

# Genetic Drift

A common conception about evolution is that the features of an organism have evolved due to random (undirected) change.

Some processes in biology are random – like mutation.

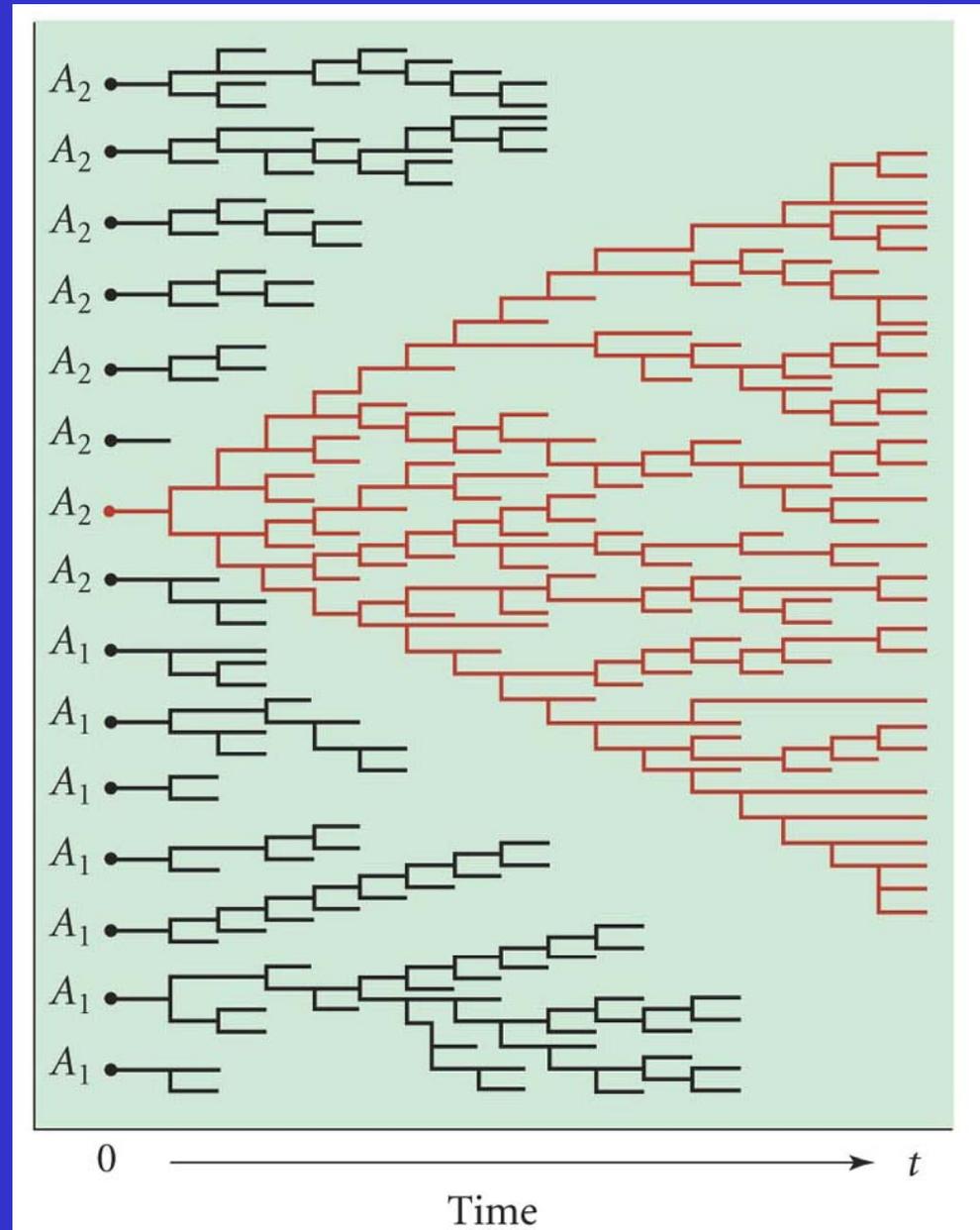
Natural selection is not random. Natural selection is the nonrandom preservation of random variation.

Genetic drift is a random process that can be important in the evolution of some populations.

One of the requirements for the maintenance of allele frequencies in populations is a very large population size. Genetic drift is the consequence of finite population size.

Alleles that do not affect fitness fluctuate randomly in frequency. Random fluctuation eventually results in the loss of alleles (allelic extinction) from populations. One allele becomes fixed – the only allele in the population.

Sampling error (random chance) results in some gene copies being lost and others continuing.



### Parents

$A_2A_1$   $A_2A_1$   
 $A_1A_1$   $A_1A_2$   
 $A_1A_2$   $A_2A_1$   
 $A_1A_1$   $A_2A_2$   
 $A_2A_2$   $A_2A_1$

In this example, there are  $N = 10$  parents and the frequency of the  $A_1$  allele is 0.5

### Very large gamete pool

$A_1A_1A_1A_1$   
 $A_1A_1A_1A_1A_1A_1A_1$   
 $A_1A_1A_1A_1A_1A_1A_1A_1A_1$   
 $A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1$   
 $A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1A_1$   
 $A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2$   
 $A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2$   
 $A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2$   
 $A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2A_2$   
 $A_2A_2A_2A_2A_2$

Allele frequencies in the gamete pool *exactly* reflect the allele frequencies in the parental population

### Small number of gamete pairs

$A_1$   $A_1$   
 $A_1$   $A_1$   
 $A_1$   $A_2$   
 $A_1$   $A_1$   
 $A_2$   $A_2$   
 $A_1$   $A_1$   
 $A_1$   $A_2$   
 $A_2$   $A_1$   
 $A_1$   $A_1$   
 $A_1$   $A_1$

Draw  $2N$  gametes at random from the gamete pool—that is, 10 pairs of gametes. Because of random chance, allele frequencies in this sample may not be exactly the same as allele frequencies in the gamete pool itself

### Offspring

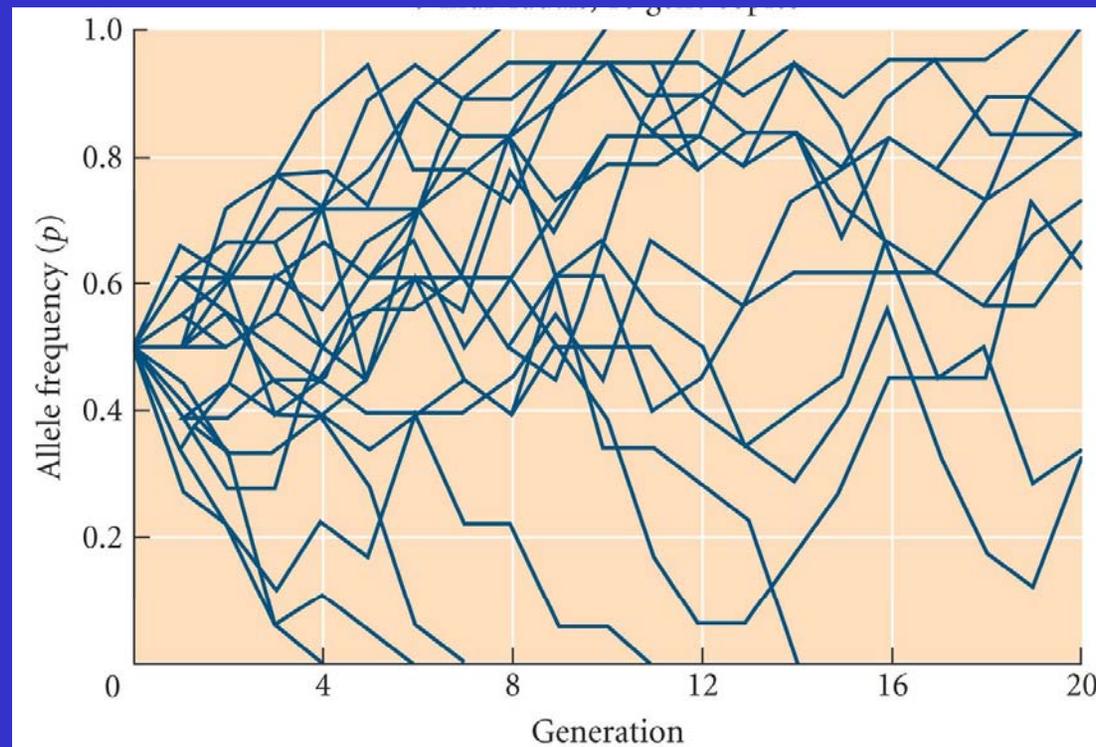
$A_1A_1$   $A_1A_1$   
 $A_1A_1$   $A_1A_2$   
 $A_1A_2$   $A_2A_1$   
 $A_1A_1$   $A_1A_1$   
 $A_2A_2$   $A_1A_1$

