ISU BIOI 1202
General Biology II lecture

CHAPTER 23
The Evolution of Populations
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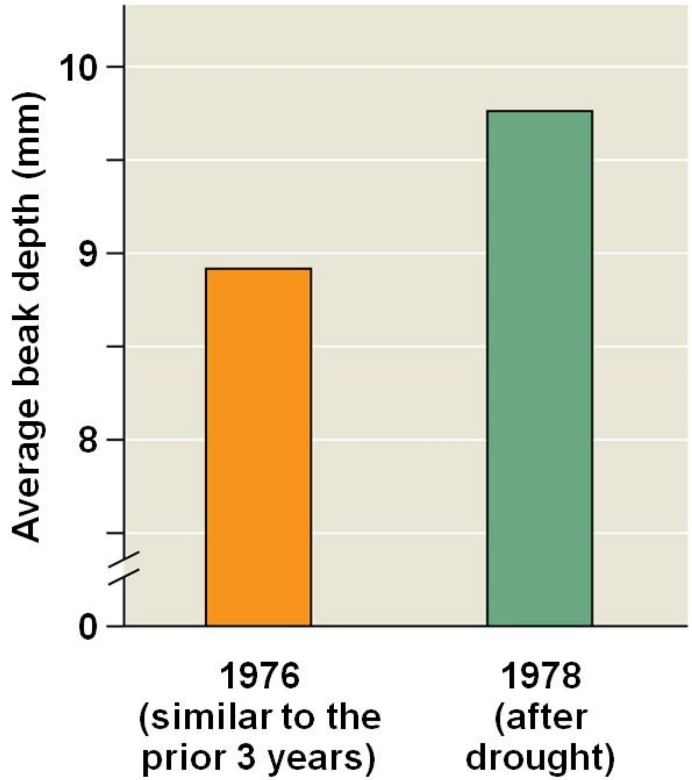
CH 23 learning Objectives

1. Describe how genetic variation arises and explain why it is a prerequisite for evolution.
2. Use allele-frequency data to predict the genotype frequencies of a population in Hardy-Weinberg equilibrium.
3. Differentiate between how natural selection, genetic drift, and gene flow affect allele frequencies in a population.
4. Explain how natural selection can lead to adaptation.

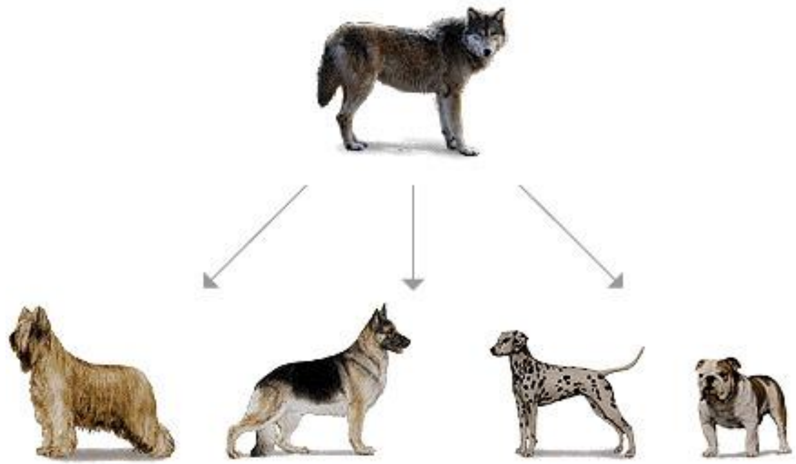
I would suggest completing the crossword puzzle to help you understand the terminology and correlate how the terms relate to topics covered in this chapter.

The Smallest Unit of Evolution

- A common misconception is that individual organisms <u>evolve</u>
- Natural selection acts on *individuals*, but only <u>**populations**</u> <u>evolve</u>
- EX: A population of medium ground finches on Daphne Major Island
  - During a drought, large-beaked birds were more likely to crack large <u>seeds and survive</u>
- So, the finch population evolved, not the <u>individual members</u>



- **Microevolution** is a change in allele frequencies in a population <u>over generations</u>



EX: All modern domestic dogs are descendants of the Gray wolf. Good article about this (<u>click me</u>)

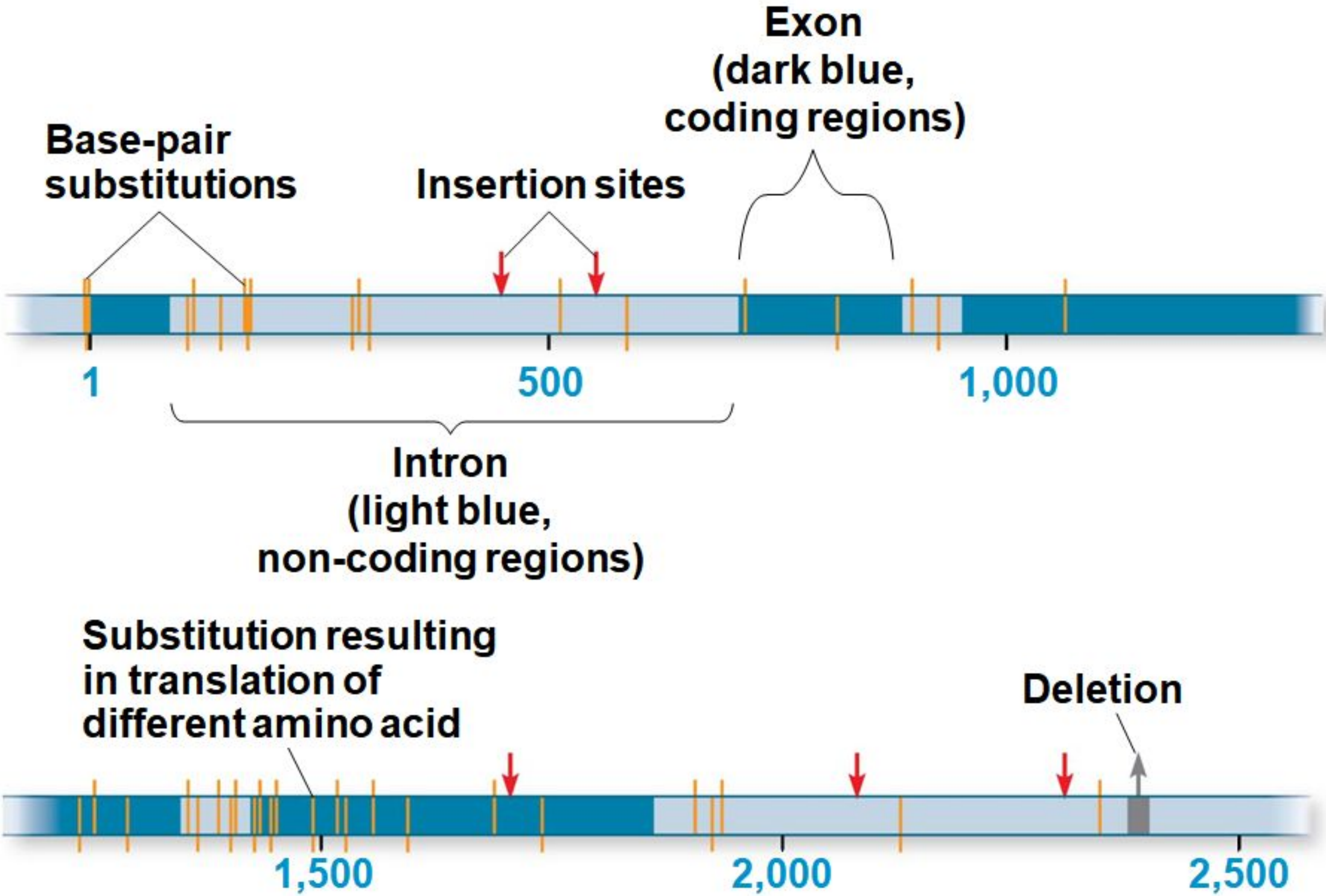
- 3 main mechanisms cause allele frequency change:
  1. <u>Natural selection</u>
  2. <u>Genetic drift</u>
  3. <u>Gene flow</u>
- Only natural selection consistently causes <u>adaptive evolution</u>

Concept 23.1: Genetic variation makes evolution possible

- **Genetic variation** among individuals is caused by differences in genes or other DNA segments
- Variation in heritable traits is a prerequisite for evolution by natural selection
- Phenotype is the product of inherited genotype and environmental influences
- Some phenotypic differences are determined by a single gene and can be classified on an "either-or" basis
- Other phenotypic differences are determined by the influence of two or more genes and vary along a continuum within a population

