

Inbreeding

BIOL3110 Conservation and Evolutionary Genetics



Invasion & Population Genetics

ISLAND *ANOLIS* LIZARDS



Invasion & Population Genetics

ISLAND *ANOLIS* LIZARDS



- Bahamas: Great Exuma Island + archipelago

Invasion & Population Genetics

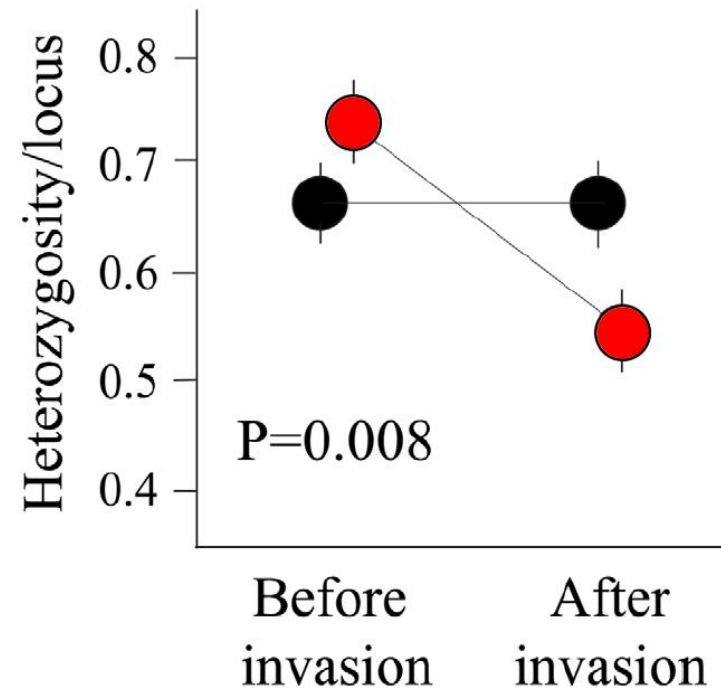
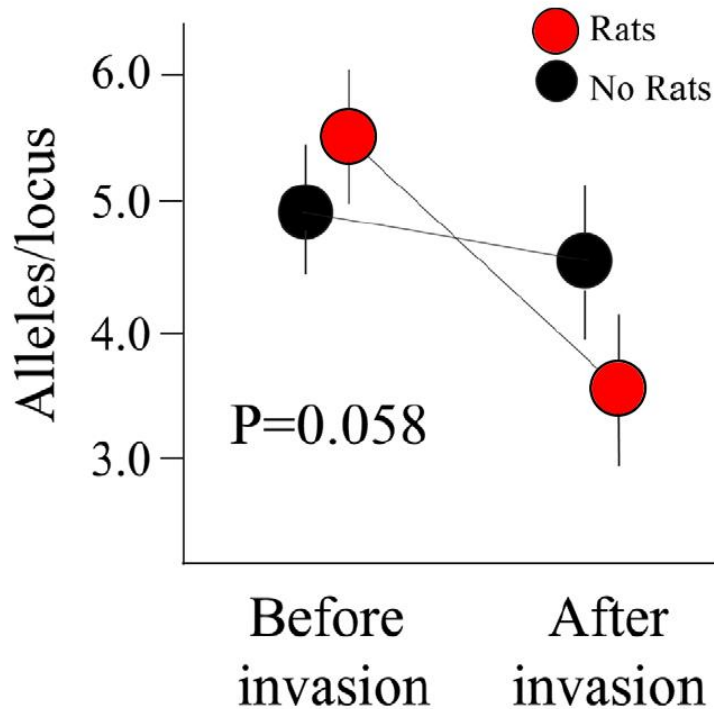
ISLAND *ANOLIS* LIZARDS



- Rats **infested** 1 island for 12-mo, then exterminated, leaving 13 individuals
- Nearby **non-infested** island served as a control

Invasion & Population Genetics

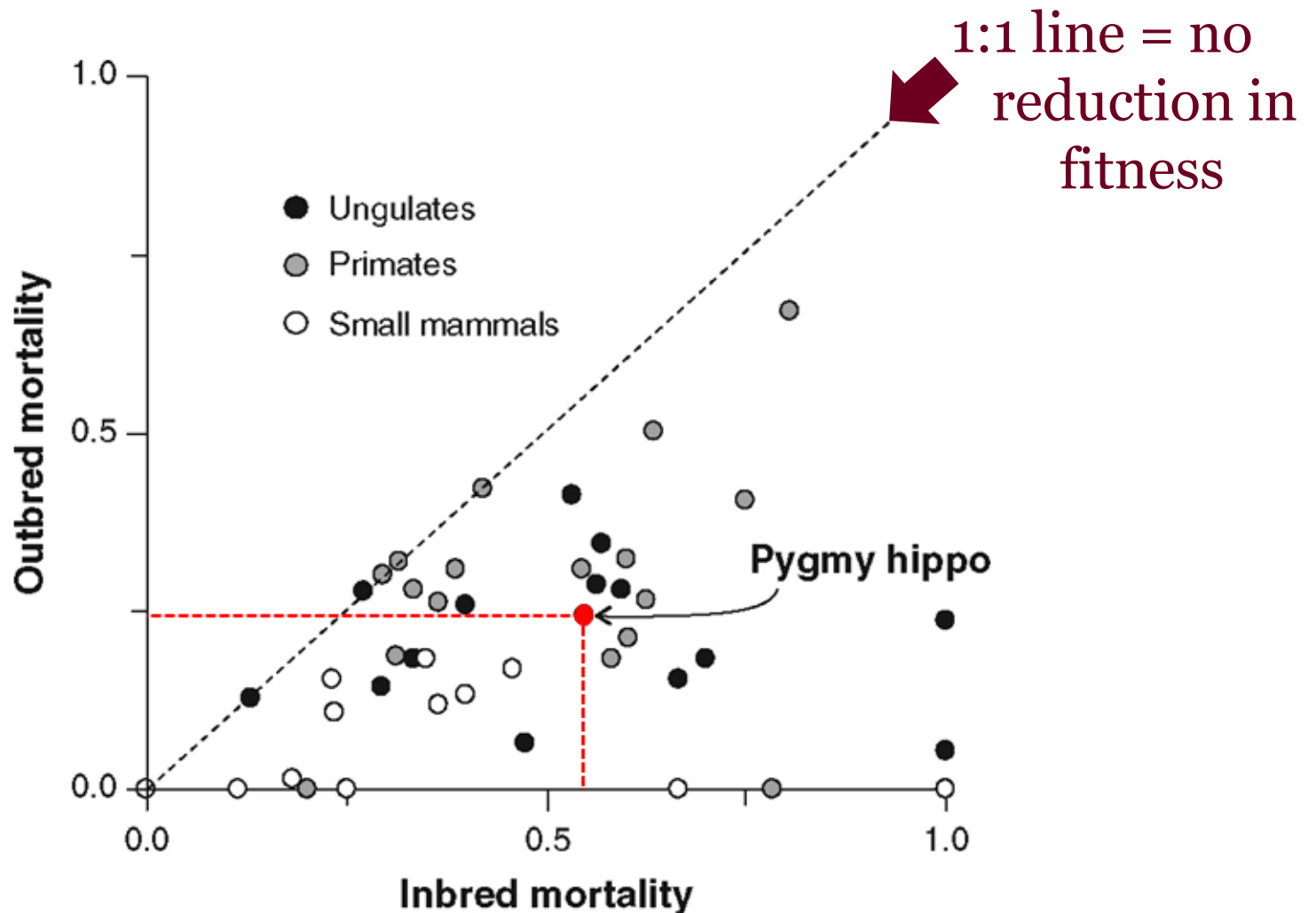
ISLAND *ANOLIS* LIZARDS



- Significant reductions in V_G post-population “recovery”

