

# Allele frequency & the gene pool

AP.BIO: EVO-1 (EU), EVO-1.K (LO), EVO-1.K.1 (EK), EVO-1.K.2 (EK)

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*How to find allele frequency and how it's different from genotype frequency. What a gene pool is.*

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## Key points:

- **Microevolution** is a change in the frequency of gene variants, alleles, in a population, typically occurring over a relatively short time period.
  - **Population genetics** is the field of biology that studies allele frequencies in populations and how they change over time.
  - **Allele frequency** refers to how common an allele is in a population. It is determined by counting how many times the allele appears in the population then dividing by the total number of copies of the gene.
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- The **gene pool** of a population consists of all the copies of all the genes in that population.

## Darwin meets Mendel—not literally

When Darwin came up with his theories of [evolution and natural selection](#), he knew that the processes he was describing depended on heritable variation in populations. That is, they relied on differences in the features of the organisms in a population and on the ability of these different features to be passed on to offspring.

[Read a quick recap of evolution and natural selection.](#)

Darwin did not, however, know how traits were inherited. Like other scientists of his time, he thought that traits were passed on via blending inheritance. In this model, parents' traits are supposed to permanently blend in their

offspring. The blending model was disproven by Austrian monk [Gregor Mendel](#), who found that traits are specified by non-blending heritable units called genes.

Although Mendel published his work on genetics just a few years after Darwin published his ideas on evolution, Darwin probably never read Mendel's work. Today, we can combine Darwin's and Mendel's ideas to arrive at a clearer understanding of what evolution is and how it takes place.

## Microevolution and population genetics

*Microevolution*, or evolution on a small scale, is defined as a change in the frequency of gene variants, alleles, in a population over generations. The field of biology that studies allele frequencies in populations and how they change over time is called *population genetics*.

Microevolution is sometimes contrasted with **macroevolution**, evolution that involves large changes, such as formation of new groups or species, and happens over long time periods. However, most biologists view microevolution and macroevolution as the same process happening on different timescales. Microevolution adds up gradually, over long periods of time to produce macroevolutionary changes.

Let's look at three concepts that are core to the definition of microevolution: populations, alleles, and allele frequency.

### Populations

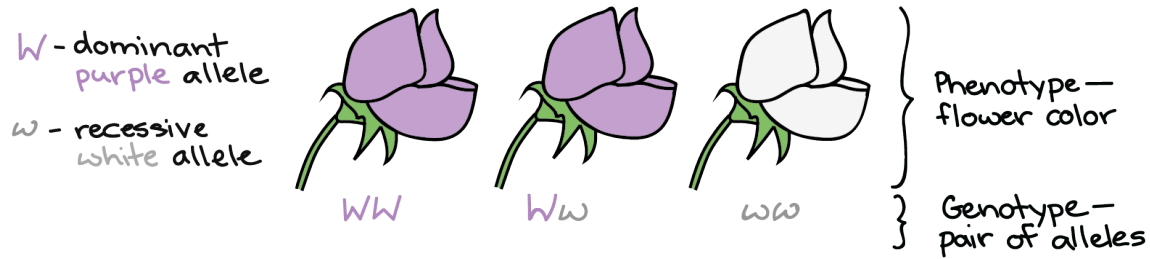
A **population** is a group of organisms of the same species that are found in the same area and can interbreed. A population is the smallest unit that can evolve—in other words, an individual can't evolve.

### Alleles

An **allele** is a version of a **gene**, a heritable unit that controls a particular feature of an organism.

For instance, Mendel studied a gene that controls flower color in pea plants. This gene comes in a white allele,  $w$ , and a purple allele,  $W$ . Each pea plant

has two gene copies, which may be the same or different alleles. When the alleles are different, one—the **dominant** allele,  $W$ —may hide the other—the **recessive** allele,  $w$ . A plant's set of alleles, called its **genotype**, determines its **phenotype**, or observable features, in this case flower color.



## Allele frequency

*Allele frequency* refers to how frequently a particular allele appears in a population. For instance, if all the alleles in a population of pea plants were purple alleles,  $W$ , the allele frequency of  $W$  would be 100%, or 1.0. However, if half the alleles were  $W$  and half were  $w$ , each allele would have an allele frequency of 50%, or 0.5.