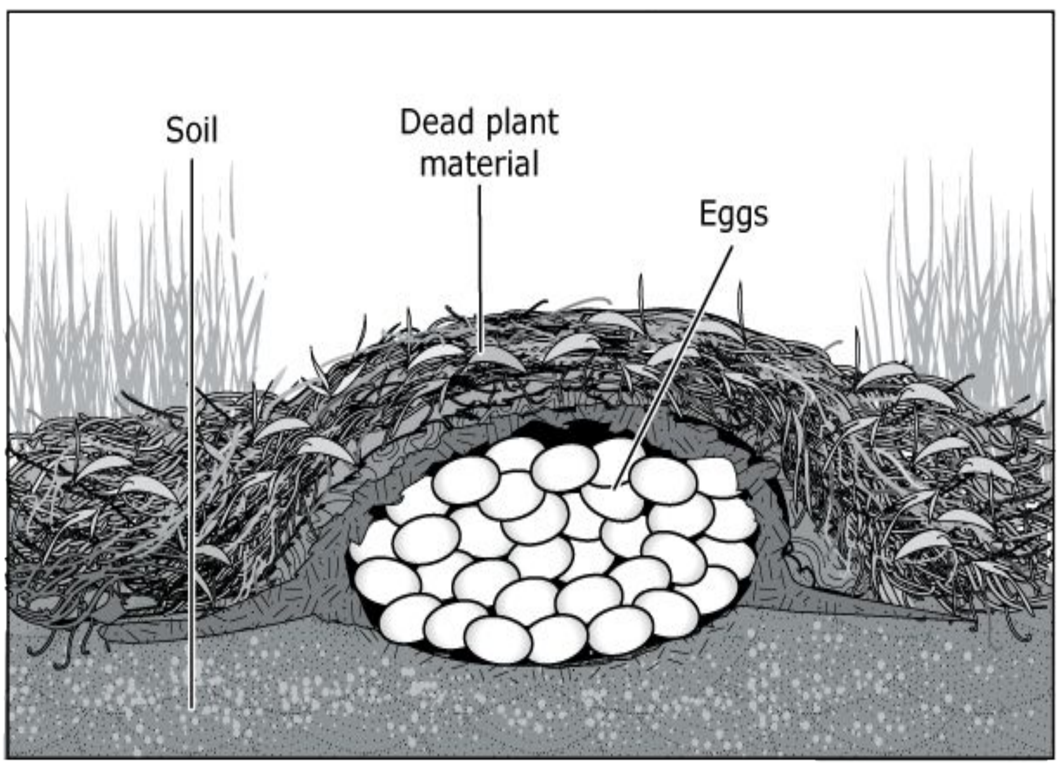
- Genetic variation can be measured as gene variability or nucleotide variability
- For gene variability, average heterozygosity measures the average percent of loci that are heterozygous in a population
- Nucleotide variability is measured by comparing the DNA sequences of two or more individuals
- Most differences occur in noncoding regions (introns, ~90% of the human genome)
- Variations that occur in coding regions (exons, ~10% of the human genome) rarely change the amino acid sequence of the encoded protein

Figure 23.4


Exon
(dark blue,
coding regions)
Base-pair
substitutions
Insertion sites
1
500
1,000
Intron
(light blue,
non-coding regions)
Substitution resulting
in translation of
different amino acid
Deletion
1,500
2,000
2,500

- Some phenotypic variation does not result from genetic differences among individuals, but rather from <u>environmental influences</u>
- Only genetically determined variation can <u>have evolutionary consequences</u>

Cross Section of an Alligator Nest

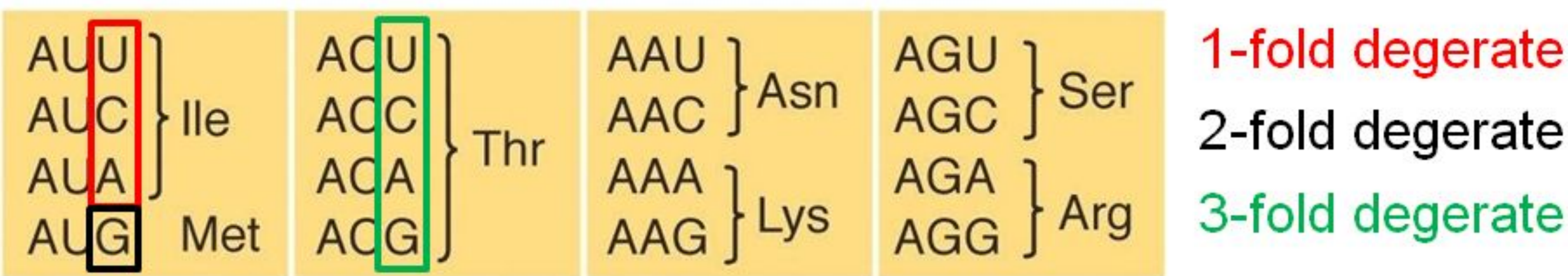


The temperature at which alligator eggs develop determines their sex. Eggs hatched between **90° F to 93° F become MAIES**, and those hatched between **82° F to 86° F become FEMAIES**. Intermediate temperature ranges produces a mix of both

Formation of New Alleles

- New alleles arise by mutation, a change in the <u>nucleotide sequence of DNA</u>
- New genes and alleles can arise by <u>gene duplication</u>
- Sexual reproduction can result in genetic variation by <u>recombining existing alleles</u>
- Only mutations in cells that produce gametes can be <u>passed to offspring</u>
- A point mutation is a change in a single nucleotide in a <u>DNA sequence</u>

- The effects of point mutations can vary
  - Mutations that alter the phenotype are often harmful
  - Harmful mutations can be hidden from selection in recessive alleles
  - Mutations that result in a change in phenotype are sometimes, though rarely, beneficial
  - Point mutations in non-coding regions (introns) generally result in **neutral variation**, conferring no selective advantage or disadvantage
  - Mutations to genes can be neutral because of redundancy in the genetic code (3,1,4 below?)



Altering Gene Number or Position

- Chromosomal mutations that delete, disrupt, or rearrange <u>many loci are typically harmful</u>
- Duplication of small pieces of DNA increases genome <u>size and is usually less harmful</u>
- Duplicated genes can take on new functions by <u>further mutation.</u>
- An ancestral odor-detecting gene has been duplicated many times: Humans have 380 copies of the gene, and <u>mice have 1,200</u>

Rapid Reproduction

- Mutation rates are <u>low in animals and plants</u>
- The average is about one mutation in every <u>100,000 genes per generation</u>
- Mutation rates are often lower in prokaryotes, but short generation times allow <u>mutations to accumulate rapidly</u>
- Viruses have both high mutation rates and <u>short generation times</u>
  - EX: HIV has a <u>very high mutation rate</u>

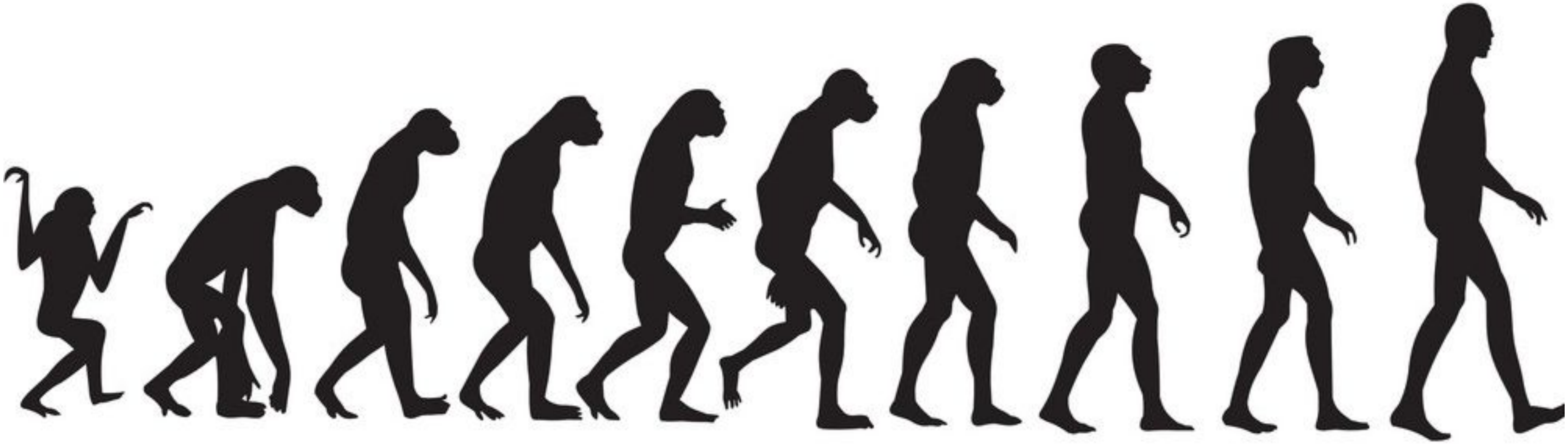
Sexual Reproduction

- In organisms that reproduce sexually, most genetic variation results from <u>recombination of alleles</u>
- Sexual reproduction can shuffle existing alleles into new combinations through three mechanisms

1. **Crossing over**: <u>this accounts for MOST of the variation</u>
2. **Independent assortment**: <u>random alignment and separation of chromosomes</u>
3. **Fertilization**: <u>Which gametes united during fertilization, but more so which one?</u>

