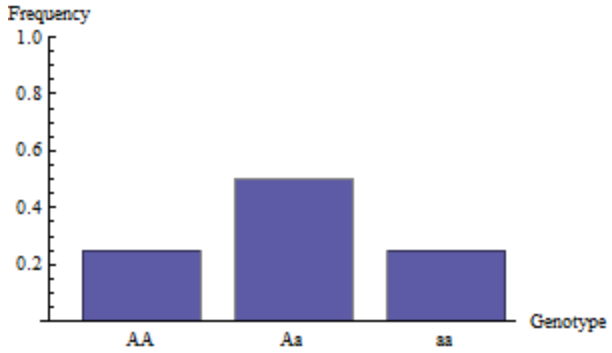
Exam Thursday

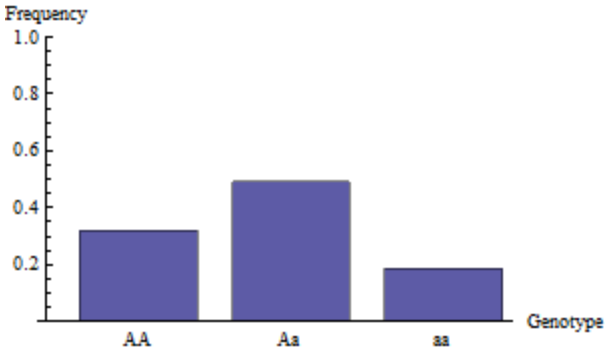
- **Covers material through Today's lecture**
- **Practice problems and answers are posted**
- **Bring a calculator**
- **5 questions, answer your favorite 4**
- **Please use clear, short sentences!**
- **Comments on Equations…**

