

# The plant of the day



# Today's Topics

Non-random mating

Genetic drift

Population structure

# Big Questions

- What are the causes and evolutionary consequences of non-random mating?
- What is genetic drift and what are its evolutionary consequences?
- How do we determine if these mechanisms are acting in a population?



# Non-random mating

**Assortative mating** – mating with individuals that are similar or dissimilar for a given trait.





# Positive Assortative Mating

If the mating phenotype is genetically-based, what will **positive assortative mating** (mating with similar individuals) do to homozygosity at the loci affecting the trait?

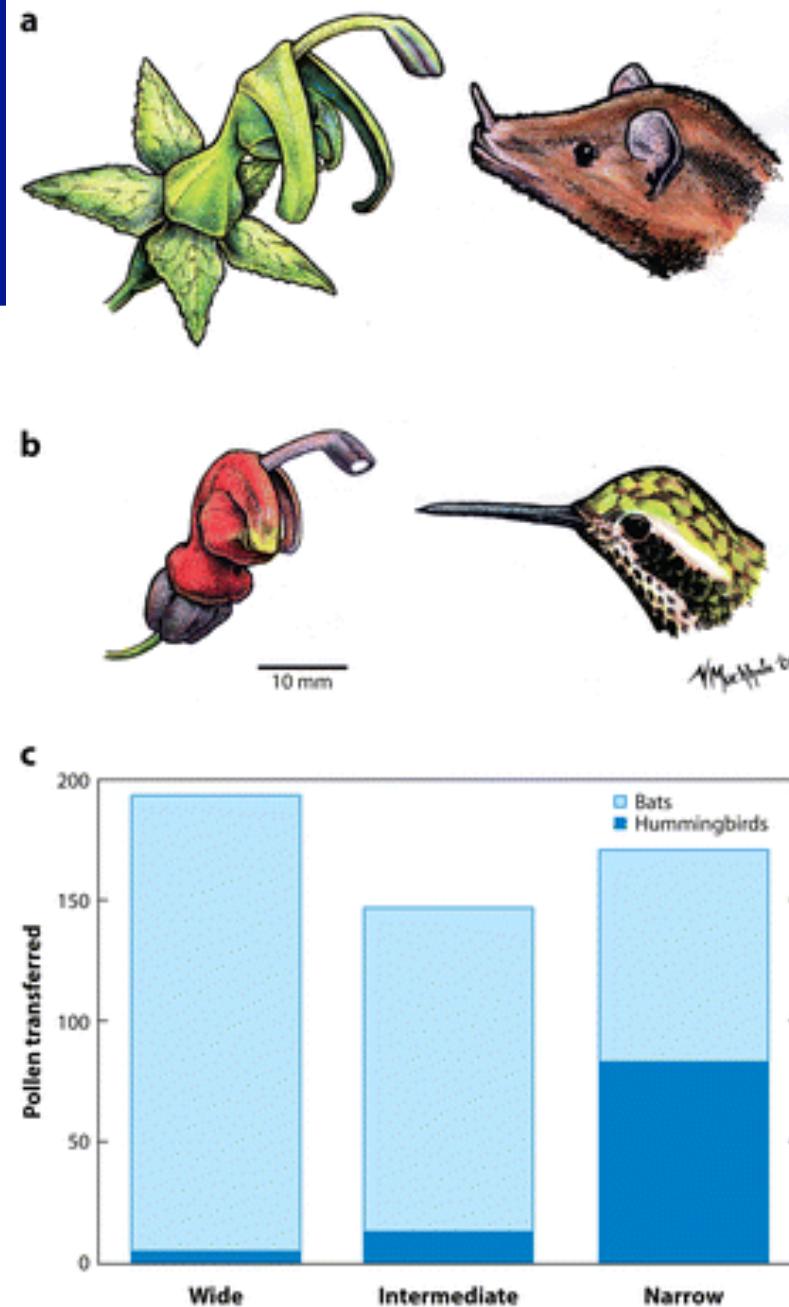
<u>AA</u>	<u>Aa</u>	<u>aa</u>
red	pink	blue
<b>AA</b>	<b>1/4 AA: 1/2 Aa: 1/4 aa</b>	<b>aa</b>



# Positive Assortative Mating

## An example

In the genus *Burmeistera*, bats are more efficient at moving pollen between wide flowers, whereas hummingbirds excel at pollen transfer between narrow flowers.