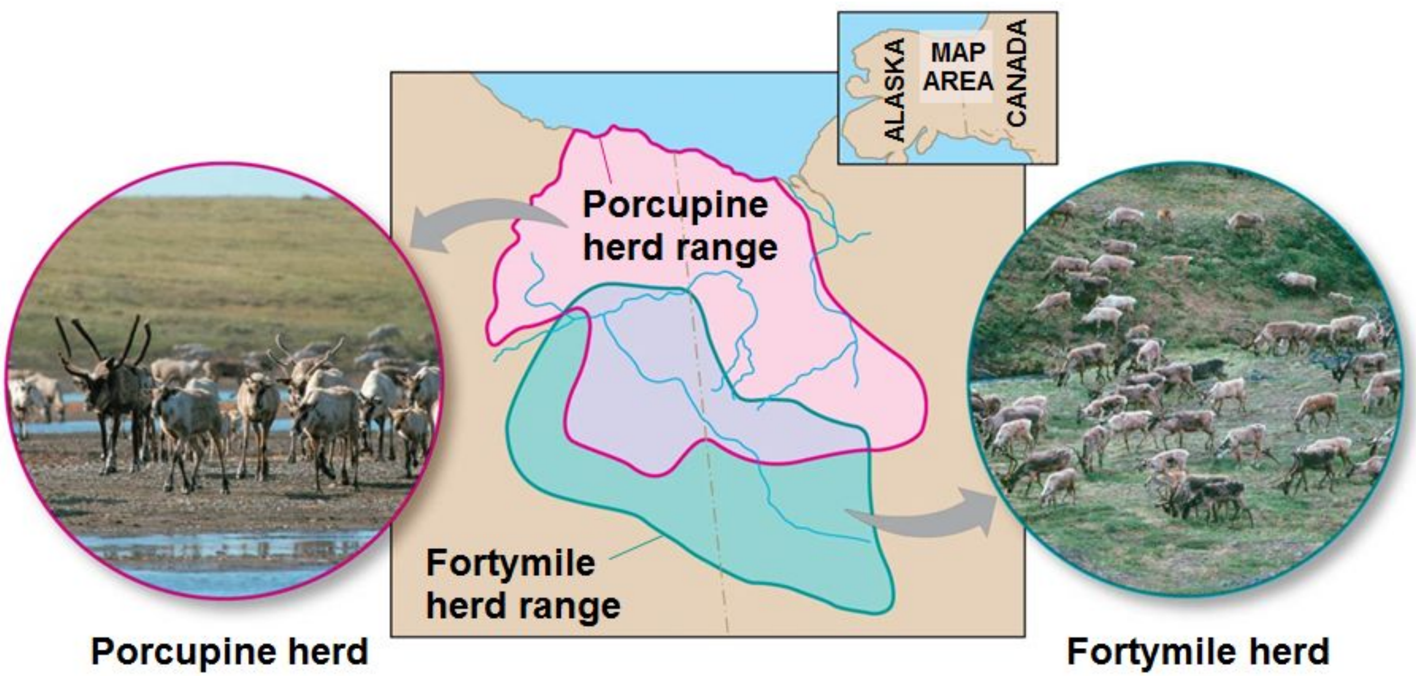
Concept 23.2: The Hardy-Weinberg equation can be used to test whether a population is evolving

- Genetic variation is required for a population to evolve, but <u>does not guarantee that it will</u>
- One or more factors that cause evolution must be at work for <u>a population to evolve</u>



Gene Pools and Allele Frequencies

- A **population** is a localized group of individuals capable of <u>interbreeding and producing fertile offspring</u>
- Populations are not always geographically isolated, but individuals typically only breed with <u>members of their own population</u>



- A **gene pool** consists of all the alleles for all loci in a population
- A locus is fixed if all individuals in a population are homozygous for the same allele
- If there are two or more alleles for a locus, diploid individuals may be either homozygous or heterozygous
- This example of flower color illustrates **INCOMPIETE** dominance (or “blending”)

C^RC^R

C^WC^W

C^RC^W

- The frequency of an allele in a population can be calculated
  - For diploid organisms, the total number of alleles at a locus is the <u>total number of individuals times 2</u>
  - The total number of dominant alleles at a locus is two alleles for each homozygous dominant individual plus one allele for each heterozygous individual; the same logic applies <u>for recessive alleles</u>
- If there are two alleles at a locus, *p* and *q* are used to represent their frequencies (where "p" if the dominant allele and "q" is the recessive allele)
- The frequency of all alleles in a population will add up to 1
  - So……. $\underline{p + q = 1}$

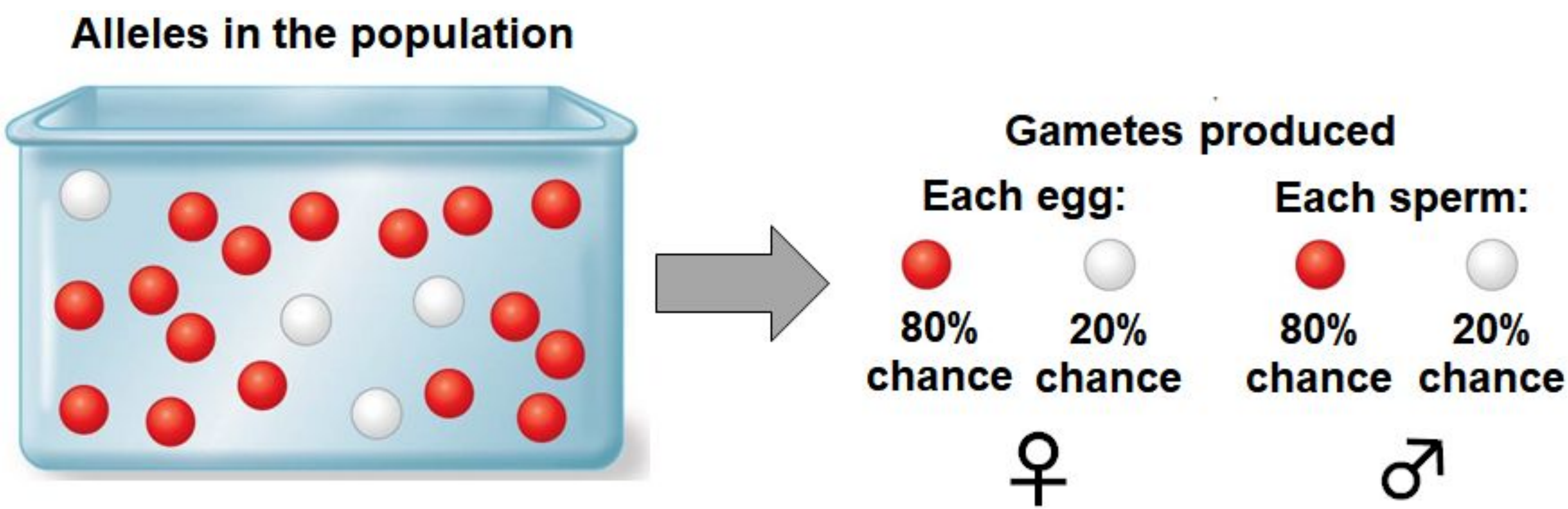
- EX: Wildflowers color is incompletely dominant
  - 320 red flowers (C^RC^R)
  - 160 pink flowers (C^RC^W)
  - 20 white flowers (C^WC^W)
- Calculate the number of copies of each allele
  - $C^R = (320 \times 2) + 160 =$
  - $C^W = (20 \times 2) + 160 =$
- Calculate the frequency of each allele
  - p = frequency of $C^R = 800/(800 + 200) = 0.8$ (80%)
  - $q = 1 - p = 0.2$ (20%)
- The sum of alleles is always 1 (100%)
  - $0.8 + 0.2 = 1.0$ (or 100%)