In general, we can define allele frequency as

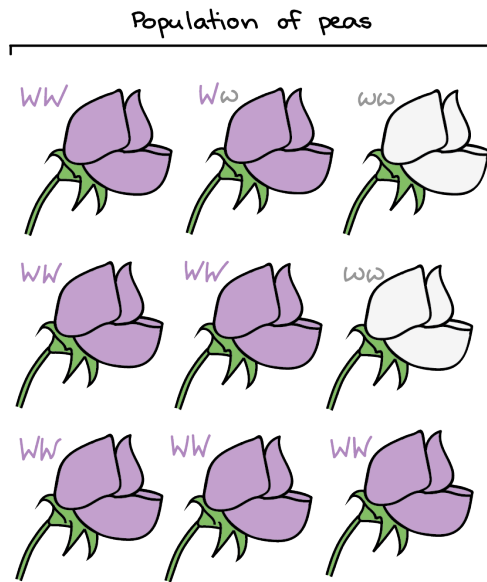
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Sometimes there are more than two alleles in a population (e.g., there might be  $A$ ,  $a$ , and  $c$  alleles of a gene). In that case, you would want to add up *all* of the different alleles to get your denominator.

It's also possible to calculate **genotype frequencies**—the fraction of individuals with a given genotype—and **phenotype frequencies**—the fraction of individuals with a given phenotype. Keep in mind, though, that these are different concepts from allele frequency. We'll see an example of this difference next.

## Example: Finding allele frequency

Let's look at an example. Consider the very small population of nine pea plants shown below. Each pea plant has two copies of the flower color gene.



If we look at the two gene copies in each plant and count up how many  $W$  copies are present, we find there are 13. If we count up how many  $w$  copies are present, we find that there are five. The total number of gene copies in the whole population is .

We can divide the number of copies of each allele by the total number of copies to get the allele frequency. By convention, when there are just two alleles for a gene

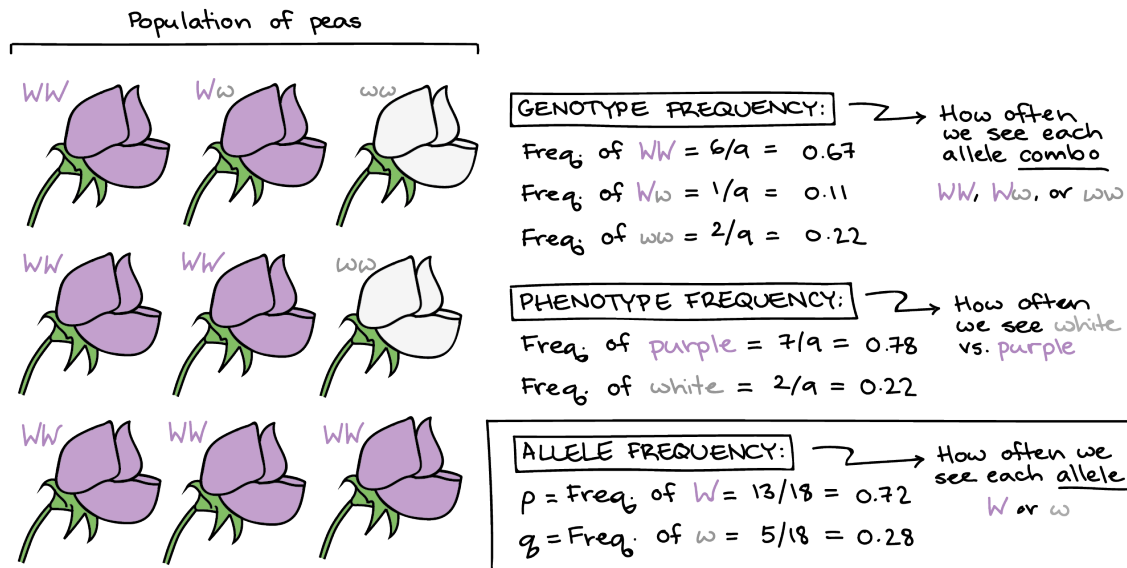
in a population, their frequencies are given the symbols and :