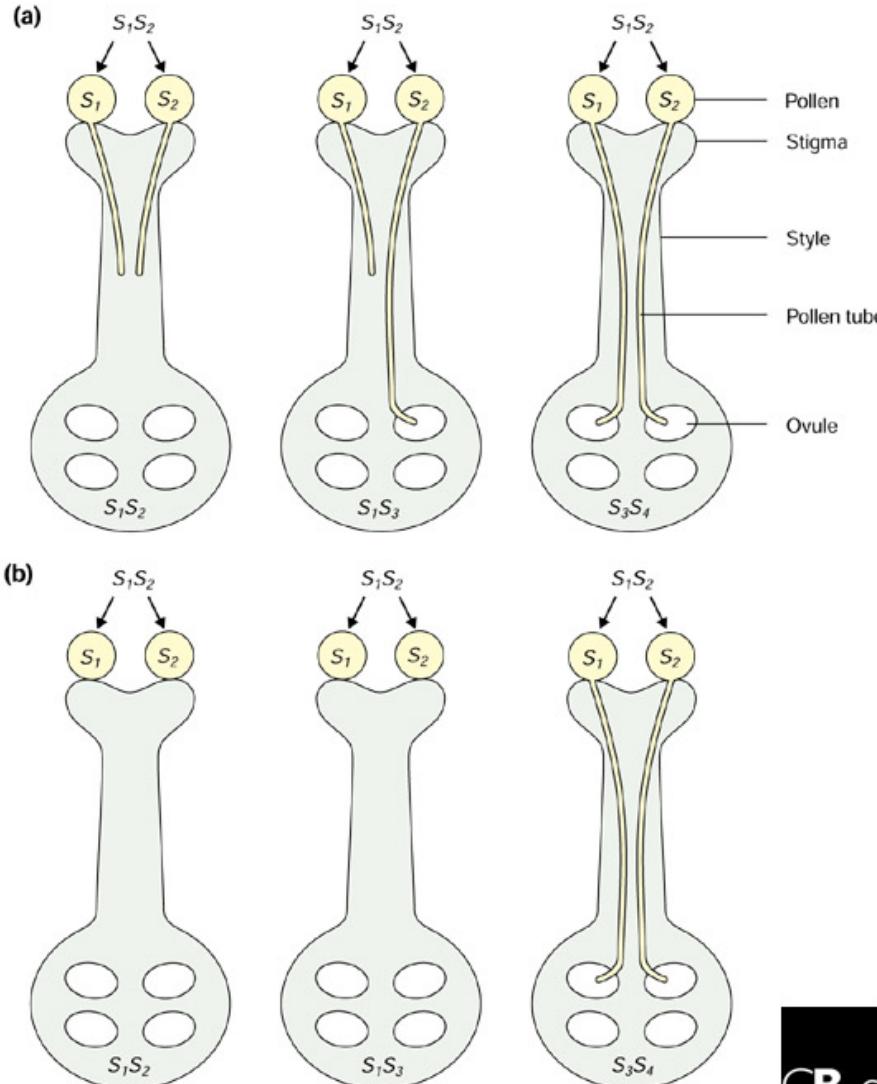
# Negative Assortative Mating

**Negative assortative mating** is preferential mating with dissimilar individuals, which has the opposite effect on heterozygosity in a population.





# Negative Assortative Mating



Plant self-incompatibility systems lead to negative assortative mating.

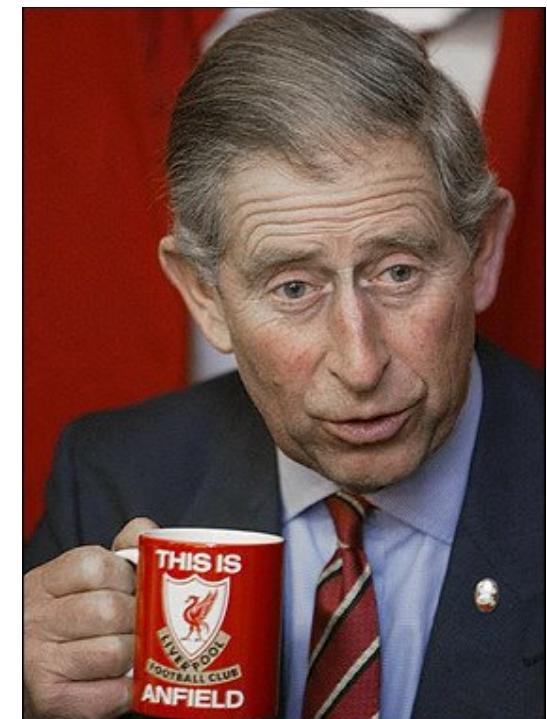
Examples: Sunflowers  
Cocoa tree  
Blue bells  
*Brassica rapa*  
(field mustard)



# Inbreeding

Inbreeding: mating with a close relative

Biparental: two different individuals are involved

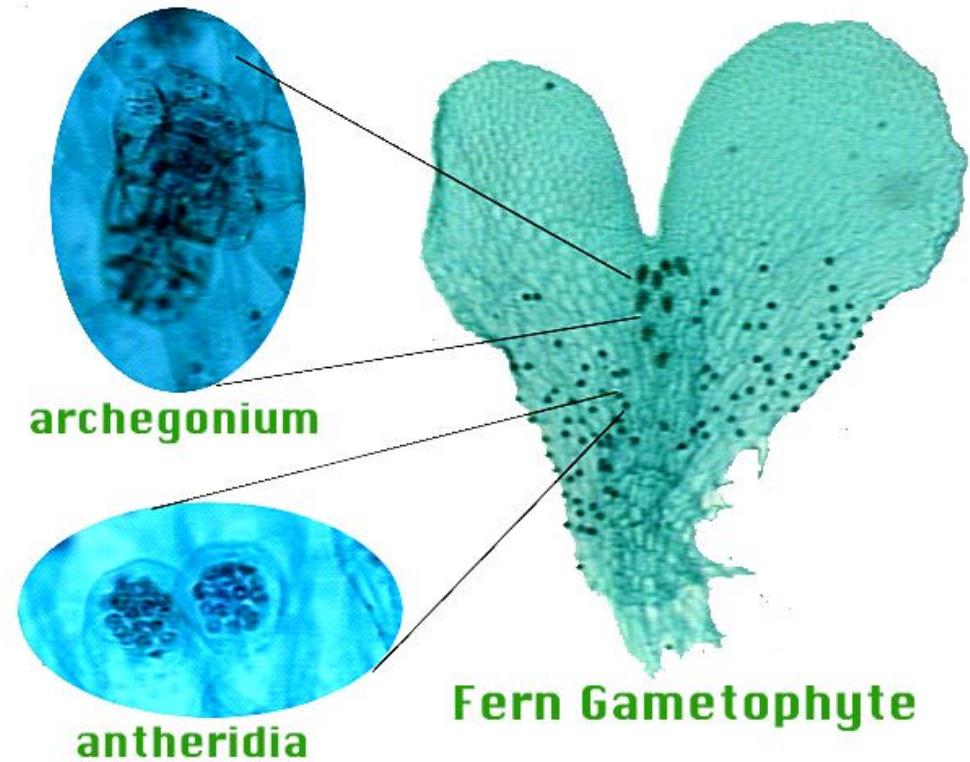




# Extreme inbreeding

Intragametophytic selfing: mating between gametes produced from the same haploid individual

- 100% homozygosity in one generation!
- some ferns and mosses





## Effect of inbreeding on genotype frequencies

### Selfing

P:	Aa x Aa		
F1:	25% AA	50% Aa	25% aa
F2:	37.5% AA	25% Aa	37.5% aa
F3:	43.75% AA	12.5% Aa	43.75% aa

Fewer heterozygotes and more homozygotes

Is this evolution?