The Hardy-Weinberg Equation

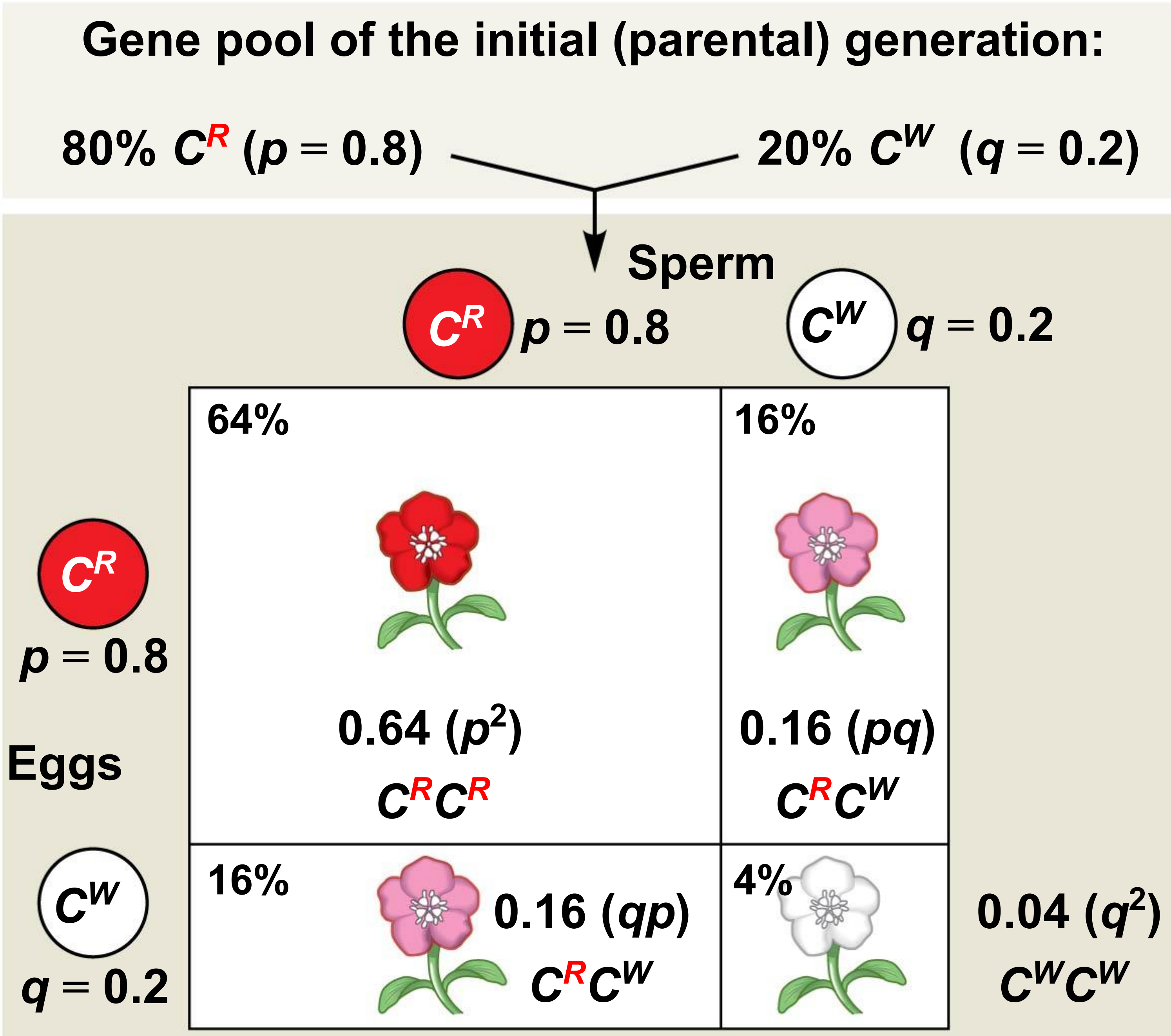
- The Hardy-Weinberg (HW) equation describes the genetic makeup we expect for a population that is *not* evolving at a particular locus
- In a population where gametes contribute to the next generation randomly and Mendelian inheritance occurs, allele and genotype frequencies remain constant from generation to generation
- Such a population is in HW equilibrium
- If the observed genetic makeup of the population differs from expectations under HW, it suggests that the population may be evolving

Hardy-Weinberg Equilibrium

- HW equilibrium describes the constant frequency of alleles in such a gene pool
- Consider, for example, the same population of 500 wildflowers and 1,000 alleles where
  - p = frequency of C^R (dominant allele) = 0.8
  - q = frequency of C^W (recessive allele) = 0.2



- The frequency of genotypes can be calculated
  - $C^{R}C^{R} = p^2 = 0.8 \times 0.8 = \underline{0.64}$
  - $C^{R}C^{W} = 2pq = 2 \times 0.8 \times 0.2 = \underline{0.32}$
  - $C^{W}C^{W} = q^2 = 0.2 \times 0.2 = \underline{0.04}$
- The frequency of genotypes can be confirmed using a Punnett square



Gene pool of the initial (parental) generation:
80% C^R (p = 0.8)
20% C^W (q = 0.2)
Sperm
C^R p = 0.8
C^W q = 0.2
Eggs
C^R p = 0.8
C^W q = 0.2
64%
0.64 (p^2)
C^RC^R
16%
0.16 (pq)
C^RC^W
16%
0.16 (qp)
C^RC^W
4%
0.04 (q^2)
C^WC^W

- If p and q represent the relative frequencies of the only two possible alleles in a population at a particular locus, then
  - $p^2 + 2pq + q^2 = 1$
  - p^2 = frequency of the homozygous dominant genotype
  - q^2 = frequency of the homozygous recessive genotype
  - $2pq$ = frequency of the heterozygous genotype

p^2	$+$	$2pq$	$+$	q^2	$=$	1
Expected frequency of genotype C^RC^R		Expected frequency of genotype C^RC^W		Expected frequency of genotype C^WC^W		

Let's say that people either have brown or blue eyes and we surveyed the class for their eye color.

16% blue eyes

Another Example

Then…
84% have brown eyes

$$q^2 = 0.16$$

So $q = 0.4$

$$p + q = 1.0$$

So $p = 0.6$

$$p^2 = 0.36$$

Blue (bb) eyes = 16% of people

Brown (B_) eyes = 84% of people

Homozygous dominant **brown** eyes (BB) = 36% of people

Heterozygous **brown** eyes (Bb) = 2pq = 2(0.6)(0.4) = 48% of people

PRACTICE HOMEWORK HANDOUT

Conditions for Hardy-Weinberg Equilibrium

- The HW approach describes a population that is <u>not evolving</u>
- In real populations, allele and genotype frequencies often <u>do change over time</u>
- Changes occur when one or more of the conditions for HW equilibrium are <u>not met</u>
- Natural populations can evolve at some loci while being in HW equilibrium <u>at other loci</u>
- The HW equation can be used to test whether evolution is <u>occuring in a population</u>
- It is also used to determine the percentage of a population <u>carrying a specific allele</u>

Table 23.1 Conditions for Hardy-Weinberg Equilibrium

Condition	Consequence if Condition Does Not Hold
1. No mutations	The gene pool is modified if mutations occur or if entire genes are deleted or duplicated.
2. Random mating	If individuals mate within a subset of the population, such as near neighbors or close relatives (inbreeding), random mixing of gametes does not occur and genotype frequencies change.
3. No natural selection	Allele frequencies change when individuals with different genotypes show consistent differences in their survival or reproductive success.
4. Extremely large population size	In small populations, allele frequencies fluctuate by chance over time (a process called genetic drift).
5. No gene flow	By moving alleles into or out of populations, gene flow can alter allele frequencies.

- EX: We can assume that the locus that causes phenylketonuria (PKU) is in HW equilibrium because:
- PKU is caused by a defect in a gene that helps create the enzyme needed to break down the amino acid phenylalanine in the body

1. The PKU gene mutation rate is low
2. Mate selection is random with respect to whether or not an individual is a carrier for the PKU allele
3. Natural selection can only act on rare homozygous individuals who do not follow dietary restrictions
4. The population is large
5. Migration has no effect, as many other populations have similar allele frequencies

- The occurrence of PKU is one per 10,000 births
  - $q^2 = 0.0001$, so $q = 0.01$
- The frequency of normal alleles is
  - $p = 1 - q = 1 - 0.01 = 0.99$
- The frequency of carriers is
  - $2pq = 2 \times 0.99 \times 0.01 = 0.0198$
  - or approximately 2% of the U.S. population

The blood sample for PKU is usually taken from a baby's heel (called a heel stick).

Concept 23.3: Natural selection, genetic drift, and gene flow can alter allele frequencies in a population

- Three major factors alter allele frequencies and bring about most evolutionary change:

1. natural selection
2. genetic drift
3. gene flow

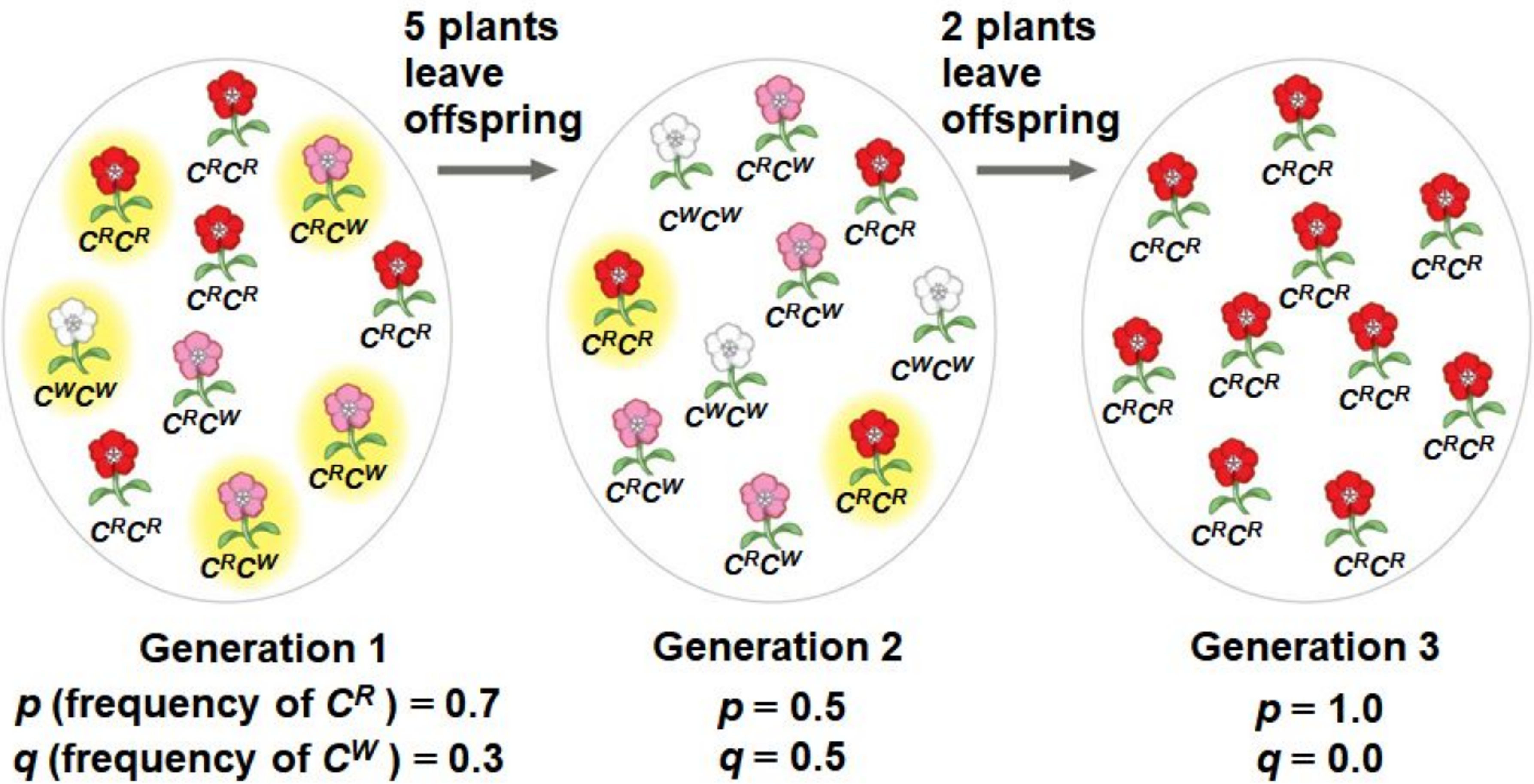
1. Natural Selection

- Selection results in alleles being passed to the next generation in proportions that differ from <u>those in the present generation</u>
- EX: An allele that confers resistance to DDT in fruit flies increased in frequency after <u>DDT was used widely in agriculture</u>
- Natural selection can cause **adaptive evolution**, a process in which traits that enhance survival or reproduction <u>increase in frequency over time</u>

2. Genetic Drift

- The smaller a sample, the greater the chance of random deviation from a predicted result
- **Genetic drift** describes how allele frequencies fluctuate unpredictably from one generation to the next
- Genetic drift tends to reduce genetic variation through the random loss of alleles
- Two main types of genetic drift
  1. Founder effect
  2. Population bottleneck

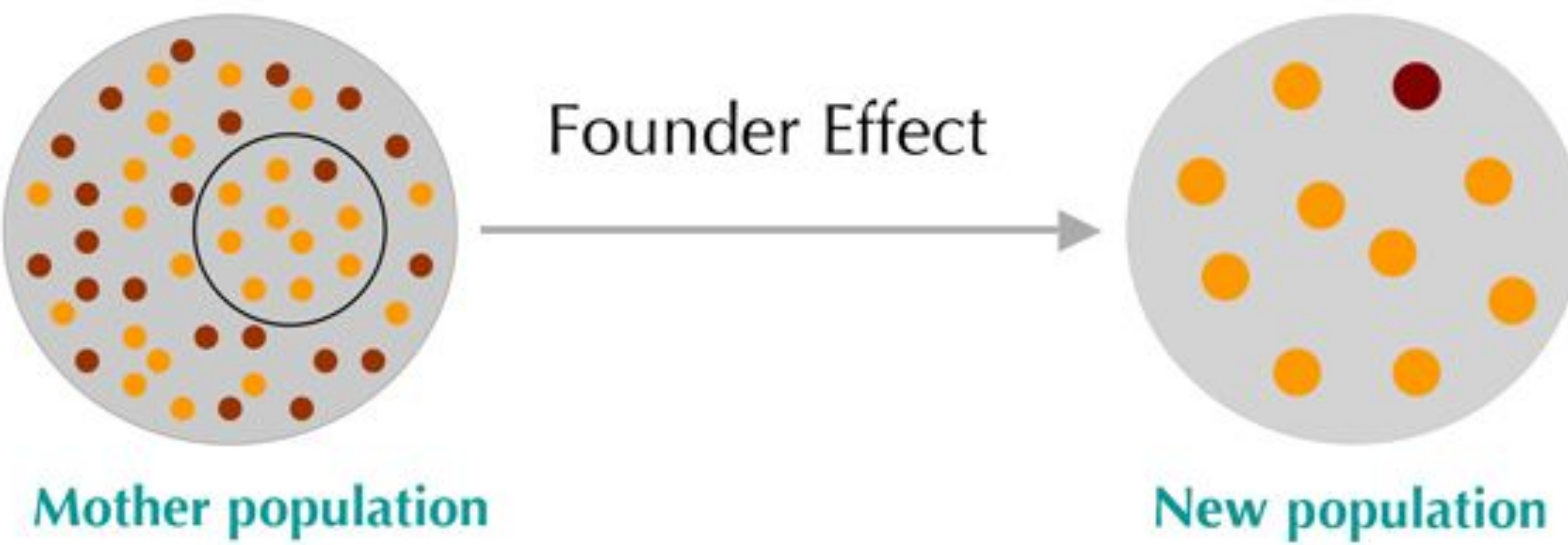
Figure 23.9_3



5 plants leave offspring
2 plants leave offspring
C^RC^R
C^RC^W
C^WC^W
Generation 1
p (frequency of C^R) = 0.7
q (frequency of C^W) = 0.3
Generation 2
p = 0.5
q = 0.5
Generation 3
p = 1.0
q = 0.0

Founder Effect

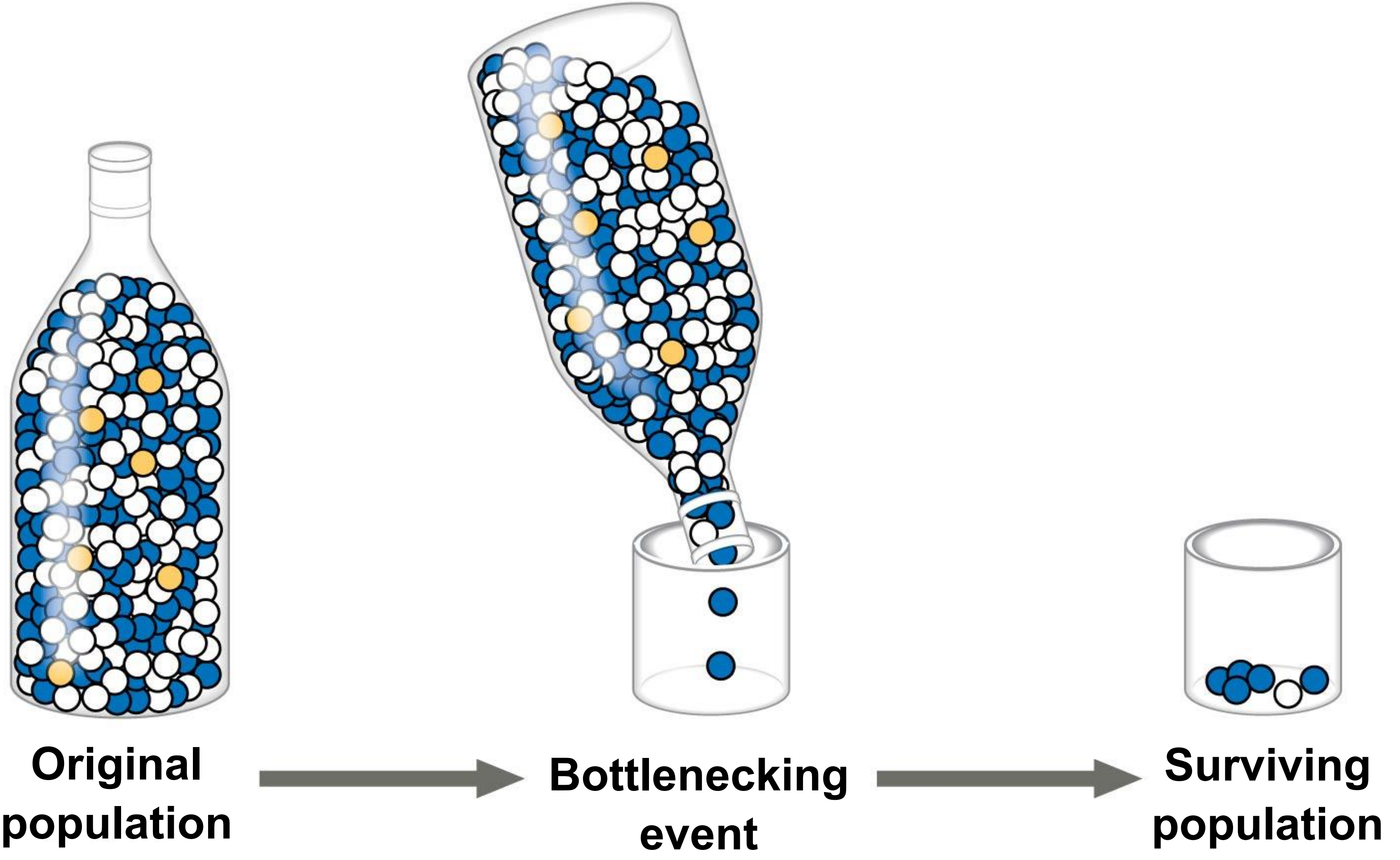
- The **founder effect** occurs when a few individuals become ***isolated*** from a larger population or ***leave*** a population and move to a new area
- Allele frequencies in the small founder population can be different from those in the larger parent population



