BIOL334 Conservation & Ecological Genetics

LECTURE 9: MUTATION, MIGRATION & SELECTION II

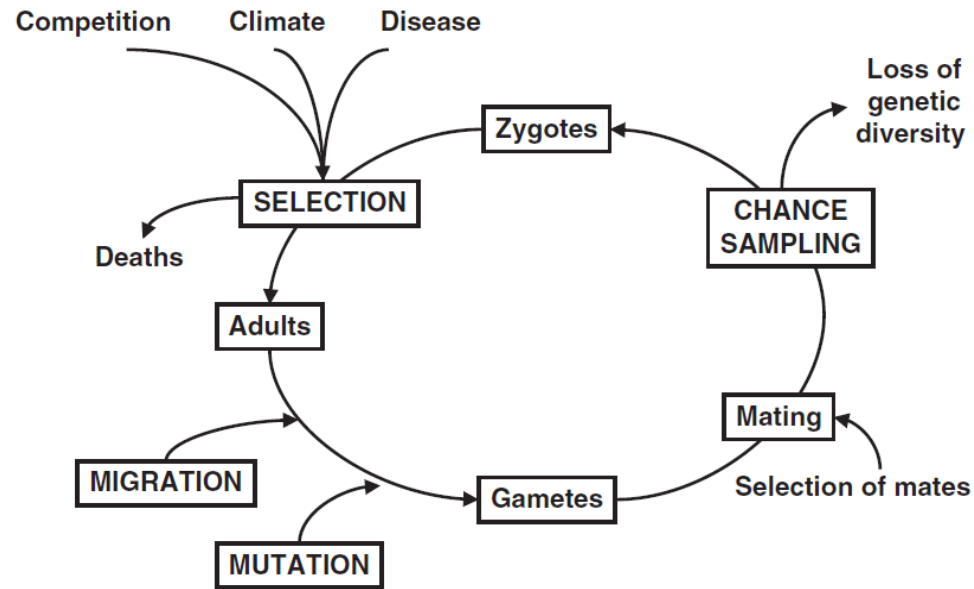MACQUARIE University

Assignment #1 grades on iLearn

Continuing from Lecture 8...

Fig. 6.1 An evolving population as a complex system.
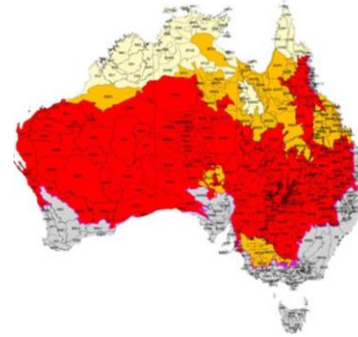
Genetics & Population size

LARGE vs SMALL POPS

<u>Large N</u>

High levels of V_G
    = "variant" alleles
    = **resilience** to change

High mutation potential
    = **NEW** V_G

Power for selection (all forms)
    = **adaptive potential**

Rabbit
N~10 Billion (1920)

Water buffalo
N~100,000

Genetics & Population size

LARGE vs SMALL POPS

Large N

High levels of V_G
    = "variant" alleles
    = **resilience** to change

High mutation potential
    = **NEW** V_G (over time)

Power for selection (all forms)
    = **adaptive potential**

Small N

1. Low V_G
= **vulnerable** to change

2. few new mutations, **BUT** existing mutations exposed

3. **Selection** overpowered by **genetic drift...**

Genetics & Population size

GENETIC DRIFT

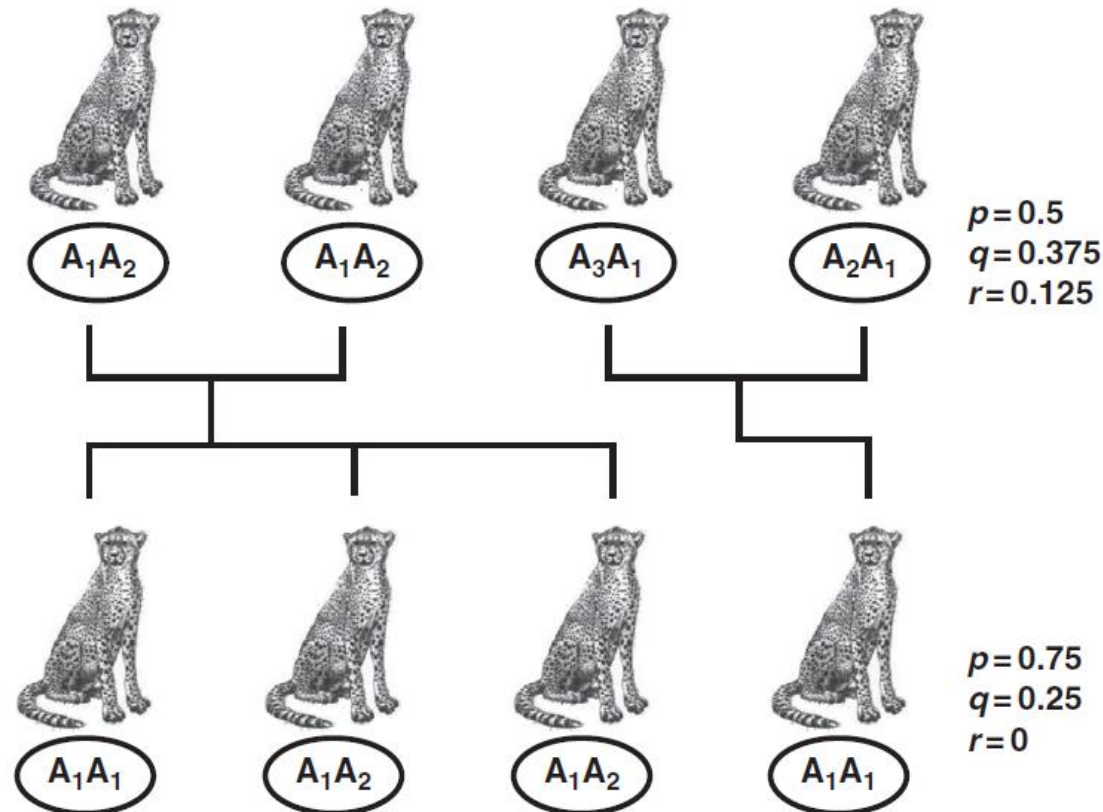Random **luck of the draw**…

Chance decides allele frequencies from one generation to the next;

These effects accumulate – once a rare gene is lost, it is gone forever!

