

# **CAIE Biology A-level**

## **Topic 17: Selection and evolution**

### Notes

This work by [PMT Education](https://www.pmt.education) is licensed under [CC BY-NC-ND 4.0](https://creativecommons.org/licenses/by-nc-nd/4.0/)



**Phenotype** – the **characteristics of an organism**, which result from the **interaction of the genes of the organism with the environment** in which it lives.

### Types of variation

- **Continuous variation** is variation within a range and it includes mass and height.
- **Discontinuous variation** can only take particular values – such as sex or blood group.

Variation in genotype has an effect on variation in phenotype. Some characteristics are influenced by one gene only and are known as **monogenic**. Such characteristics show **discontinuous variation**. Sometimes several genes at different loci are involved in determining a characteristic – this is known as **polygenic inheritance and often gives rise to continuous variation**.

Some characteristics are influenced by both genotype and the environment.

- **Height** is a polygenic characteristic. However, an organism might not reach its maximum height due to **poor nutrition** which is an environmental factor.
- Some people may be more susceptible to **lung cancer** due to mutations affecting **proto-oncogenes** that regulate the cell cycle. Smoking exposes lung cells to chemicals that convert these genes into active oncogenes, thus leading to **uncontrolled cell division** in the lungs which can result in lung cancer.
- **Animal hair colour**, for example Siamese cat hair colour, is determined by both genotype and environment. Siamese cats have a gene coding for enzyme **tyrosinase** which darkens the fur which is active only below 31 °C. Therefore, only the body **extremities** of Siamese cats are dark.

The **student's T-test** can be used to compare the mean values of two sets of data. This is the formula:

$$t = \frac{|\bar{x}_1 - \bar{x}_2|}{\sqrt{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)}}$$

**Key to symbols:**

- $\bar{x}$  = mean
- $s$  = sample standard deviation
- $n$  = sample size (number of observations)

The **null hypothesis** will state that there is **no significant difference** between the two means. The **alternative hypothesis** will state that there is a significant difference between the two means.

You compare the value you get from the T-test to the **critical value** (which depends on the level of significance).

- If **t is greater** than the critical value, you **reject** the null hypothesis (and accept the alternative hypothesis).
- If **t is less** than the critical value, you **accept** the null hypothesis, which means there is no significant difference between the two means.



## Natural selection and evolution

The **niche** of a species is **its role within the environment**. Species which share the same niche compete with each other and the better adapted species survive. This is the basis of **natural selection**.

### Organisms are adapted to their environment in various ways

- **Anatomical adaptations** are **physical adaptations**, either external or internal. For example, the presence of loops of Henlé allows desert mammals to produce concentrated urine and minimise water loss.
- **Behavioural adaptations** are **changes in behaviour** which improve the organism's chance of survival e.g. mating calls.
- **Physiological adaptations** are **processes inside an organism's body** that increase its chance of survival e.g. regulation of blood flow through the skin.

**Natural selection** is the process in which **fitter individuals** who are better adapted to the environment **survive and pass on advantageous alleles to future generations**. Evolution is the process by which the **frequency of alleles in a gene pool changes over time, often as a result of natural selection**. You can find out more about **evolutionary relationships** between species by looking at **DNA sequences**.

### Evolution via natural selection

- There are a **variety of phenotypes** within a population.
- An **environmental change occurs** and as a result of that the **selection pressure changes**.
- Some individuals possess **advantageous alleles which give them a selective advantage and allow them to survive and reproduce**.
- The **advantageous alleles are passed on to their offspring**.
- Over time, **the frequency of alleles in a population changes** and this leads to evolution.

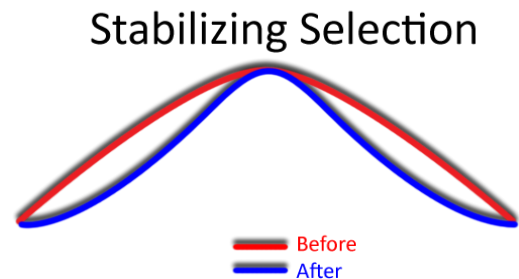


## Types of Selection

Selection describes how **allele frequencies change** in a population over time because some phenotypes have a **reproductive or survival advantage**.

### 1. Stabilising Selection

- Acts **against extreme phenotypes** at both ends of a distribution.
- **Favours the average phenotype**.
- Reduces variation in the population.
- Occurs in **stable environments** where the average phenotype is most advantageous.

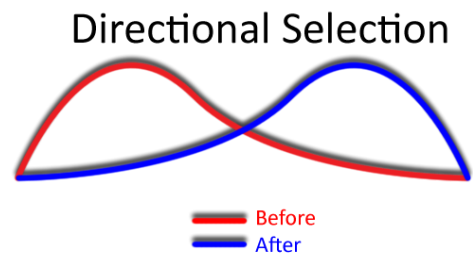


Example:

Human birth weight - very low or very high weights have higher mortality; intermediate weights have higher survival.

