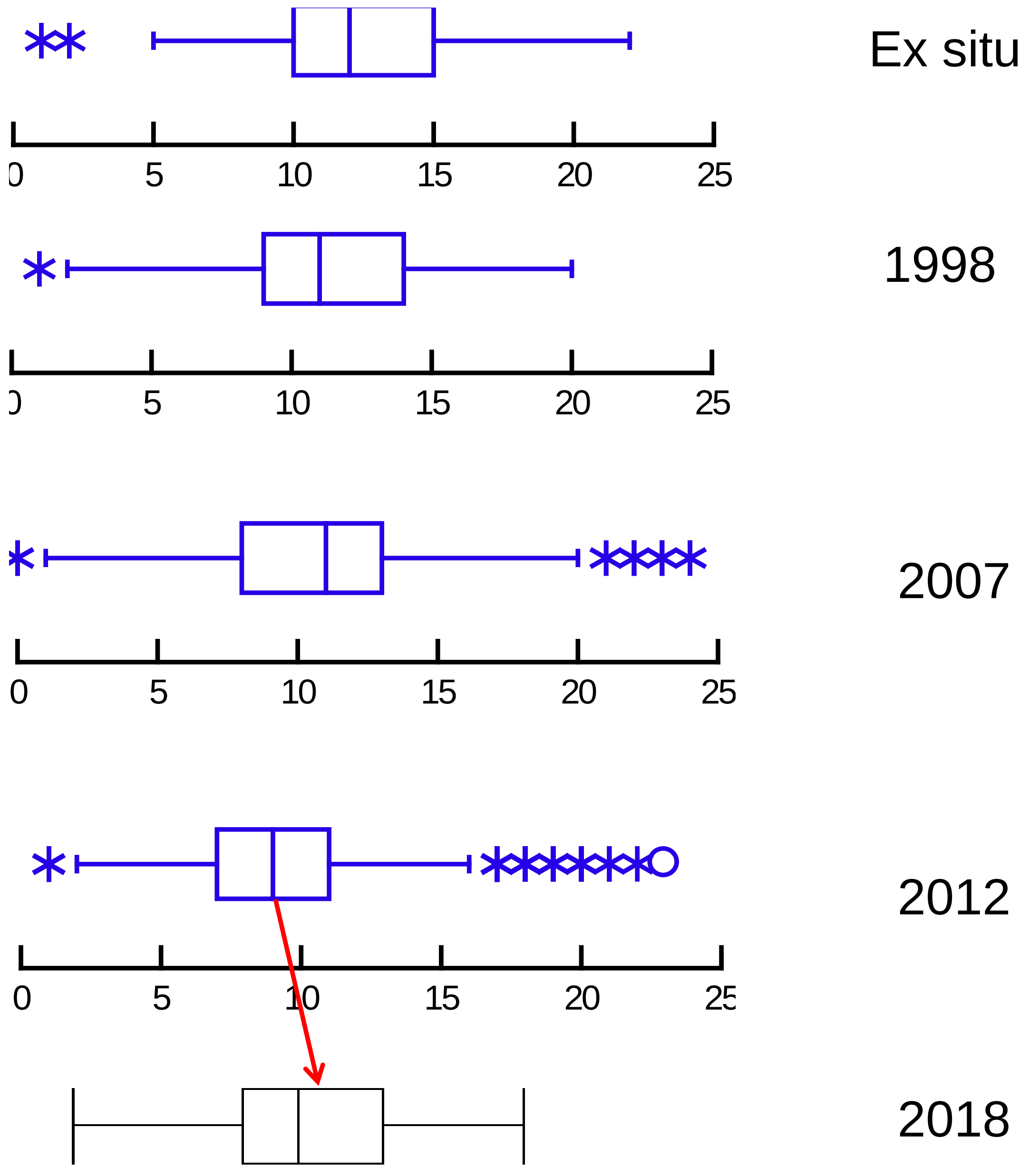
# 20% decline in mean pairwise Genetic Dissimilarity in 3 generations



Evidence for heterozygote advantage in natural recruits surviving at *G. scapigera* translocation site in 2018



Increase in Pairwise Genetic Dissimilarity in 2018 survivors



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## Conclusions:

- Genetic erosion stabilised post-2007.

- Pairwise genetic dissimilarity declined (1998-2012), rebounded with heterozygote advantage (2012-2018).

- Although mean dissimilarity decreased, range increased – (e.g. 23% of 2012 cohort more outbred than the mean for 1998).

- Mass flowering + pollinator services = very high seed set (>1M/year).

- Therefore, alot of outbred seed to survive the inbreeding depression filter. Thresholds?

- Benefits to be gained from targeting relatively outbred individuals – promote wide outcrossing

# Keys to successful translocation of *Grevillea scapigera*

- a 30-year journey
- mass flowering of hundreds of plants in multiple sites
- abundant insect pollinators
- mass seed set
- long-lived high-viability seed bank
- natural recruitment
- genetics managed for high diversity
- multiple secure sites = metapopulation
- floristically diverse, fenced, weed-free sites
- apparently now self sustaining
- *ex situ* collections (seed, tissue culture, cryo)
- underpinned by research
- dedicated volunteers

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