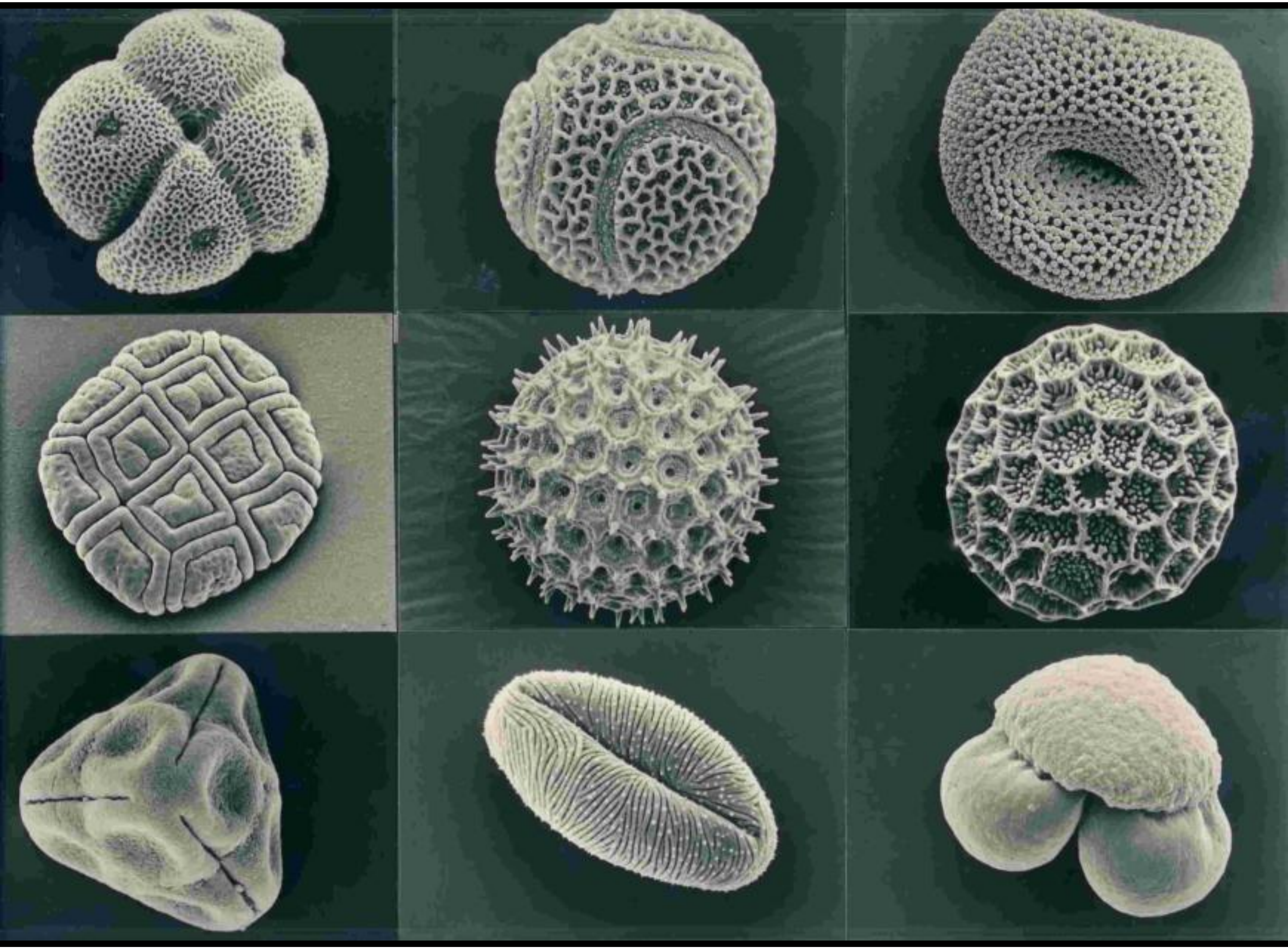
Plant of the Day

Drosera rotundifolia

a tiny carnivore native to bogs!

Big Questions

- How do plants exchange genes between populations?
- How do we measure gene flow?
- How does the spread of a beneficial allele via gene flow differ from that of a neutral allele?



Gene flow

Gene flow is the transfer of genetic material between populations resulting from the movement of individuals (**migration**) or their gametes.

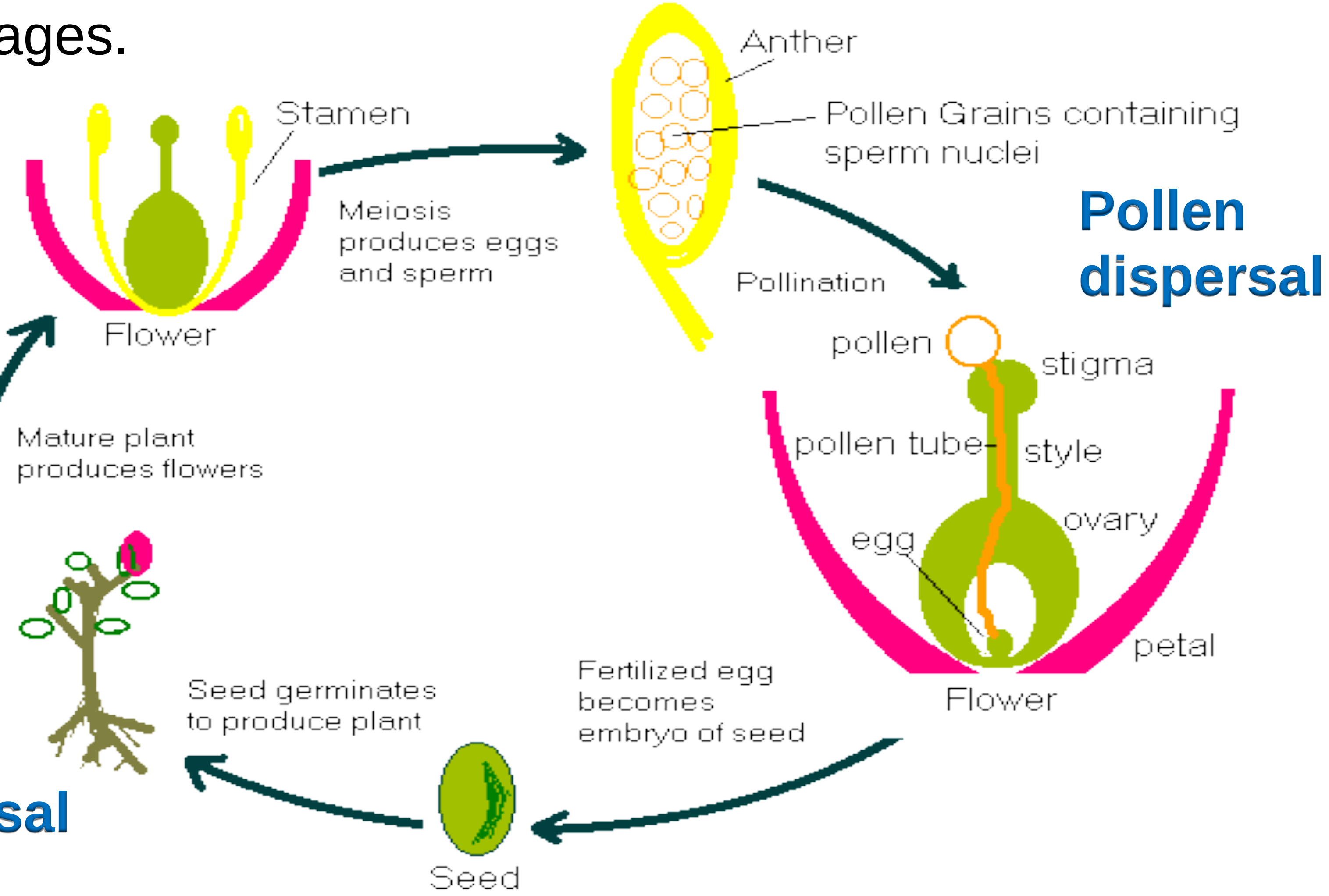
Gene flow may add new alleles to a population or change the frequencies of alleles already present

Gene flow connects the populations of a species, enabling them to evolve collectively (as a unit).