Genetic Drift

Adaptive evolution



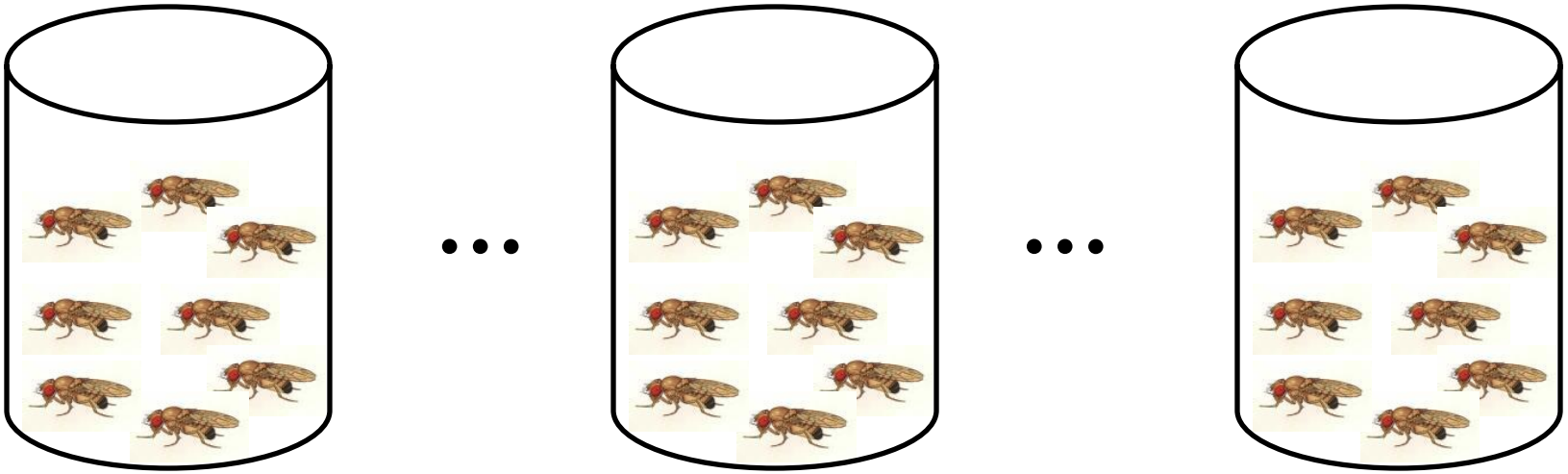
Non-adaptive evolution



In both cases above, AA genotypes are favored by natural selection

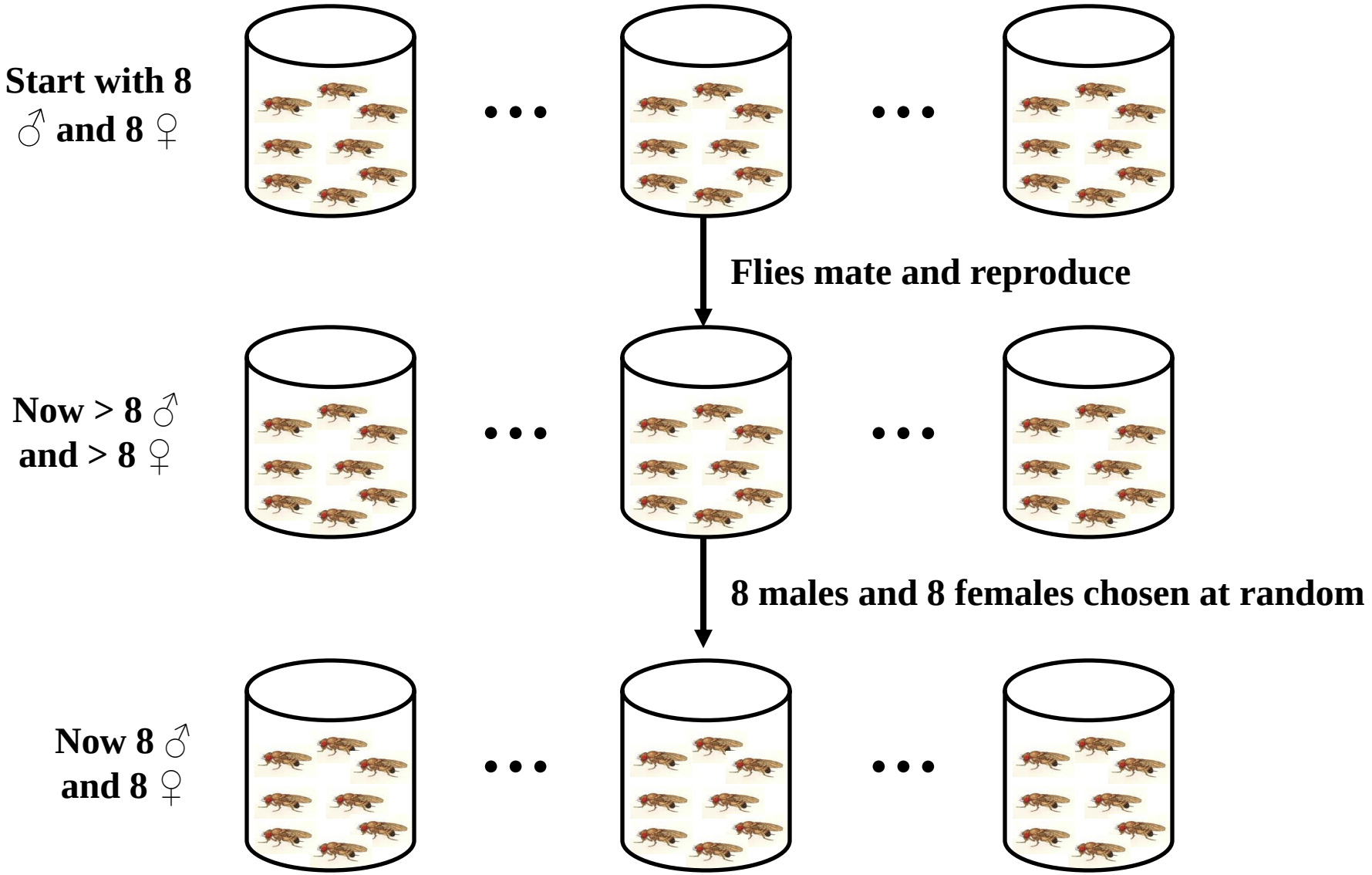
What happened in the right-hand population?