Bottleneck Effect

- The **bottleneck effect** occurs when there is a drastic ***reduction*** in population size due to <u>a sudden change in the environment</u>
- The resulting gene pool may no longer be reflective of the <u>original population's gene pool</u>
- If the population remains small, it may be further affected by <u>genetic drift</u>
- Understanding the bottleneck effect can increase understanding of how <u>human activity affects other species</u>

Figure 23.10_3



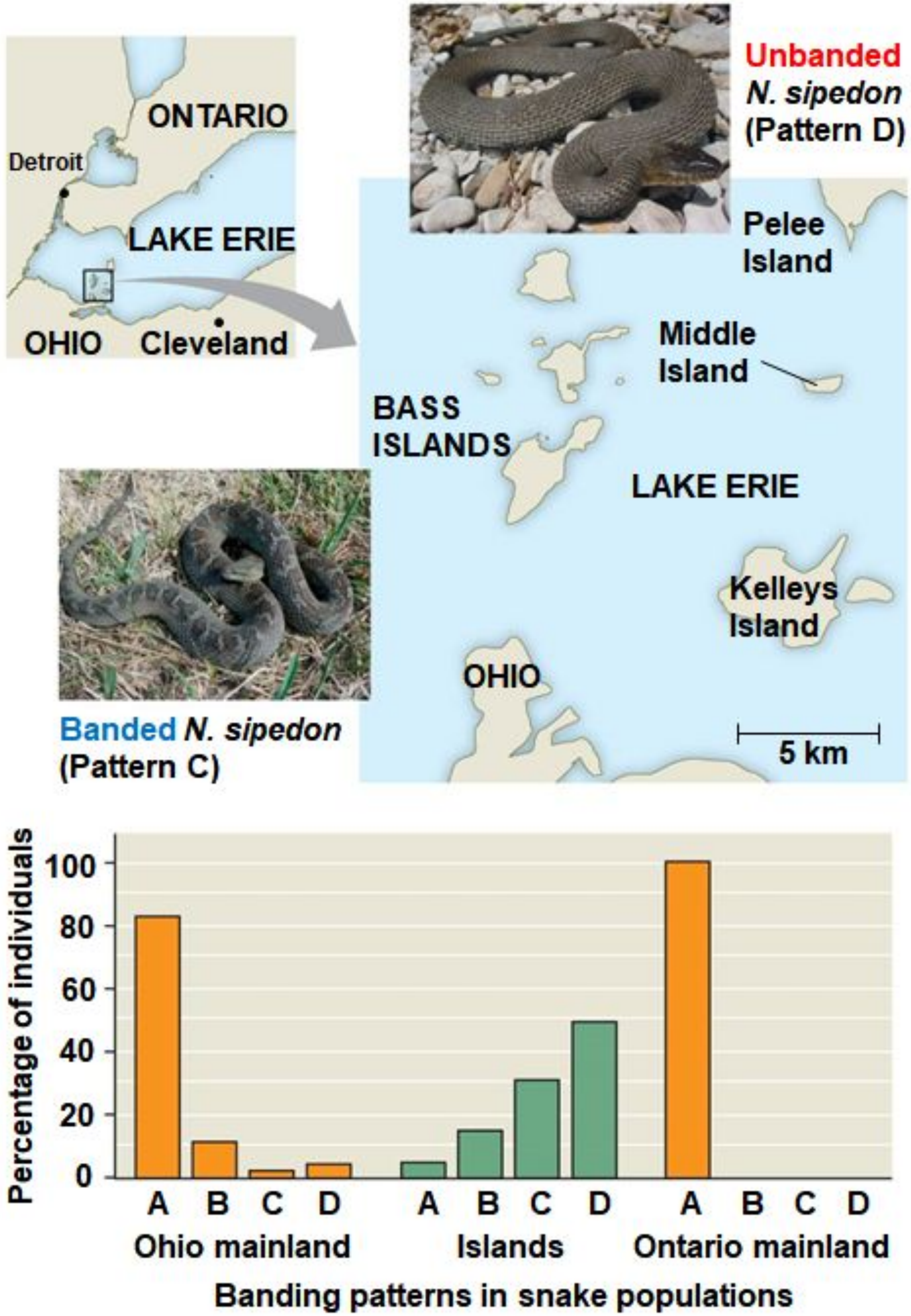
Effects of Genetic Drift: *A Summary*

1. Genetic drift is <u>significant in small populations</u>
2. Genetic drift can cause allele frequencies to <u>change at random</u>
3. Genetic drift can lead to a <u>loss of genetic variation within populations</u>
4. Genetic drift can cause <u>harmful alleles to become fixed</u>

3. Gene Flow

- Consists of alleles moving between populations
- Alleles can be transferred through the movement of fertile individuals or gametes (EX: pollen)
- Gene flow can reduce population variation over time
- Gene flow can affect adaptation to local environments
- EX: banding pattern in lake Erie water snakes represents adaptation to mainland and island habitats
  - Most snakes on the mainland are strongly banded; most island snakes are un-banded or intermediate
  - Un-banded snakes are better camouflaged on islands, but migration of banded snakes from mainland to the islands maintains alleles in island population

Figure 23.12



ONTARIO
Detroit
LAKE ERIE
OHIO
Cleveland
Unbanded
N. sipedon
(Pattern D)
Pelee
Island
Middle
Island
BASS
ISLANDS
LAKE ERIE
Kelleys
Island
OHIO
5 km
Banded N. sipedon
(Pattern C)
Percentage of individuals
100
80
60
40
20
0
A B C D
Ohio mainland
A B C D
Islands
A B C D
Ontario mainland
Banding patterns in snake populations

- Gene flow can increase the fitness of a population
- EX: Spread of alleles for resistance to insecticides
  - Insecticides have been used to target mosquitoes that carry West Nile virus and malaria
  - Alleles have evolved in some populations that confer insecticide resistance to these mosquitoes
  - The flow of insecticide resistance alleles into a population can cause an increase in fitness
- Gene flow is an important agent of evolutionary change in modern human populations

Concept 23.4: Natural selection is the only mechanism that consistently causes adaptive evolution

- Evolution by natural selection involves both chance and "sorting"
  - New genetic variations arise by chance
  - Beneficial alleles are "sorted" and favored by natural selection
- Only natural selection consistently increases the frequencies of alleles that provide reproductive advantage
- Natural selection brings about adaptive evolution by acting on an organism's phenotype