Reductions in gene flow may lead to speciation.

Gene flow in plants

(Seed) plants disperse their genes during two independent life cycle stages.



Pollen dispersal agents: biotic

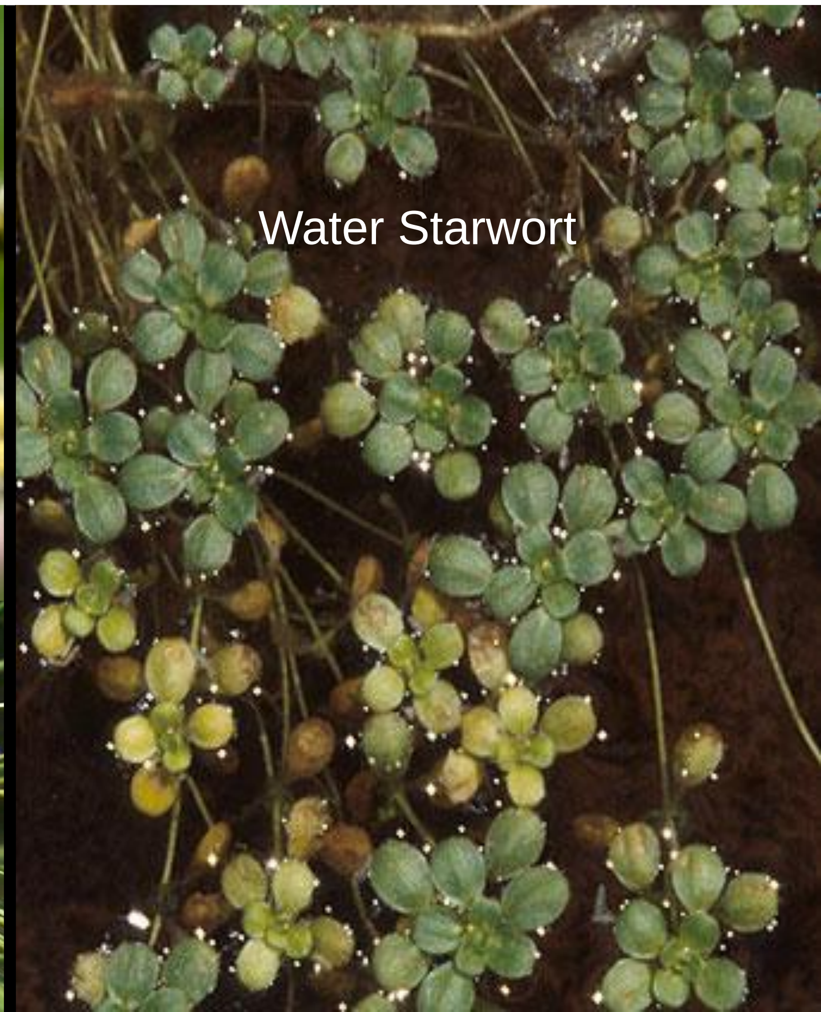
Insects

Vertebrates

Pollen dispersal agents: abiotic

Wind

Water



Seed dispersal agents

Gene flow

<u>Think – Pair – Share</u>

Describe a scenario where knowing gene flow rates is important.

Write down 1–2 sentences.
Discuss with a neighbor.
Report back to class.

Measuring gene flow: direct methods

(1) Observe movement of dispersal agents

• *Shortcomings: may e.g. underestimate dispersal because of pollen and seed carryover. Can't tell if pollen is successfully incorporated into new population.*

(2) Mark dispersing objects with dyes, paint, or radioactive tracers and monitor movement

• *Alternative: naturally polymorphic dispersing objects.*

• *Shortcomings: marking may affect dispersal. Can't tell if pollen is successfully incorporated into new population.*

Measuring gene flow: direct methods

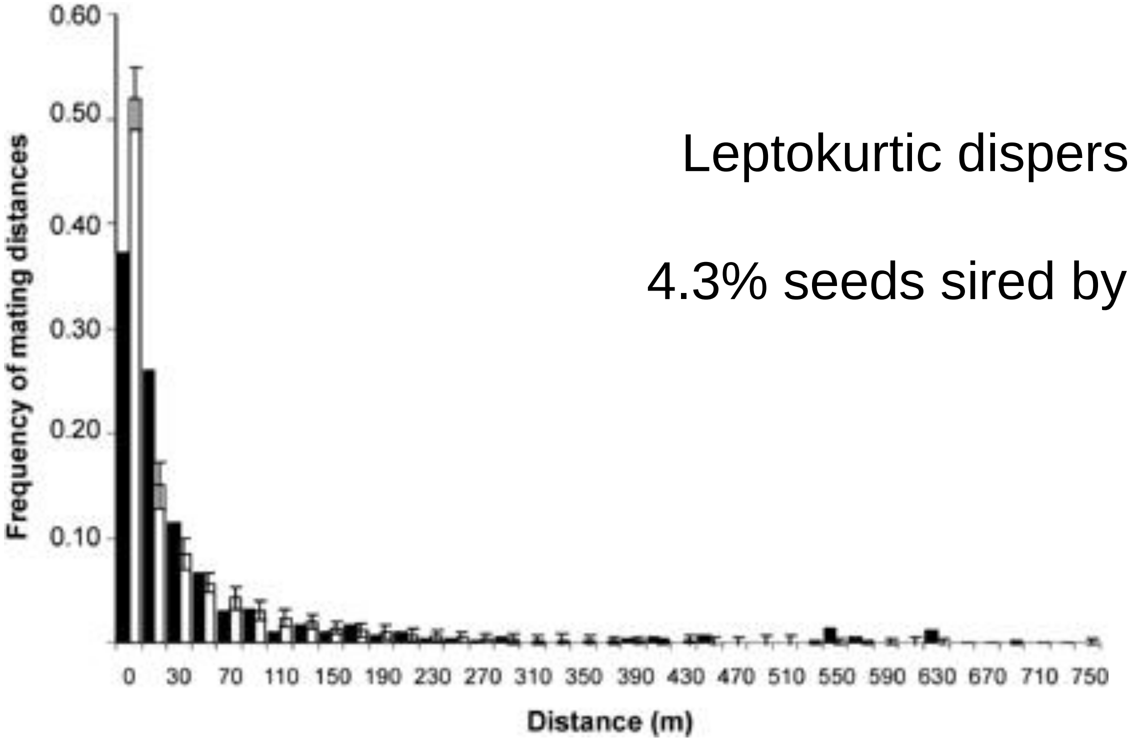
(3) Track unique molecular marker from source plant(s) in progeny of nearby plants

- *Shortcomings: Need to identify marker and genotype all potential progeny, limited to specific source.*

Data from first three methods indicates that most pollen and seeds are dispersed close to source. These results suggest that gene flow rates between plant populations are very low (< 1% per gen.).

