Natural Selection—an Interactive PhET simulation

Deoxyribonucleic acid (DNA) is organized in the form of long molecules called **chromosomes**. **Genes** are small sections of these chromosomes; a gene is the basic physical and functional unit of **heredity** and represents instructions to make proteins. **Diploid** organisms such as humans have two copies or **alleles** of each gene, one inherited from each parent. Humans have 46 chromosomes which exist as 23 pairs, 22 of which are non-sex chromosomes or **autosomes** and one is made up of **sex-determining chromosomes**. In humans, the sex chromosomes are **X** and **Y**; females carry two X chromosomes, males carry one X and one Y chromosome.

Alleles are versions of the same gene that exist at a locus or position on a chromosome. In humans, each pair of alleles represents the **genotype** of a specific gene. If there are two identical alleles at a given locus, the genotype is described **homozygous**. If there are two different alleles at a locus, the genotype is described **heterozygous**. Alleles contribute to the outward appearance of an organism, called the **phenotype** of the organism.

Characteristics or **traits** can be **dominant** or **recessive**. **Dominant traits** appear more frequently whereas **recessive traits** are masked by other traits and are expressed only when the genotype is homozygous.

Alleles can be **dominant** or **recessive**. A **dominant phenotype** can arise in organisms that are i) **homozygous** at a given locus and carry two dominant alleles or ii) if an organism is **heterozygous** at a particular locus and carries one dominant and one recessive allele. But the heterozygous organism will be considered a **carrier of the recessive allele**. For an organism to express the **recessive phenotype**, it should have **two copies of the recessive allele**.

Mutations are changes in the nucleotide sequence of the genome or other genetic elements. They arise due to errors in DNA replication or due to damage to DNA by radiation or carcinogens. **Somatic** mutations occur in non-reproductive cells and will not be passed onto offspring. **Germline** mutations occur in reproductive cells such as eggs or sperm and are passed onto offspring. Mutations may or may not lead to visible changes in the phenotype of an organism.

Genetic conditions caused by mutations in a single gene can inherited in any of the following patterns: **autosomal dominant, autosomal recessive, X-linked dominant, X-linked recessive, Y- linked, codominant** and **mitochondrial**. Pedigree analysis allows the study of inheritance of genes, especially when progeny data from many generations is limited and the species of interest has a long generation time.

Camouflage describes the ways adopted by animals so that they are not easily detected by their prey and predators. It can be any of the following types:

i) **Background matching** using coloration and patterning to resemble their environment, *e.g.,* the snowshoe hare that is white against the snow in winter and brown in spring and summer .

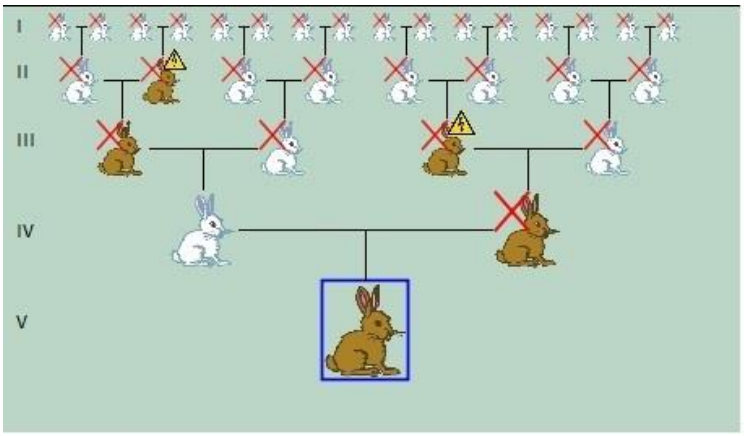
ii) **Disruptive camouflage** where patterns of light and dark patches, stripes and spots on the individual make it difficult to see the outline or shape of the animal, *e.g.*, tiger.

iii) **Mimicry** where the individual mimics the appearance or behavior of another object or species, *e.g.*, stick insects that sway like sticks moving in the wind.

iv) **Adaptive camouflage** where the animals change their color, pattern, shape and texture according to their environment, *e.g.*, chameleon.

v) **Motion dazzle** where animals use light and dark patterns and stripes to disguise their direction, speed and size when they move, *e.g.*, zebra.

vi) **Countershading** where animals are darker on top and paler underneath so they blend into darker backgrounds when seen from above and blend into paler backgrounds (such as the sky) when seen from below, e.g., Adelie penguins.
The reverse of countershading (darker beneath and light on top) enhances contrast and is seen in animals that can defend themselves, *e.g.*, skunks.



Consider the above **pedigree chart** for the rabbit framed in the blue rectangle. Each row of rabbits has been assigned a roman numeral from I to V. From left to right, we assign Arabic numerals to the animals so that the third rabbit from the left in row III (a brown one) is III-3.

What if we wanted to find out the genotype of III-3 and find out the pattern of inheritance for brown fur in the above pedigree chart?

First, let us assume that the left animal in each mating pair, linked by a horizontal line, is male and the right one is female.

III-3 is a brown male rabbit. It has a yellow triangle next to it which means that the brown fur mutation took place in this rabbit (as opposed to being transmitted).

Let us assume that inheritance of brown fur was dominant in this instance and check if our assumption is correct. For this assumption, let us use B to denote brown fur and b to denote white fur.

Parents of III-3 are II-5 and II-6, both white rabbits. Let us draw a **Punnett square** and write the alleles for II-6 (mother) horizontally on top and for II-5 (father) vertically on the side. As both II-5 and II-6 are white and we have assumed brown fur to be a dominant mutation, an

animal with white fur must be homozygous and have the recessive allele b. So the female II-6 must be X_b X_b and the male II-5 must be X_b-Y.

	X_b	X_b
X_b	X_bX_b	X_bX_b
Y	X_bY	X_bY

As seen in the Punnett square, the progeny (children) of II-5 and II-6 can be female or male but they will all be white. So the genotype of III-3, a male rabbit, has to be X_bY, which means that according to the Punnett square prediction, it should be white. However, III-3 is a brown rabbit. However, the yellow triangle indicates that it underwent a mutation after which its fur became brown and become X_BY.

The pedigree analysis we just did for III-3 assumed that inheritance of the brown fur mutation was dominant. When the observation matched the prediction, we inferred that the inheritance pattern for the brown fur mutation was indeed dominant. Hence, we can analyze pedigree and determine the genotypes of individuals in different generations to find out inheritance patterns of mutations.