

# Genetic Variation

Meerkats are mammals that live in the deserts of Africa. They live together in cooperative groups.

**FIGURE 2:** Meerkats stand alert to look for predators.



## Gather Evidence

Record the similarities and differences you see between the meerkats in Figure 2. Why do traits vary between individuals in a population?

## Differences in the Gene Pool

As you looked at the physical traits, or phenotypes, of the meerkats, you might have noticed variations in some of their traits. For instance, some are smaller than others. One has a light underside, while most have a darker underside. A few have more white on their faces, and others have more brown.

The phenotypic differences that you observed among the meerkats are due to differences in genes that code for those traits. Certain differences may offer a competitive advantage compared to the rest of the population. A particular phenotype may allow individuals to survive longer and reproduce more efficiently, both of which increase the total number of offspring produced. So, over time the phenotype becomes more prevalent. This gradual favoring of advantageous traits within a population is called natural selection, and it directly affects the population's gene pool. A **gene pool** is the collection of alleles found in all of the individuals of a population.

The different alleles in a gene pool ultimately result from mutations. When mutations occur during meiosis, the gametes that result may carry these mutations. Genetic variation may also be a result of crossing over and recombination, which occur during meiosis. During this process, chromosomes condense and homologous chromosomes align. Homologous chromosomes have the same genes but could have different alleles. During the alignment, an exchange of genetic material may take place. This exchange could alter the rearrangement of the linked genes in the chromosomes. As a result, the gametes are not genetically identical.



**Collaborate** Meerkats have a range of fur colors, from very light brown with more silver to a medium brown with less silver. Imagine a plant species with similar colors to the darker brown meerkats starts to grow in their habitat. With a partner, discuss what would happen to the meerkats and why.



## Explain

How can mutations in gametes become widespread in the gene pool?

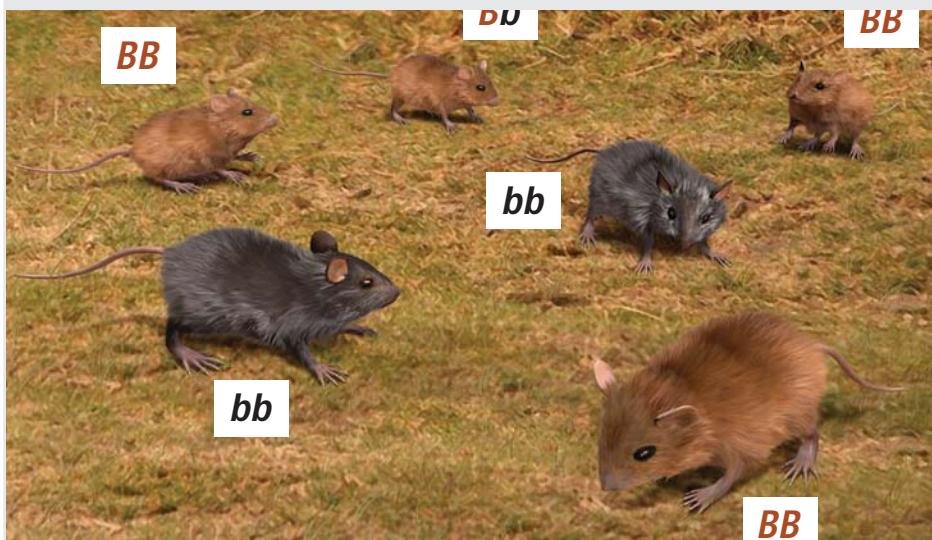
## Variation in Alleles

Different combinations of alleles in a gene pool can be formed when organisms mate and have offspring. Alleles are different forms, or versions, of genes. For example, mice with either one or two copies of the dominant *B* allele have brown fur, while mice with two recessive *b* alleles have black fur, shown in Figure 3.

### Gather Evidence

Use the image to determine how many total alleles, dominant alleles (*B*), and recessive alleles (*b*), are in the gene pool of this mouse population.

**FIGURE 3:** Differences in fur color in mice are due to differences in allele combinations.



### Math Connection



Use Figure 3 and the allele frequency equation to answer the following questions:

1. What is the allele frequency of the dominant allele *B*? Express your answer as a decimal rounded to the thousandths place and as a percentage.
2. What is the allele frequency of the recessive allele *b*? Express your answer as a decimal rounded to the thousandths place and as a percentage.