Measuring gene flow: direct methods

(4) **Parentage analyses**: highly polymorphic markers are used to screen seeds to determine what fraction of seeds had fathers or mothers from outside the population.



Leptokurtic dispersal curve in Scots Pine

4.3% seeds sired by individuals outside of the population

Robledo-Arnuncio & Gi 2005

Measuring gene flow: direct methods

Paternity analyses suggest that populations spatially isolated by hundreds or thousands of meters are not genetically isolated and gene flow rates often are high (> 1% per gen.)

How to resolve this conflict?

Measuring dispersal from a source (i.e. as in Methods 1-3) misses rare, long distance dispersal events. The tails of these dispersal curves were missing.

Measuring gene flow: direct methods

Final caveat:

All direct methods provide **contemporary** estimates of gene flow only, which are not necessarily related to **historical** gene flow levels.

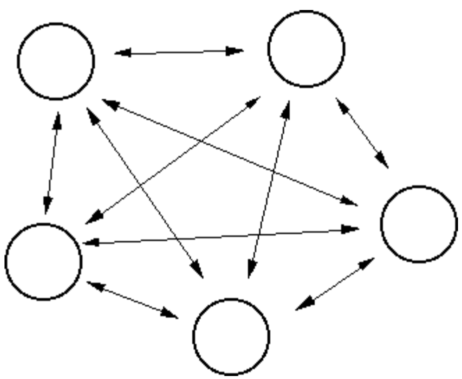
Why is this, from our perspective as evolutionary biologists, problematic?

Measuring gene flow: indirect methods

Historical gene flow can be inferred from population genetic structure (e.g. from F_{ST}). What could high F_{ST} between two populations indicate?

Statistical methods exist to relate genetic distance estimates to the parameter ***Nm*** (the average number of realized immigrants per generation).

Wright's F_{ST}



Island model

$$F_{ST} = \frac{1}{4Nm + 1}$$

Measuring gene flow: indirect methods

Nm is a critical value because it tells us how much gene flow is required to overcome the effects of genetic drift.

Nm > 4 : gene flow wins
Nm < 1 : genetic drift wins and populations diverge
Nm between 1 and 4 : neither prevails

Caveats:

1) Tells us about historical gene flow, not contemporary gene flow.
2) The real world is not like the island model (most assumptions are violated in most species).

Thus, indirect estimates must be viewed with caution.

Measuring gene flow: indirect methods

Nm = 0.24

Selfers

Nm = 0.90

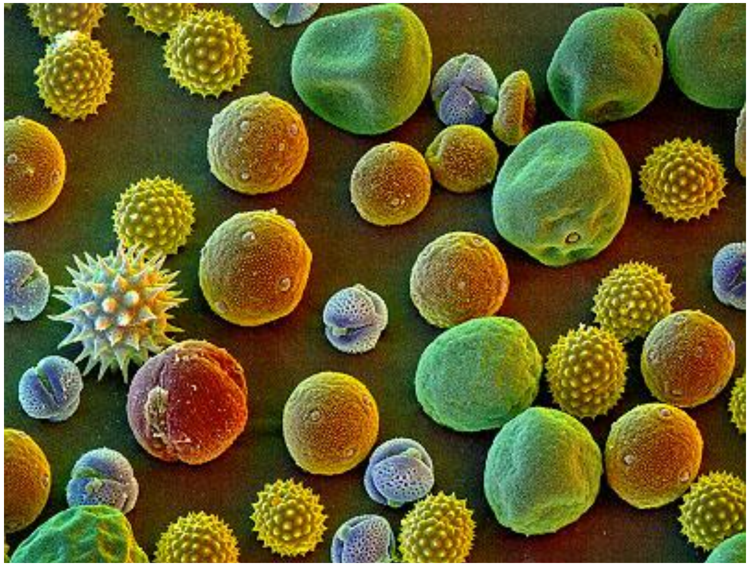
Mixed maters

Nm = 1.43

Outcrossers

Hamrick and Godt 1996

Pollen versus seed dispersal



How do these direct and indirect methods deal with the two modes of dispersal?

Pollen versus seed dispersal

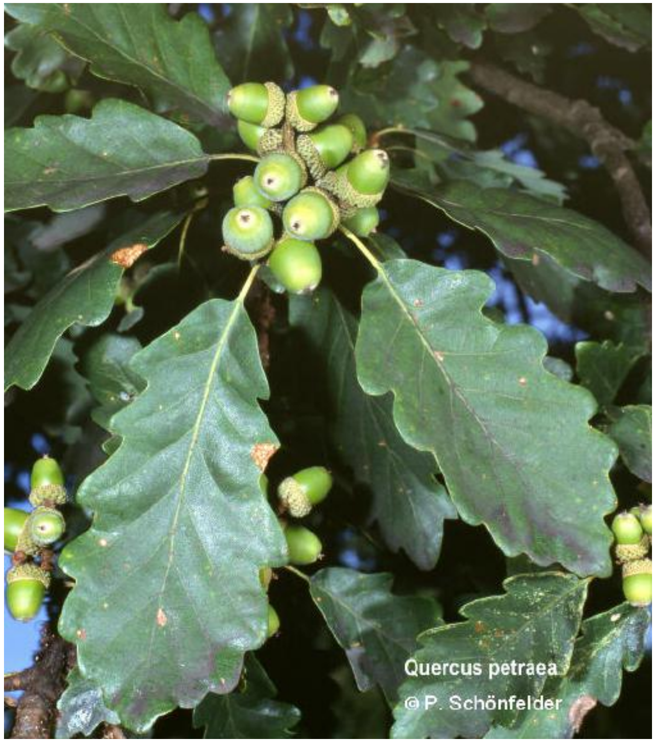
Direct estimates from parentage analyses have generally documented fairly high rates of seed immigration rates, ranging from 2.1% in honey locust to 40% in Magnolias

How can we differentiate the relative contributes of gene flow from seeds versus gene flow from pollen?

We could compare levels of interpopulational differentiation (e.g. F_{ST}) for maternal versus bi-parentally inherited genes.

Pollen versus seed dispersal

Ratios of pollen to seed flow from indirect measures range from 4 (for selfing annual, wild barley) to 400 for wind-pollinated sessile oak.



Evolution and gene flow

CONSERVATIVE ROLE (emphasized by Mayr):

- Prevents differentiation due to random processes (i.e. genetic drift).
- Prevents adaptive genetic differentiation (if $m > s$).

CREATIVE ROLE:

- Enables the spread of new mutations.

Gene flow: unifying effects

How strong is gene flow in nature?