Causes small populations to evolve in 'random' directions – i.e. to **drift…**
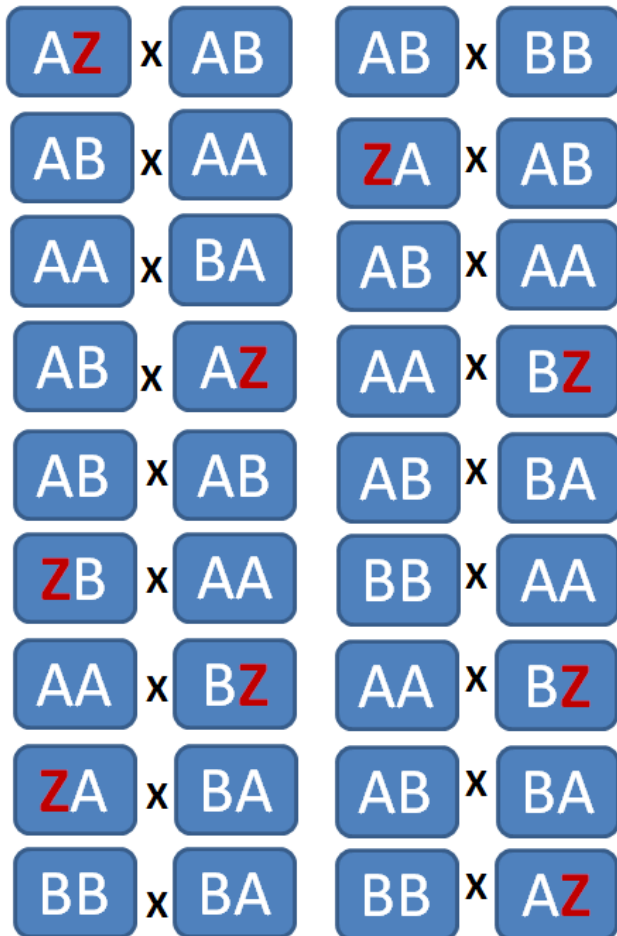
Loss of rare alleles via drift

Fig. 8.1 Genetic drift in allele frequencies in a small population of cheetahs. p, q and r are the frequencies of alleles A_1, A_2 and A_3, respectively. Allele A_3 is lost by chance. Further, the frequencies of A_1 and A_2 change from one generation to the next, with A_1 rising and A_2 falling.

Genetics & Population size

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GENETIC DRIFT

Population N=36

AZ x AB		AB x BB	
AB x AA		ZA x AB	
AA x BA		AB x AA	
AB x AZ		AA x BZ	
AB x AB		AB x BA	
ZB x AA		BB x AA	
AA x BZ		AA x BZ	
ZA x BA		AB x BA	
BB x BA		BB x AZ	

Allele frequencies

A: 36 (50.0%)
B: 27 (37.5%)
Z: 9 (12.5%)
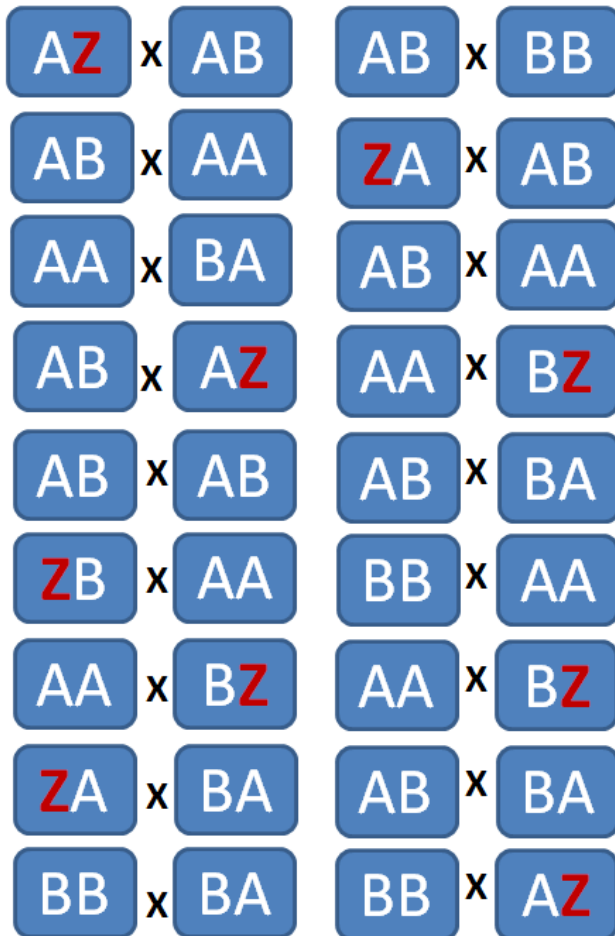
Gen +1