A classic experiment

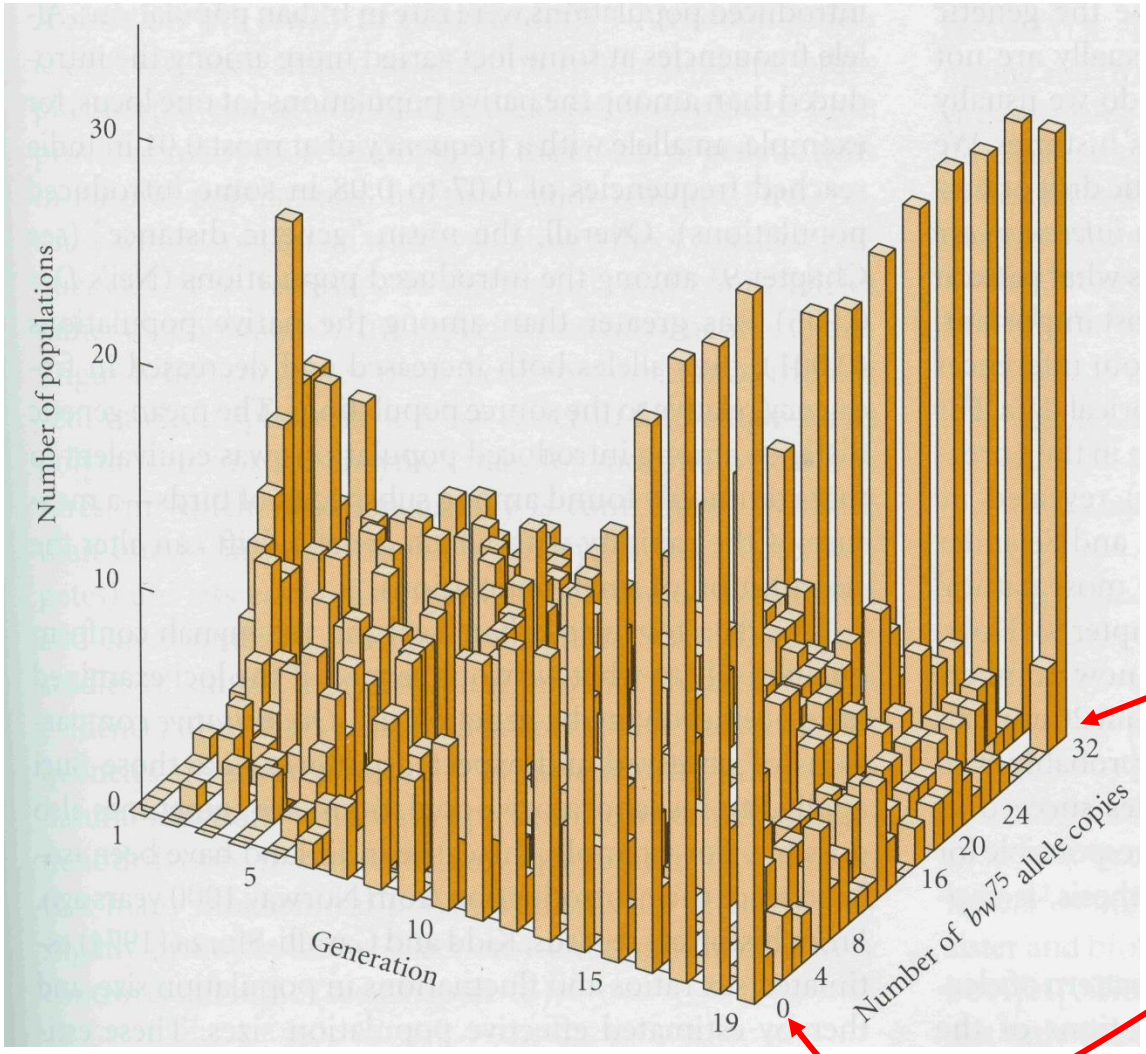


- **Initiated 107 experimental populations of *Drosophila*, each with 8 males and 8 females heterozygous for the eye color alleles *bw* and bw^{75} (Buri, 1956). Since all individuals were heterozygous, the initial allele frequency of the *bw* allele was ½.**

Propagated the 107 populations for 19 generations



What happened?



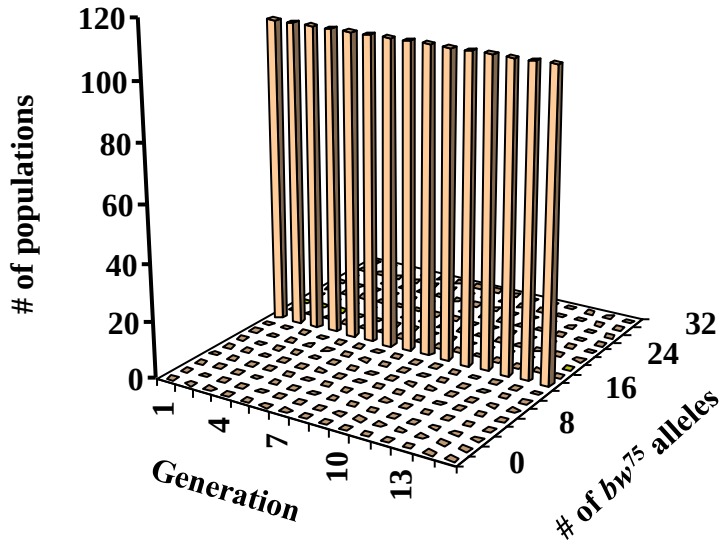
Populations fixed for bw^{75}

Populations fixed for bw

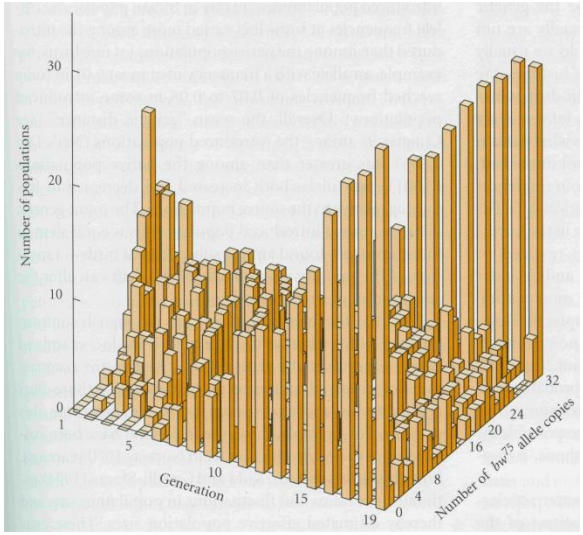
Almost all of the populations became fixed for one of the two alleles!

What happened to Hardy-Weinberg?

Expected under Hardy-Weinberg



Data actually observed



WHY???

What happened to Hardy-Weinberg?

- **Random mating** ✓
- **No selection** ✓
- **Infinitely large population**
- **No gene flow** ✓
- **No mutation** ✓

Why does violating this assumption matter?

- **In a finite population, the alleles present in the next generation are a random sample**

- **This random sampling causes deviations from the population mean**

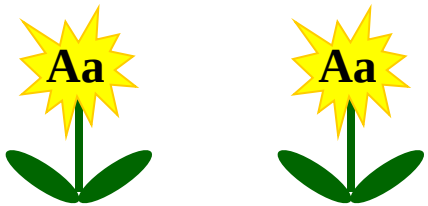
- **It is this *sampling error* that causes GENETIC DRIFT**

Genetic drift – Random changes in the frequencies of two or more alleles or genotypes within a population

A simple example of drift in a diploid population

Imagine a diploid population with a constant size of two individuals. If the population is initially composed of two heterozygous individuals:

Parental generation (*p* =.5):



Gametes:

Offspring generation:

# of A alleles	Allele frequency, *p*	Probability
0	0	$(1-1/2)^4 = .0625$
1	.25	$4(1/2)(1-1/2)^3 = .25$
2	.5	$6(1/2)^2(1-1/2)^2 = .375$
3	.75	$4(1/2)^3(1-1/2) = .25$
4	1	$(1/2)^4 = .0625$

The probability of becoming fixed for the A or the a allele is .125 in a single generation!

