

# POPULATION GENETICS

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# Genetic Variation

Genetic variation can be defined as the genetic makeup of organisms within a population change.

Genes are inherited segments of DNA that contain codes for the production of proteins.

Genes exist in alternate versions, or alleles that determine distinct traits that can be passed on from parents to offspring.

Genetic variation is important to the processes of natural selection and biological evolution.

The environment determines which genetic variations are more favorable or better suited for survival.

As organisms with these environmentally selected genes survive and reproduce, more favorable traits are passed on to the population as a whole.

# Causes of Genetic Variations

Genetic variation occurs mainly through

- DNA mutation
- Gene flow (movement of genes from one population to another)
- Sexual reproduction

Due to the fact that environments are unstable, populations that are genetically variable will be able to adapt to changing situations better than those that do not contain genetic variation.



A true albino squirrel

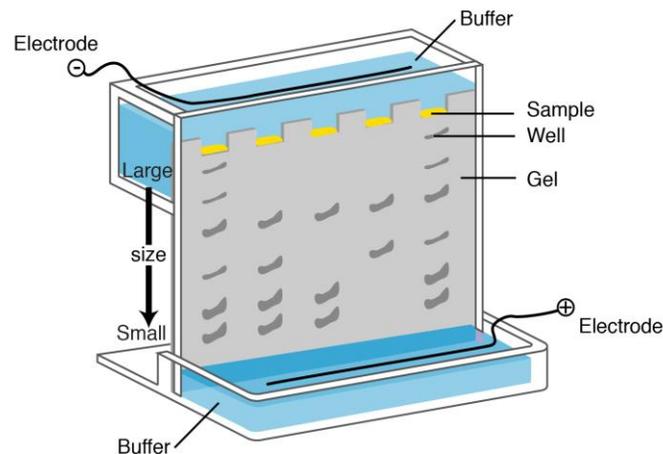
A person's skin color, hair color, dimples, freckles, and blood type are all examples of genetic variations that can occur in a human population. Examples of genetic variation in plants include the modified leaves of carnivorous plants and the development of flowers that resemble insects to lure plant pollinators. Gene variation in plants often occurs as the result of gene flow. Pollen is dispersed from one area to another by the wind or by pollinators over great distances.

Examples of genetic variation in animals include albinism, cheetahs with stripes, snakes that fly, animals that play dead, and animals that mimic leaves. These variations enable the animals to better adapt to conditions in their environments.

# Gel Electrophoresis

- It is a technique that can identify variations in the physical and chemical properties of proteins.
- Protein samples are readily obtained from extracts of tissues such as blood. The individual proteins in these samples can be separated from each other by passing them through a carbohydrate sieve.
- The carbohydrates are formed in the gel, saturated with a buffering solution and attached to an electric current.
- Protein samples inserted into slots at one end of the gel are then moved through the gel by electric force.
- The rate of movement is determined by the electric charge on the protein and this in turn depend on the protein's amino acid sequence.

- Thus, if two forms of proteins have slightly different sequence, and if this cause them to have different charges then they will move at different rates through the gel
- When the electric current is turned off, the gel can be treated with the specific stain to reveal mobility difference in the protein molecules.
- Form of the same protein that are separated in this way are called **ALLOZYMES**.
- Because Allozymes are specified by different alleles, allozymic variations is a direct reflection of underlying genetic variation.



The extent of this variation have been documented in various studies.

- About one third of all soluble proteins in human being show allozymic variations.
- In many other species, the frequency of loci with allozymic variations is 20-30% but in some it is much lower.
- One example is African Cheetah in which 4% of enzyme-coding loci are segregating different alleles. This lack of variability is probably the result of bottleneck in the size of Cheetah population. Such bottleneck are expected to reduce genetic variability by causing the loss of rare alleles in the species.

# ALLELE FREQUENCY

- Allele frequency (also called gene frequency) is the term used to describe the fraction of gene copies that are of a particular allele in a defined population.

In a population in equilibrium there are 1000 people. There are 160 recessive homozygous and 480 heterozygous genotypes. Calculate the frequency of the dominant allele.

$$\begin{array}{l} \text{AA} \quad \text{Aa} \quad \text{aa} \\ 360 + 480 + 160 = 1000 \\ \quad \quad \quad \nearrow 240 \quad \quad \quad \nwarrow 240 \nearrow \\ \text{A} \quad 600 \quad \quad \quad \text{a} \quad 400 \\ \quad 60\% \quad \quad \quad \quad 40\% \\ \quad 0.6 \quad \quad \quad \quad 0.4 \end{array}$$

$\frac{D}{D} = 100\%$   
 $A + a = 1$   
 $0.6 + 0.4 = 1$

Let us consider, for example, a population of 100 diploid individuals. Each individual carries two copies of each gene, so there are a total of 200 gene copies in the population of 100 people. Now let us say that 20 individuals in this population are heterozygous for allele A (with a second allele of some other type), and 5 individuals are homozygous for allele A. Each homozygote would contribute two copies of the allele toward the total fraction, while each heterozygote would only contribute one copy toward the total fraction. So the total number of A alleles in the population would be  $20 + 10$ , for a total of 30. The allele frequency would be this number divided by the total number of gene copies ( $30/200$ ) to yield 0.15, which is the allele frequency. Allele frequencies can always be determined in this way when the numbers of homozygotes and heterozygotes in a population are known. When heterozygotes cannot be distinguished because an allele expresses a recessive trait, it is still possible to use Hardy–Weinberg statistics to estimate the allele frequency if certain assumptions about breeding practices are made.