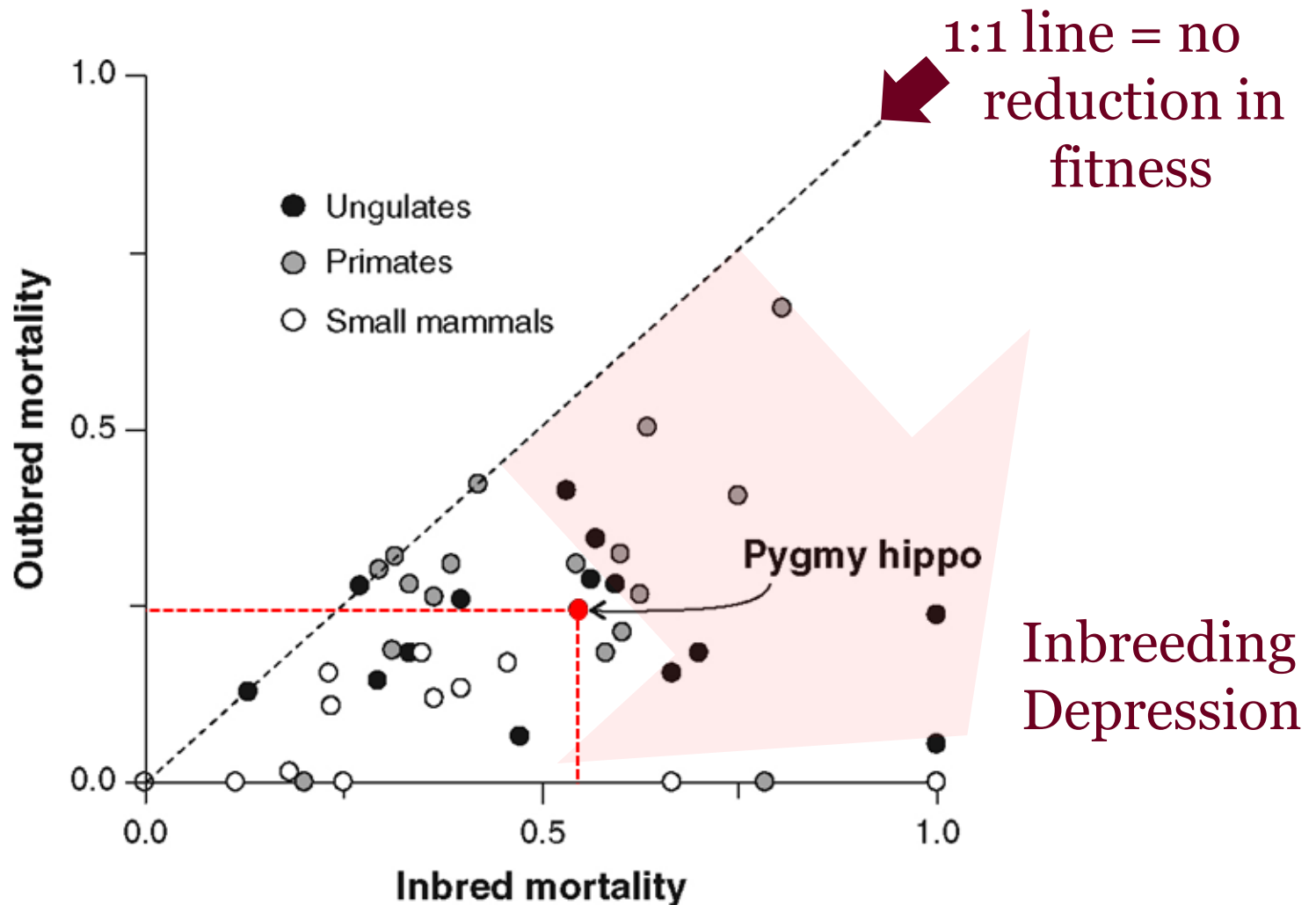
Inbreeding

SPECIES VARIATION IN INBREEDING DEPRESSION



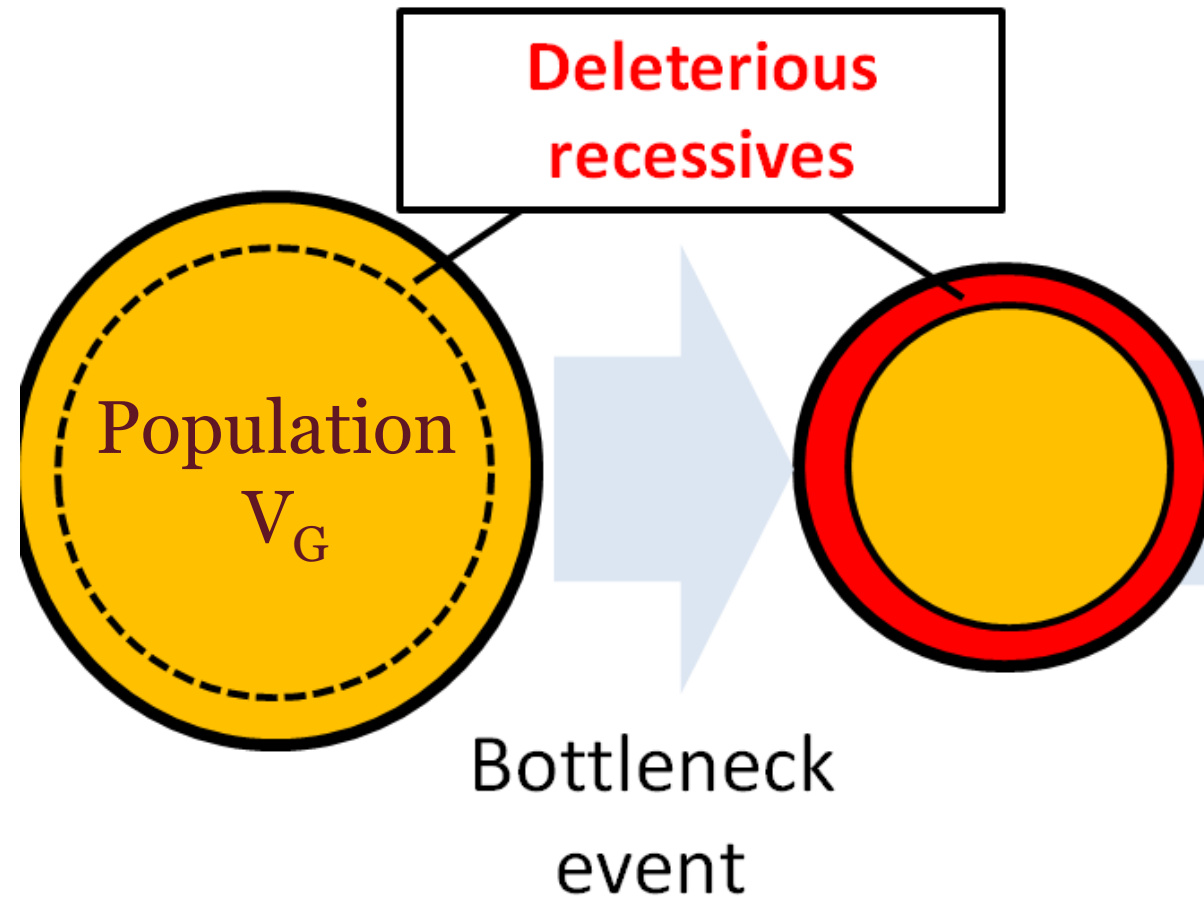
Inbreeding

SPECIES VARIATION IN INBREEDING DEPRESSION



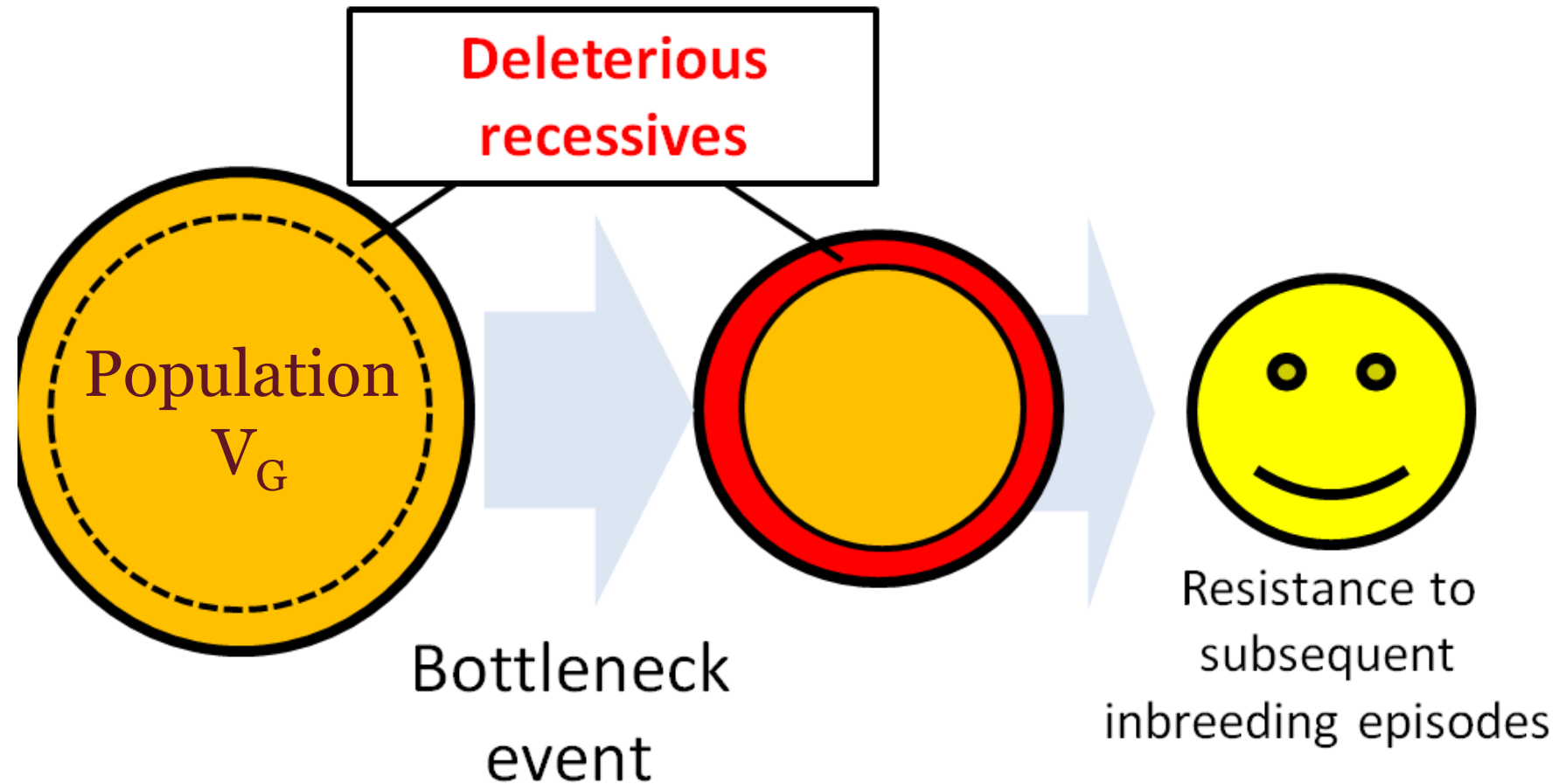
Inbreeding:

Mutational load exposed & purged



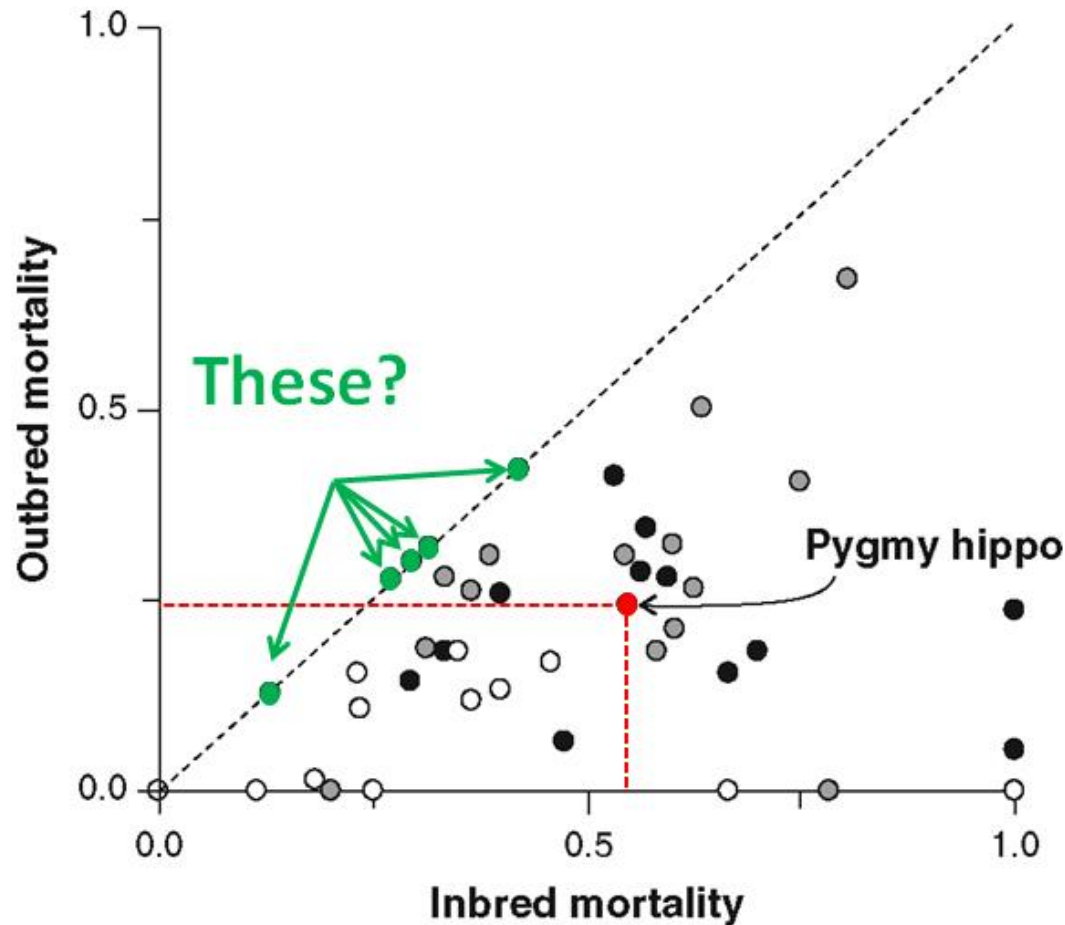
Inbreeding:

Mutational load exposed & purged



Inbreeding:

Mutational load exposed & purged



Inbreeding

Inbreeding & Evolutionary Potential

e.g. *Evolution* **66**:2384–2398

ORIGINAL ARTICLE

doi:10.1111

RESPONSE TO SELECTION ON COLD TOLERANCE IS CONSTRAINED BY INBREEDING

Anneke Dierks,^{1,2} Birgit Baumann,¹ and Klaus Fischer¹

¹Zoological Institute and Museum, University of Greifswald, J.-S.-Bachstraße 11/12, D-17489 Greifswald, Germany

²E-mail: anneke.dierks@uni-greifswald.de



Inbreeding & Evolutionary Potential

ORIGINAL ARTICLE

doi:10.1111/j.1558-5646.2012.01604.x

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No inbreeding
($F = 0.00$)

Some inbreeding
($F = 0.25$)