Together, these observations reveal three basic facts about genetic drift

1. **The expected change in allele frequency due to drift is 0. This is because allele frequencies increase and decrease with equal probability.**

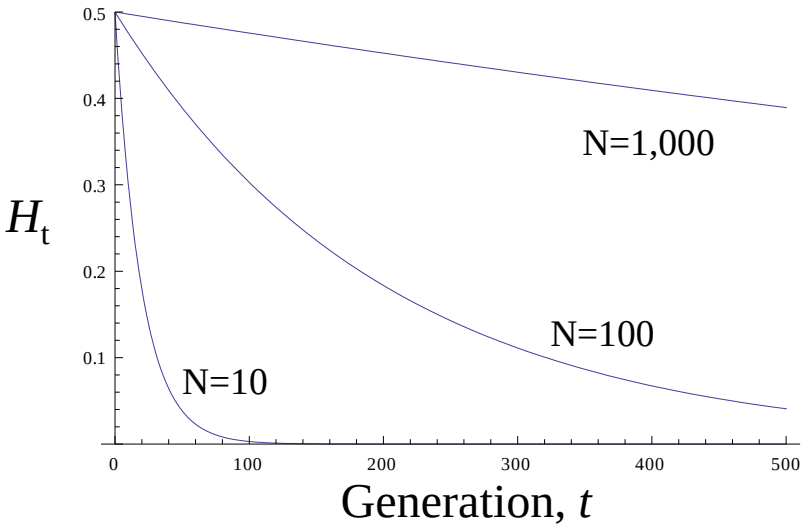
2. **Drift decreases the genetic variance within a population. Eventually a single allele will become fixed.**

3. **Drift increases the genetic variance between populations. Eventually populations become fixed for different alleles.**

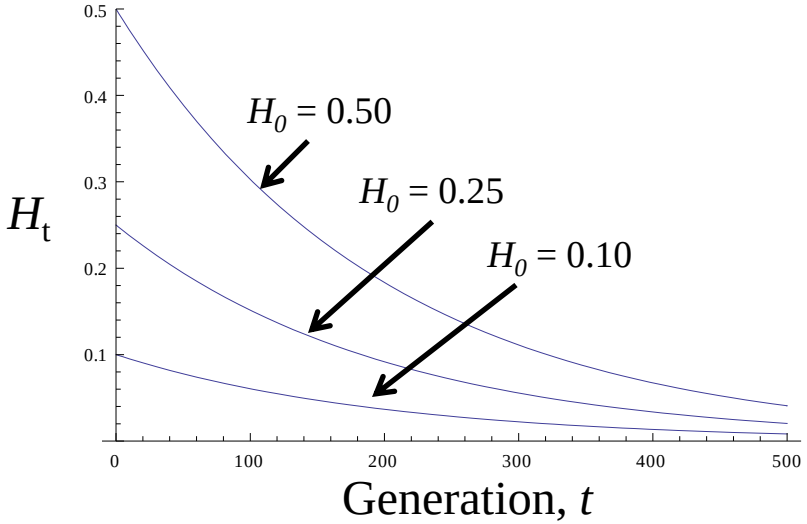
The rate of drift I: Heterozygosity

$$H_t = H_0\left(1-\frac{1}{2N}\right)^t$$

Effect of population size



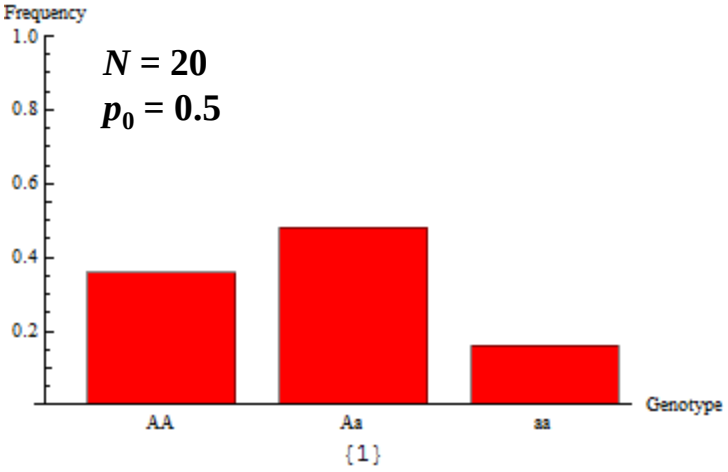
Effect of initial heterozygosity

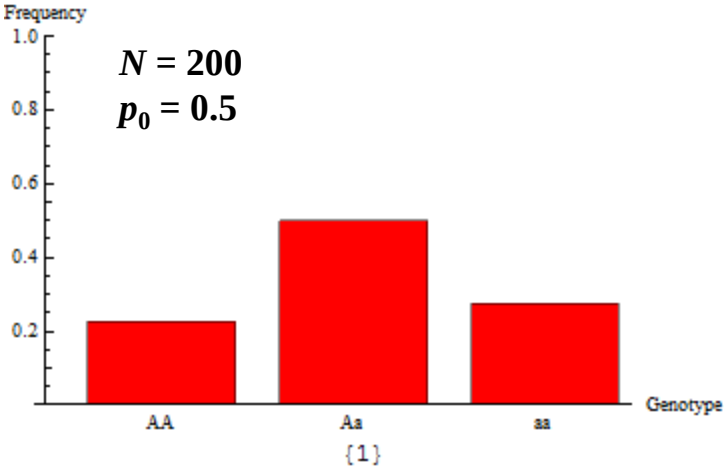


H_t is the heterozygosity of the population at time t – The probability of drawing a heterozygous individual at random from the population.