Nine 50:50 chances of retaining the **Z** allele

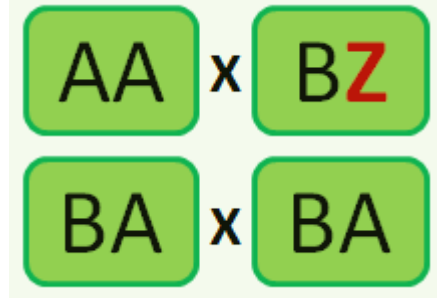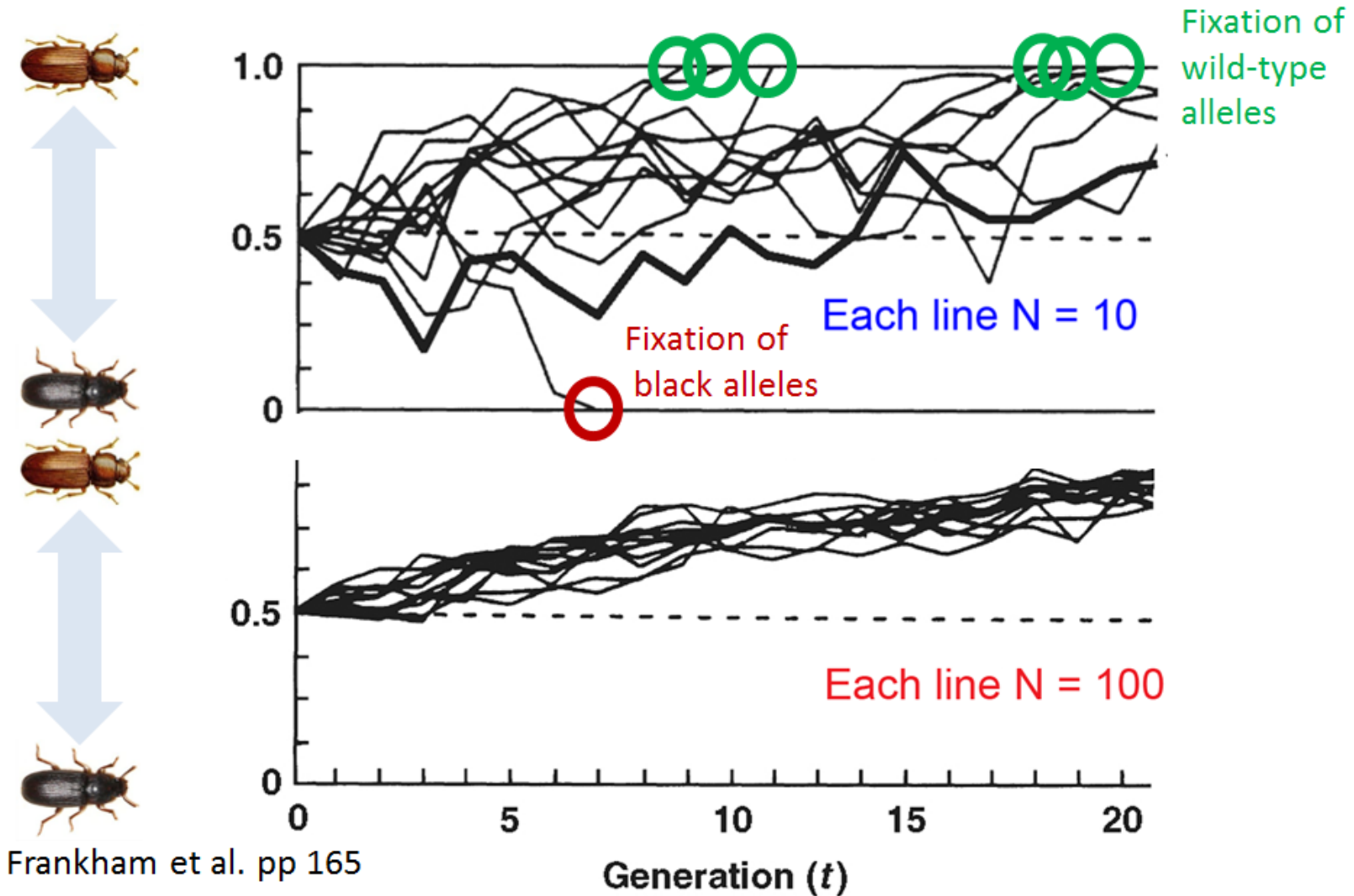# Genetics & Population size

GENETIC DRIFT

Population N=36

AZ x AB	AB x BB
AB x AA	ZA x AB
AA x BA	AB x AA
AB x AZ	AA x BZ
AB x AB	AB x BA
ZB x AA	BB x AA
AA x BZ	AA x BZ
ZA x BA	AB x BA
BB x BA	BB x AZ

Allele frequencies

A: 36 (50.0%)
B: 27 (37.5%)
Z: 9 (12.5%)

Gen +1 →

Nine 50:50 chances of retaining the **Z** allele

AA x BZ
BA x BA

N = 4 (8 alleles)
A: 8 (50.0%)
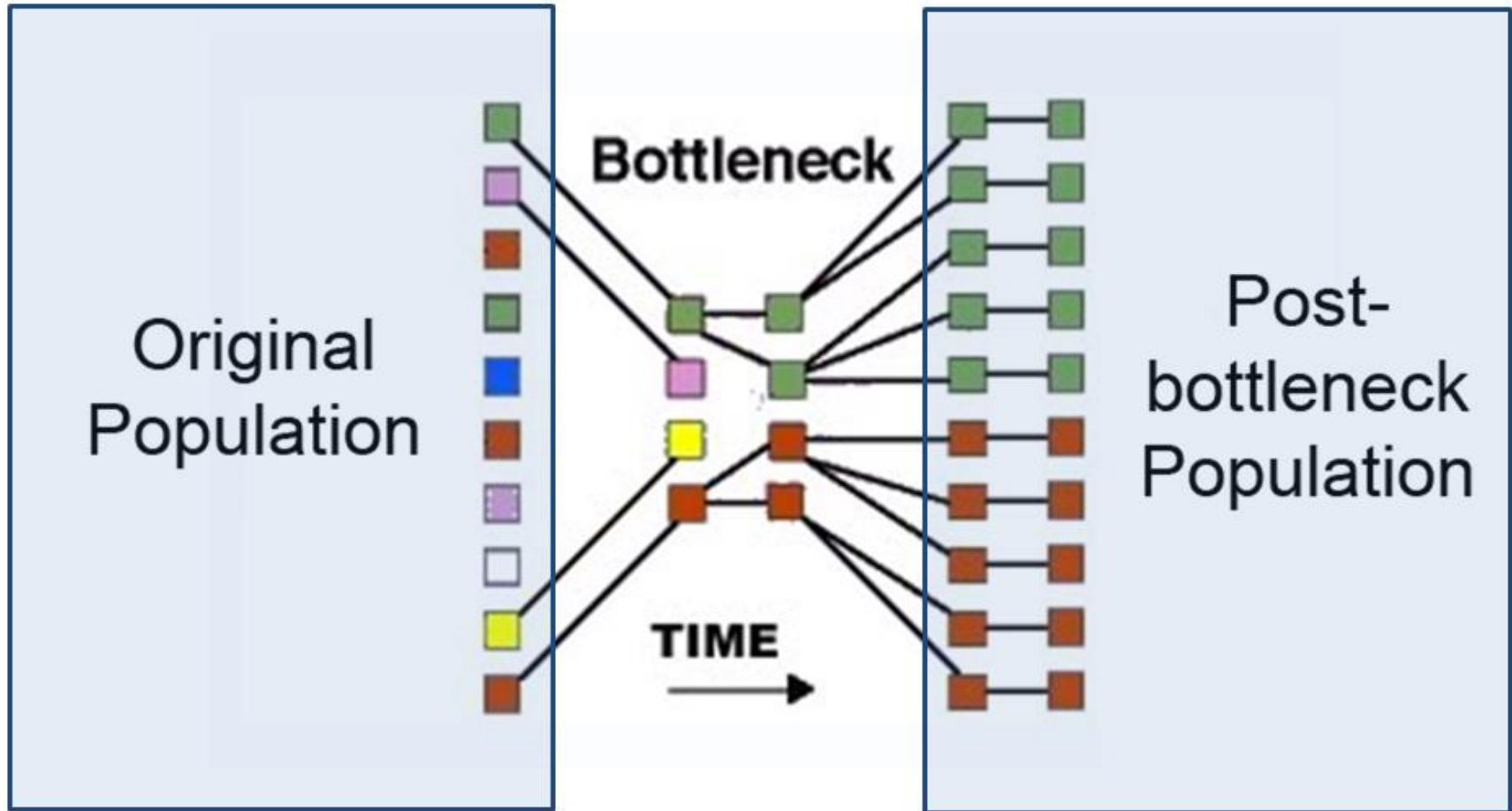B: 7 (37.5%)
Z: 1 (12.5%)