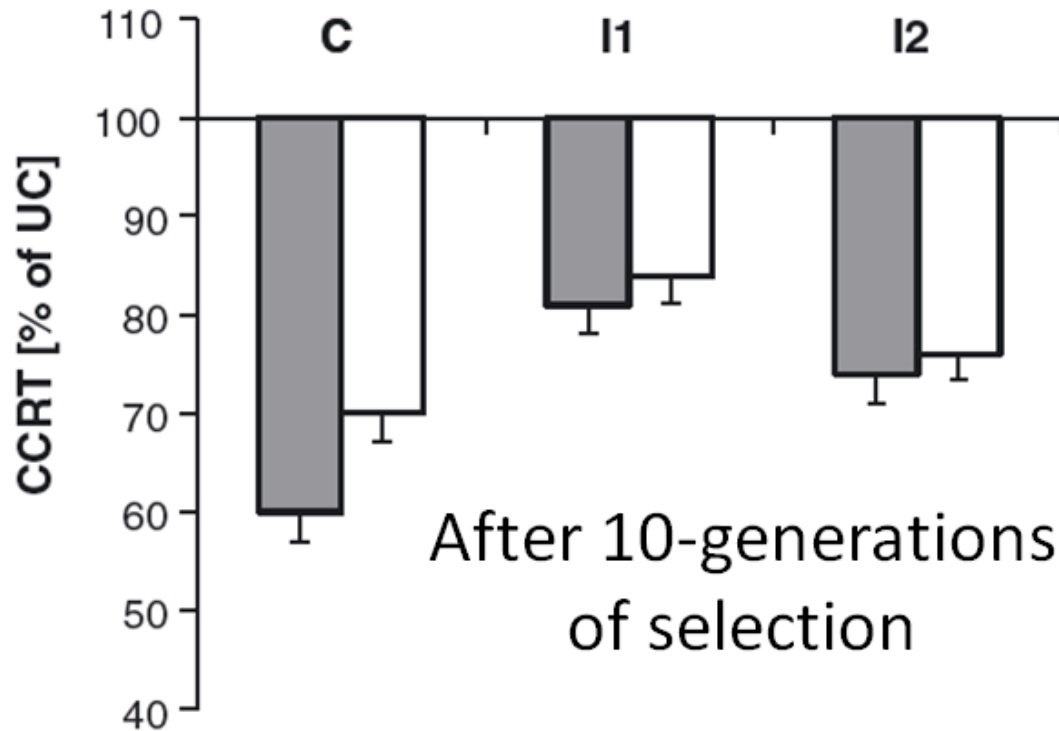
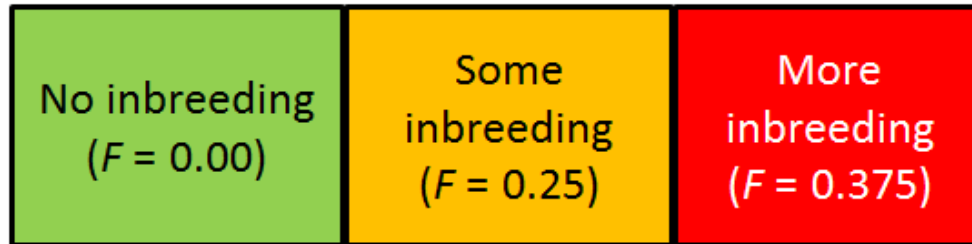
More inbreeding
($F = 0.375$)

10 Generations of
directional selection for
cold tolerance

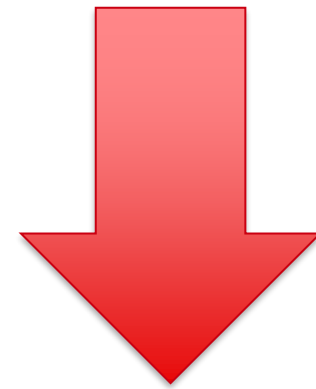
Assessed:

- Cold tolerance
- Other stuff, such as:
 - Heat tolerance
 - Fecundity
 - Egg hatching
 - Develop time
 - Adult size
 - Growth rate

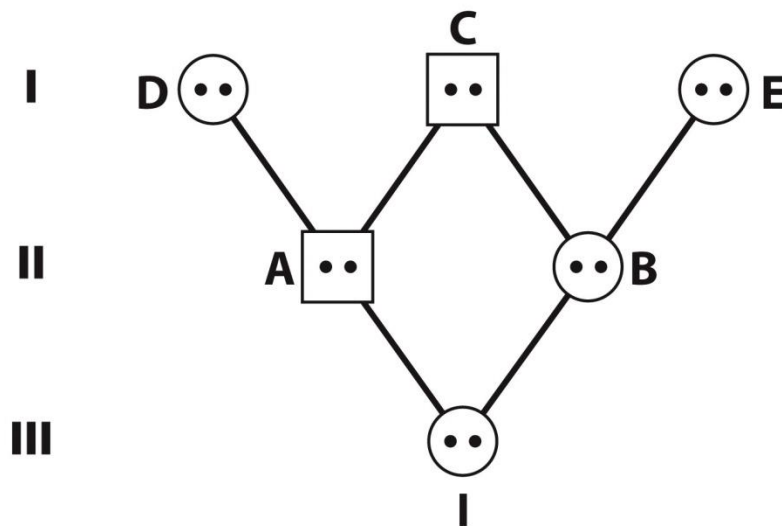
Inbreeding & Evolutionary Potential



Selective
response



Genetic Analysis of Inbreeding

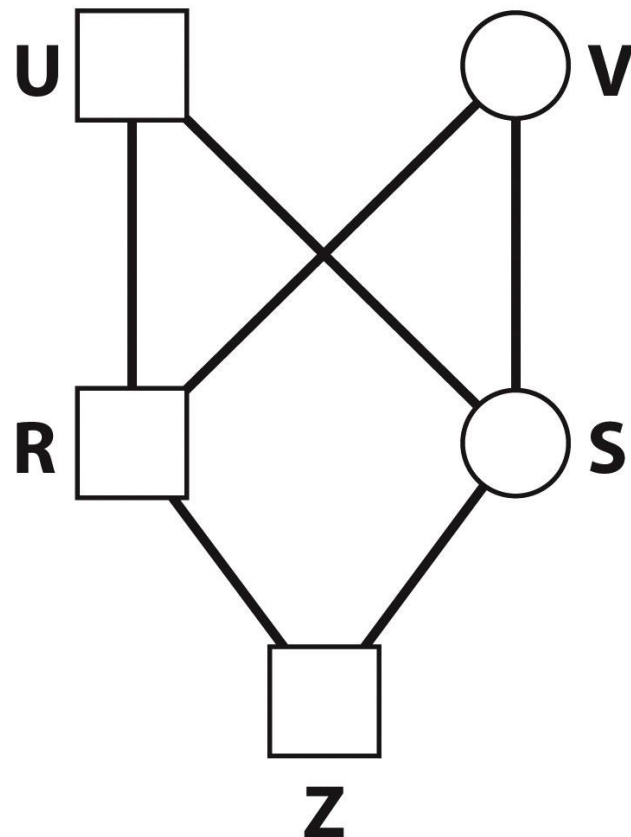


- Individuals A and B are half-siblings.
- Their offspring, I, is inbred, and inherited one copy of her genes from A and one copy from B.
- These copies may be **identical by descent** if they are identical copies inherited from individual C.
- C is the common ancestor of I.