The gamete pairs will form  $N$  offspring (in this case, 10 offspring); here the frequency of the  $A_1$  allele has by chance increased to 0.75

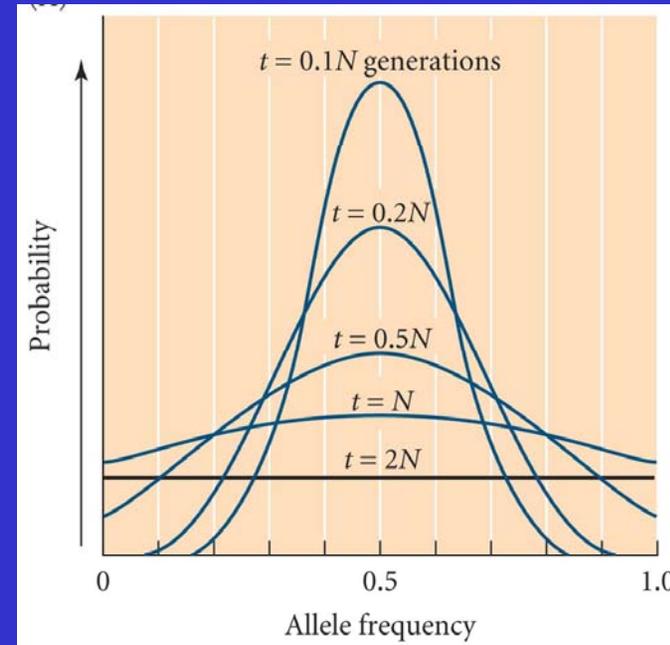
Different populations will lose different alleles.

The probability that a particular allele will be fixed in a population in the future equals the frequency of the allele in the population. If there are two alleles in a population,  $A$  and  $a$ , with frequencies  $p$  and  $q$ , the probability that the allele  $a$  will be lost at some point in the future is  $p$  and the probability that allele  $A$  will be lost is  $q$ .

If a large number of populations is considered, each drifting, the total heterozygosity overall will decrease.

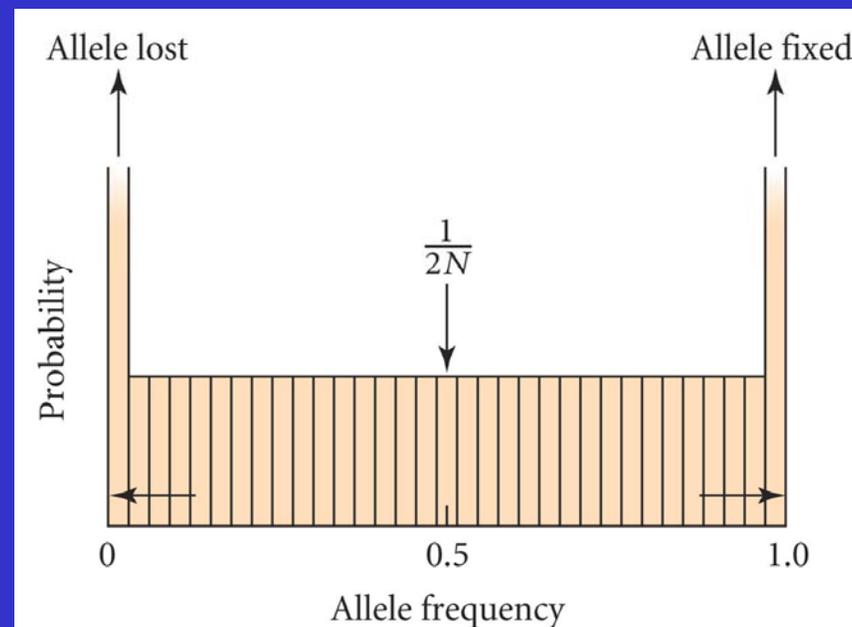


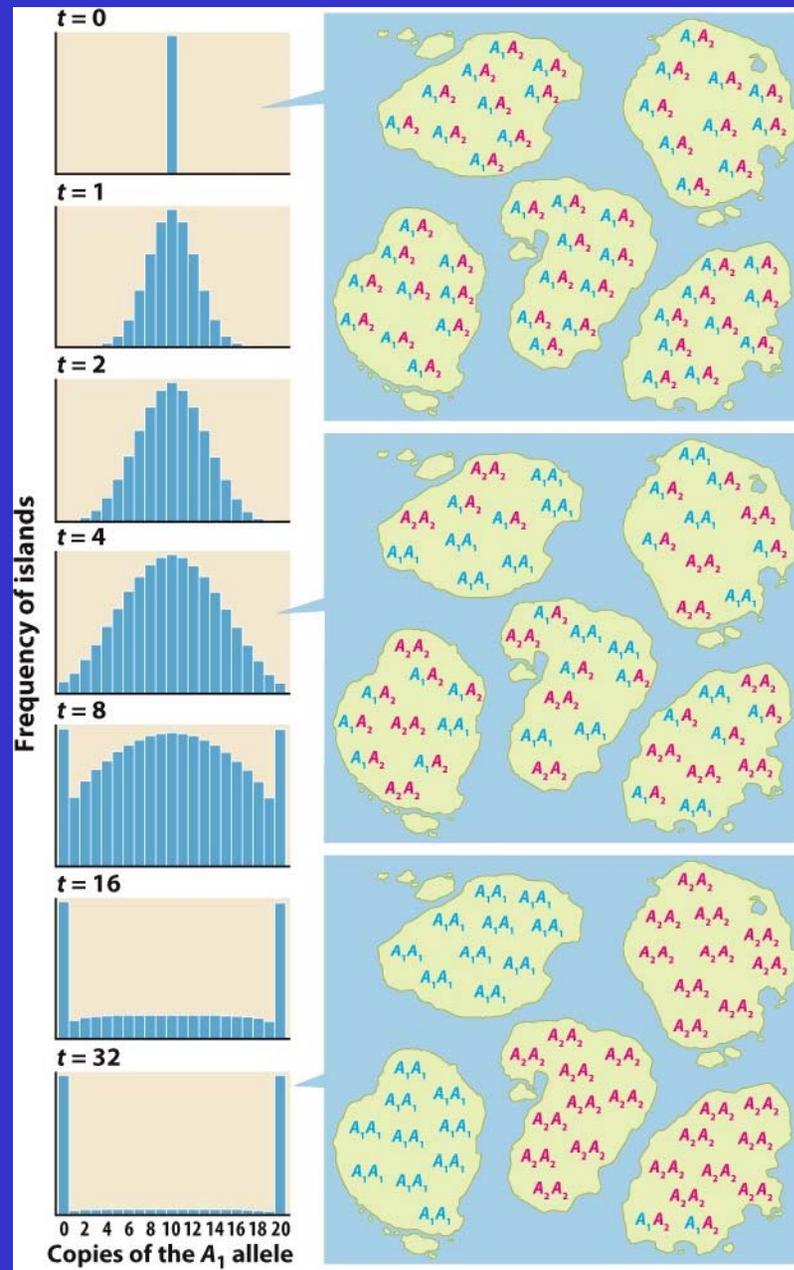
Starting with a population size of  $N$  with two alleles in equal frequencies  $p$  and  $q$ , the likely magnitude of divergence from the initial frequencies increases with time.