You can use the total number of alleles, the number of dominant alleles, and the number of recessive alleles to find the allele frequency in a population. **Allele frequency** is the proportion of one allele, compared with all the alleles for that trait, in the gene pool. To find the frequency of a particular allele, divide the number of times the allele is present by the total number of alleles in the population.

$$\text{Allele Frequency} = \frac{\text{Number of particular allele}}{\text{Total number of alleles}}$$

Allele frequency can also be expressed as a percentage by multiplying the frequency by 100. The frequencies of all the different alleles in a population should equal 1.0, or 100 percent.

Allele frequency is used to track genetic variation in populations and detect changes in alleles. Imagine that periodic fires blacken the ground in the field mice habitat in Figure 3. The black mice may be better camouflaged, providing more protection against predators. If they survive and reproduce more effectively than brown mice, the frequency of the *b* allele may increase over time relative to the *B* allele frequency.

## Analyzing Population Evolution

Some chickens, ducks, and other birds can lay eggs that have either white or blue shells. Blue eggshells are dominant and are coded for by allele *O*. White eggshells are recessive and are coded for by allele *o*. The outcome of a heterozygous-heterozygous cross for eggshell color can be determined by creating a Punnett square. We can create a Punnett square to represent any dominant or recessive allele in a population for this type of cross. In this generic Punnett square, *p* represents any dominant allele and *q* represents any recessive allele. The Punnett square that gives the possible genotypes of the offspring of heterozygous parents for eggshell color is shown in Figure 4.

The Punnett square shows that the genotypic frequency of  $OO$  is represented as  $p^2$ ,  $Oo$  is represented as  $2pq$ , and  $oo$  is represented as  $q^2$ . The frequency of all possible genotypes in a population must equal 1. If allele frequency can be found using the equation  $p + q = 1$ , then  $p^2 + 2pq + q^2 = 1$ . Scientists use these equations to predict the genotypic frequencies in a population. Then, they compare the predicted frequencies to the actual frequencies in a population.



**Predict** What could a scientist conclude if the genotypic frequencies in a population are different from the predicted values?

**FIGURE 4:** In this Punnett square,  $p$  represents any dominant allele and  $q$  represents any recessive allele.

$O (p)$	$o (q)$	
$O (p)$	$OO (p^2)$	$Oo (pq)$
$o (q)$	$Oo (pq)$	$oo (q^2)$



## Data Analysis

In a population of 1,000 chickens, 840 hens lay blue eggs and 160 hens lay white eggs. Use the equation  $p^2 + 2pq + q^2 = 1$  to determine the predicted genotypic frequencies for this population. Then compare those values with the actual genotypic frequencies in the population.

**STEP 1** Solve for  $q^2$  by dividing the number of  $oo$  chickens by 1,000.

$$q^2 = \frac{160}{1000} = 0.16$$

**STEP 2** Solve for  $q$  by taking the square root of each side of the equation.

$$q = \sqrt{0.16} = 0.4$$

**STEP 3** Determine  $p$  by substituting the value of  $q$  in the equation  $p + q = 1$ :

$$p + 0.4 = 1$$

$$p = 1 - 0.4 = 0.6$$

These are the predicted allele frequencies:  $p = 0.6$  and  $q = 0.4$ .

**STEP 4** Calculate the predicted genotypic frequencies from the predicted allele frequencies:

$$p^2 = (0.6)^2 = 0.36$$

$$2pq = 2(0.6)(0.4) = 0.48$$

$$q^2 = (0.4)^2 = 0.16$$



**Analyze** Answer the following questions in your Evidence Notebook:

- What percentage of this population is expected to be  $OO$ ,  $Oo$ , and  $oo$ ? What do these values mean?
- Through genetic analysis, scientists discovered the actual genotypic frequencies for the above population to be  $OO = 0.60$ ,  $Oo = 0.14$ , and  $oo = 0.26$ . What can you infer by comparing these data to the values predicted above?