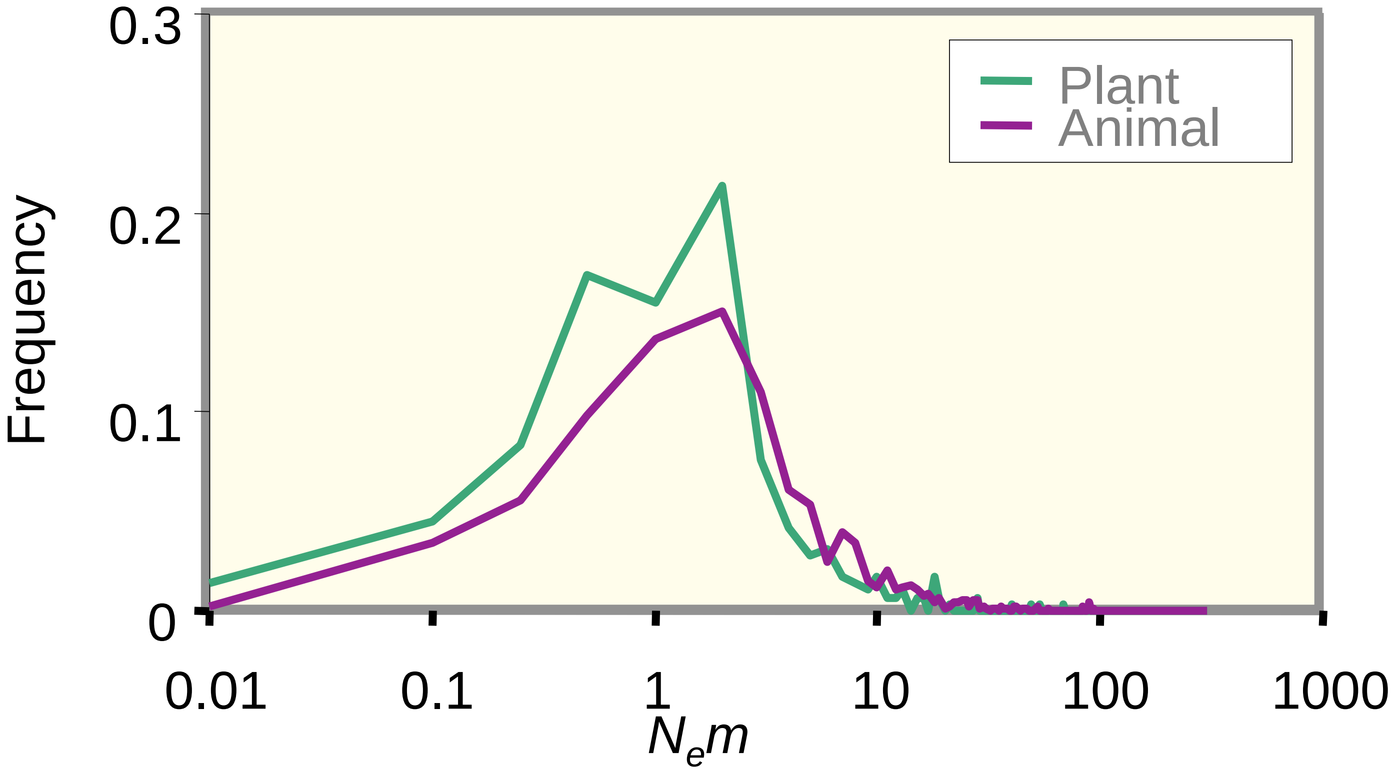
Traditional View:

- Species held together by gene flow

Opposing View (Ehrlich and Raven, 1969):

- Species-wide gene flow is too low
- Populations are the units of evolution
- Species are merely aggregates of evolving units

Gene flow: unifying effects

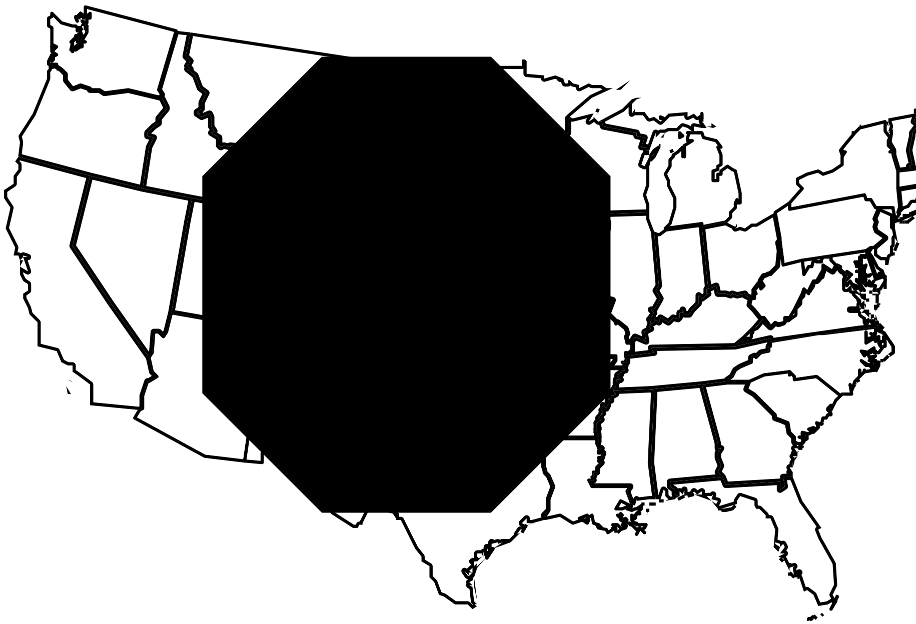


What is a typical number of migrants per generation for most species? What does this tell us?