After  $2N$  generations, all allele frequencies are equally likely.

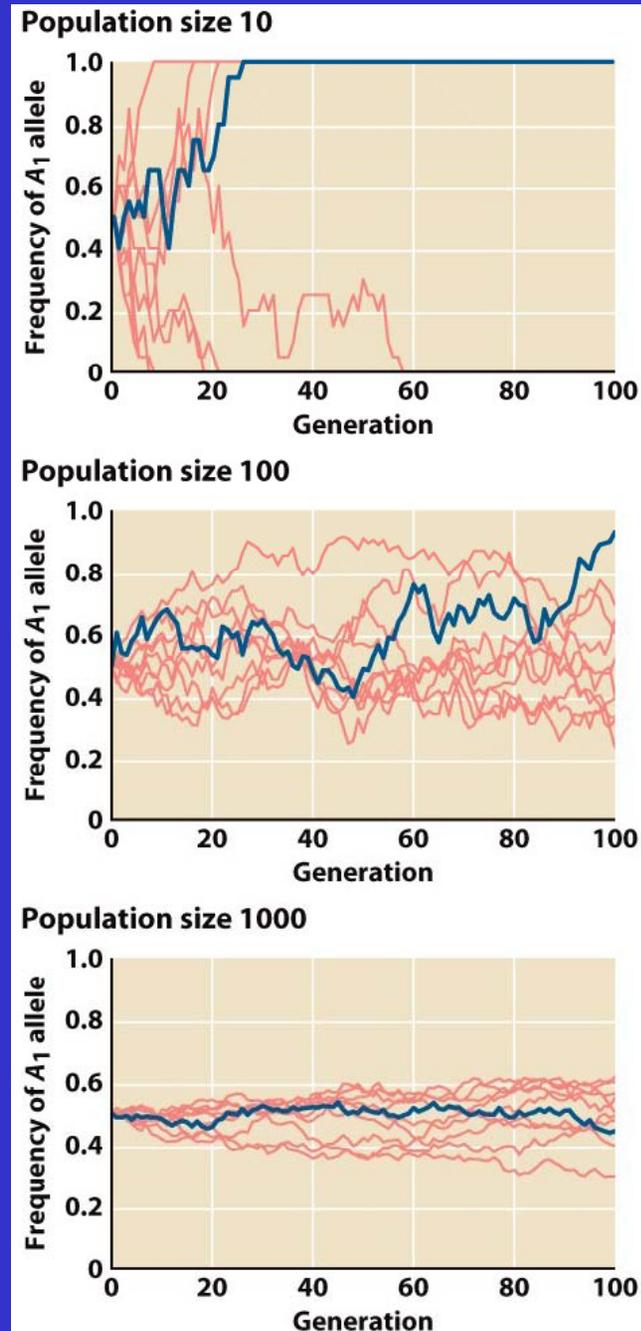
The average time to fixation of one of the alleles is  $4N$  generations.





The effective population size is the number of individuals in the population that successfully pass genes to the next generation. This is usually smaller than the actual number (census number) in the population.

The smaller the effective population size, the faster a population will drift, and the faster one of the alleles in the population will become fixed.



The effective population size ( $N_e$ ) is affected by biological parameters other than the number of individuals in the population.

Variation in offspring number among individuals can reduce  $N_e$ . If some individuals produce more offspring than others their alleles, even those that have no effect on fitness, will be passed on at higher rates.

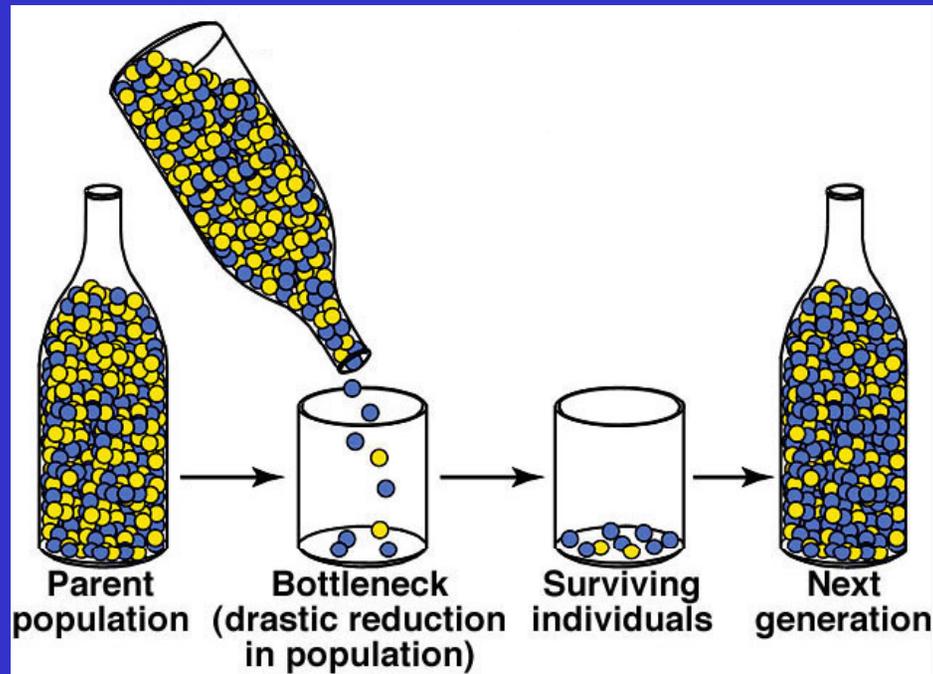


A sex ratio other than 1:1 produces a similar reduction in  $N_e$

Natural selection at one gene can produce differences in offspring number among individuals and reduce  $N_e$

Inbreeding within or between generations reduces the number of different copies of a gene passed to the next generation and effectively reduces  $N_e$

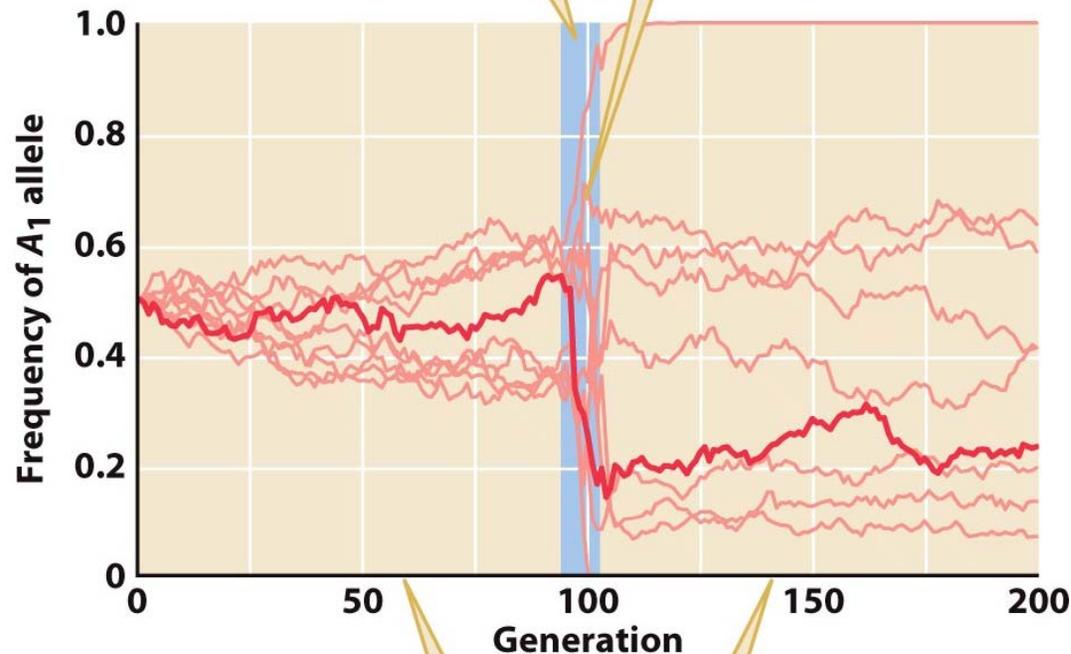
Fluctuations in population size reduce  $N_e$ . Temporary decreases in population size have greater effects than temporary increases in population size.