# Inbreeding

Inbreeding does NOT change allele frequency by itself

Inbreeding coefficient ( $F$ ):

measures the extent to which populations depart from the expectations of the Hardy-Weinberg equilibrium

$H_e$  = Expected heterozygosity, HW ( $2pq$ )

$H_o$  = Observed heterozygosity

$$F = (H_e - H_o) / H_e$$

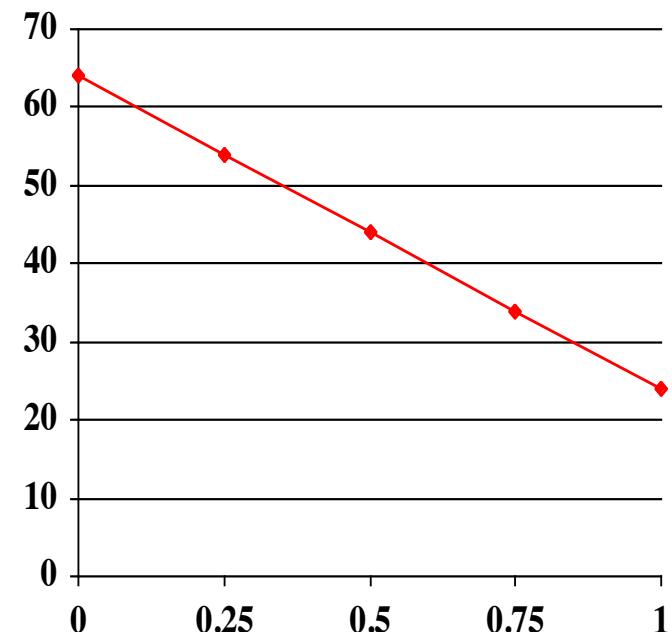
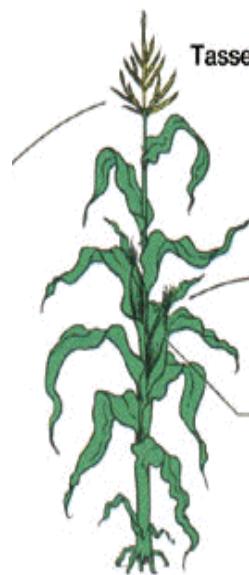


# Evolutionary Consequences of Inbreeding

In large, random mating populations, most individuals carry recessive deleterious alleles as heterozygotes

Under inbreeding, increased homozygosity for these recessive deleterious alleles results in reduced population mean fitness

Corn yield in relation to Inbreeding



Inbreeding Coefficient



# Evolutionary Consequences of Inbreeding

*Think – Pair – Share*

**When is inbreeding beneficial? Is inbreeding depression universal?**

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



# Genetic drift

**Definition:** Changes in the genotypic composition of populations due to random sampling.

One of the requirements for the maintenance of stable allele frequencies in populations is a very large population size.

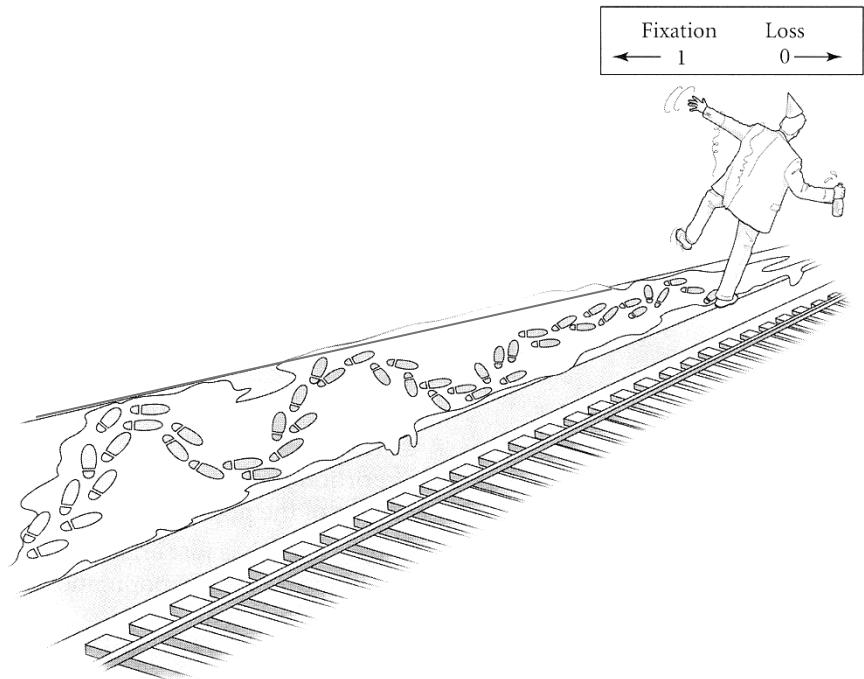
Genetic drift is the consequence of finite population size.



# Genetic drift

## Classic model:

Alleles that do not (necessarily) affect fitness fluctuate randomly in frequency, which eventually results in the loss of alleles from populations.



Futuyma *Evolution* 2009, fig. 10.2

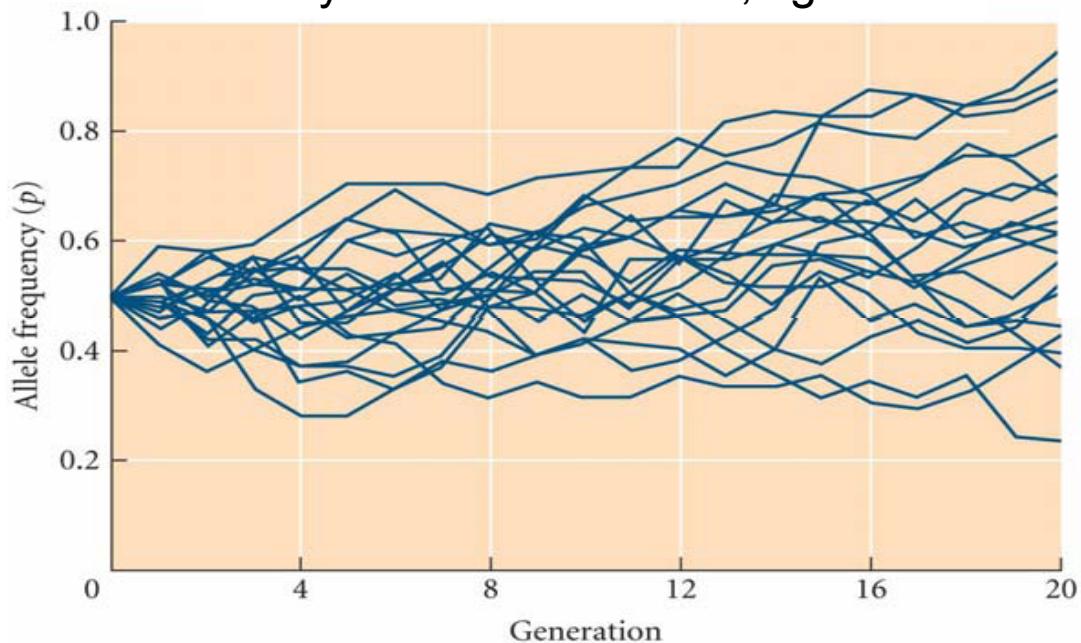


# Genetic drift

Different populations will lose different alleles.