Morjan & Rieseberg 2004

Gene flow: how favorable mutations are spread

Common sunflower, *Helianthus annuus,* and its primary dispersal agent



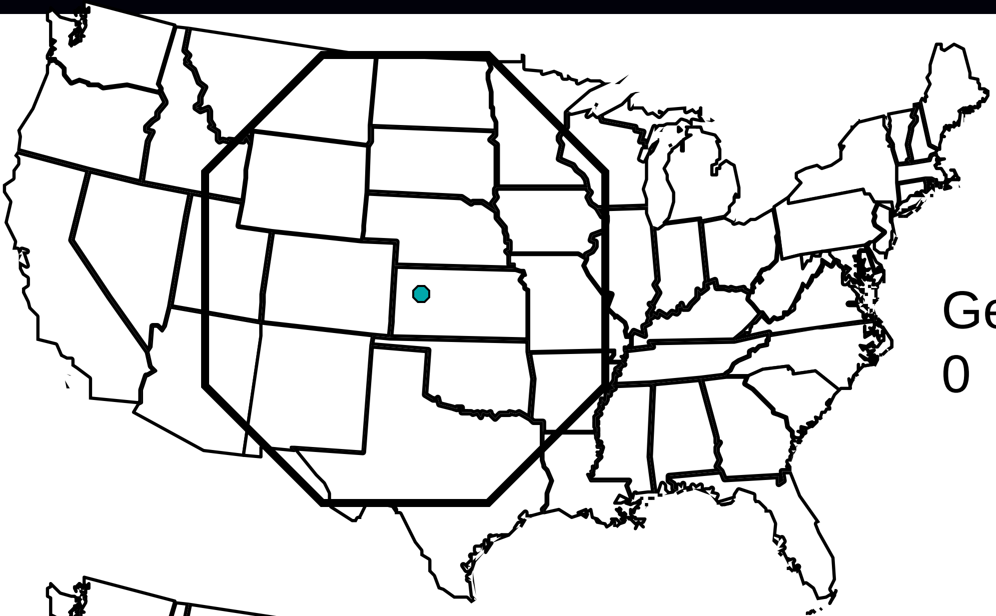
Prehistoric range of common sunflower

Spread of mutant alleles across the range of a widespread species

Advantageous mutation

Strength of selection
S = 0.10

Number of migrants
Nm = 1

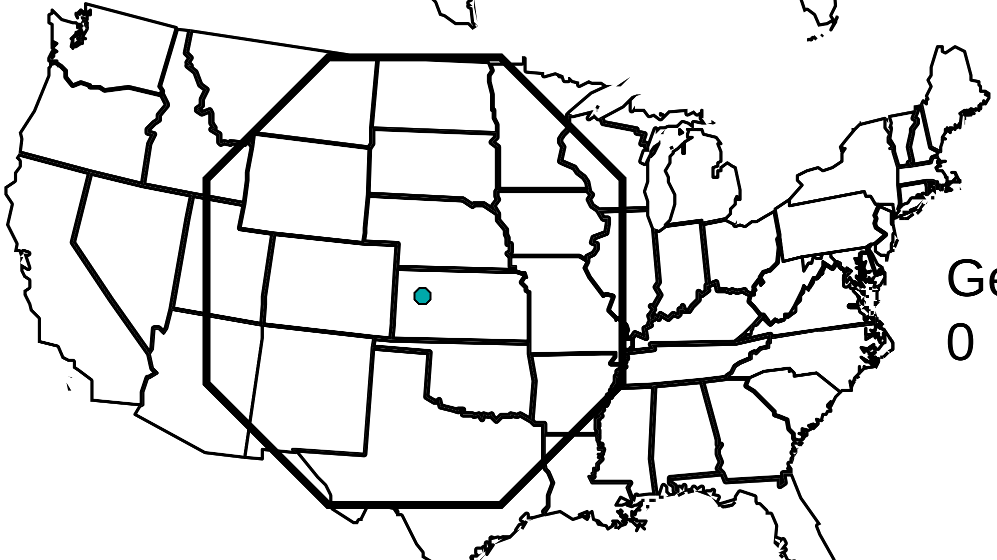


Generation
0

Near neutral mutation

Strength of selection
S = 0.0001

Number of migrants
Nm = 1



Generation
0

Spread of mutant alleles across the range of a widespread species

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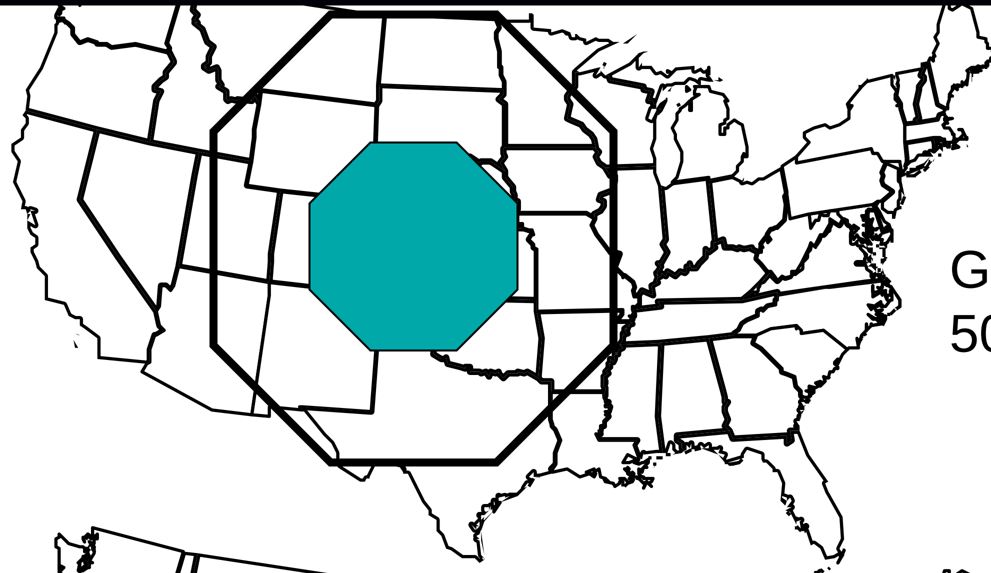
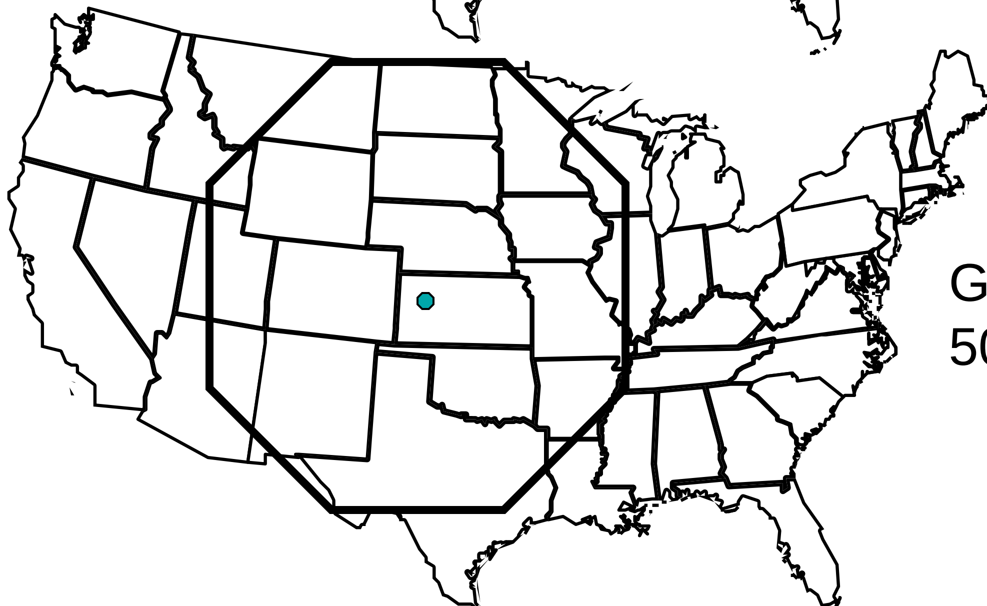