A temporary reduction in population size is called a **bottleneck**.

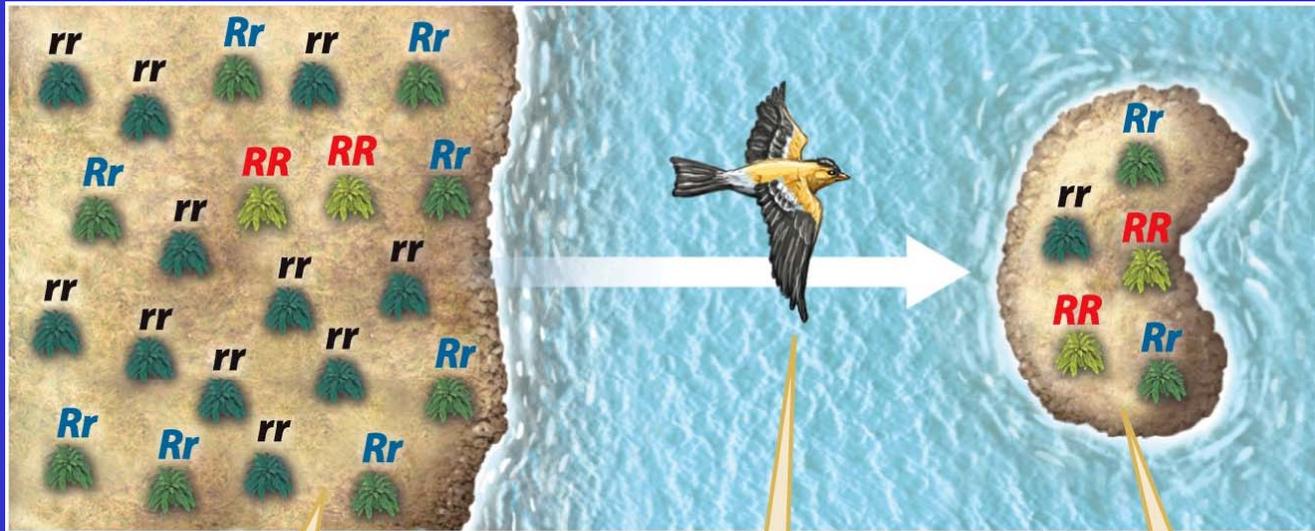
Populations experience a bottleneck in size during the period indicated by the shaded region and return to the original size of 1000 individuals afterward

Allele frequencies fluctuate much more during the bottleneck than before or after



The bottleneck causes divergence between populations. Before the bottleneck, allele frequencies are similar in all populations. After the bottleneck, allele frequencies differ greatly from one population to the next

Read: A Strong Bottleneck Reduced the Heterozygosity of Elephant Seals



Allele frequencies  
on the mainland are  
 $R = 0.3$   $r = 0.7$

Migrating bird carries five  
seeds to a previously  
uncolonized island

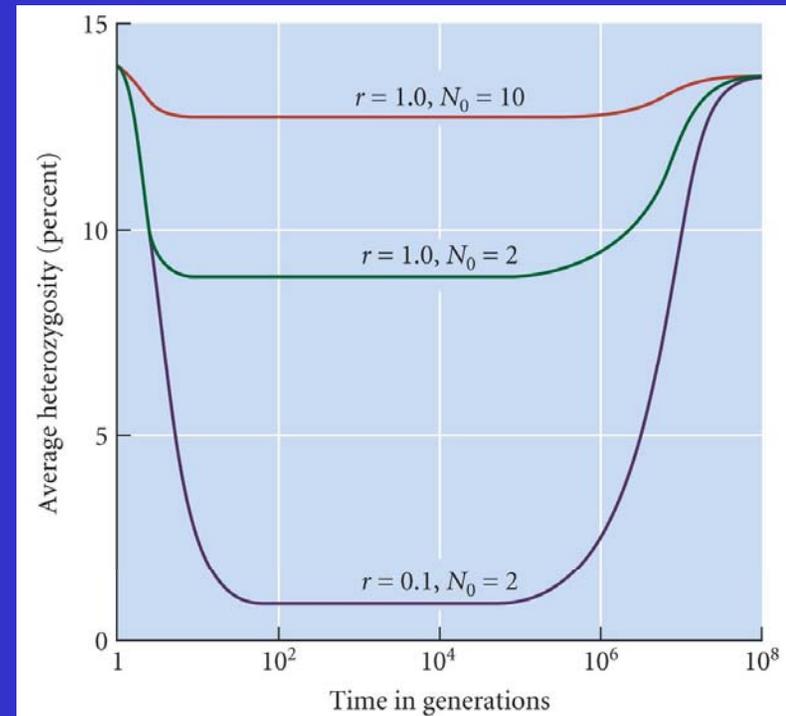
Allele frequencies  
on the island shift  
to  $R = 0.6$   $r = 0.4$

When a small number of individuals from a source population establish a new population genetic variation can be lost. The loss of genetic variation due to such an extreme bottleneck is called the **founder effect**.

Founder effects may make formerly rare alleles common.

Simulations of founder effects suggest that a small number of founders and a small population growth rate ( $r$ ) result in greater loss of genetic diversity.