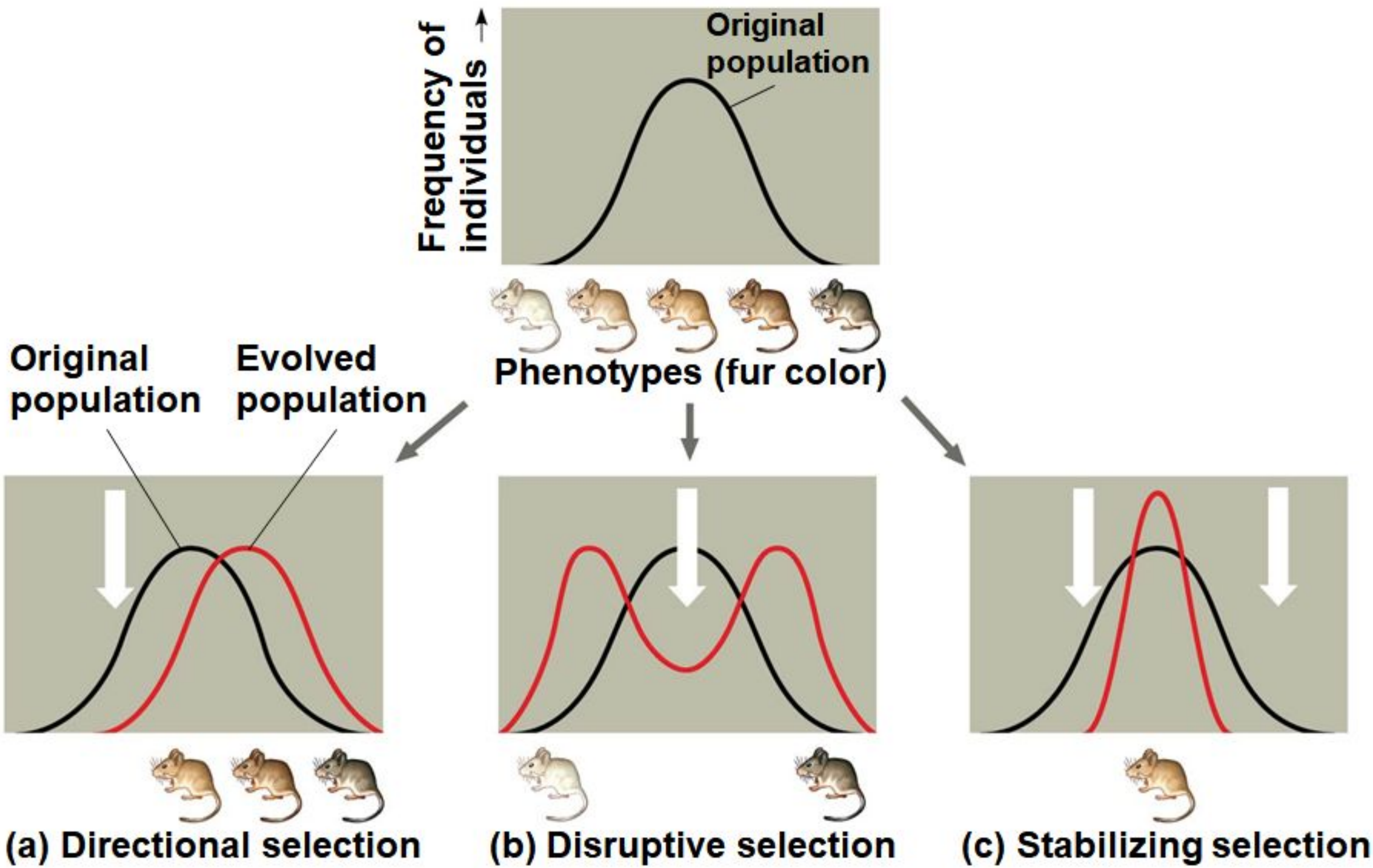
Relative Fitness

- The phrases “struggle for existence” and “survival of the fittest” are misleading, as they imply <u>direct competition among individuals</u>
- Reproductive success is generally more subtle and depends on <u>many factors</u>
- **Relative fitness** is the contribution an individual makes to the gene pool of the next generation relative to the <u>contributions of other individuals</u>
- Selection favors certain genotypes by acting on the <u>phenotypes of individuals</u>

Directional, Disruptive, and Stabilizing Selection

- There are three modes of selection:
  1. **Directional selection** favors individuals at one <u>extreme end of the phenotypic range</u>
  2. **Disruptive selection** favors individuals at <u>both extremes of the phenotypic range</u>
  3. **Stabilizing selection** favors intermediate variants and acts <u>against extreme phenotypes</u>

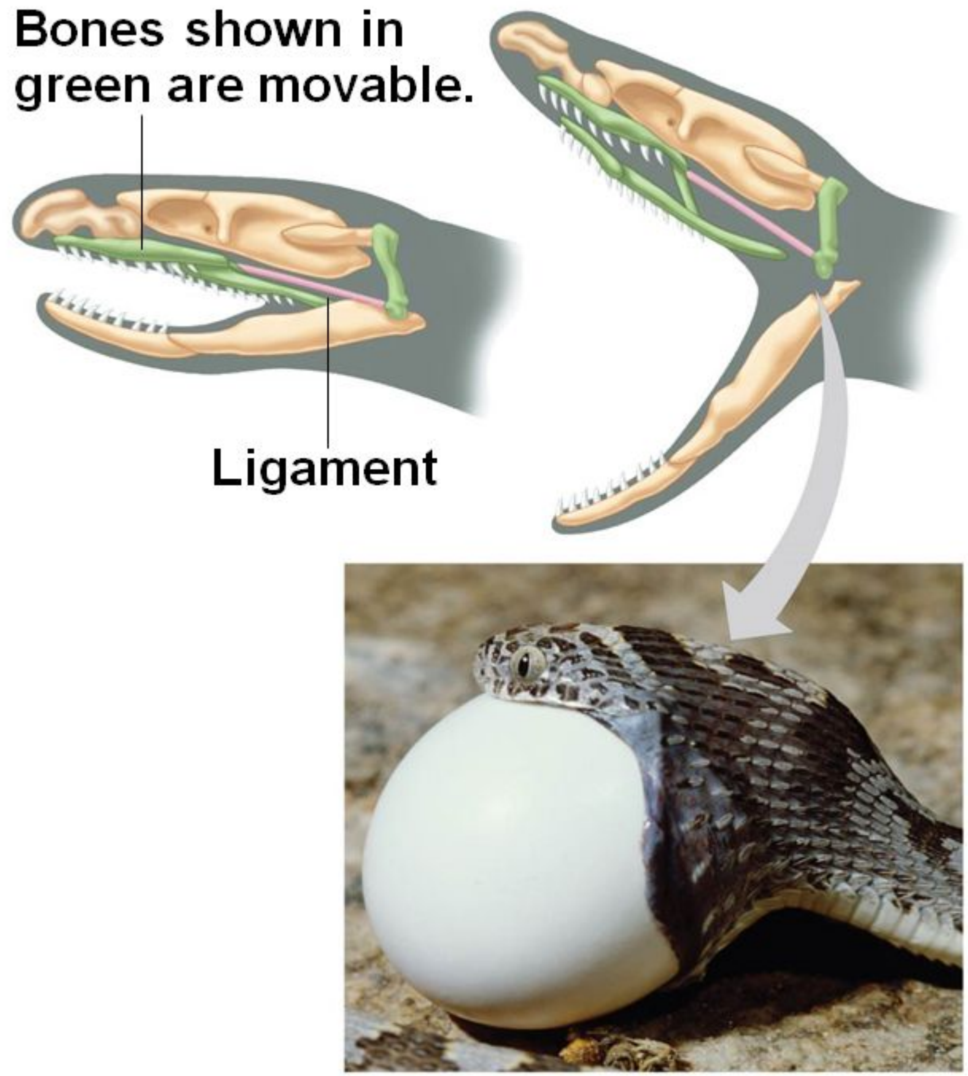
Figure 23.13



Frequency of individuals
Original population
Phenotypes (fur color)
Original population
Evolved population
(a) Directional selection
(b) Disruptive selection
(c) Stabilizing selection

The Key Role of Natural Selection in Adaptive Evolution

- Striking adaptations have arisen by <u>natural selection</u>
  - EX: certain octopuses can change color rapidly for <u>camouflage</u>
  - EX: the jaws of snakes allow them to swallow prey <u>larger than their heads</u>



- Natural selection increases the frequencies of alleles that <u>enhance survival and reproduction</u>
- Adaptive evolution occurs as the degree to which a species is well suited for life in <u>its environment improves</u>
- Because the environment can change, adaptive evolution is a <u>continuous process</u>
- Genetic drift and gene flow do not consistently increase the frequency of alleles that enhance <u>survival and reproduction</u>
- Both processes may increase or decrease the frequency of <u>beneficial alleles in a population</u>

Sexual Selection

- Process in which individuals with certain inherited characteristics are more likely to acquire mates than other individuals of the same sex
- It can result in **sexual dimorphism**, marked differences between the sexes in secondary sexual characteristics

Male

Female

- **Intra-sexual selection** is direct competition among individuals of one sex (often males) for mates of the opposite sex
- **Inter-sexual selection**, often called mate choice, occurs when individuals of one sex (usually females) are choosy in selecting their mates
- Showiness of male appearance can increase a male's chances of attracting a female while decreasing his chances of survival
- How do female preferences evolve?
- The "good genes" hypothesis suggests that if a trait is related to male genetic quality, both the male trait and female preference for that trait should increase in frequency

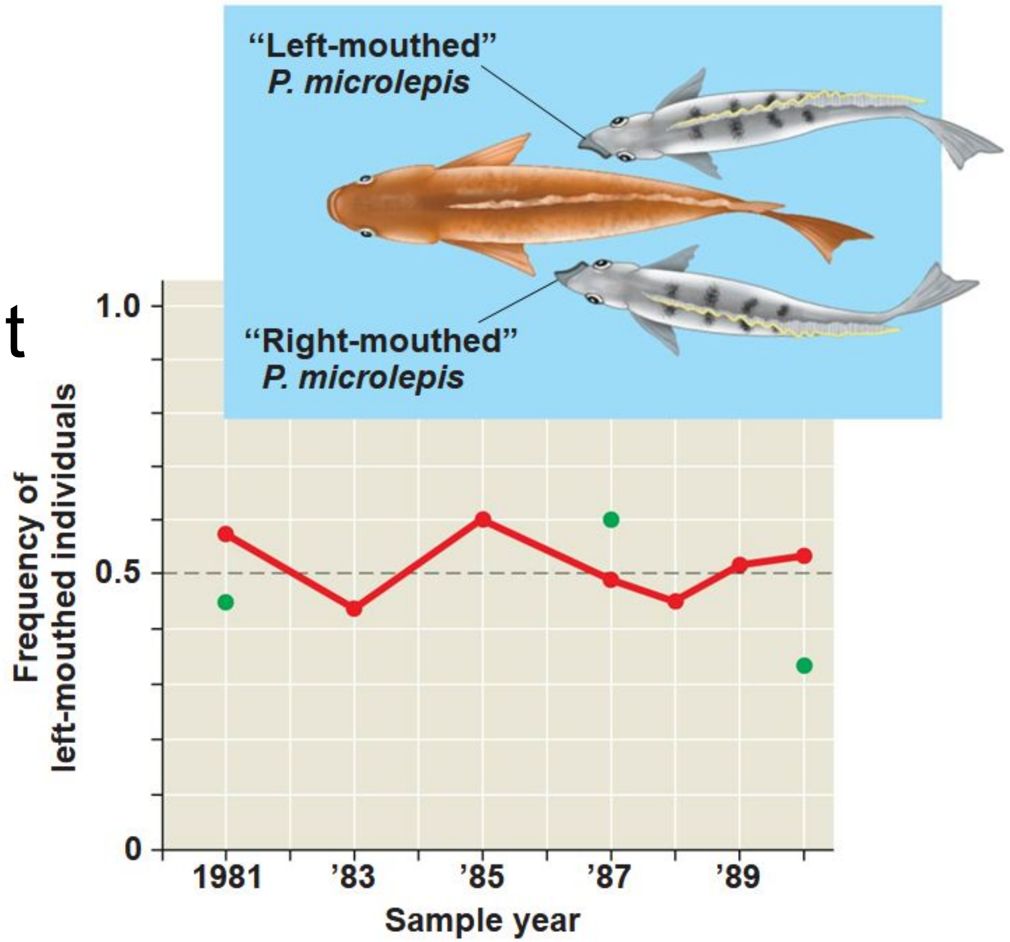
Balancing Selection

- Diploidy maintains genetic variation in the form of recessive alleles hidden from <u>selection in heterozygotes</u>
- **Balancing selection** occurs when natural selection maintains stable frequencies of two or more <u>phenotypic forms in a population</u>
- Balancing selection includes
  1. <u>Frequency-dependent selection</u>
  2. <u>Heterozygote advantage</u>