Generation
50

Near neutral mutation

Strength of selection
$S = 0.0001$

Number of migrants
Nm = 1



Generation
50

Spread of mutant alleles across the range of a widespread species

Advantageous mutation

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S = 0.10

Number of migrants
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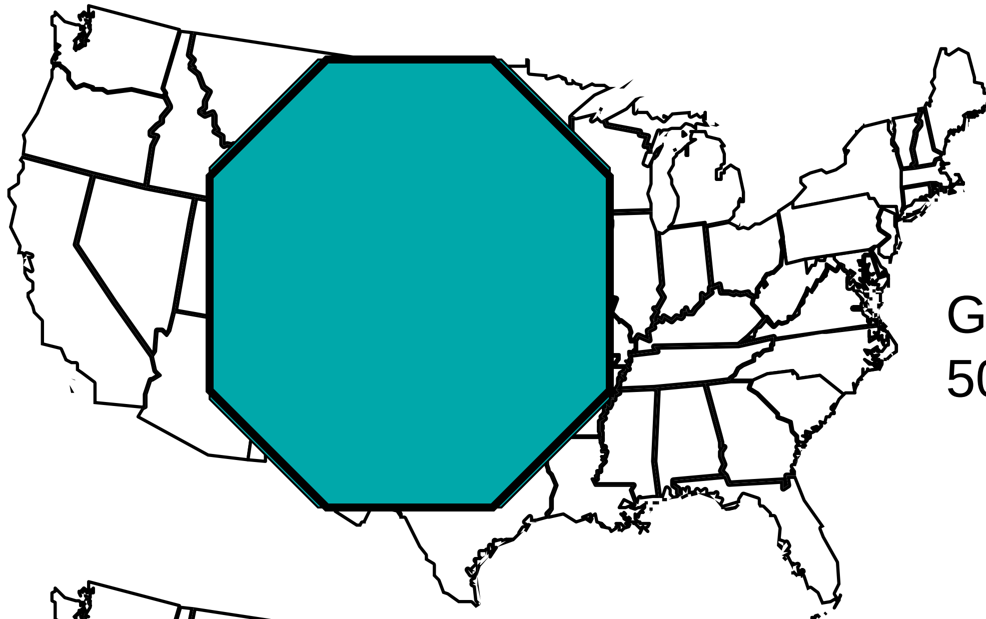
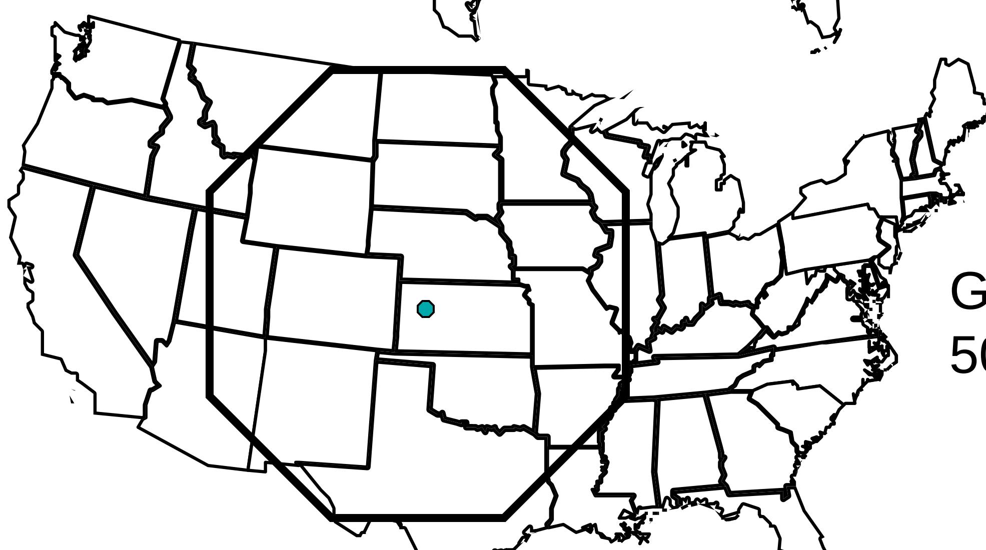