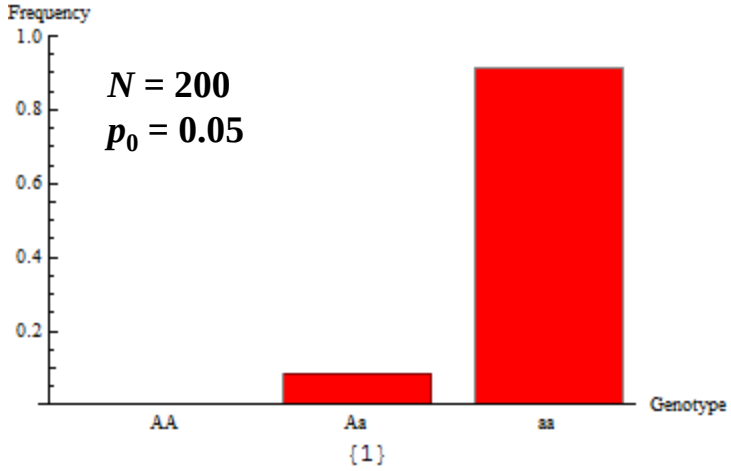
The rate of drift II: Allele frequencies

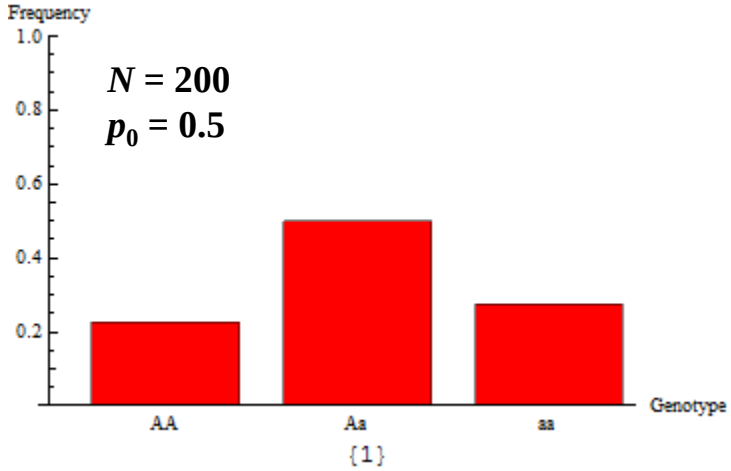
Effect of population size





Effect of initial allele frequency





Summary of drift

1) **The larger the population size, *N*, the longer polymorphism and heterozygosity will persist.**

   → Genetic drift is weak in large populations

2) **The closer the initial allele frequency is to ½, the longer heterozygosity and polymorphism will persist.**

Practice Problem

A team of scientists working on a species of marine crab was interested in determining whether natural selection was favoring increased shell thickness as a defense against predators. The same team was also interested in predicting whether increased shell thickness would evolve as a result. To this end, the scientists measured the average shell thickness of all crabs in the population at the beginning of the year and found it to be $\bar{x}_T = 10mm$. At the end of the year, before the crabs mated and produced the next years offspring, the scientists measured the average shell thickness of the surviving crabs (those that were not killed by predators), estimating the mean shell thickness of these selected parents as $\bar{x}_S = 12mm$. In a previous study, the same group of scientists had estimated that the slope of a regression of mid-parent shell thickness on offspring shell thickness was 0.50. Use this information to answer the following questions.

A. What is the heritability (narrow sense) of shell thickness?

B. What is the selection differential acting on shell thickness?

C. What will the response to selection exerted by predators be?

D. What do you estimate the shell thickness of the crabs will be in the next generation?

The interaction between drift and mutation

- **Drift acts to remove polymorphism from a population**
- **Mutation acts to regenerate polymorphism**
- **In a large population, mutation introduces new alleles as rapidly as they are eliminated by genetic drift.**
- **As a consequence, substantial genetic polymorphism can be maintained!**

More specifically, we expect the equilibrium heterozygosity at a locus to be:

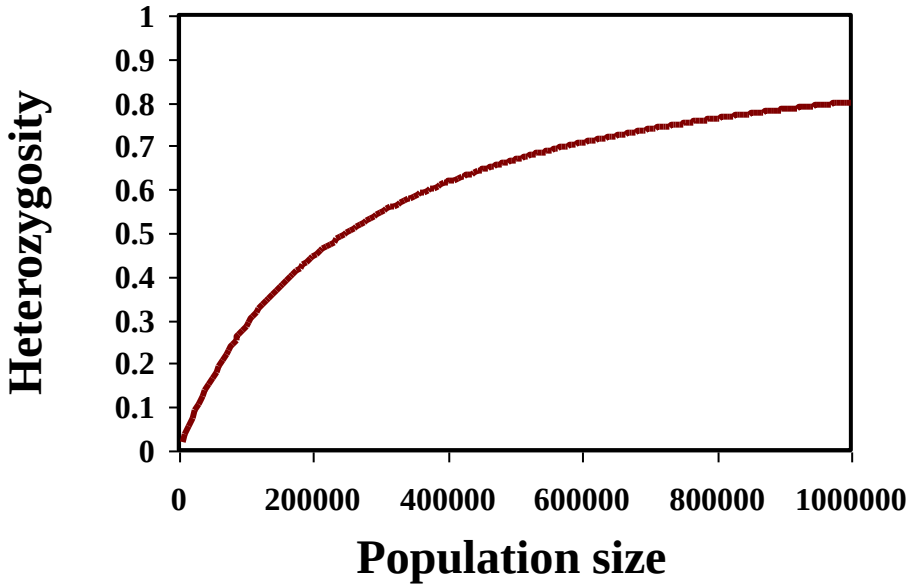
$$\hat{H} = \frac{4N\mu}{1+4N\mu}$$

Where *N* is the population size, and μ is the per locus mutation rate

The balance between mutation and drift

$$\hat{H} = \frac{4N\mu}{1+4N\mu}$$

Based on an infinite alleles model



It doesn't take a huge population to maintain substantial polymorphism/heterozygosity!