### 2. Directional Selection

- Favours **one extreme phenotype** over the other.
- Shifts the **mean phenotype** in one direction.
- Common in **changing environments**.

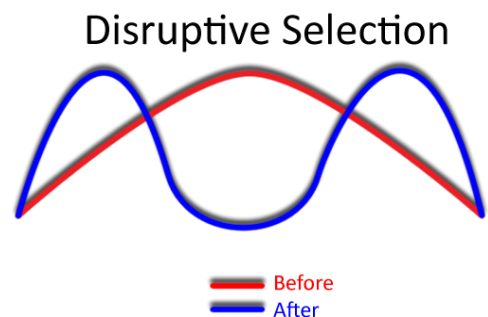


Example:

Antibiotic resistance - bacteria with alleles for drug resistance have a selective advantage under antibiotic use.

### 3. Disruptive Selection

- Favours **both extremes** of the trait distribution.
- Acts **against the average phenotype**.
- Increases variation in the population.
- Can lead to **polymorphism** or even **speciation** if extremes become reproductively isolated.



Example:

Beak size in birds - if both small and large seeds are available but intermediate sizes are rare, birds with small or large beaks are favoured over intermediate beak sizes.



## Factors that can affect the evolution of a species

- **Genetic drift** – a phenomenon where there is a small change in allele frequency that occurs because not all individuals in a population reproduce. This effect is amplified in very small groups, isolated from the rest of the population.
- **Genetic bottleneck** – rapid reduction in population size that affects genetic variation in future generations.
- **Founder effect** – decrease in genetic diversity which occurs when the population descends from a small number of ancestors.

**Speciation** is the process by which new species arise after a **population becomes separated** and **cannot interbreed**. For instance, **allopatric speciation** occurs when a **physical barrier** reduces **gene flow** between populations. Each group experiences a different selection pressure as the environment they live in is different. Over time, the frequency of alleles changes through **natural selection** and the two populations **can no longer interbreed and they become separate species**. The cause of allopatric speciation is genetic isolation. Another type of speciation is **sympatric speciation**, where new species evolve from a **single ancestral species** when **inhabiting the same geographic region**. For example, a **chromosomal error during cell division** can lead to **reproductive isolation**.

**Antibiotic resistance** is an example of natural selection. A **random mutation** occurs in the bacteria which makes it resistant to the antibiotic. The bacteria with the mutation are able to **survive and reproduce, passing** the mutant allele over many generations. This means the antibiotic becomes less effective in killing the bacteria. This can lead to bacteria like MRSA, which is resistant to a wide variety of antibiotics. To prevent antibiotic resistance, the whole antibiotic course must be finished and doctors will prescribe antibiotics only when necessary.

The **Hardy-Weinberg Equation** can be used to **estimate the frequency of alleles in a population** and to see whether a **change in allele frequency is occurring in a population over time**.

### equation 1:

$$p + q = 1$$

### equation 2:

$$p^2 + 2pq + q^2 = 1$$

### Key to symbols:

$p$  = frequency of the dominant allele, e.g. **A**

$q$  = frequency of the recessive allele, e.g. **a**

$p^2$  = frequency of homozygous dominant genotype, e.g. **AA**

$2pq$  = frequency of heterozygous genotype, e.g. **Aa**

$q^2$  = frequency of homozygous recessive genotype, e.g. **aa**

For a population in genetic equilibrium:

**$p + q = 1.0$**  (The sum of the frequencies of both alleles is 100%.)

Hardy–Weinberg equilibrium assumes **a large population, random mating, no mutation, no migration, and no selection**.



## Artificial selection

**Artificial selection** is the process where selection pressures are artificially created by humans, allowing the breeding of the desired characteristics.

An example of artificial selection is the **dairy cow**. The milk yield of each cow is measured and recorded to identify the cows with the highest milk yields. This enables the identification of the best quality bulls. The cows with the highest yields may be treated with hormones to increase ovulation rate and allow multiple embryos to be produced. The eggs are fertilised in vitro and subsequently implanted into **surrogate** mothers.

**Examples of crop improvement by selective breeding include:**

- introduction of **disease resistance** to varieties of wheat and rice.
- the **incorporation of mutant alleles for gibberellin synthesis** into dwarf varieties so increasing yield by having a greater proportion of energy put into grain.
- **inbreeding and hybridisation** to produce vigorous, uniform varieties of maize.