The probability that a particular allele will be fixed in a population in the future equals the frequency of the allele in the population.

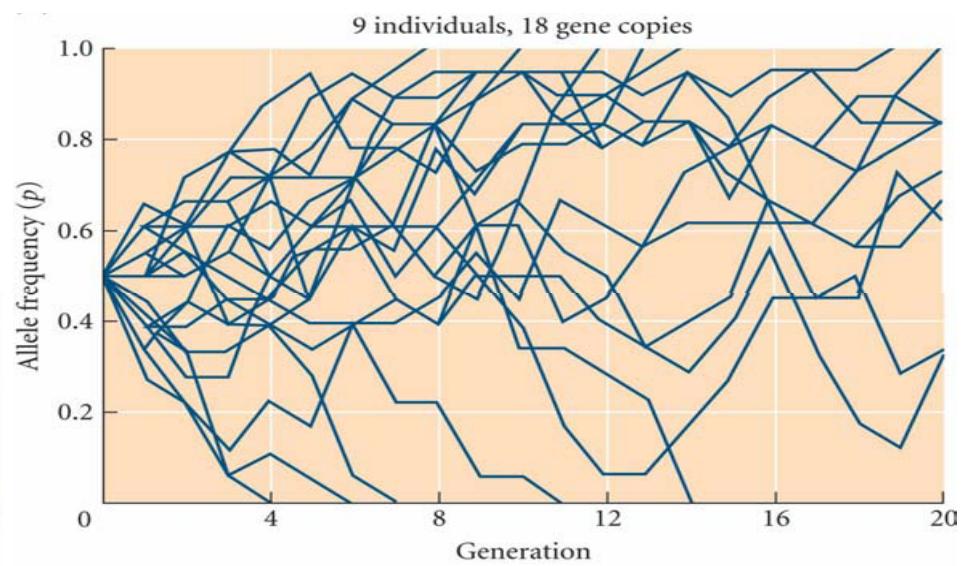
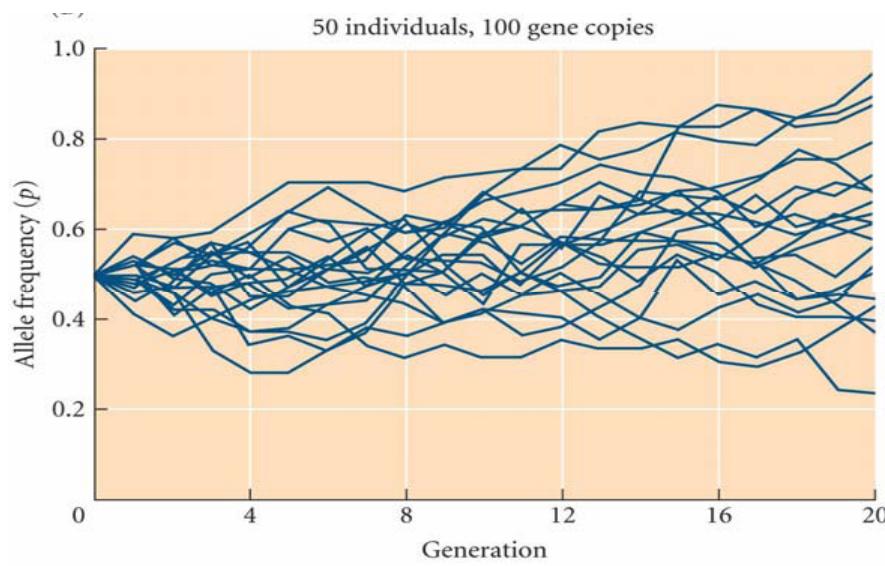
Futuyma *Evolution* 2009, fig. 10.3b





# Genetic drift

(Population) size matters. Why?





# Effective population size, $N_e$

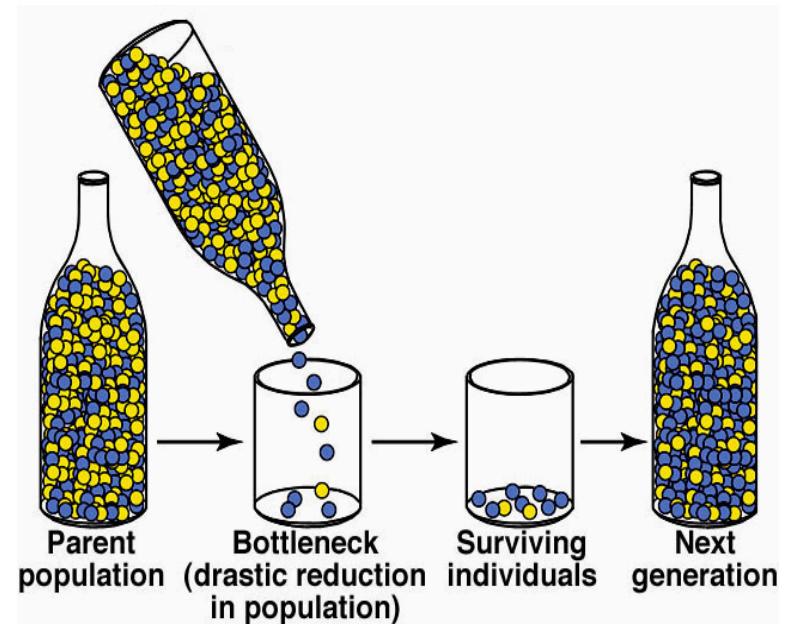
- number of individuals in the population that successfully pass genes to the next generation
- usually smaller than the actual population (census) size
- affected by biological parameters other than the number of breeding individuals in the population