A quick historical refresher…

- **Prior to 1966, the majority of evolutionary biologists believed that almost all alleles differed in their effects on an organism's fitness.**

- **If this were the case, polymorphism would be quite rare since natural selection, acting in isolation, rapidly removes polymorphism and genetic variation.**

- **Studies based on molecular data reported in 1966 and 1968 shattered this conventional view, suggesting that many alternative alleles may be neutral with respect to an organisms fitness.**

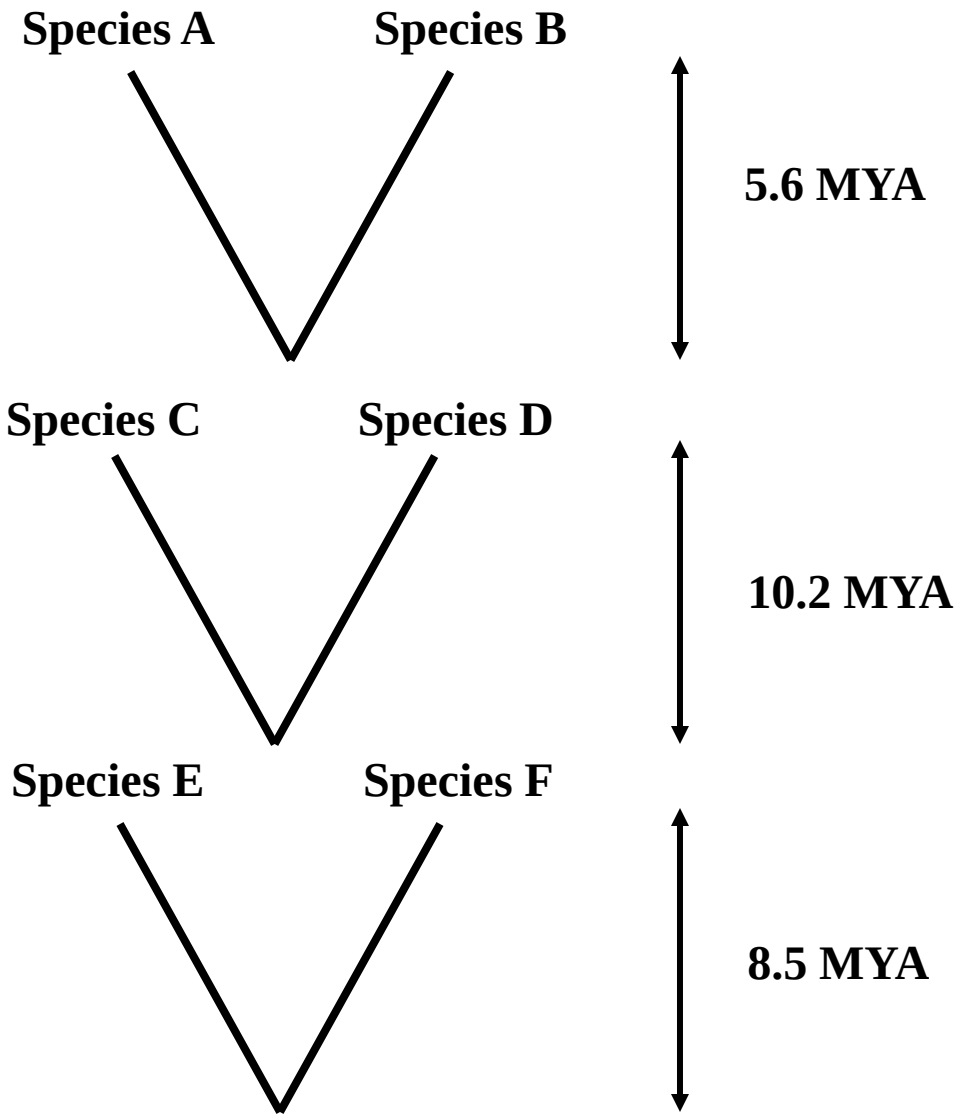
Study 1: Lewontin and Hubby, 1966

	NUMBER OF SPECIES EXAMINED	AVERAGE NUMBER OF LOCI PER SPECIES	AVERAGE PROPORTION OF LOCI	
			POLYMORPHIC PER POPULATION	HETEROZYGOUS PER INDIVIDUAL
Insects				
Drosophila	28	24	0.529	0.150
Others	4	18	0.531	0.151
Haplodiploid wasps[a]	6	15	0.243	0.062
Marine invertebrates	9	26	0.587	0.147
Marine snails	5	17	0.175	0.083
Land snails	5	18	0.437	0.150
Fishes	14	21	0.306	0.078
Amphibians	11	22	0.336	0.082
Reptiles	9	21	0.231	0.047
Birds	4	19	0.145	0.042
Rodents	26	26	0.202	0.054
Large mammals[b]	4	40	0.233	0.037
Plants[c]	8	8	0.464	0.170

$$\overline{H} = .096$$

Observed levels of polymorphism are too great to be compatible with fitness differences among alleles