Frequency-Dependent Selection

- In **frequency-dependent selection**, the fitness of a phenotype depends on <u>how common it is in the population</u>

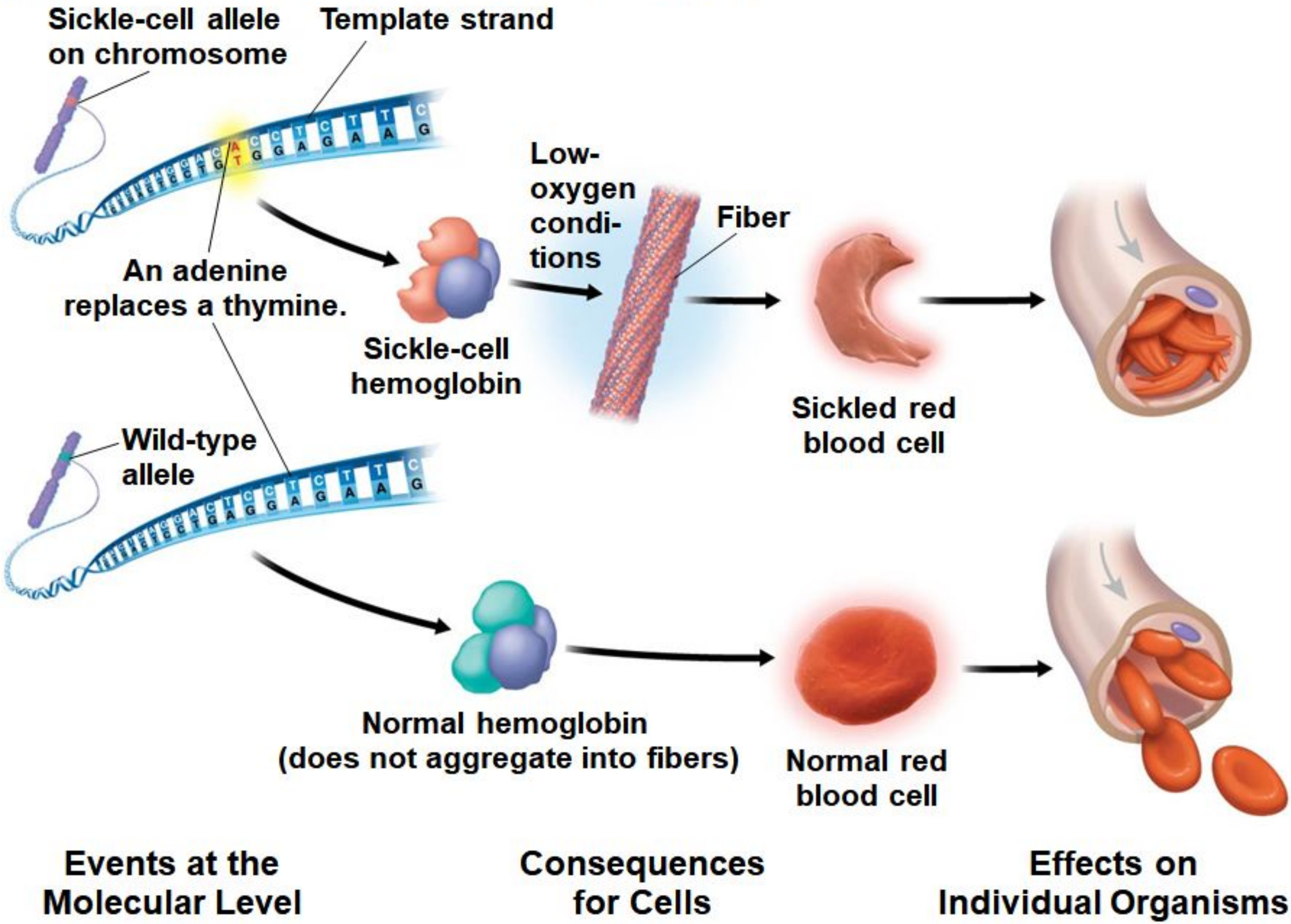
- EX: frequency-dependent selection results in approximately equal numbers of “right-mouthed” and “left-mouthed” <u>scale-eating fish</u>



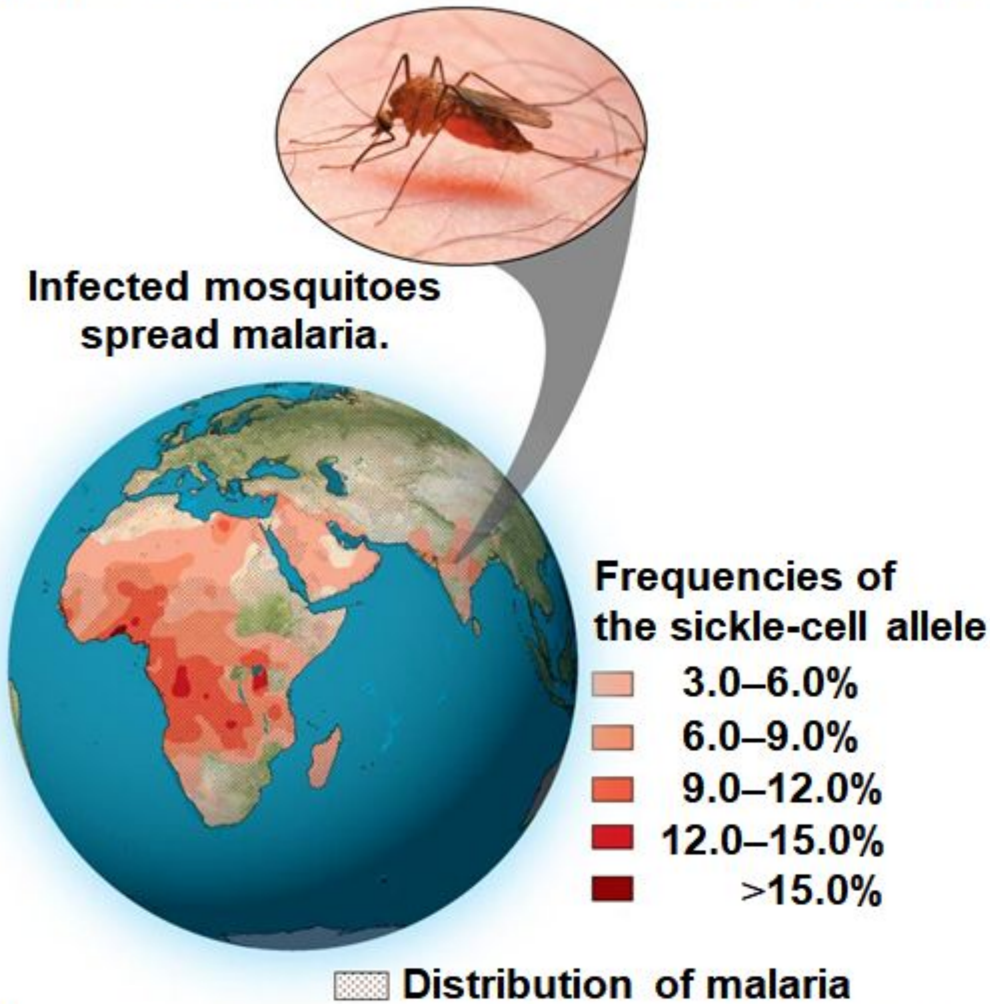
Heterozygote Advantage

- **Heterozygote advantage** occurs when heterozygotes have a higher fitness than both homozygotes
- Natural selection will tend to maintain two or more alleles at that locus
- Heterozygote advantage can result from stabilizing or directional selection
- A mutation in an allele that codes for part of the hemoglobin protein causes sickle-cell disease, but also confers malaria resistance
- In regions where the malaria parasite is common, selection favors individuals heretozygous for the sickle-cell allele

Make Connections: The Sickle-Cell Allele



Make Connections: The Sickle-Cell Allele



Heterozygotes are more likely to survive malaria.

This child has sickle-cell disease, a genetic disorder.

Evolution in Populations

Why Natural Selection Cannot Fashion Perfect Organisms

1. Selection can act only on existing variations
2. Evolution is limited by historical constraints
3. Adaptations are often compromises
4. Chance, natural selection, and the environment interact