## VARIABLES

$p$  = frequency of  $O$   
(dominant allele, blue shell)

$q$  = frequency of  $o$   
(recessive allele, white shell)

$p^2$  = frequency of chickens with  $OO$   
(homozygous dominant genotype)

$2pq$  = frequency of chickens  $Oo$   
(heterozygous genotype)

$q^2$  = frequency of chickens with  $oo$   
(homozygous recessive genotype)

The equation  $p^2 + 2pq + q^2 = 1$  is known as the Hardy-Weinberg equation. A Hardy-Weinberg population is in equilibrium, meaning it is stable and not evolving. Five conditions must be met for a population to be in equilibrium: no mutations, very large population, no natural selection, no new genetic material is introduced, and individuals are equally likely to mate with any other individual in the population.



## Cause and Effect

**FIGURE 5:** Peppered Moths



## Selection on Peppered Moth Populations

The peppered moth *Biston betularia* found in the English countryside, ranges in color from light (*Biston betularia typica*) to dark (*Biston betularia carbonaria*). Before the Industrial Revolution, light moths were more prevalent than dark moths. During the Industrial Revolution, trees became covered in dark soot from coal burned in factories. Over time, scientists observed that the number of dark moths increased relative to light moths. More recently, clean air laws returned the trees to their lighter coloring, and the dark colored moths decreased in frequency (Figure 6).

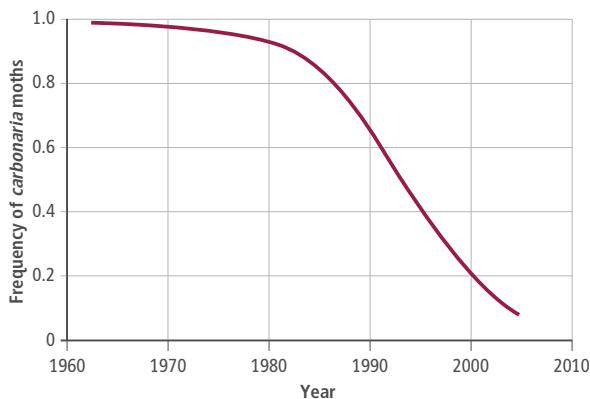
Recent studies found bird predation was one possible driving force behind the population shift. When trees were covered with soot, birds preyed on light moths. When the soot faded, birds preyed on dark moths (Figure 7). Other factors, such as migration, may have also influenced the population and require further study.



**Analyze** Create a graph of the shift observed in the peppered moth population. Place the color range on the x-axis and frequency of the trait on the y-axis.

**Frequency of dark moths around Leeds, England, from 1970-2000**

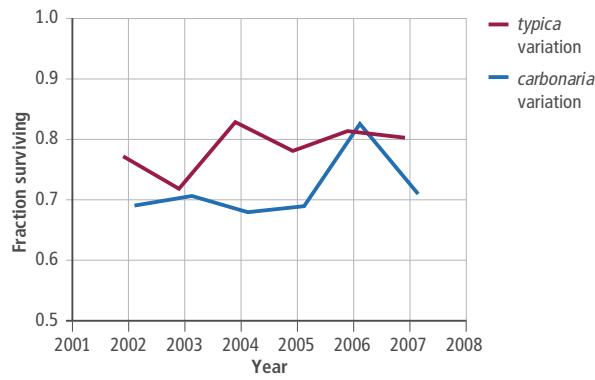
**FIGURE 6:** Frequency of Dark Moths



Source: John N. Thompson, *Relentless Evolution* (2013): 57, quoted in <http://phenomena.nationalgeographic.com/2013/10/09/evolution-in-color-from-peppered-moths-to-walking-sticks/>

**Effect of bird predation on the population of light and dark moths**

**FIGURE 7:** Effect of Bird Predation



Source: Cook, L. M., B. S. Grant, and I. J. Saccheri, J. Mallet. "Selective bird predation on the peppered moth: the last experiment of Michael Majerus." *Biol. Lett.* 2012. Published 8 February 2012. doi: 10.1098/rsbl.2011.1136.



**Explain** How does the Hardy-Weinberg equilibrium equation use genetic variation and allele frequencies in a population to describe whether a population is evolving?