## DNA Sequence Data & Evolutionary Relationships

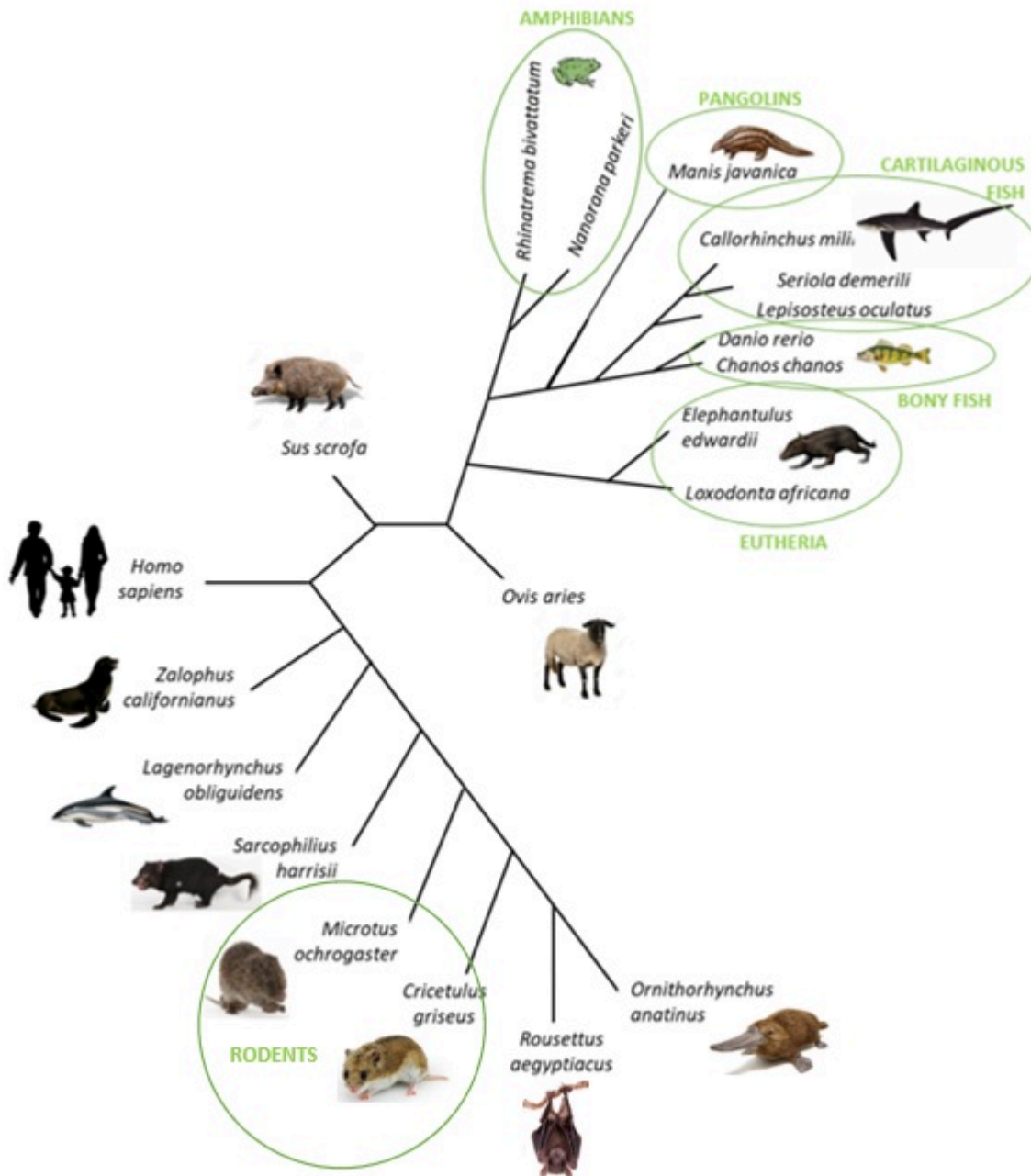
DNA sequence data provides strong evidence for **evolutionary relationships** by allowing direct comparison of the **base sequences of DNA** between different species. Species that share a **recent common ancestor** have DNA sequences that are **more similar**, whereas species that diverged longer ago show **greater differences** due to the accumulation of mutations over time.

DNA from different species can be **sequenced and aligned**, and the number of **base differences** can be counted. A **small number of differences** indicates a **close evolutionary relationship**, while a larger number indicates a **more distant relationship**. These comparisons can be made using **specific genes, non-coding DNA**, or **entire genomes**, depending on the level of resolution required.

Because **mutations accumulate at an approximately constant rate**, DNA sequence differences can be used as a **molecular clock**. By comparing the number of base substitutions between species, scientists can estimate the **time since divergence from a common ancestor**. This allows evolutionary timelines to be constructed and compared.

DNA sequence data is used to produce **phylogenetic trees**, where species with the most similar DNA sequences are placed **closest together**. Branch points represent **common ancestors**, and the length of branches may reflect the number of genetic differences. Phylogenetic trees based on DNA data are generally **more reliable** than those based on morphology alone.





An important advantage of using DNA sequence data is that it is **objective and quantitative**, and is **not affected by convergent evolution**, where unrelated species evolve similar characteristics due to similar selection pressures. This makes DNA comparisons a powerful tool for determining evolutionary relationships and provides strong evidence for **evolution by common descent**.