# Effective population size

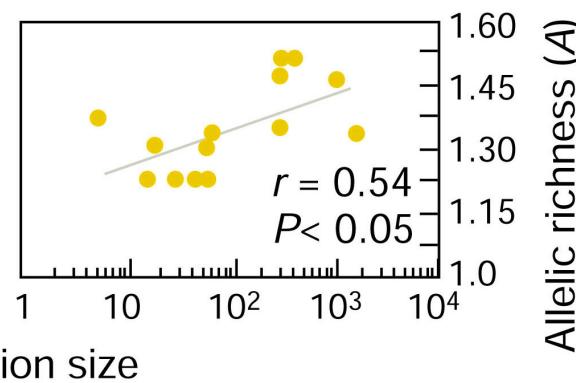
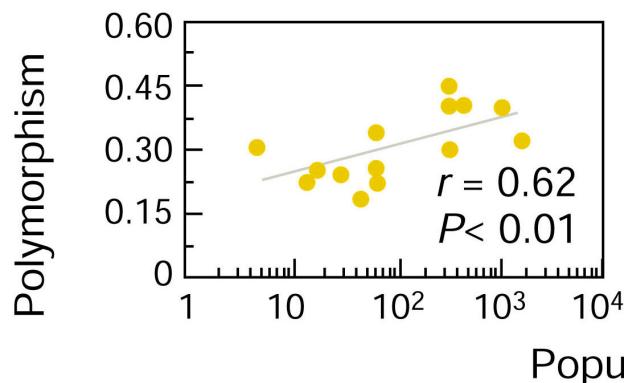
Factors that affect  $N_e$ :

- Variation in offspring number among individuals
- Natural selection
- Uneven sex ratios
- Inbreeding (reduces the number of different copies of a gene passed to the next generation)
- Fluctuations in population size

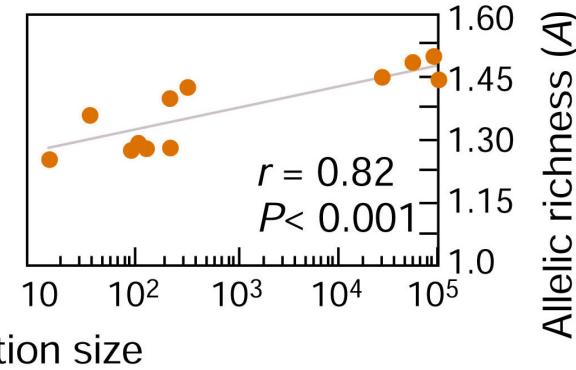
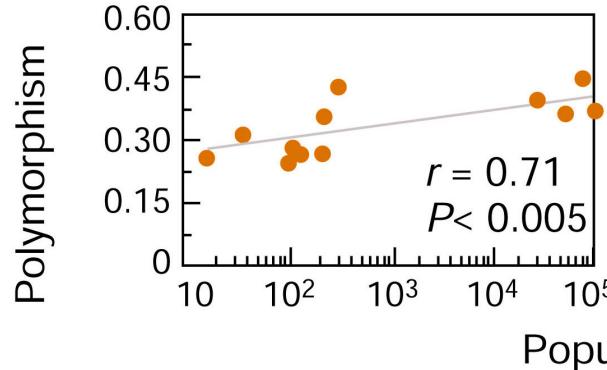




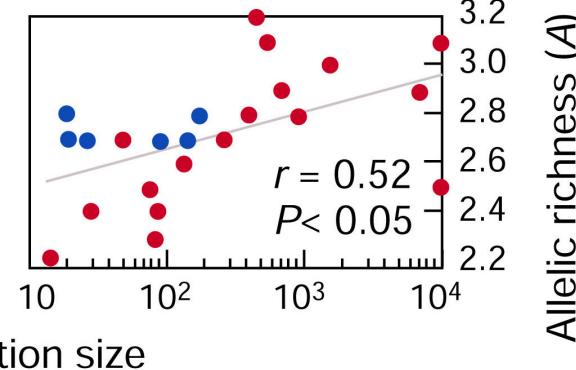
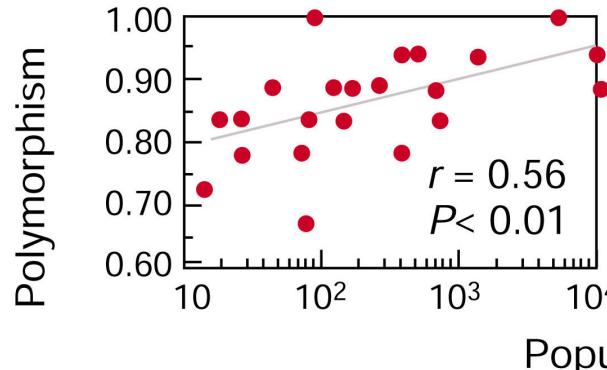
(a) *Salvia pratensis*