ONE 50:50 chance of retaining the **Z** allele
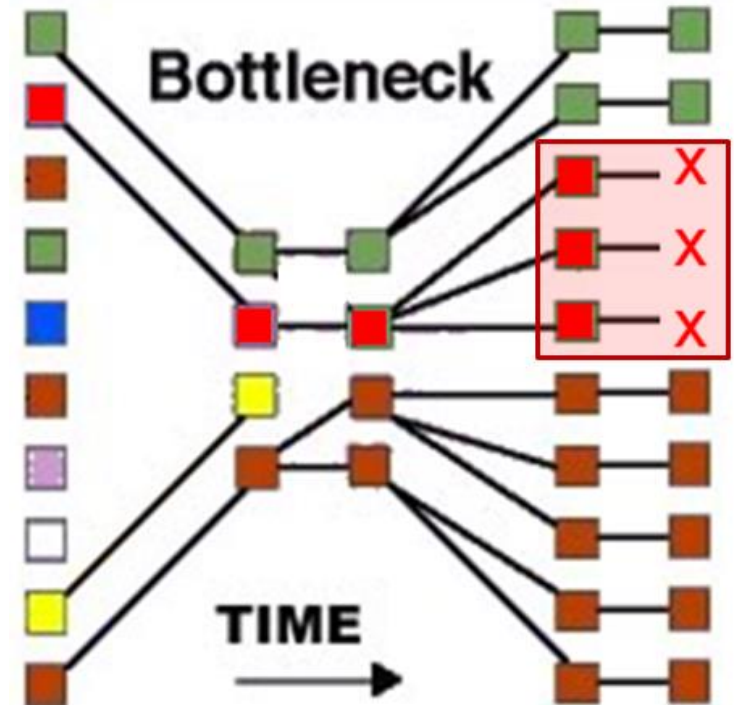
Genetics & Population size

Frankham et al. pp 165

Genetics & Population size

BOTTLENECKS IN THE PAST…
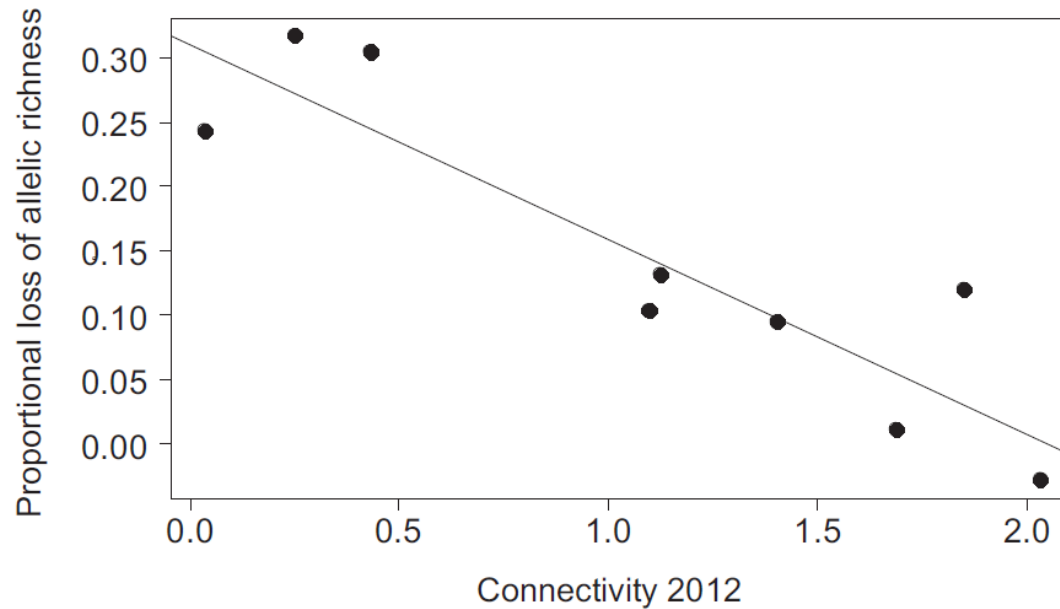
Genetics & Population size