Study 2: Kimura, 1968



- **Estimated dates of divergence from the fossil record**

- **Counted the number of amino acid differences between species for a given protein. *e.g.*, γ interferon:**

  Human: Met Lys Try Thr Ser…
  Mouse: Met Asn Ala Thr His…

- **From this data, Kimura estimated evolutionary rates for each protein in the various lineages**

Study 2: Kimura, 1968

- **Kimura found that a given protein evolved at a similar rate in different lineages**

- **Kimura concluded that natural selection was an unlikely explanation**

- **Instead, Kimura concluded that the data could be best explained by mutation and genetic drift**

The neutral theory of molecular evolution

Motoo Kimura

- Most mutations are selectively neutral
- Fixation of these mutations occurs through genetic drift not selection
- As a consequence, the substitution of alleles at the molecular level proceeds at a constant rate

The neutral theory predicts a constant rate of evolution at the molecular level

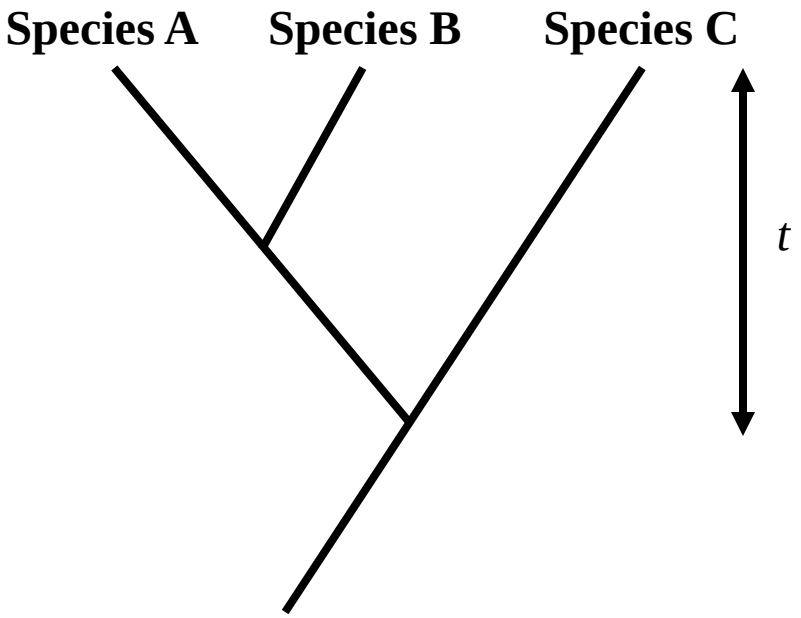
- **The frequency of a new mutation is $1/(2N)$**
- **The probability that a new mutation fixes due to drift is then $1/(2N)$**
- **In every generation we expect there to be $2N\mu$ new mutations**

<u>We can then draw the following conclusion:</u>

Once a steady state is reached, we expect $2N\mu$ $[1/(2N)] = \mu$ new mutations to become fixed in any generation. In other words, the rate of evolution at a locus is equal to the mutation rate at that locus

This prediction suggests the existence of a 'molecular clock'

Utility of the molecular clock



- **Estimate the mutation rate, μ, for a locus**
- **Estimate the # of allelic substitutions at that locus between two species**
- **From this it is possible to estimate how long ago the species diverged**

<u>Example:</u>

Imagine there have been 42 allelic substitutions between Species B and Species C, and that the mutation rate at this locus has been independently estimated at $1X10^{-6}$. We could then estimate the date of species divergence, *t*, as $42/(2*1X10^{-6})$ or 21 million years ago!

Practice Problem

$$\Delta\bar{z} = R = h_N^2 \,\mathrm{cov}[z, w] = h_N^2 S$$

Define each piece of the equation above means, how each might be measured, and why each is important for evolution by natural selection

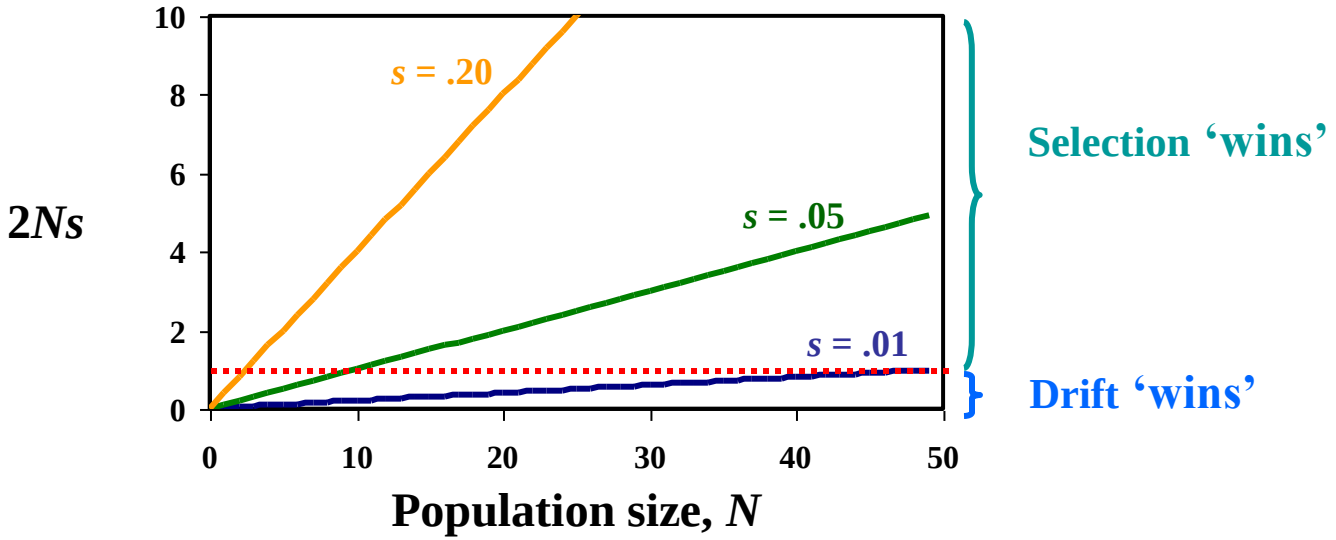
But what about loci that are not ‘neutral’?