(b) *Scabiosa columbaria*

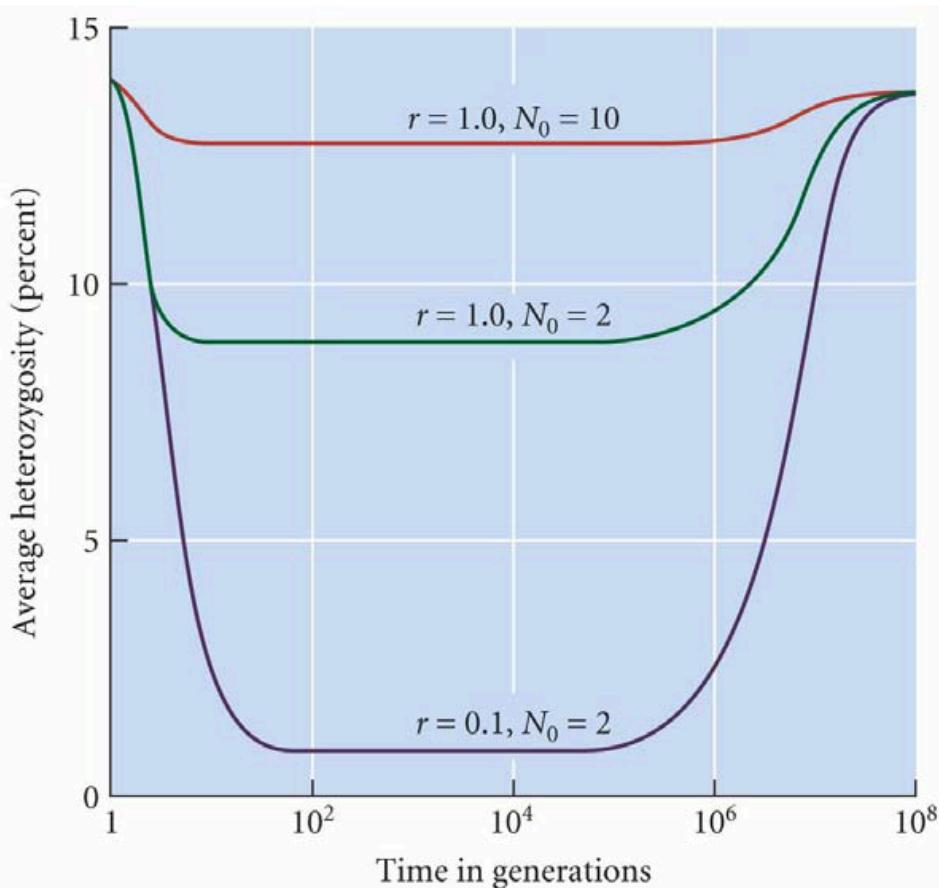


(c) *Eucalyptus albens*





# Founder effects



When a small number of individuals from a source population establish a new population, genetic variation can be lost.

Fewer founders and a small population growth rate ( $r$ ) result in greater loss of genetic diversity.

Eventually, genetic variation will be restored in a founding population. Why?

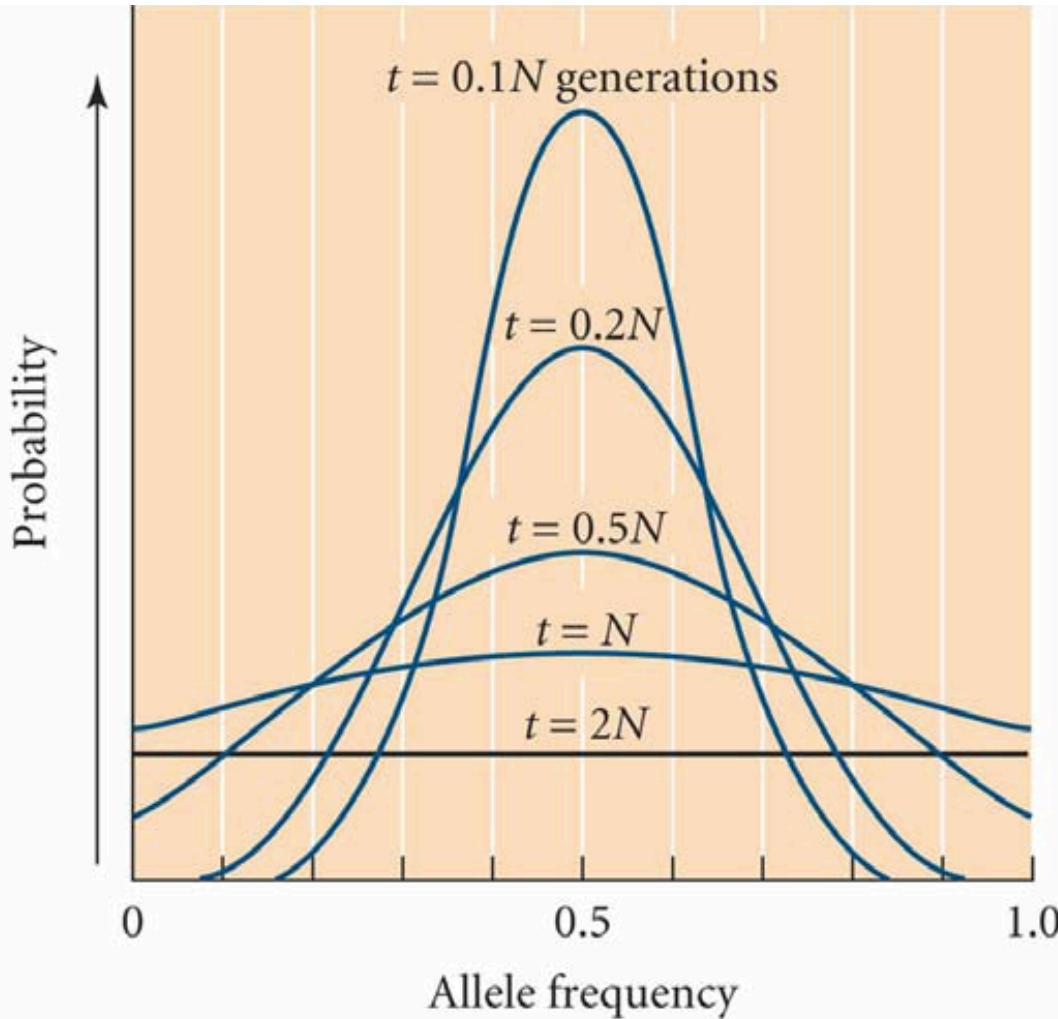


## Genetic drift: Concept check!

What is the approximate probability of fixation of a new neutral mutation that arises in an effective population of 1500 diploid *Arabidopsis thaliana* individuals?