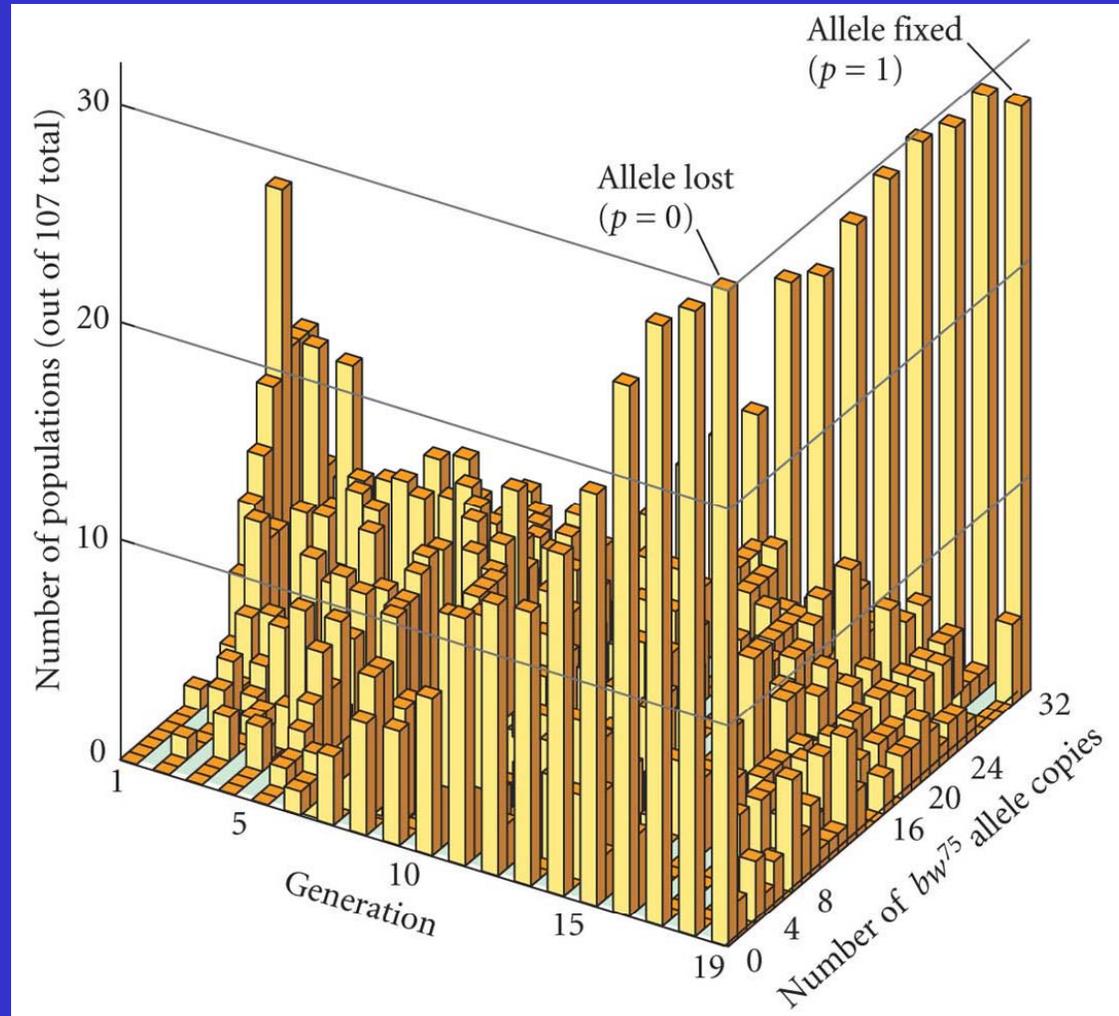
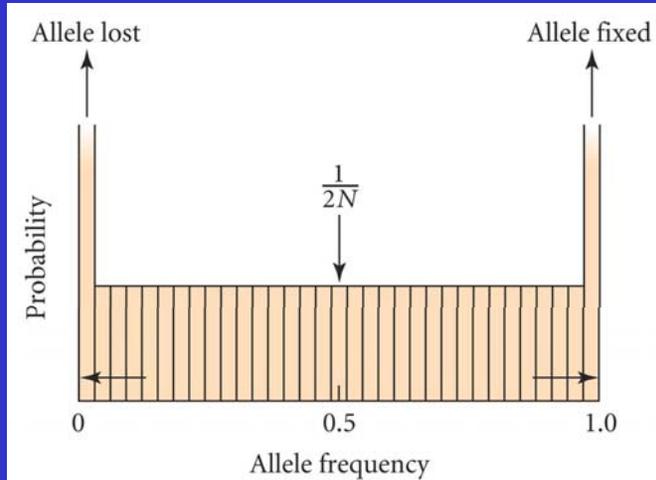
Eventually mutation will restore genetic variation in a founding population.



Studies of laboratory and natural populations confirm the theoretical expectations of genetic drift models.

107 populations of fruit flies each started with 16 heterozygotes, 8 males and 8 females.

8 randomly chosen males and females were used to start each generation.



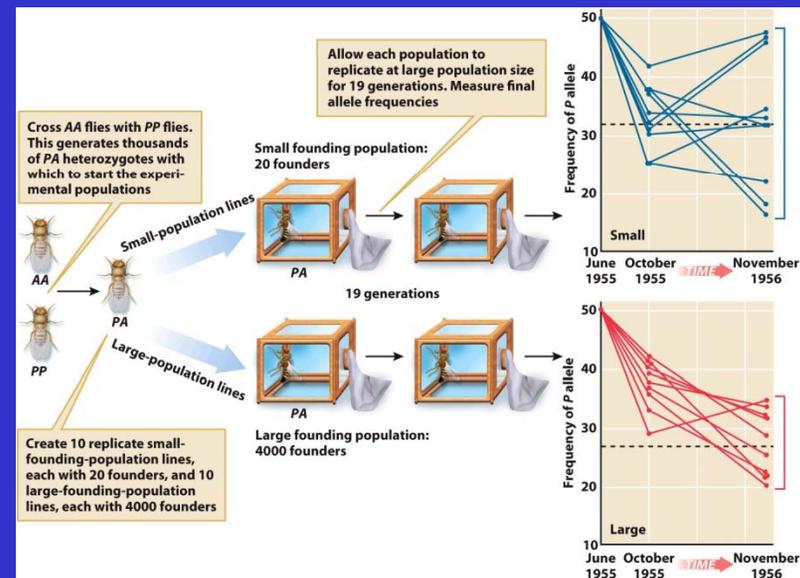
## Genetic Drift and Natural Selection

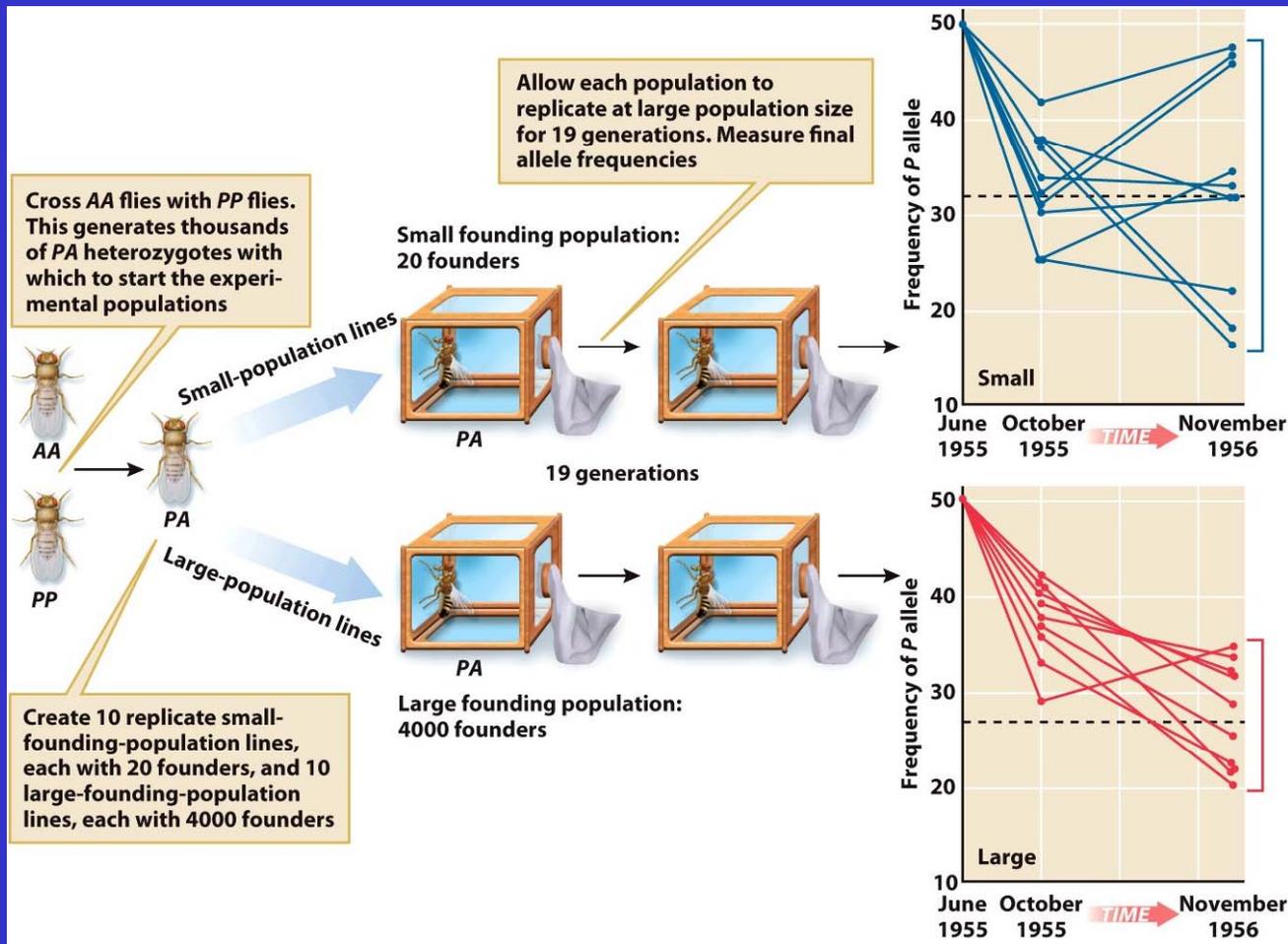
- Directional selection will cause the frequency of alleles that confer high fitness to increase.
- In small populations drift may increase or decrease allele frequencies independent of the fitness they confer.
- Very strong selective regimes may make drift negligible
- Very small population sizes may make the effects of drift so large that selection is negligible.