, or

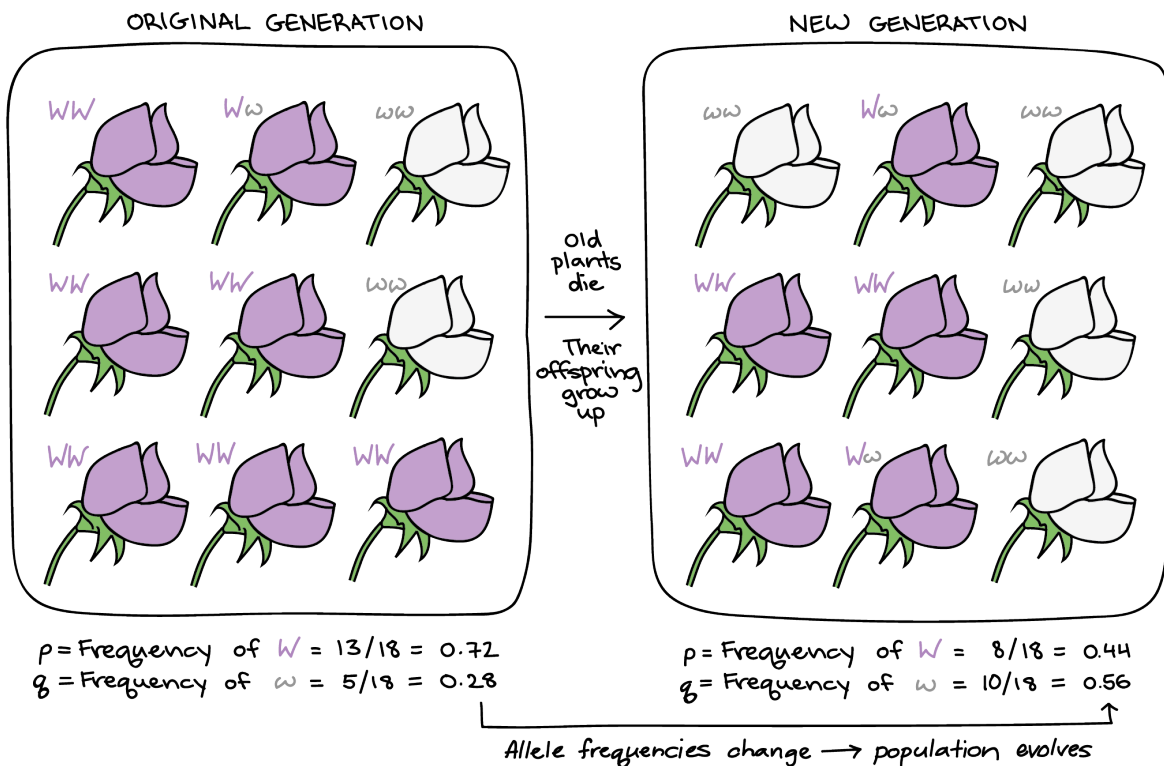
, or

The frequencies of all the alleles of a gene must add up to one, or 100%.

Allele frequency is different from genotype frequency or phenotype frequency. Genotype and phenotype frequencies can also be calculated and are important for understanding how populations evolve, but they are not the same thing as allele frequency. The diagram below shows the difference:



Now, let's suppose we come back a generation later and check the genotypes of the new pea plants that now make up the population. To find the allele frequencies, we again look at each individual's genotype, count the number of copies of each allele, and divide by the total number of gene copies. Now, we find the frequency of  $W$  has dropped to , or 44%, and the frequency of  $w$  has risen to , or 56%.



There has been a change in allele frequencies in the population over generations, so—by the definition of microevolution—we can say that the

population has evolved. If we were actually doing research, we might want to use a statistical test to confirm that these proportions were really different. We'll examine the factors that cause a population to evolve, including natural selection, genetic drift—random change—and others factors, in the rest of this tutorial.

## The gene pool

The total set of gene copies for all genes in a population is referred to as its *gene pool*. The gene pool gets its name from the idea that we are essentially taking all the gene copies—for all genes—in the individuals of a population and dumping them into one large, common pool.

What would this look like? In the example above, we went through all nine individuals in the population and looked at their copies of the flower color gene. There were 18 individual gene copies, each of which was a *W* or a *w* allele. Now, imagine that we went through this same process for every single gene in the pea plant, including genes that control height, seed color, seed shape, metabolism, etc. There would be 18 copies of each gene pulled out and dumped into the common pool. At the end of this process, the common pool of gene copies will be the gene pool of our population.

By looking at all the copies of all the genes in a population, we can see globally how much genetic variation there is in the population. The more variation a population has, the better its ability to adapt to changes in its environment through natural selection. If there is more variation, the odds are better that there will be some alleles already present that allow organisms to survive and reproduce effectively under the new conditions.