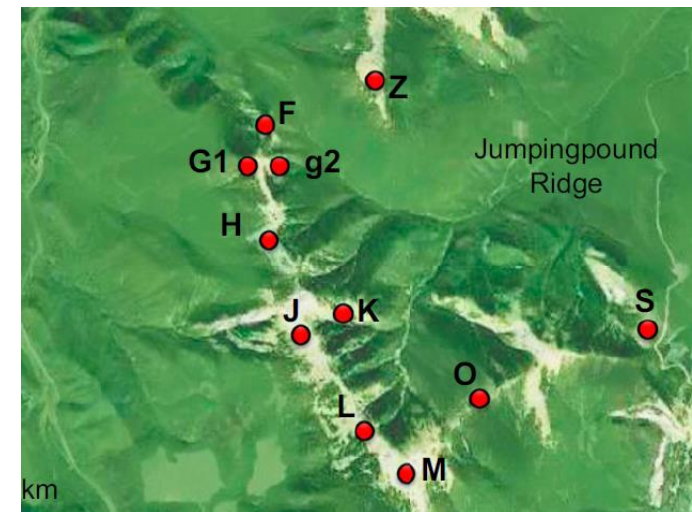SUBHEADING

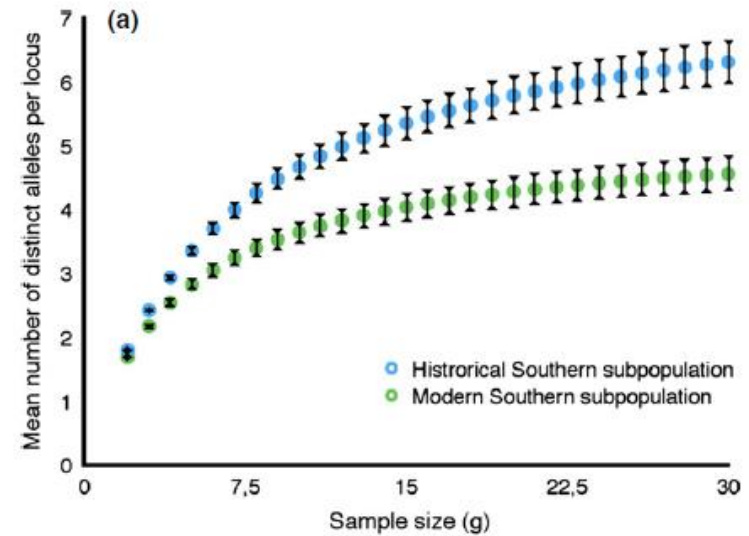**Northern Elephant Seal:**
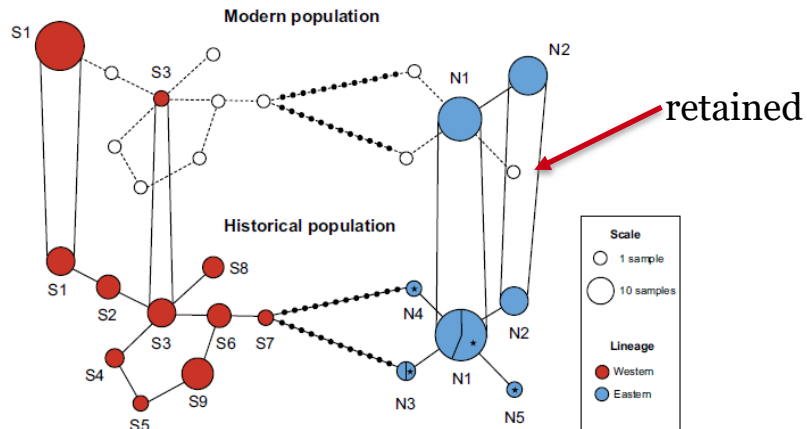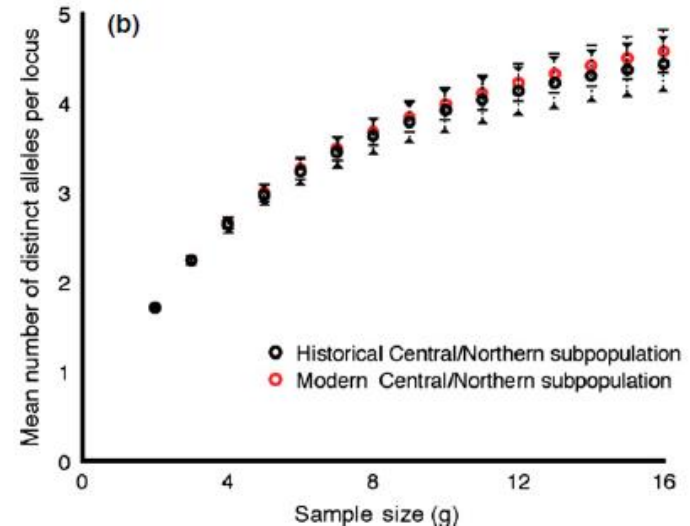20-30 individuals in late 1800s
>175,000 now

Importance of connectivity

Jangjoo et al. 2016 PNAS

Magnitude of bottleneck effects vary across a distribution

retained

Xenidoudakis et al. 2015 Mol Ecol

Genetics & Population size
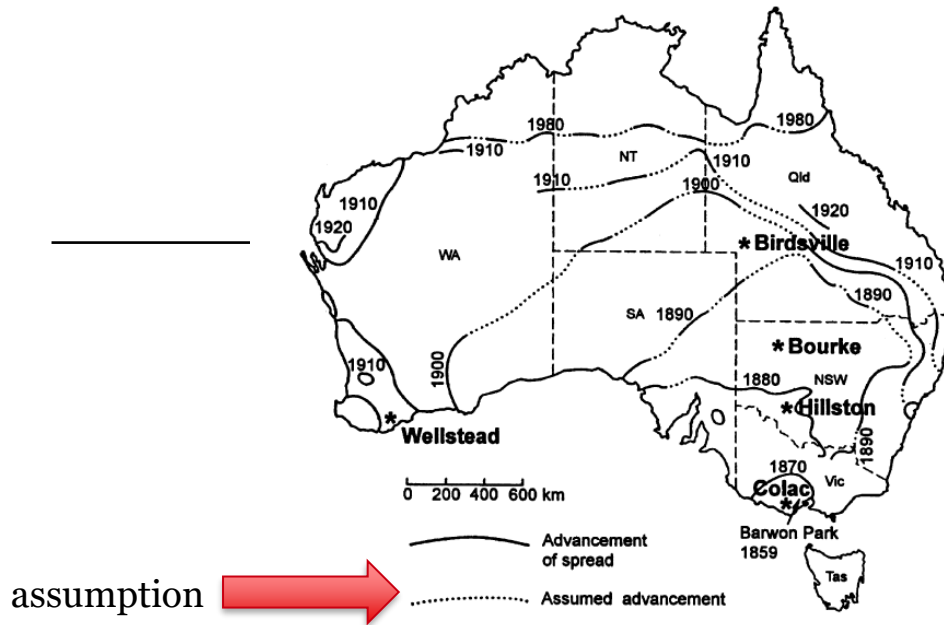
LARGE vs SMALL POPS

Original release by Thomas Austin in 1859 (Vic).

Austin hunted rabbits on his weekends in England. Upon arriving in Australia, Austin requested **12 grey rabbits, 5 hares, 72 partridges and some sparrows** to fuel his hobby.
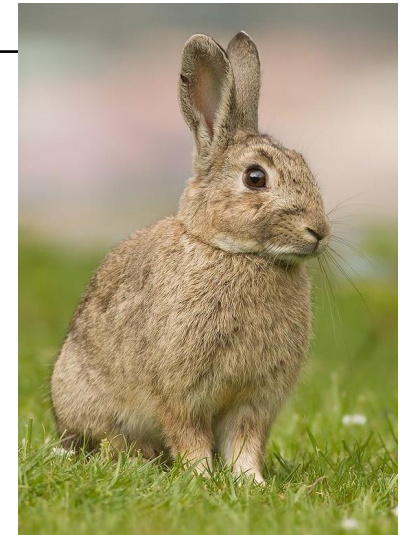
His nephew sent **grey & domestic rabbits** to meet this order.

Many other releases of rabbits following Austin.

Fig. 1 The summary spread of the rabbit over mainland Australia (after Stodart & Parer 1988). Map also shows geographical location of sample sites.

assumption

No sequential loss in variation?