The Inbreeding Coefficient

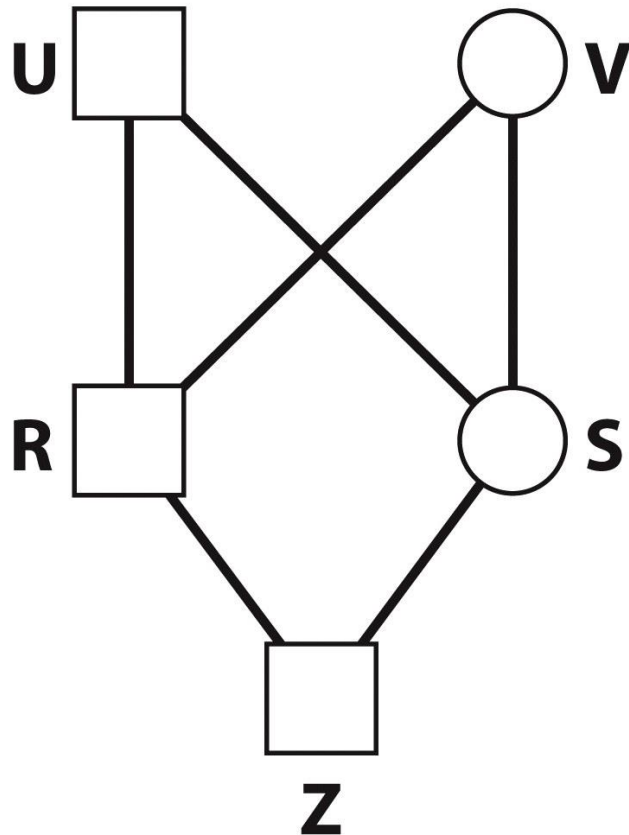
- The Inbreeding Coefficient, F , is the probability that the two gene copies in an individual are identical by descent from a common ancestor.
- Calculation of the Inbreeding Coefficient
 - 1) Identify the common ancestor(s) of an inbred individual.
 - 2) Count the number of linkages between individuals (n) in each inbreeding loop.
 - 3) Calculate the quantity $2 \times (1/2)^n$ for each inbreeding loop and sum the results.

Calculating F for a Full-Sibling Mating



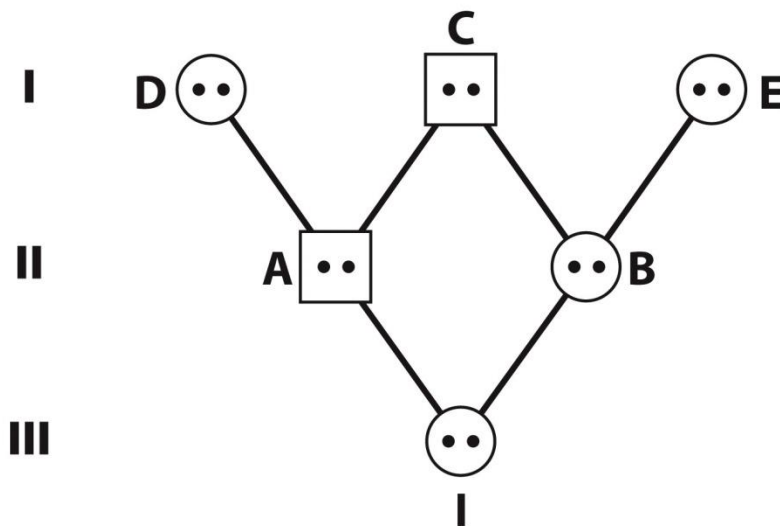
- 1) Identify the common ancestor(s).
 - U and V are both common ancestors, so there are two inbreeding loops.
- 2) Count the number of links between individuals in each inbreeding loop.
 - Loop 1: U, R, S, Z;
 $n=4$
 - Loop 2: V, R, S, Z
 $n=4$)

Calculating F for a Full-Sibling Mating

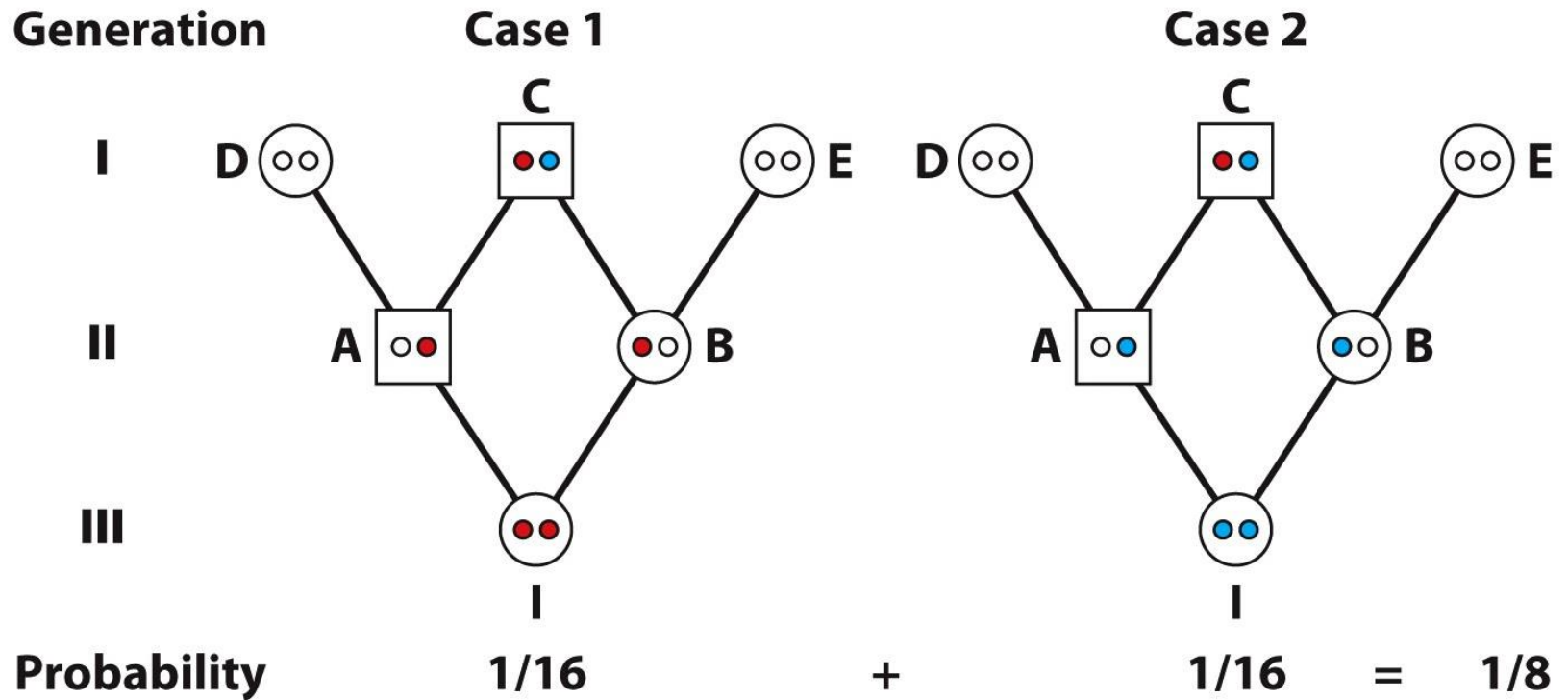


- 3) Each individual is diploid...therefore the probability of Z receiving two copies of either allele from a common ancestor is $(1/2)^n \times 2$ for each loop and sum the results.
- Loop 1: $(1/2)^4 \times 2 = 1/8$
 - Loop 2: $(1/2)^4 \times 2 = 1/8$
 - $F = 1/8 + 1/8 = 1/4$

Calculating F for a Half-Sibling Mating

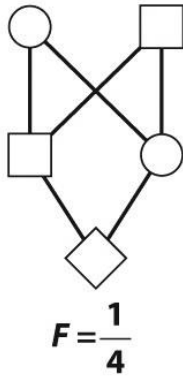


- 1) Identify the common ancestor(s).
 - C is the common ancestor, so there is one inbreeding loop.
- 2) Count the number of linkages between individuals in each inbreeding loop.
 - The Loop includes C, A, and B; $n=4$
- 3) Calculate $(1/2)^n$ for each loop and sum the results.
 - There is only one loop in this case
 - $(1/2)^4 \times 2 = 1/8$, so $F = 1/8$