Dobzhansky and Pavlovsky's experiment:

- Used fruit flies with two different inversions P and A.
- Created heterozygotes for both inversions – PA hybrids
- They knew that PA hybrids had higher fitness than homozygotes
- And, fitness of AA homozygotes was greater than PP homozygotes.
- So, they expected the P allele to decrease in cultures

Started 10 replicates of populations with 20 flies – the high drift treatment  
Started 10 replicates of populations with 4000 flies – the low drift treatment.

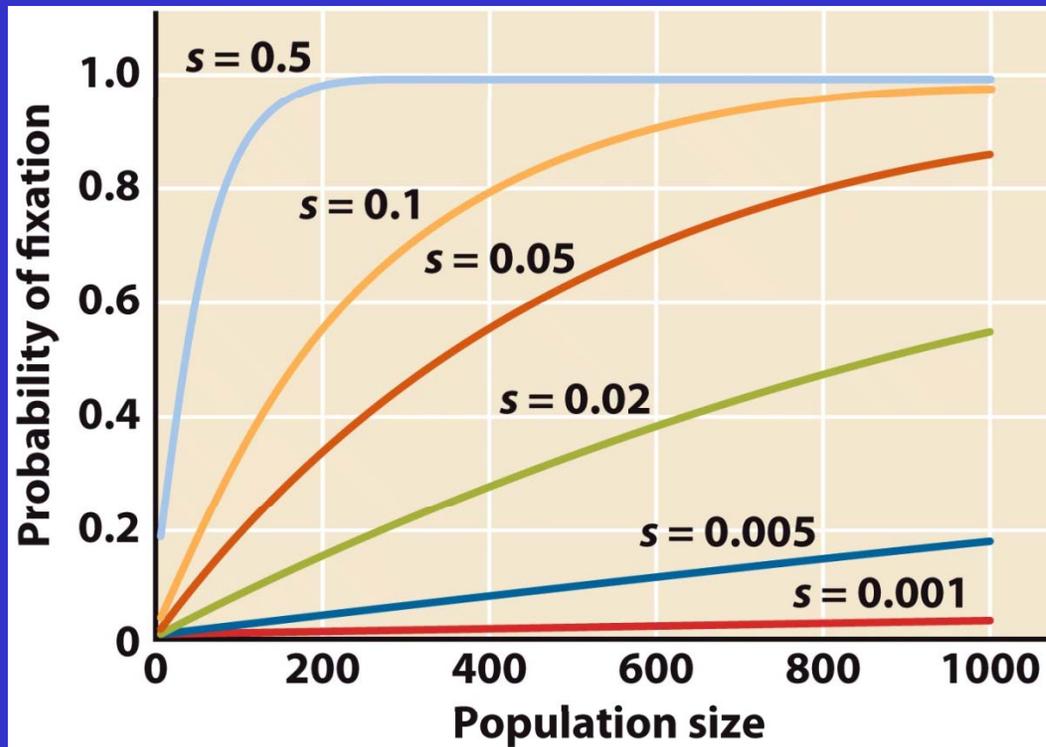




They found frequencies of the two types varied among cultures much more in the high drift treatment

But, the average frequency of the P allele in the two treatments was nearly the same at the end of the experiment.

Kimura showed mathematically that selection is more important if the selection coefficient ( $s$ ) is greater than  $1/2N_e$ .



The probability of fixation of a favored allele due to natural selection increases with increased fitness advantage and with increased population size.

When techniques for analysis of molecular variation became available (protein electrophoresis and then later gene sequencing) the amount of genetic variation within and between populations was surprising. It had been expected that there would be little variation within natural populations because natural selection would have caused the fixation of high fitness alleles.

The **neutral theory of molecular evolution** holds that although some genetic variation is selectively advantageous or disadvantageous and can result in natural selection, most genetic variation is effectively neutral.

The neutral theory predicts that most of the variation between populations or species is selectively neutral.

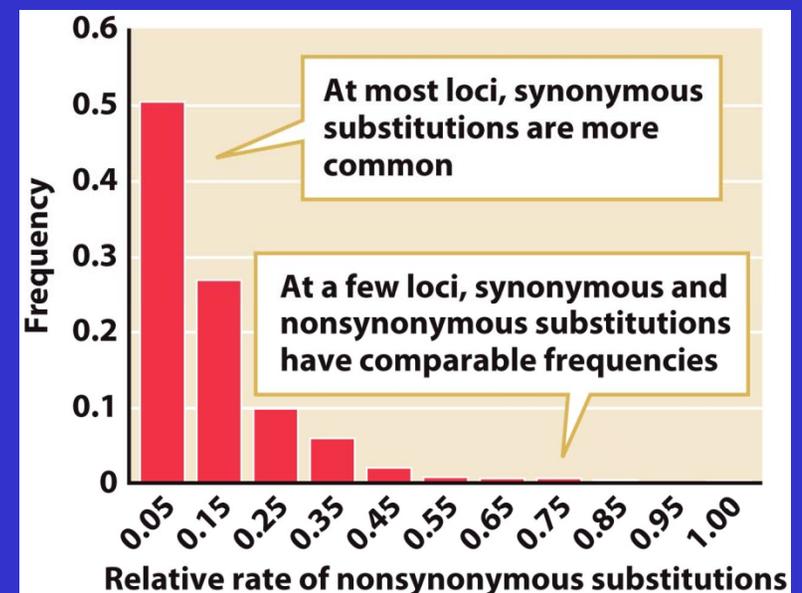
Alleles of a gene can be selectively neutral due to

- synonymous codon changes
- nonsynonymous changes that have little functional effect
- changes in noncoding regions

		Second							
		U		C		A		G	
U	U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
		UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys
		UUA	Leu	UCA	Ser	UAA	Stop	UGA	Stop
		UUG	Leu	UCG	Ser	UAG	Stop	UGG	Trp
C	C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
		CUC	Leu	CCC	Pro	CAC	His	CGC	Arg
		CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg
		CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg
A	A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
		AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser
		AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg
		AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg
G	G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly
		GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly
		GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly
		GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly

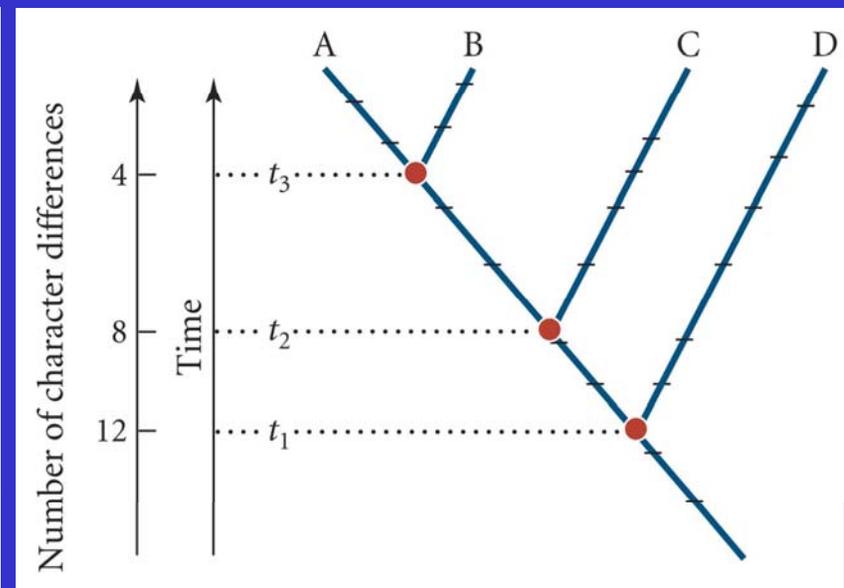
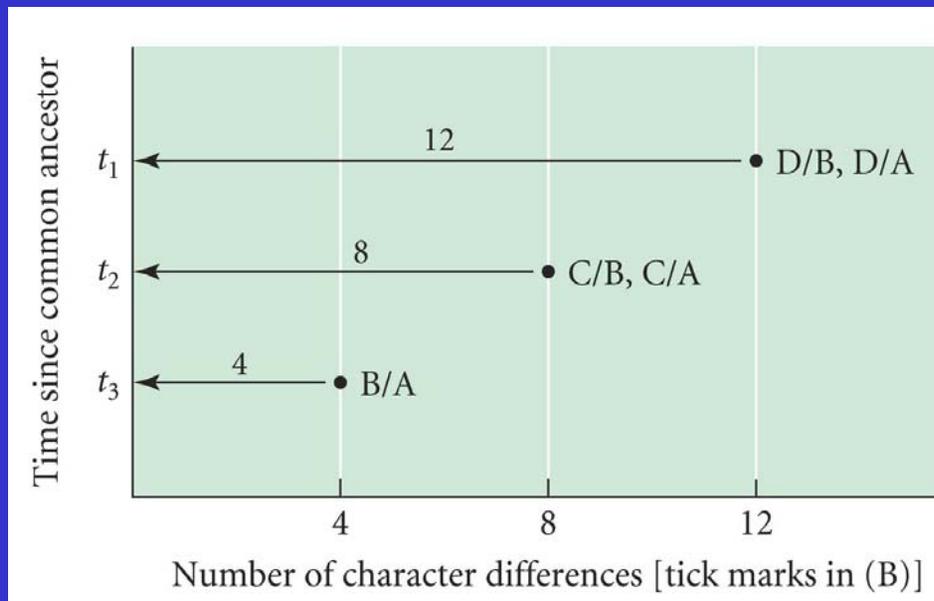
Third

- Coded by 6 codons
- Coded by 4 codons
- Coded by 3 codons
- Coded by 2 codons



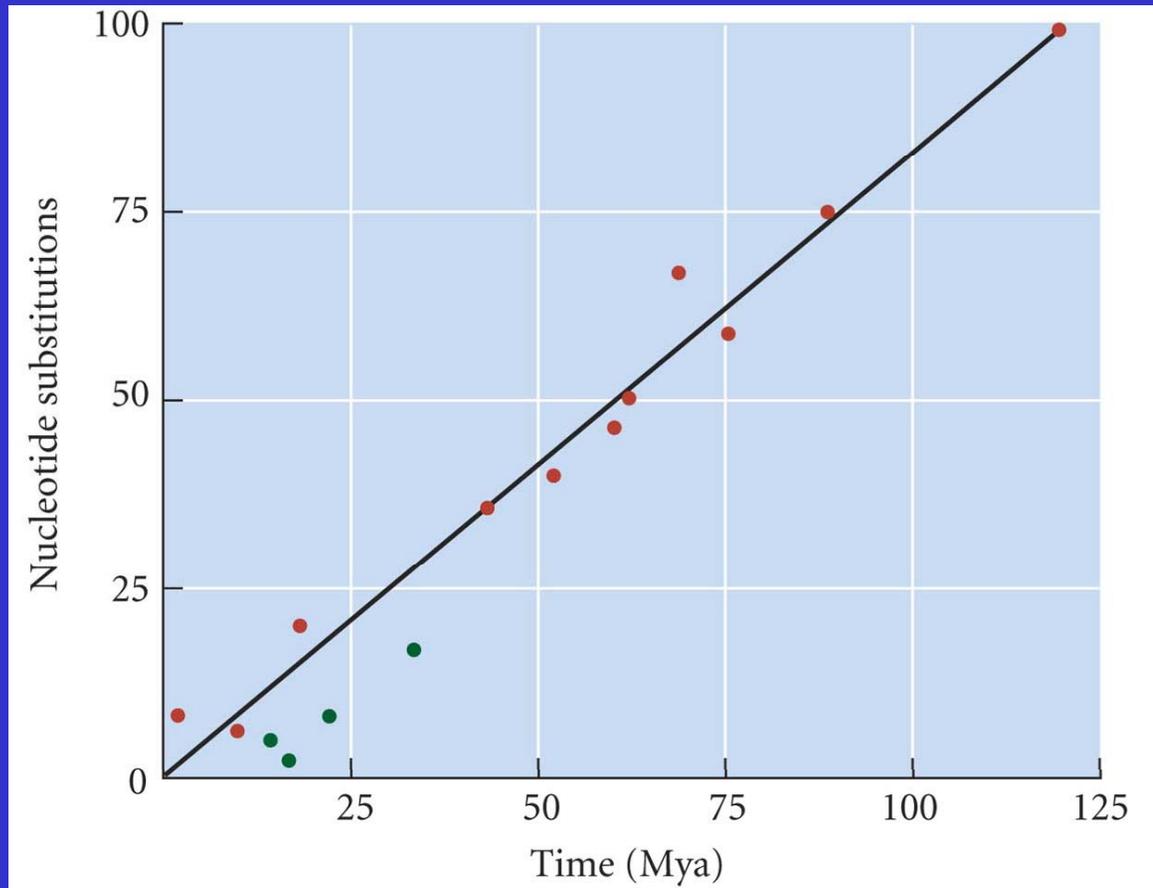
**The Molecular Clock** - early in the history of the study of molecular evolution it was hypothesized that molecular evolution may be different than morphological evolution. Molecular evolution may proceed at a constant rate.

If the molecular clock hypothesis is true, the time since divergence of two species could be estimated by the number of DNA base pair differences between species.