Table 1 Estimates of genetic diversity (Mean ± SE) for rare alleles (rA; = 0.05 frequency), number of alleles (A), observed and expected heterozygosity (H_O and H_E) and unique alleles (uA) across all loci for all countries (bold) and across individual Australian populations. Results of heterozygosity excess test (HET), mode shift and M ratio analysis where '−' indicates no significant reduction in N_e

| Sample location	n	rA	A	H_O	H_E	uA	HET TPM	Mode shift	M ratio§ (M)
Spain†	110	4.10 ± 0.32	9.62 ± 0.39	0.66 ± 0.03	0.79 ± 0.02	4.86 ± 0.70	—	—	—
France†	257	1.23 ± 0.20	5.03 ± 0.26	0.63 ± 0.03	0.64 ± 0.03	0.86 ± 0.26	—	—	0.477–0.554*
England‡	340	1.68 ± 0.22	5.05 ± 0.29	0.44 ± 0.06	0.64 ± 0.04	1.00 ± 0.60			
Australia	252	0.97 ± 0.17	5.03 ± 0.21	0.66 ± 0.02	0.67 ± 0.01	0.29 ± 0.18			
Wellstead	49	1.84 ± 0.55	5.57 ± 0.61	0.64 ± 0.06	0.65 ± 0.03	0.71 ± 0.42	—	—	0.519*
Birdsville	49	1.14 ± 0.26	5.00 ± 0.53	0.64 ± 0.04	0.66 ± 0.03	0.43 ± 0.20	—	—	0.514*
Bourke	47	1.00 ± 0.22	4.86 ± 0.26	0.69 ± 0.04	0.68 ± 0.02	0.14 ± 0.14	—	—	0.491*
Hillston	57	0.43 ± 0.30	5.14 ± 0.46	0.72 ± 0.04	0.72 ± 0.03	0.14 ± 0.14	*	—	0.525*
Colac	50	0.43 ± 0.20	4.43 ± 0.30	0.63 ± 0.05	0.65 ± 0.01	0	*	*	0.437*

†Data obtained from Queney et al. (2001).
‡Data based on sat5, sat7 and sat8 from Surridge et al. (1999).
§Significance based on $M < M_C$ where M_C = 0.712–0.828; *$P < 0.05$.
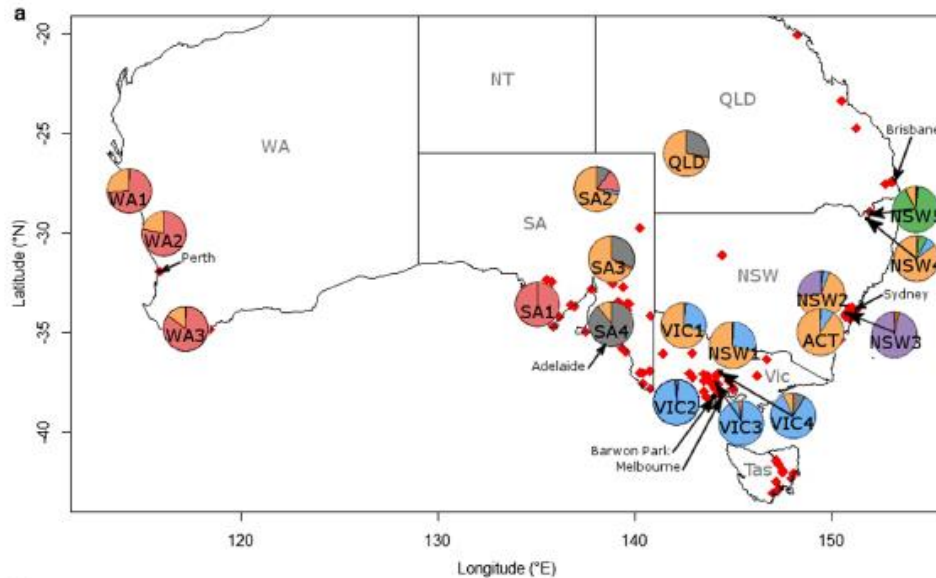
Zenger et al. 2003 Mol Ecol