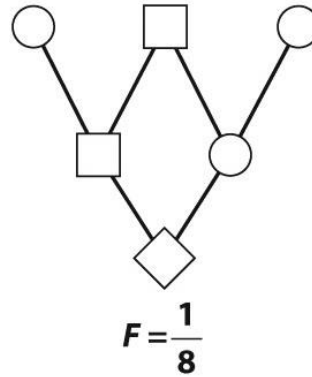




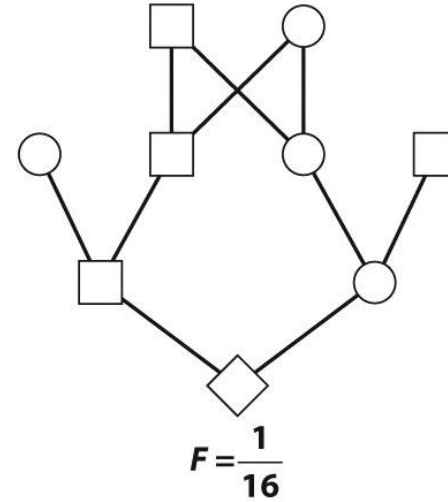
Full siblings



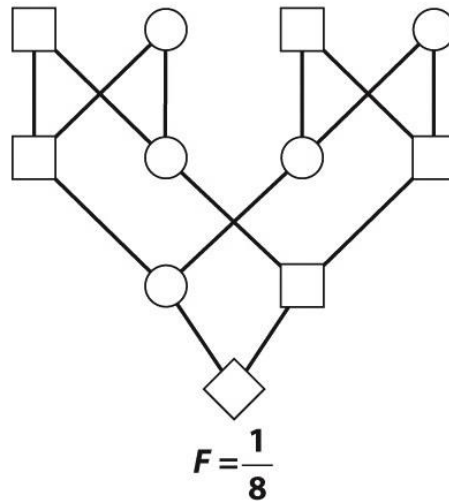
Half siblings



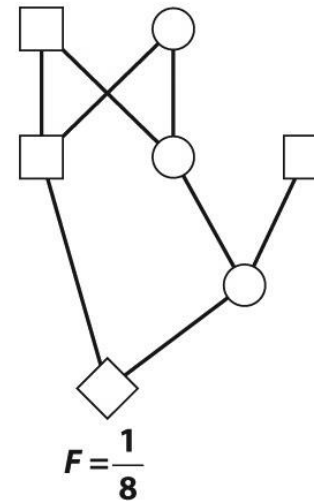
First cousins



Double first cousins

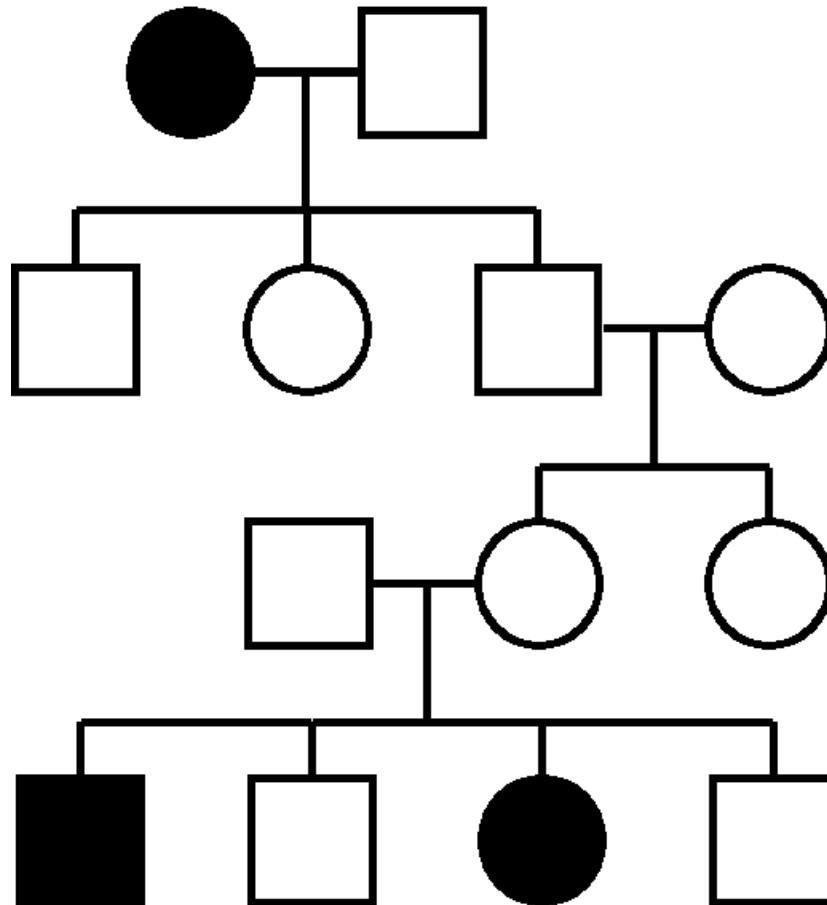


Uncle-niece



Inbreeding

TRACED VIA PEDIGREE DIAGRAMS

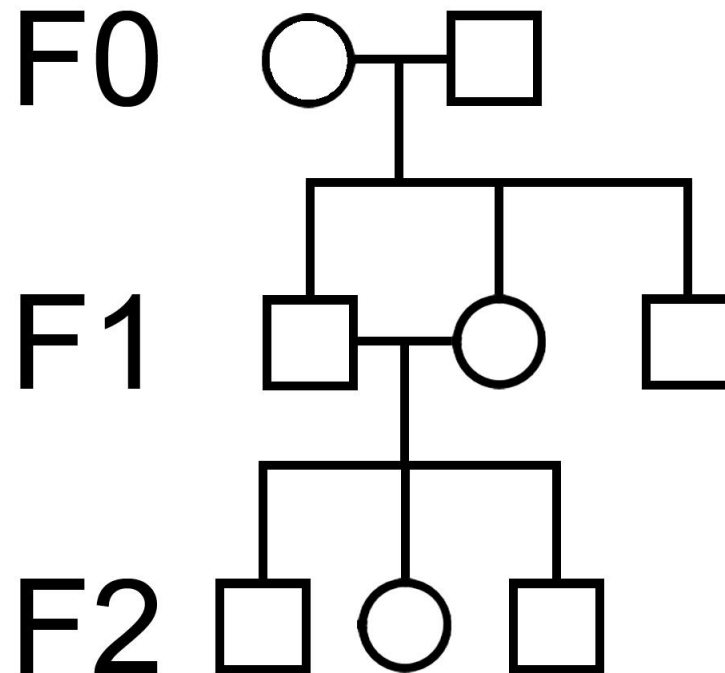


Inbreeding

SIMPLY FROM PEDIGREE DIAGRAMS:

Count the nodes:

$$F = 0.5^n$$

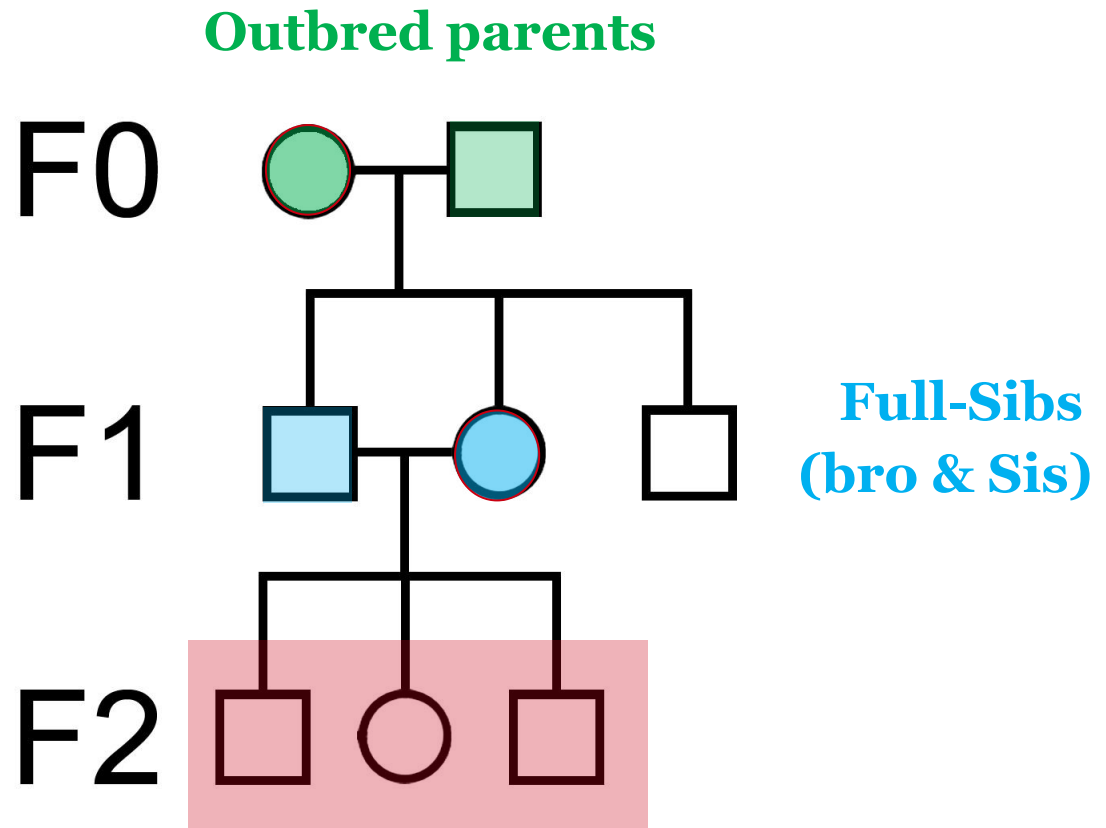


Inbreeding

OFFSPRING OF FULL-SIBLINGS:

Count the nodes:

$$F = 0.5^n$$



Inbreeding

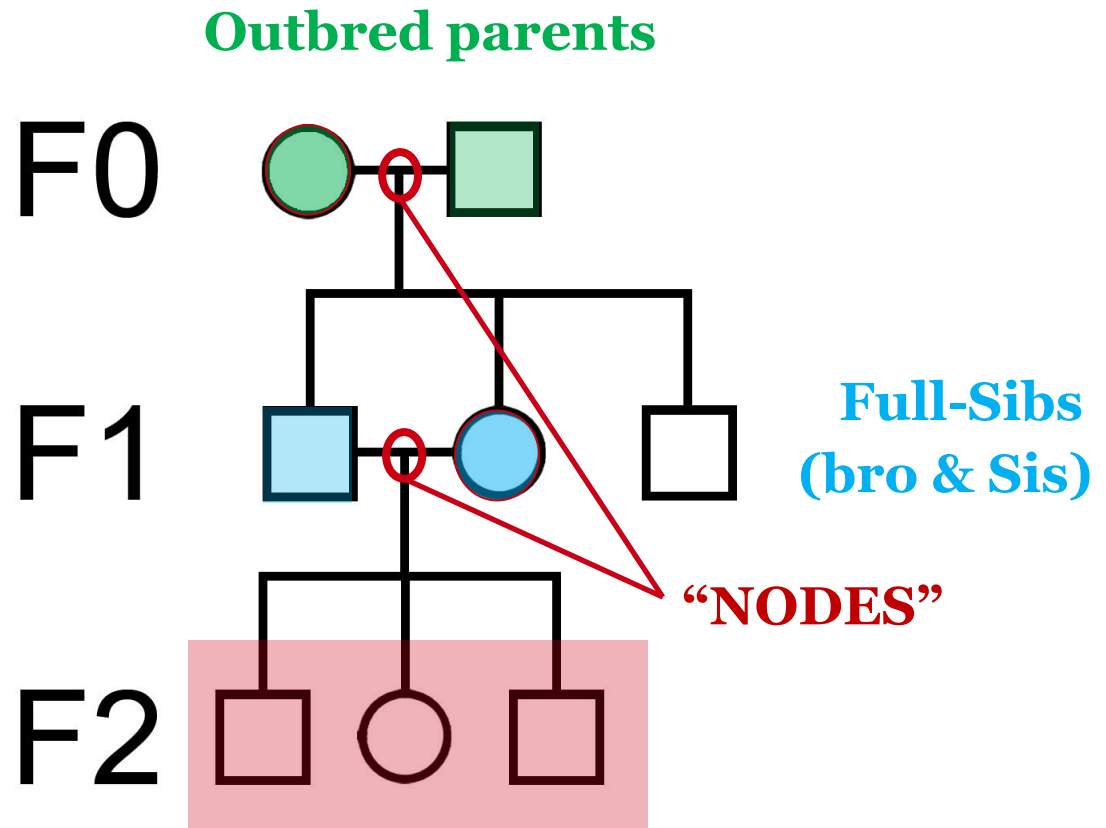
OFFSPRING OF FULL-SIBLINGS:

Count the nodes:

$$F = 0.5^n$$

$$F = 0.5^2$$

$$F = 0.25$$



Inbreeding

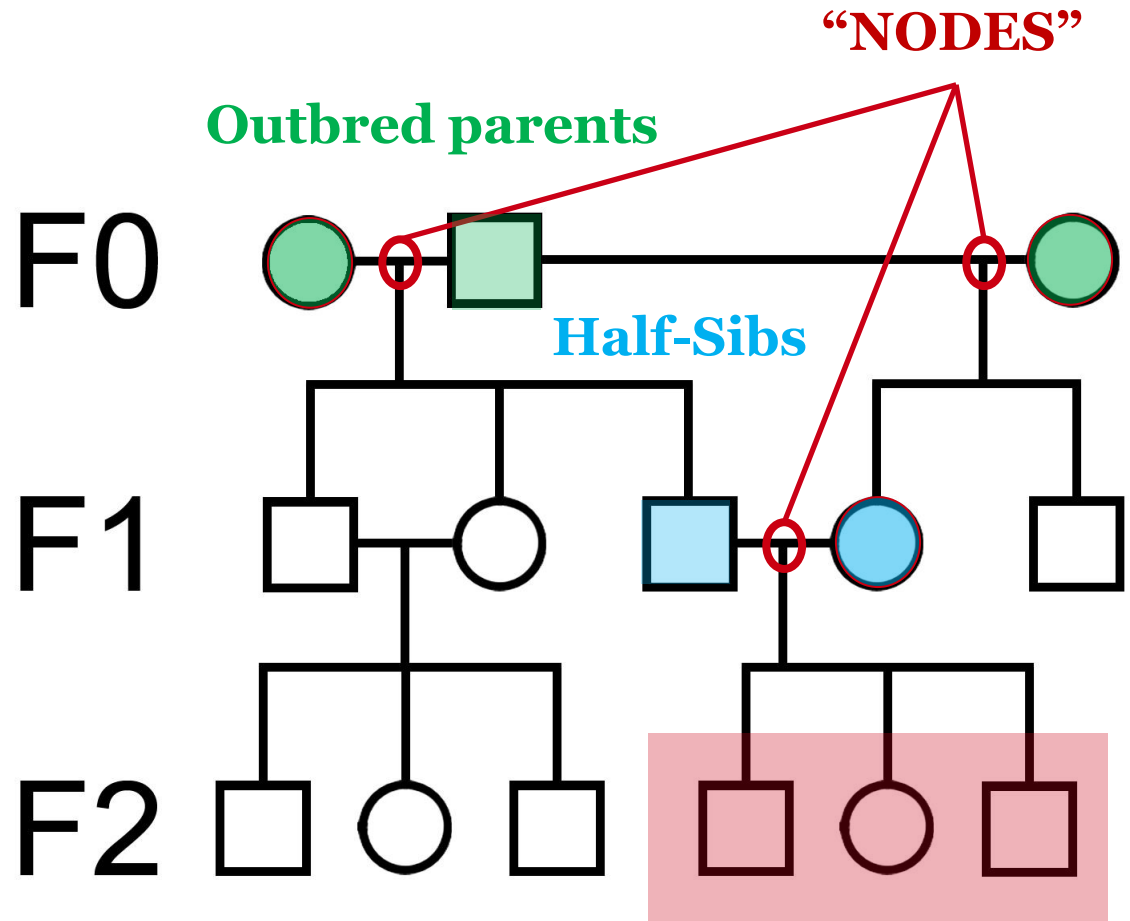
OFFSPRING OF HALF-SIBLINGS:

Count the nodes:

$$F = 0.5^n$$

$$F = 0.5^3$$

$$F = 0.125$$



Inbreeding

RELATIONSHIP TO GENETIC VARIANCE

$$F = 1 - \frac{H_{obs}}{H_{exp}}$$



H-W expected V_G

As H_{obs} nears H_{exp} F nears zero.