# Genetic drift

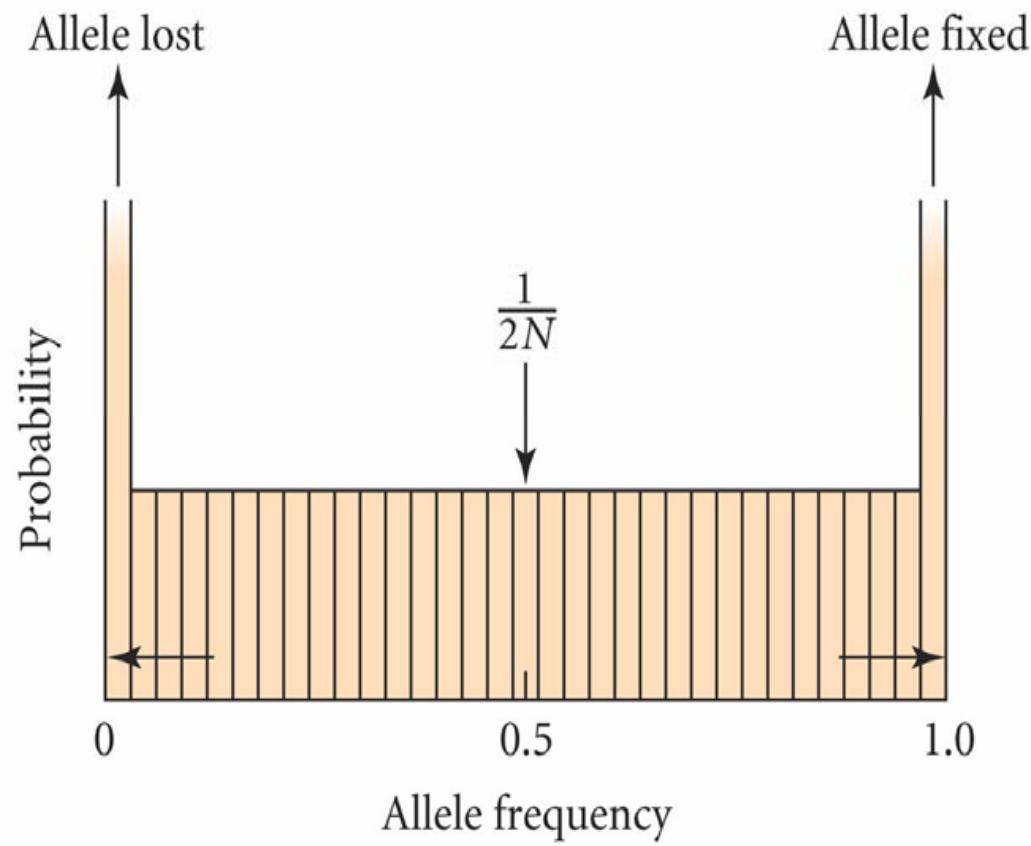


The likely magnitude of divergence from initial frequencies (here as  $p = q = 0.5$ ) increases with time and scales to population size ( $N_e$ ).



# Genetic drift

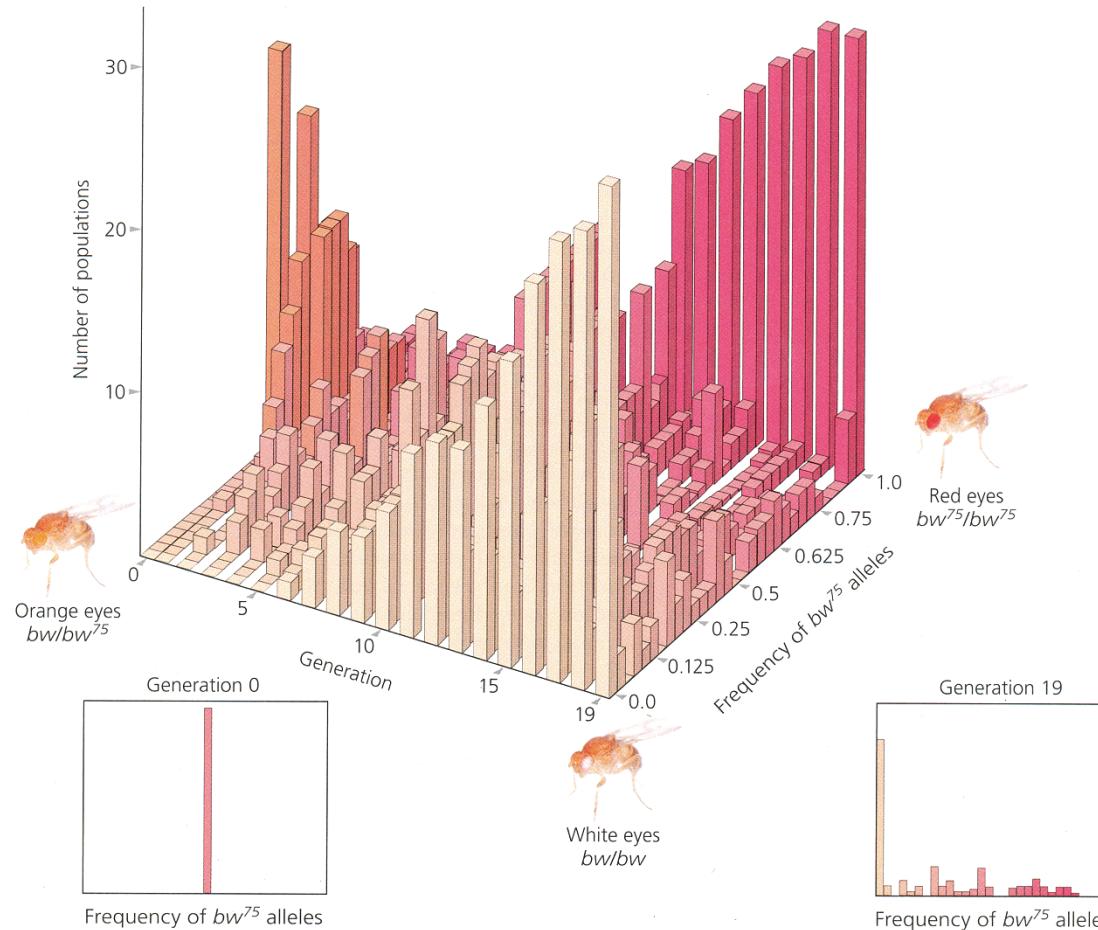
After  $2N$  generations, all allele frequencies between 0 and 1 are equally likely. Fixation or loss, however, are more likely.



Futuyma *Evolution* 2009, fig. 10.4b



# Genetic drift



Zimmer and Emlen *Evolution* 2013, fig. 6.4



# Genetic drift

In a finite population, allele frequencies are simultaneously affected by **both** selection and drift.

If  $s$  (the strength of selection) or  $N_e$  are small, then an allele will primarily evolve via genetic drift.