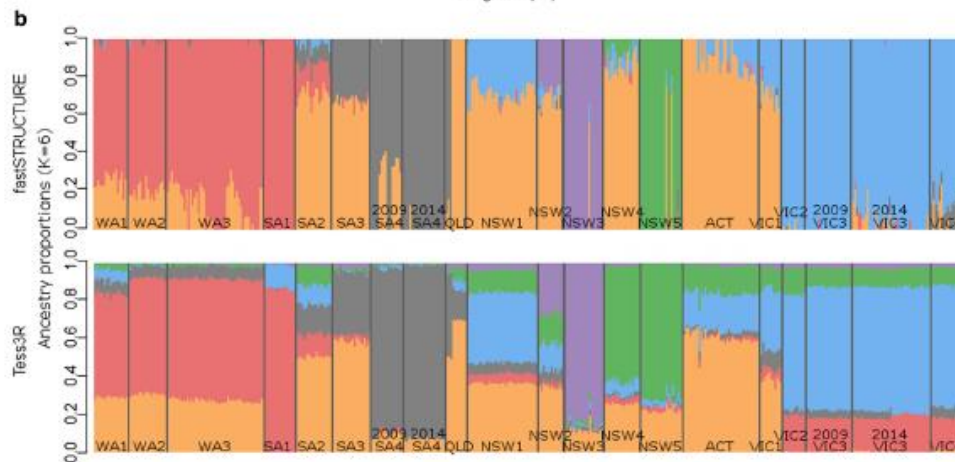# Lower Australian Vg supported by large scale SNP analysis
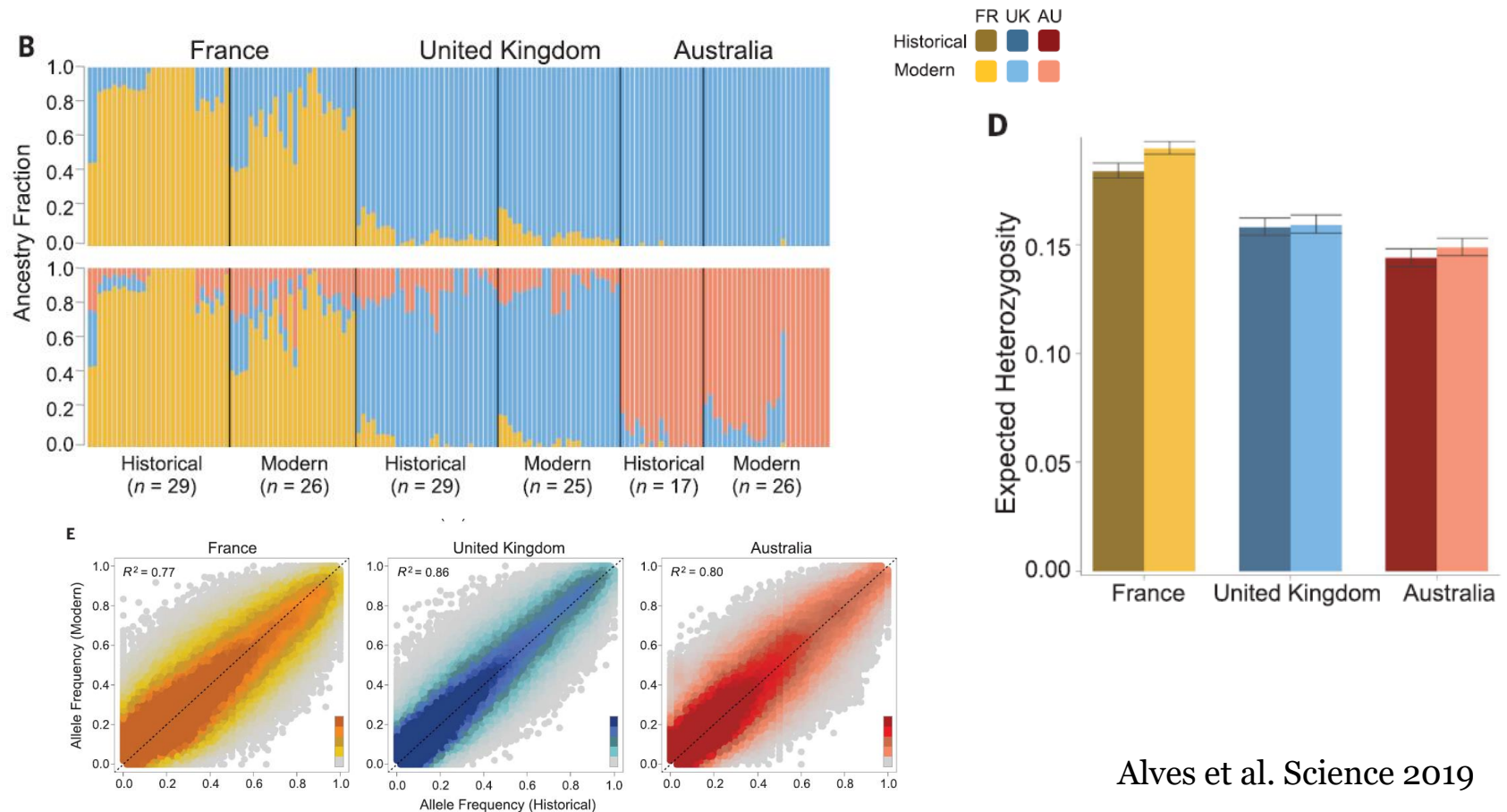
Alves et al. Science 2019
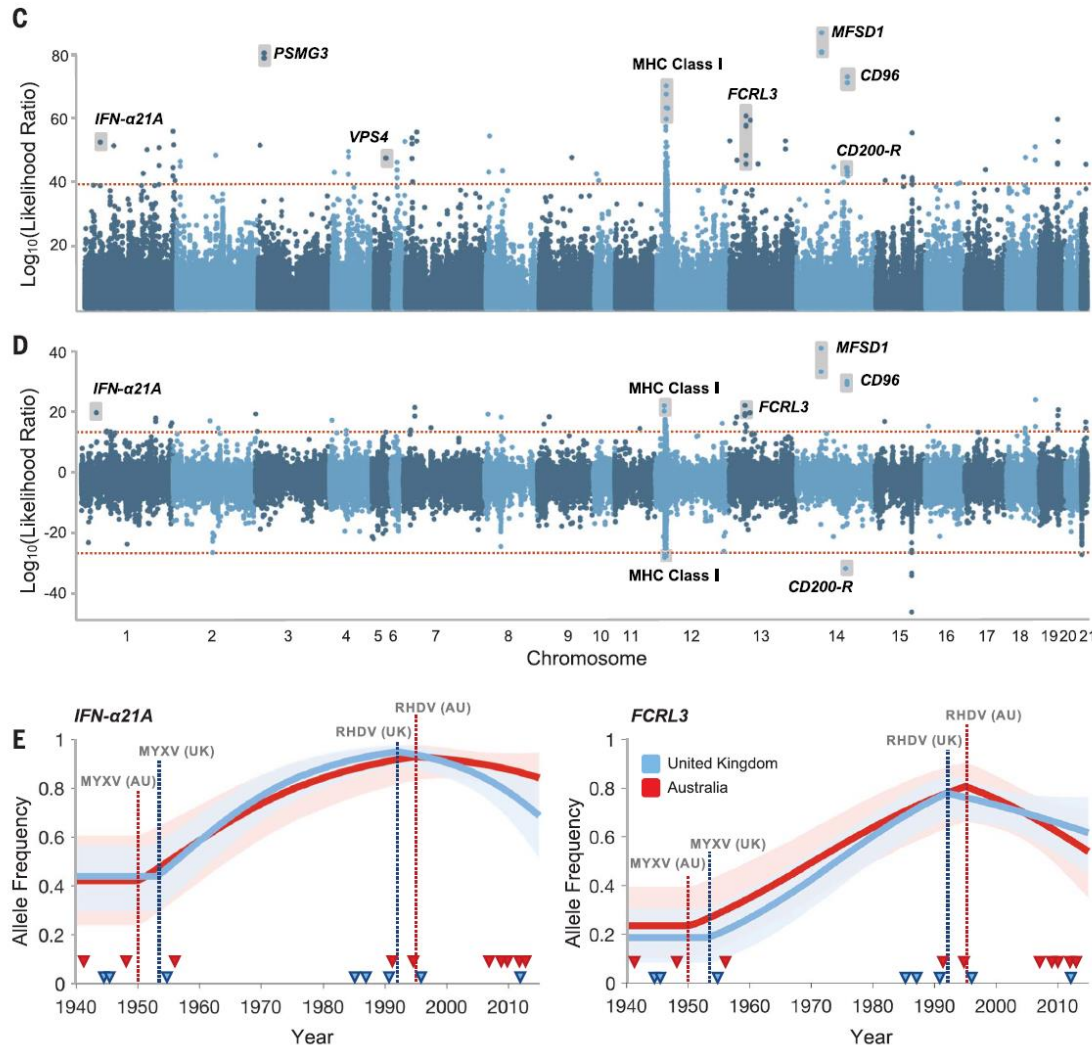
Multiple Introductions