As $H_{obs} \ll H_{exp}$ F nears one.

Inbreeding

RELATIONSHIP TO GENETIC VARIANCE

$$F = 1 - \frac{H_{obs}}{H_{exp}}$$

H-W expected V_G

$$F = 1 - \frac{H_{t=1}}{H_{t=0}}$$

Change in V_G
over time

Inbreeding

RELATIONSHIP TO (DELTA) GENETIC VARIANCE

$$F = 1 - \frac{H_{t=1}}{H_{t=0}}$$

Inbreeding

RELATIONSHIP TO (DELTA) GENETIC VARIANCE

$$F = 1 - \frac{H_{t=1}}{H_{t=0}}$$

$$\frac{H_{1997}}{H_{1974}} = \frac{0.10}{0.23} = \mathbf{0.43}$$



Inbreeding

RELATIONSHIP TO (DELTA) GENETIC VARIANCE

$$F = 1 - \frac{H_{t=1}}{H_{t=0}}$$

$$F = 1 - 0.43$$

$$F = \mathbf{0.57}$$

$$\frac{H_{1997}}{H_{1974}} = \frac{0.10}{0.23} = \mathbf{0.43}$$



Genetic problems are usually eased by restoring genetic variation

‘genetic rescue’ / ‘gene pool mixing’ works

Nearly every one of 156 cases (Frankham 2015)



Applications of Genetic Tools and Approaches in Conservation Biology and Management

CASE STUDY

Augmenting
genetic
variation
reverses
a
population
decline

Madsen *et al.* (1999)
Nature



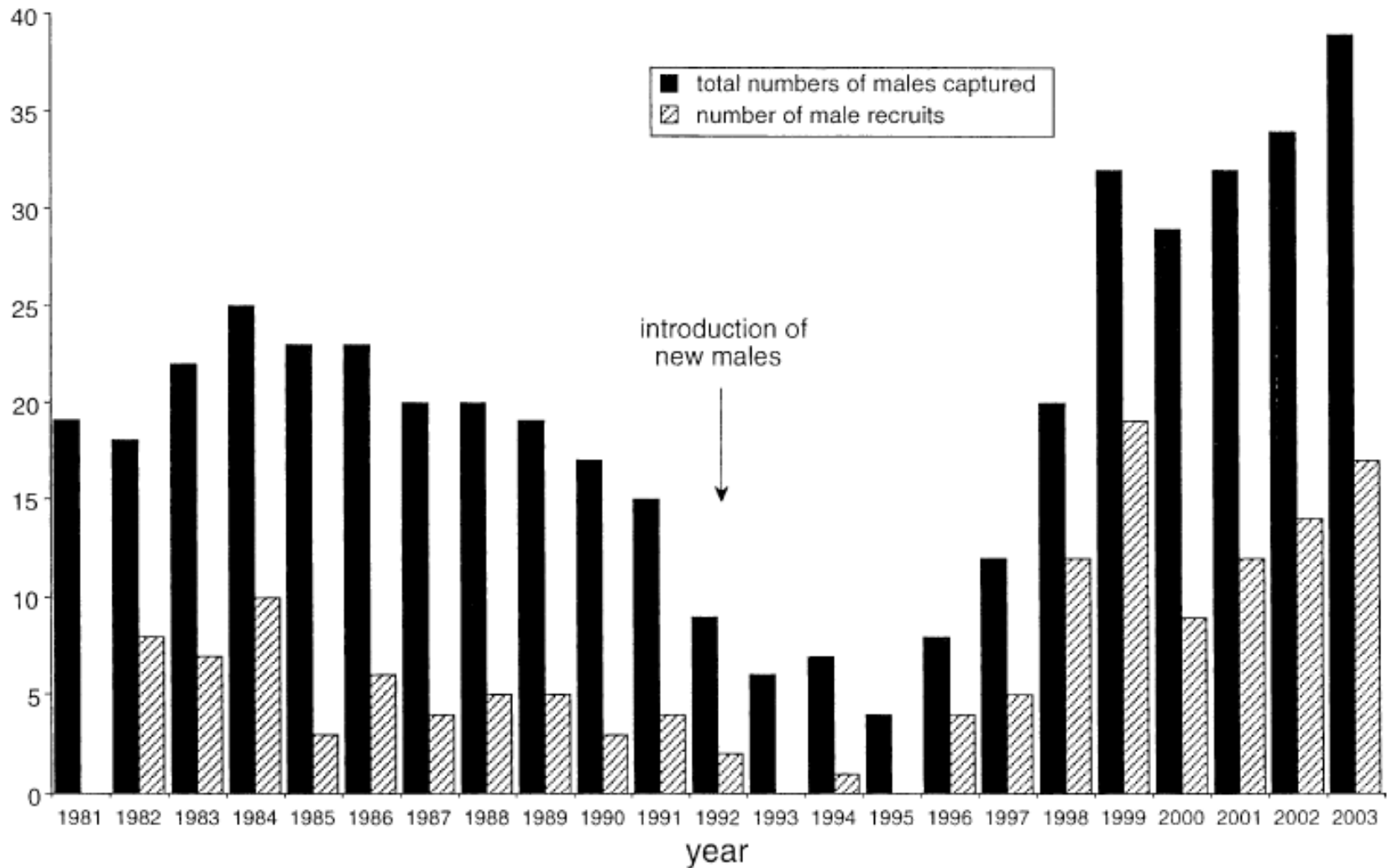
- population of adders ($N_e < 15$)
- isolated for 100 years
- pop. decline over 35 years
- high proportion of stillborn & deformed young
- low genetic variation

- added 20 males from diverse nearby population
- watched population change & re-examined genetic variation

- migrant males settled in & mated, removed after 4 breeding seasons
- from first breeding season, stillbirths declined, population began dramatic growth...

NB: numbers exclude ones added

T. Madsen et al. / Biological Conservation 120 (2004) 145–147



Many other high profile successes



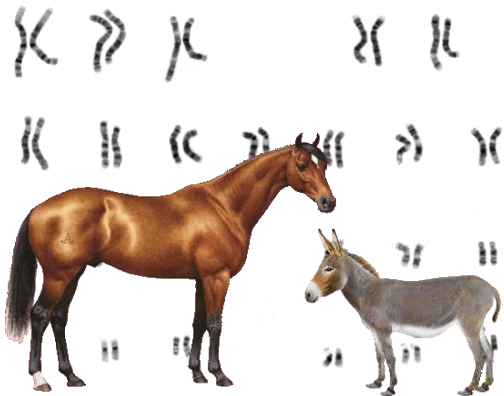
But still, genetic rescue has rarely been used

Fear of outbreeding depression, but it's

- Rare
- Usually mild / transient
- Predictable and avoidable

Three 'red flags' for outbreeding depression

Major
chromosomal
differences



Long isolation



Adaptive
differentiation



Next Lecture: Genetic consequences of Habitat Fragmentation