- **We have already considered how mutation and drift interact in the absence of selection**
- **We know, however, that many loci are not selectively neutral**
- **As a consequence, at least in some cases, we need to consider how drift and selection interact**

How do drift and selection measure up?

A general rule of thumb:

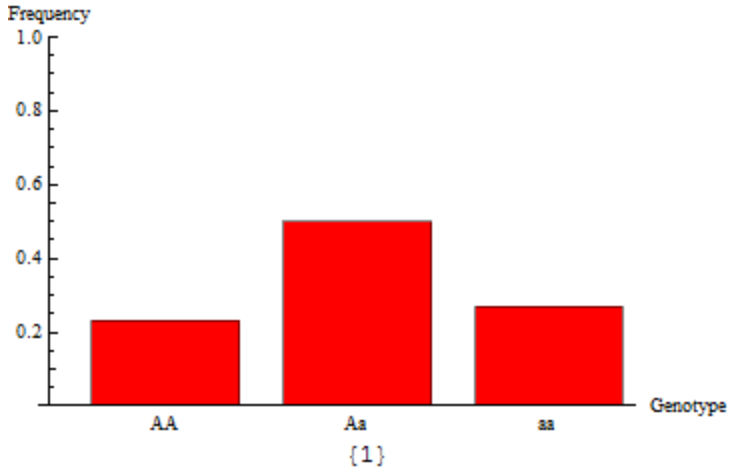
- If $2Ns >> 1$ evolution is driven by natural selection
- If $2Ns << 1$ evolution is driven by genetic drift



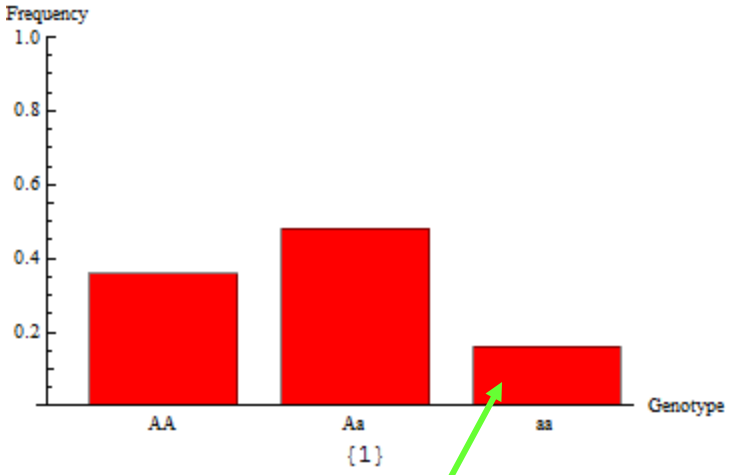
For initially frequent alleles, selection dominates drift for all but the smallest populations

An example of drift and selection

$2Ns \approx 2(500)(.05) = 50 > 1$



$2Ns \approx 2(5)(.05) = .5 < 1$



Here drift has caused 'maladaptation'

How do drift and selection measure up?

Drift is an important evolutionary force for selected loci only if:

1. Population size is small

2. Selection is weak

or

3. Alleles are very infrequent (e.g., new mutations)

Drift can cause new beneficial mutations to be lost

- The probability a new beneficial mutation reaches fixation in an infinitely large population is only:

$$\pi_{fix} \approx 2hs$$

The dominance coefficient

The selective advantage of the new mutation

- The probability of fixation for new beneficial mutations is fairly small

- The probability of fixation is greatest for beneficial mutations which are dominant ($h = 1$)

- Many new and potentially beneficial mutations are lost by chance alone!

A summary of genetic drift

1. **Genetic drift is the product of sampling error in finite populations**

2. **Genetic drift leads to the random fixation of alleles and the loss of polymorphism**

3. **Genetic drift reduces genetic variation within populations but increases genetic variation between populations**

4. **For selectively neutral loci, the interaction between drift and mutation can maintain substantial levels of heterozygosity and polymorphism**

5. **For selectively neutral loci, the interaction between drift and mutation leads to a constant rate of molecular evolution**

6. **For loci under selection, drift is only an important evolutionary force if:**
   - **Population size is small**
   - **Selection is weak**
   - **Alleles are very rare (e.g., new mutations)**

Practice problem

You are studying a small population of the plant, *Centaurea maculosa*, to evaluate the potential for this population to become invasive on the Palouse. This population is currently composed of 1087 individual plants. Your research has revealed that an allele which confers increased competitive ability is segregating within this population and is favored by selection with an estimated s = 0.012. If this allele were to spread to fixation, this population would be a serious threat as an invader; if the allele were to be lost by chance, the population would not be a serious threat.

A. If the initial allele frequency of the selectively favored allele is 0.34, does your data indicate the plant is a potential threat as an invader? Justify your response mathematically and verbally.

B. If, instead, the allele frequency of the selectively favored allele is only 1/1087, would you change your answer?