The theoretical critical value is  $4N_e s$   
( $4N_e s < 1$ , alleles are **nearly neutral**).



# Genetic Drift

- Within populations
  - Changes allele frequencies
  - Reduces variance among individuals
  - Can still predict genotype frequencies from allele frequencies using Hardy-Weinberg expectations
- Among populations (if there are many)
  - Does NOT change allele frequencies
  - Does NOT degrade diversity
  - Causes a deficiency of heterozygotes compared to Hardy-Weinberg expectations (if all populations are pooled), like inbreeding.



# The neutral theory of molecular evolution

## Observations:

- Many loci are polymorphic (Lewontin and Hubby, 1966)
- Proteins evolve at similar rates in different lineages (Kimura, 1968)

**Debate:** How much of evolution is neutral (i.e. via drift)?

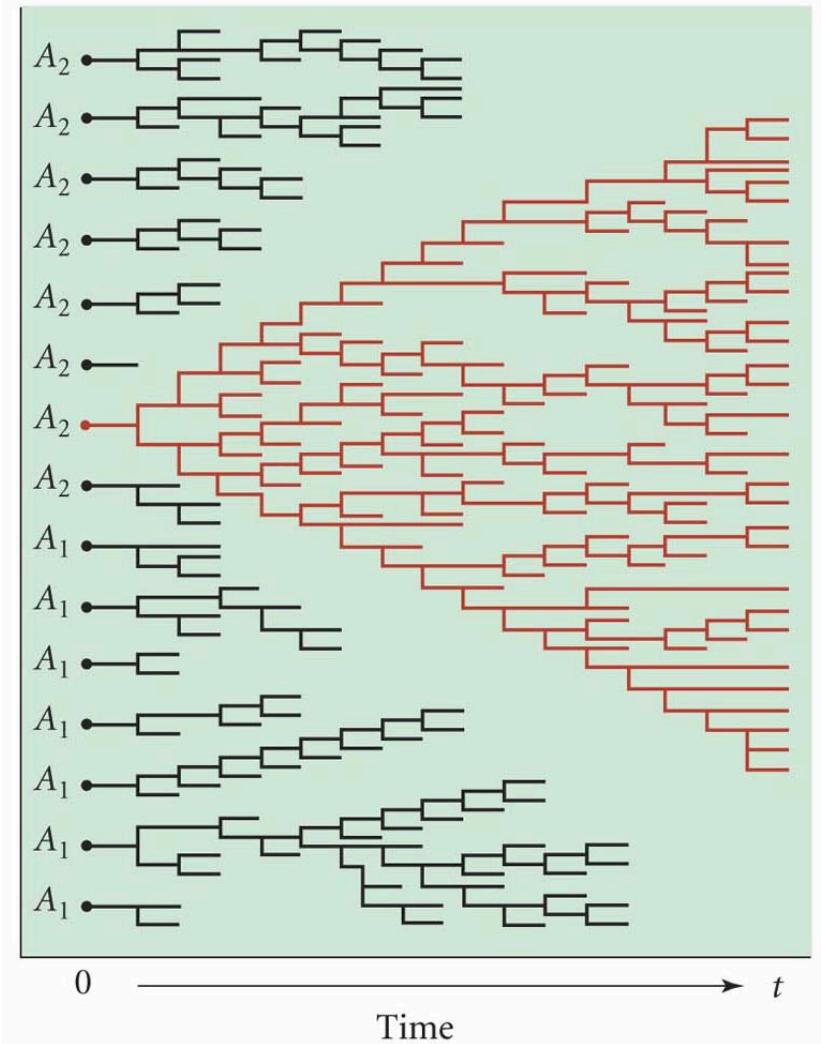
**Resolution?** The neutral theory proposes that the majority of mutations that are fixed are effectively neutral. Therefore, most genetic variation evolves via genetic drift (and at a relatively constant rate). **HOWEVER**, this does not propose that the majority of *phenotypic* variation is neutrally evolved.



# Coalescence

All gene copies in a population ultimately are descended from a single ancestral copy

(Or, all gene copies **coalesce** back to a single common ancestor)





# Population structure

How do we measure population genetic structure?



**Sewall Wright**



## Wright's fixation index

Fixation index ( $F$ ) is a measure of genetic differentiation among populations

Compares heterozygosity at different hierarchical levels. For example:

$$F_{ST} = (H_T - H_S)/H_T$$

$H_T$ : The overall expected HW heterozygosity for the **Total** set of (sub)populations

$H_S$ : The average expected HW heterozygosity among organisms within **(Sub)**populations



# *Linanthus parryae* population structure

TABLE 6.3 Hierarchical Structure of *Linanthus parryae*

Region	Subpopulations		Regions		Total	
	Allele frequency	Heterozygosity	Average allele frequency	Heterozygosity	Average allele frequency	Heterozygosity
W	0.573	0.4893	0.5153		B	
	0.717	0.4058				
	0.504	0.5000				
	0.657	0.4507				
	0.302	0.4216				
	0.339	0.4482				
C	9 × 0.000	0.0000	0.0138		C	
	0.032	0.0620				
	0.007	0.0139				
	0.008	0.0159				
	0.005	0.0100				
	0.009	0.0178				
	0.005	0.0100				
	0.010	0.0198			D	
	0.068	0.1268				
	0.002	0.0040				
	0.004	0.0080				
	0.126	0.2202				
	0.106	0.1895				
	0.224	0.3476				
	0.411	0.4842				
E	0.014	0.0276	0.1888	0.3062	0.1374	0.2371
	Average heterozygosity	$H_S = 0.1424$		$H_R = 0.1589$		$H_T = 0.2371$

What is the genetic divergence among sub populations?

What could be causing the divergence in flower colour among the sub populations?

# Unresolved Questions

- How often does genetic drift (versus natural selection) create patterns of genetic variation within species?
- What proportion of new mutations are fixed via natural selection versus genetic drift?



# Genetic drift: why is it important?

- Erodes genetic variation within populations
- Causes population differentiation
- Strength is dependent on population size
- The demographic history of populations affects patterns of genetic variation
- Can oppose selection (e.g. conservation implications)
- Provides a “neutral” model for evolutionary change and most molecular changes are effectively neutral