~ 40000 SNPs

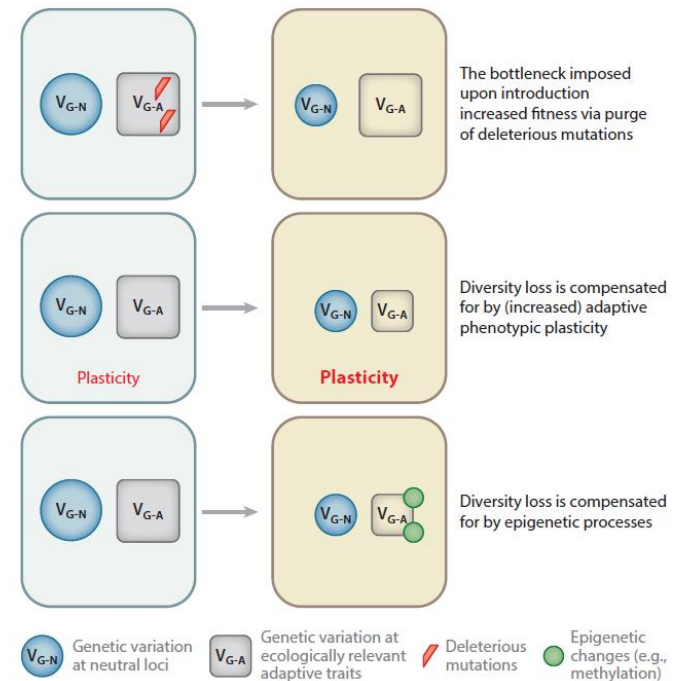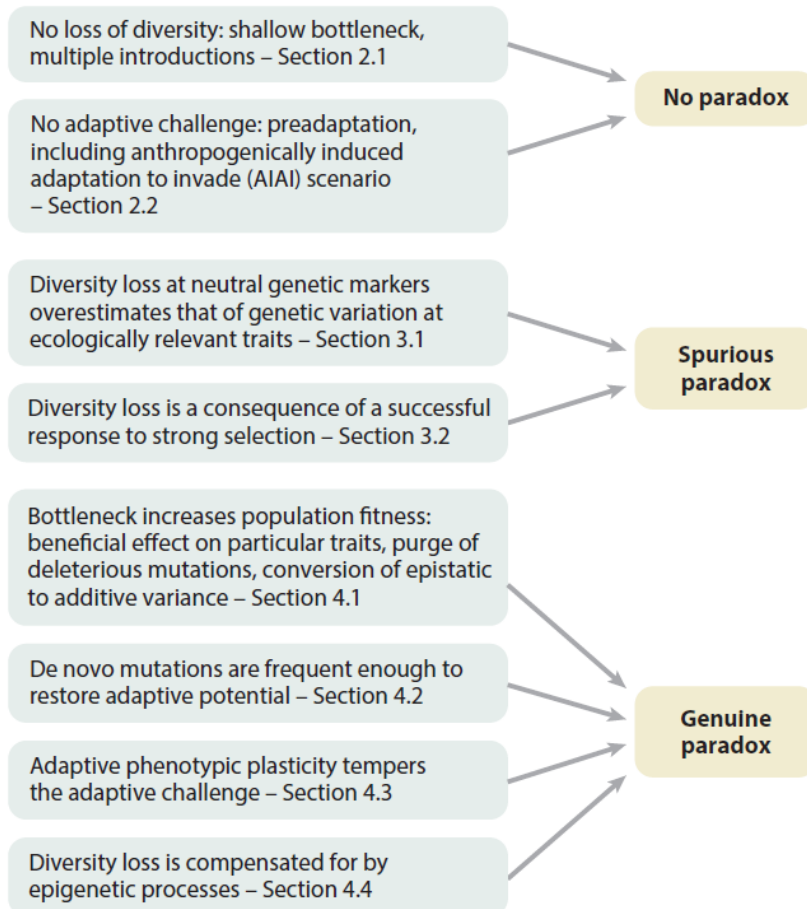Iannella et al.
Biological Invasions 2019

Enough standing genetic variation for evolution

Alleles selected for by myxoma virus

Decrease in Myxoma virulence

Invasive species success- a genetic paradox?

Estoup et al. 2016 Annual Reviews

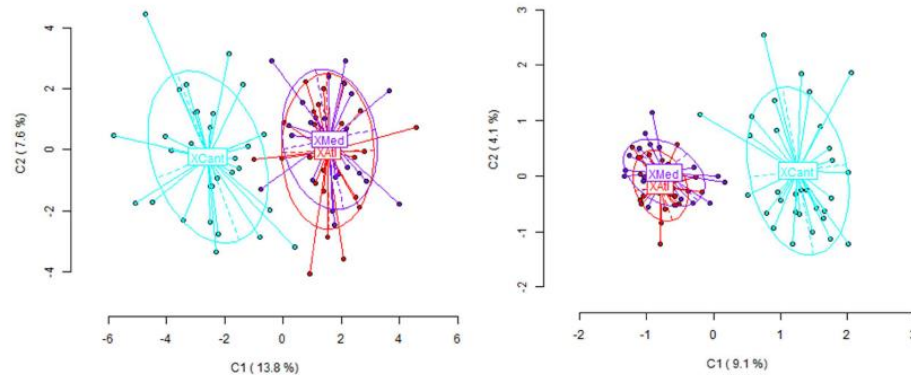# Decrease in methylation expected in new invasives

Figure 2. Two-dimensional visualization of the Principal Component Analysis (PCoA) of the detected methylation patterns in *Xenostrobus securis*, with the epigenetic variation (methylation-sensitive loci) on the left and the genetic variation (no methylated loci, NML) on the right. The individuals of each population are represented by the acronyms XAtl, XCant and XMed for the Atlantic international port, Cantabric international port and Mediterranean lagoon populations respectively.
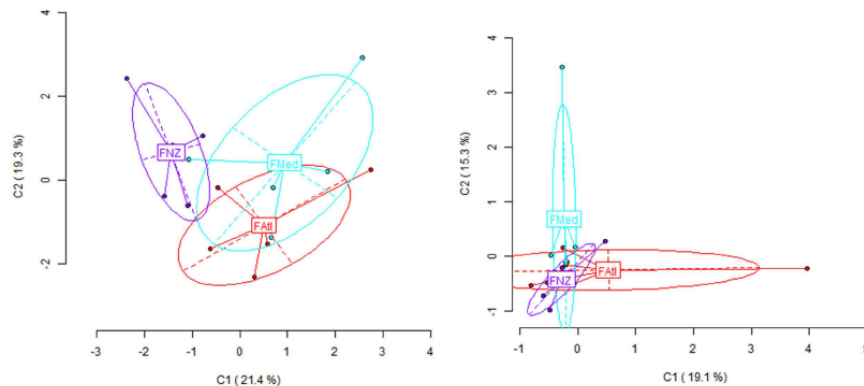
New

old

Figure 4. Two-dimensional visualization of the Principal Component Analysis (PCoA) of the detected methylation patterns in *Ficopomatus enigmaticus*, with the epigenetic variation (methylation-sensitive loci) on the left and the genetic variation (no methylated loci, NML) on the right. Each population is represented by the acronyms FNZ, FCant and FMed for samples, respectively, from the international Napier port in New Zealand, Cantabric fishing port and Mediterranean lagoon locations.

B

Next Lecture

Inbreeding