

16-1 Genes and Variation

How Common Is Genetic Variation?

Many genes have at least two forms, or alleles.

All organisms have genetic variation that is “invisible” because it involves small differences in biochemical processes.

An individual organism is heterozygous for many genes.

Variation and Gene Pools

Genetic variation is studied in populations.

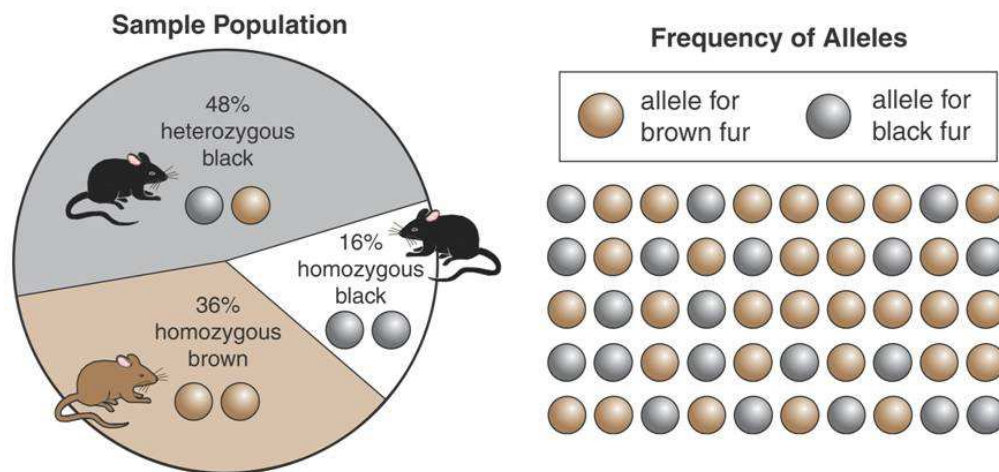
A **population** is a group of individuals of the same species that interbreed.

A **gene pool** consists of all genes, including all the different alleles, that are present in a population.

The **relative frequency** of an allele is the number of times the allele occurs in a gene pool, compared with the number of times other alleles for the same gene occur.

Relative frequency is often expressed as a percentage.

When scientists determine whether a population is evolving, they may look at the sum of the population’s alleles, or its gene pool. This diagram shows the gene pool for fur color in a population of mice.



How is evolution defined in genetic terms?

In genetic terms, evolution is any change in the relative frequency of alleles in a population.

What are the main sources of heritable variation in a population?

The two main sources of genetic variation are

- mutations and
- the genetic shuffling that results from sexual reproduction.

Mutations

A mutation is any change in a sequence of DNA.

Mutations occur because of mistakes in DNA replication or as a result of radiation or chemicals in the environment.

Mutations do not always affect an organism’s phenotype.

Gene Shuffling

Most heritable differences are due to gene shuffling.

Crossing-over increases the number of genotypes that can appear in offspring.

Sexual reproduction produces different phenotypes, but it does not change the relative frequency of alleles in a population.

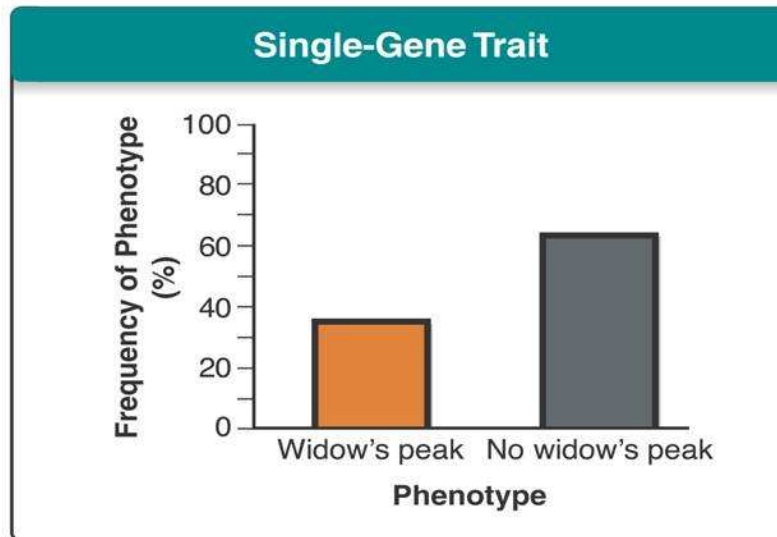
What determines the numbers of phenotypes for a given trait?

The number of phenotypes produced for a given trait depends on how many genes control the trait.

Single-Gene Traits

A **single-gene trait** is controlled by one gene that has two alleles. Variation in this gene leads to only two possible phenotypes.

In humans, a single gene with two alleles controls whether a person has a widow's peak (left) or does not have a widow's peak (right). As a result, only two phenotypes are possible. **The number of phenotypes a given trait has is determined by how many genes control the trait.**



The allele for a widow's peak is dominant over the allele for a hairline with no peak.

However, the presence of a widow's peak may be less common in a population.

In real populations, phenotypic ratios are determined by the frequency of alleles as well as by whether the alleles are dominant or recessive.

Polygenic Traits

Many traits are controlled by two or more genes and are called **polygenic traits**.

One polygenic trait can have many possible genotypes and phenotypes.

Height in humans is a polygenic trait.

- A bell-shaped curve is typical of polygenic traits.
- A bell-shaped curve is also called normal distribution.

The graph below shows the distribution of phenotypes that would be expected for a trait if many genes contributed to the trait.