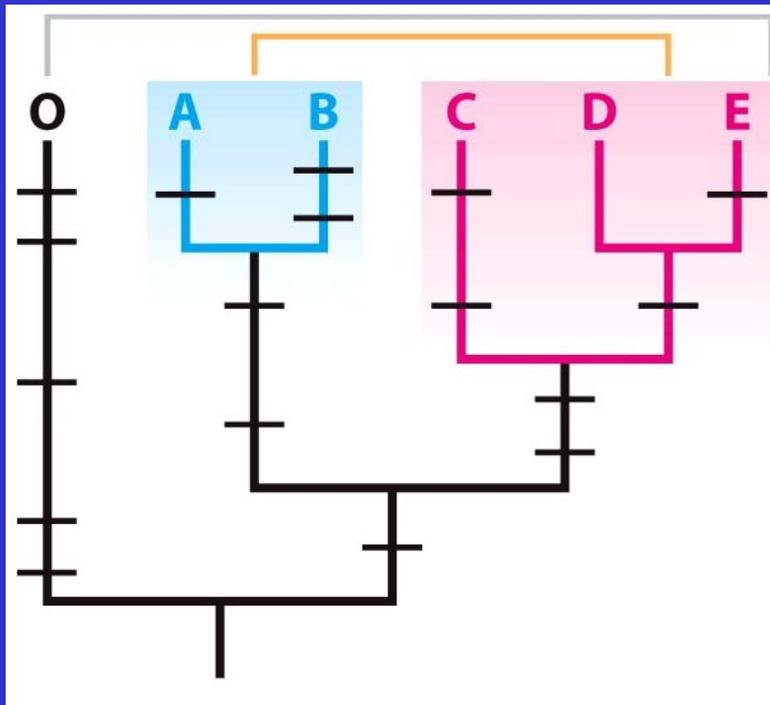
The rate of molecular evolution can be estimated by referring to the fossil record. The fossil record gives an approximate date of divergence of genetic lineages. The rate of molecular change can then be estimated.

Not all groups appear to evolve at the same rate.



## Tests of the molecular clock

If evolution is clock-like then any two pairs of species should be equally different from an outgroup

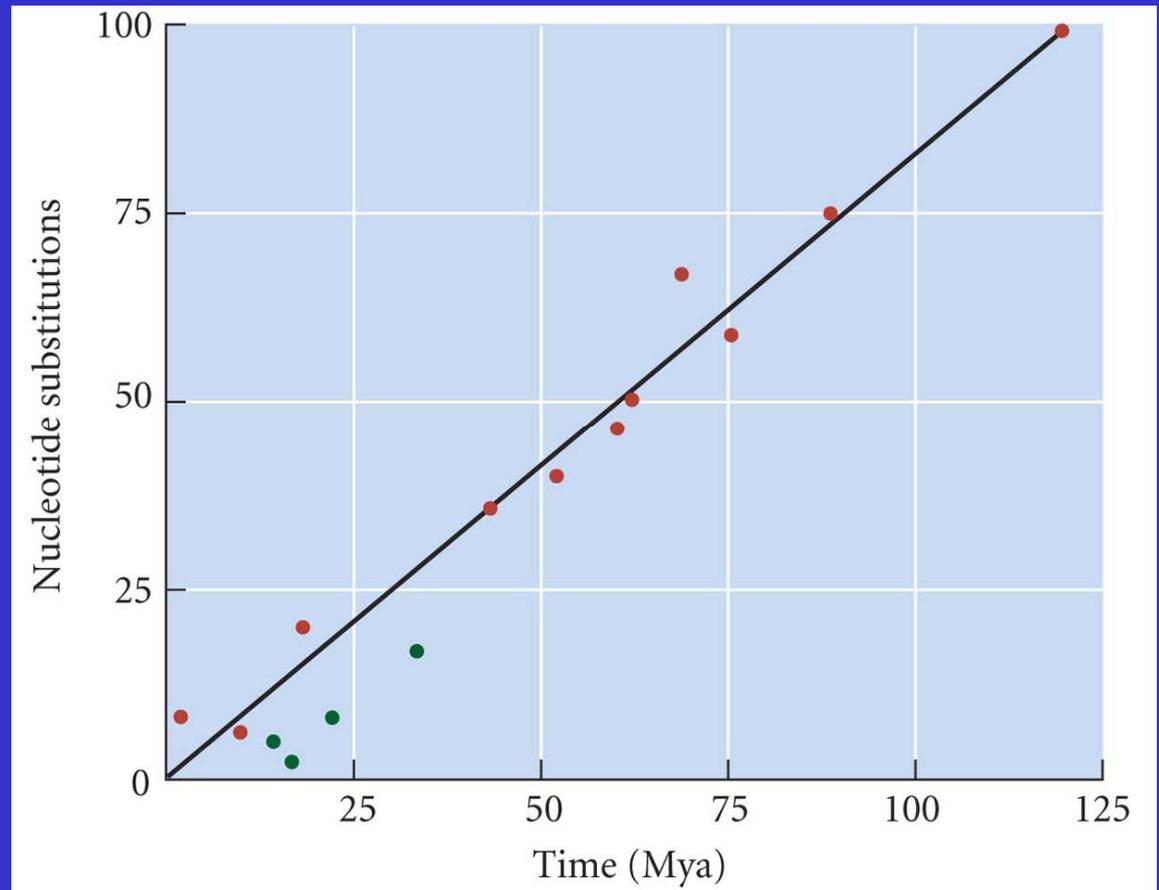


	O	A	B	C	D	E
O	—	9	10	10	9	10
A		—	3	7	6	7
B			—	8	7	8
C				—	3	4
D					—	1
E						—

This is called the **genetic equidistant principle** or the **relative rate test**.

Studies of closely related species suggest that the rate of molecular evolution is often nearly constant.

Studies of more distantly related species suggest that the rate of molecular evolution can vary greatly among groups. For example, within primates and within rodents the rates of evolution have been relatively constant. However, primates have evolved relatively slowly compared to rodents.

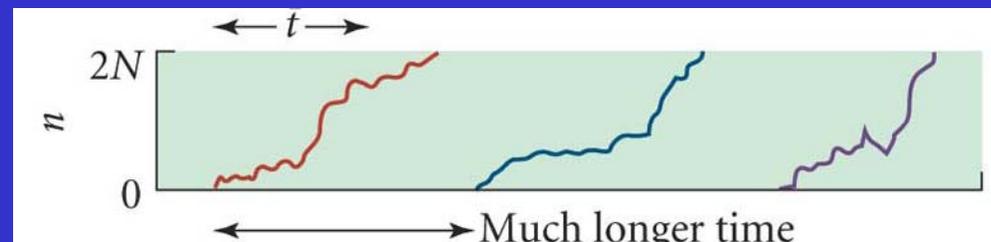
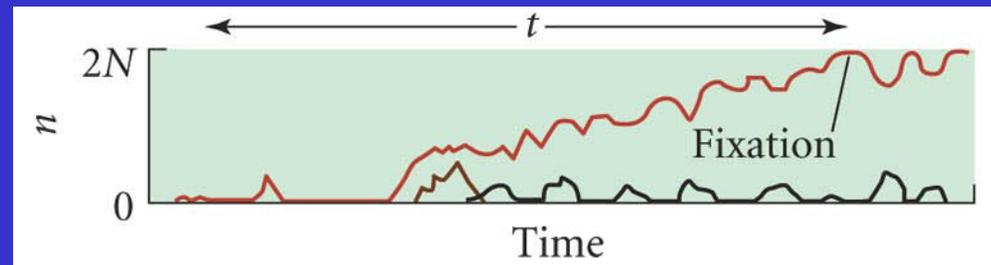


## Why should there be molecular clock?

Neutral genetic variation can be expected to evolve according to the mathematical expectations of genetic drift models

Neutral alleles arise by mutation and many are lost but some increase and become fixed.

Over long periods of time more alleles become fixed.



Since there are  $2*N_e$  copies of a gene to mutate in a population the number of new alleles in a population in each generation should be  $\mu*2*N_e$

The probability that a new neutral allele will eventually become fixed is equal to its initial frequency,  $1/(2*N_e)$

So the number of new alleles that arise in each generation that will someday become fixed is

$$\mu*2*N_e * 1/(2*N_e) = \mu$$

Thus the rate of fixation of neutral alleles is equal to the mutation rate. **This is the basis of the molecular clock.**

If we have 2 species that have diverged from a common ancestor  $t$  generations ago and have  $D$  mutational differences between them, the rate of production of neutral mutations can be estimated as  $\mu = D/2t$

Over long periods of time this estimate becomes poorer because of multiple mutations at the same site or “multiple hits” or “mutational saturation.”