Generation
500

Near neutral mutation

Strength of selection
S = 0.0001

Number of migrants
Nm = 1



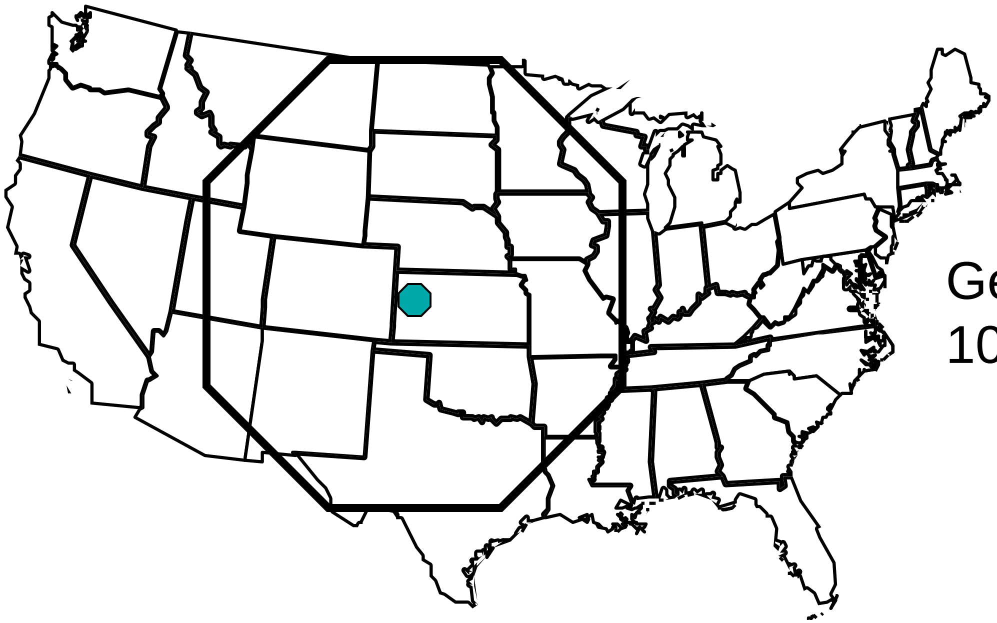
Generation
500

Spread of mutant alleles across the range of a widespread species

Near neutral mutation

Strength of selection
S = 0.0001

Number of migrants
Nm = 1



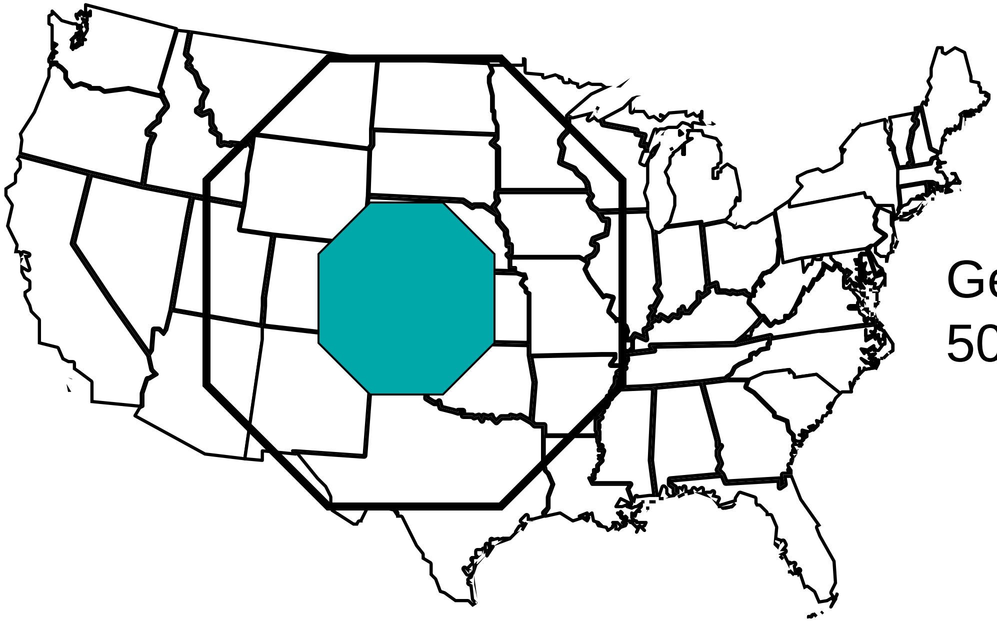
Generation
10,000

Spread of mutant alleles across the range of a widespread species

<u>Near neutral mutation</u>

Strength of selection
S = 0.0001

Number of migrants
Nm = 1



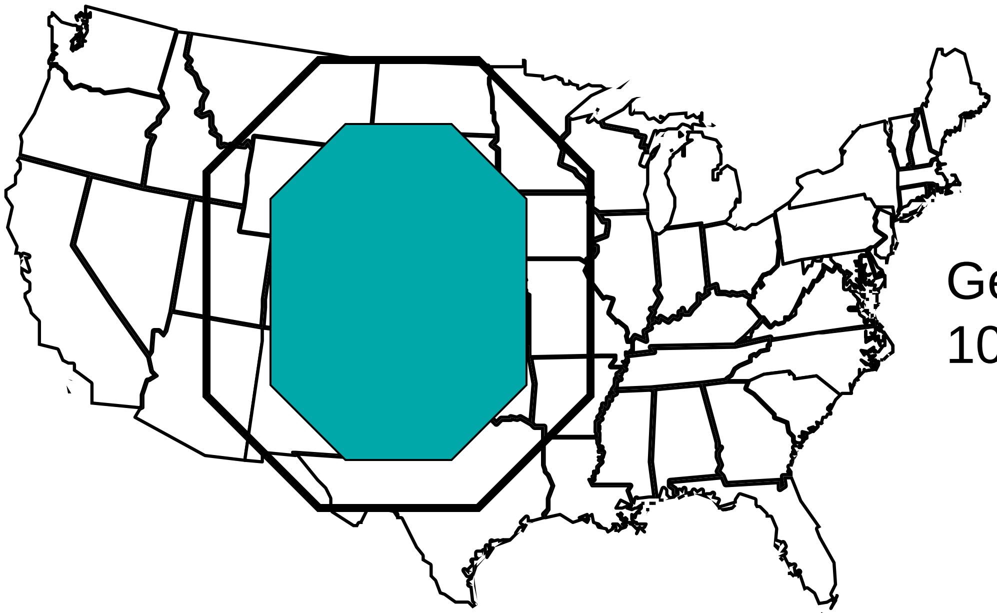
Generation
50,000

Spread of mutant alleles across the range of a widespread species

<u>Near neutral mutation</u>

Strength of selection
S = 0.0001

Number of migrants
Nm = 1



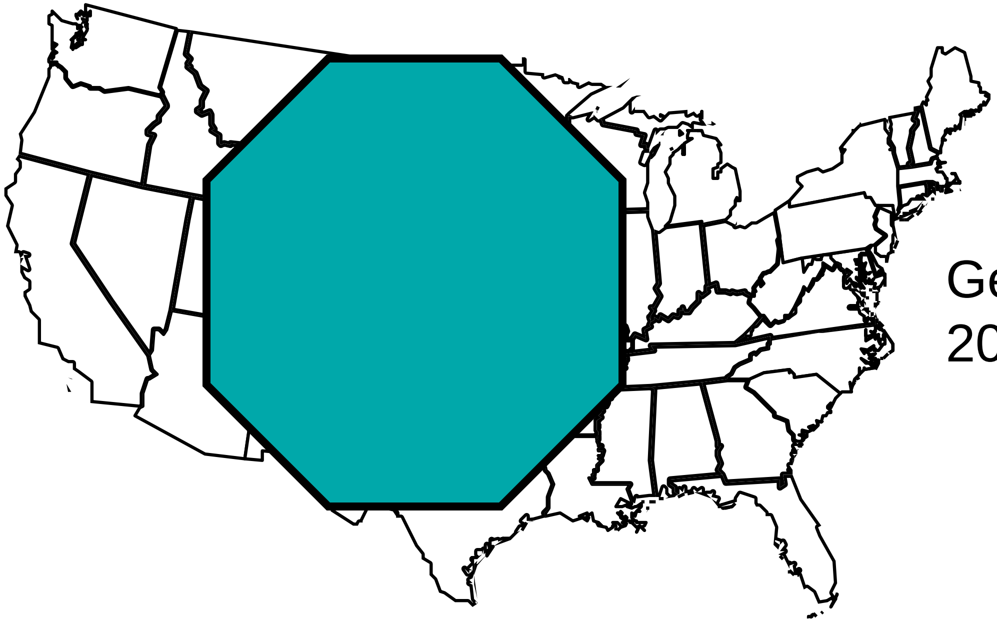
Generation
100,000

Spread of mutant alleles across the range of a widespread species

<u>Near neutral mutation</u>

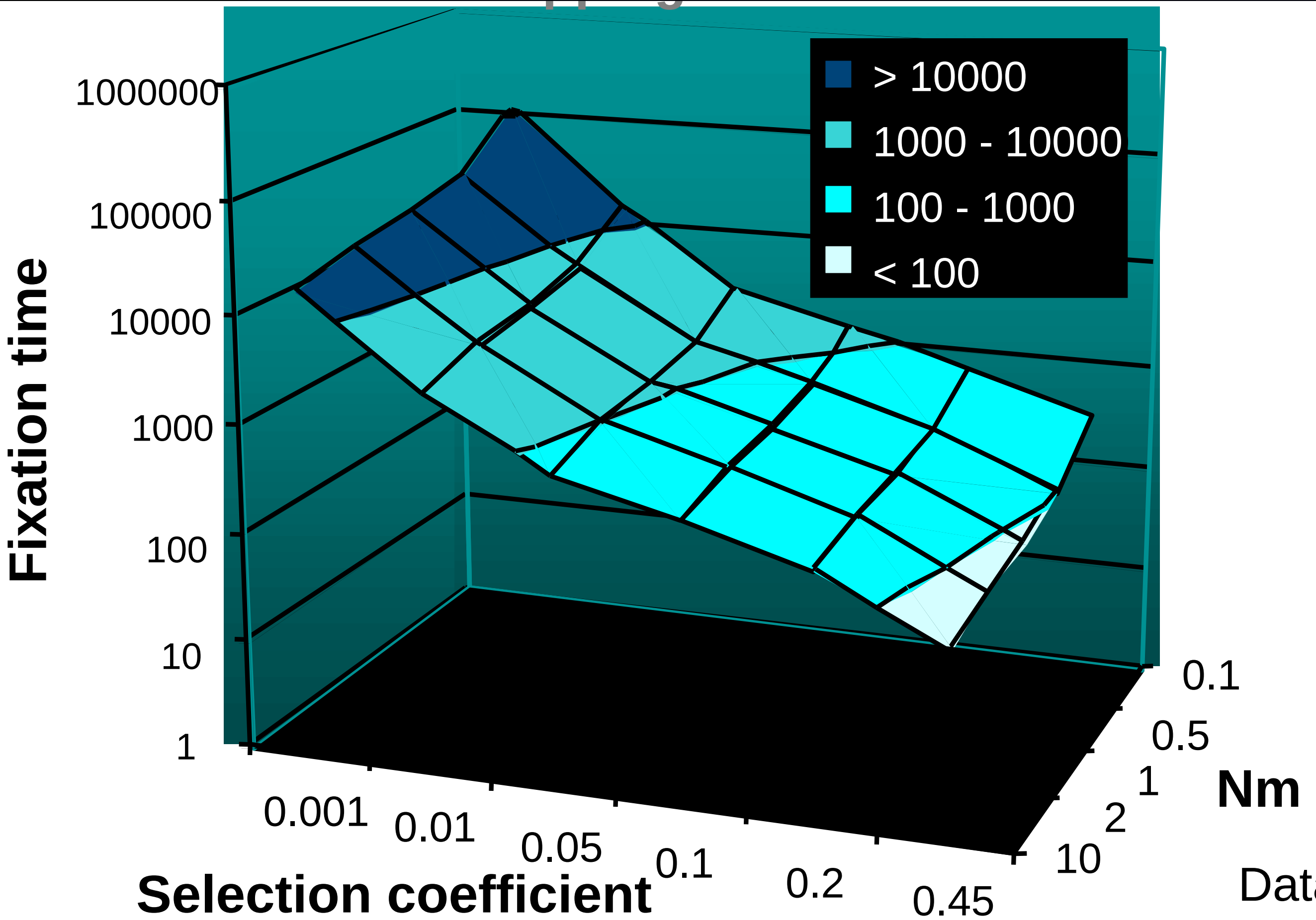
Strength of selection
S = 0.0001

Number of migrants
Nm = 1



Generation
200,000

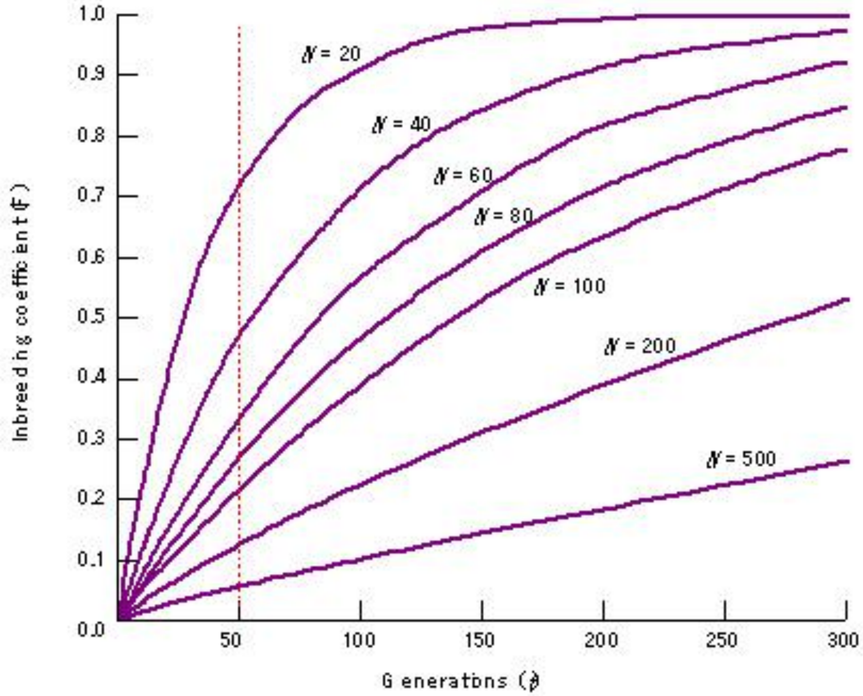
Time to fixation of a beneficial allele in a stepping stone model

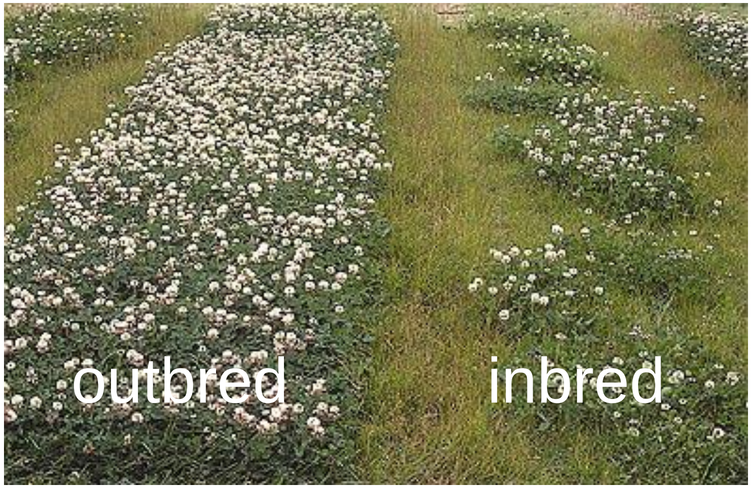


Data from Slatkin 1976

What does this new information tell us about the unification of species via gene flow?

Gene flow: implications for conservation





Small populations become inbred more rapidly than large populations

<u>Gene flow reduces inbreeding depression:</u>
migration rates into small populations are higher than into large populations

Gene flow: implications for conservation

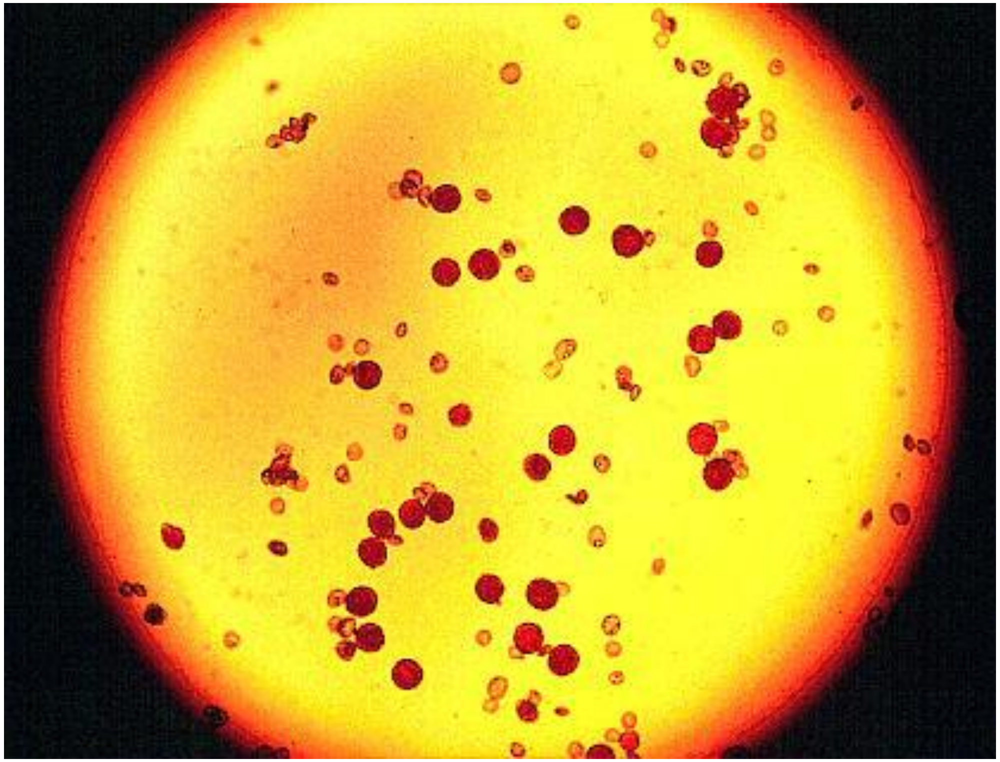
Gene flow may create heterosis or 'hybrid vigour,' which is manifested as increased size, growth rate or other parameters resulting from the increase in heterozygosity

Hybrid corn

Hybrid sunflower

Gene flow: implications for conservation

Gene flow between species (or hybridization) may result in outbreeding depression or genetic assimilation



Reduced pollen viability in interspecific hybrids

Gene flow: implications for conservation

Example of genetic assimilation:
Catalina Island Mahogany

Rieseberg et al. 1989

Gene flow: implications transgene escape

Prevalence of Crop x Wild Hybridization

Gene flow from crop plants into their wild relatives may lead to the escape of engineered genes.

Wheat	Yes	Millet	Yes
Rice	Yes	Common Bean	Yes
Maize	Yes	Rapeseed	Yes
Soybean	Yes	Groundnut	No
Barley	Yes	Sunflower	Yes
Cotton	Yes	Sugar Cane	Yes
Sorghum	Yes		

Gene escape is inevitable for most crops.

Ellstrand et al. (1999)

Gene flow: implications transgene escape

Bt protein Cry1Ac toxic to Lepidopteran Insects

Suleima helianthana
Sunflower Bud Moth (stem/developing bud)

Plagiomimicus spumosum
(developing bud; > 50% seed loss)

Gene flow: implications transgene escape

- How would you determine if a transgene is likely to spread in wild populations?

Unanswered Questions

- Is gene flow primarily conservative or creative?
- Are species tied together by gene flow as a single ‘evolutionary unit’?
- How often does gene flow impede versus assist adaptation?