CLASSIFICATION

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CLASSIFICATION SCHEMES

Variation is a defining feature of life in that no two individuals are identical in all their traits. Classification schemes are employed by scientists to collect, sort and group information about organisms. They allow for organisms to be identified and compared based on recognised characteristics, predict evolutionary patterns and show relatedness, as well as ensure that all organisms can be named according to global conventions.

TAXONOMIC RANKS

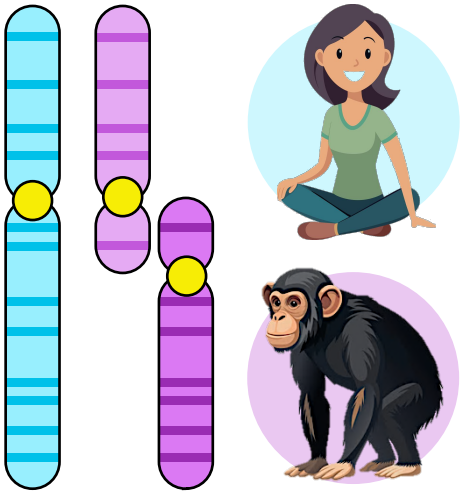
Organisms with shared characteristics are grouped according to a series of hierarchical units (called **taxa**). The more similar two organisms are, the more taxonomic ranks they will share. The taxa used to classify all living organisms are **d**omain, **k**ingdom, **p**hylum, **c**lass, **o**rder, **f**amily, **g**enus, **s**pecies (**hint:** ***d**umb **k**ids **p**ut **c**hili **o**n **f**ood – **g**et **s**mashed*). Every organism is given a scientific name that consists of both the **genus** and **species**. In this **binomial system**, genus is capitalised and the name is underlined or is in *italics*. **Example:** *Homo sapiens* (humans), *Bos taurus* (cows), *Staphylococcus albus* (bacteria).

SPECIES CONCEPT

A species represents the most precise unit of classification and is composed of organisms that will share the greatest number of morphological and genetic features. However, species are not typically defined by their structural characteristics. Non-interbreeding populations may look very different due to genetic divergence but still belong to the same species. Conversely, different species may appear phenotypically similar due to the presence of analogous structures (arising via convergent evolution). According to the **biological species** concept, a species represents a group of organisms that can *interbreed* and produce *fertile, viable offspring*. Exceptions to this definition include organisms that reproduce asexually (such as bacteria) and ring species. Additionally, it is difficult to establish breeding potential in geographically isolated populations or in fossils.

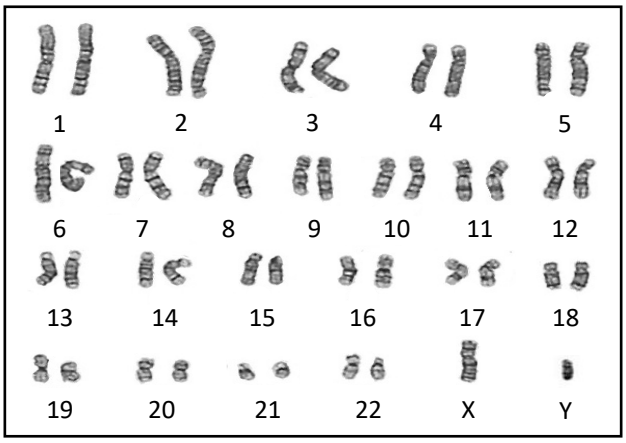
CHROMOSOME NUMBER

In order for members of a species to interbreed, they must have a **compatible genetic profile**. The genetic information of each parent must be organised onto the same number of chromosomes, with comparable sizes and gene loci positions. Organisms with different diploid numbers will be unable to interbreed as the chromosomes cannot form the homologous pairs required for meiotic division. Hence, chromosome number is a characteristic feature of members of a species and can be used to deduce evolutionary relationships. For example, humans have 46 chromosomes and chimpanzees have 48 chromosomes. It is hypothesised that chromosome 2 in humans arose from fusion of chromosomes 12 and 13 in a shared ancestor.



KARYOGRAMS

Karyotyping is the process of pairing and ordering the complete set of chromosomes within a cell to provide a snapshot of an individual genetic profile. Cells will be arrested mid-division as chromosomes are condensed, before chromosomes are arranged into pairs according to size and centromere position. Chromosome sets are then photographed to produce a **karyogram**, which can be used to identify species, sex and any abnormalities. A karyogram from a human male is shown on the right.



GENOMIC DIVERSITY

A **genome** is all of the genetic information within an organism (including both nuclear and organelle DNA). Organisms in the same species will share most of their genome, but variations such as **single-nucleotide polymorphisms** will give some diversity. Genomes vary in overall size as well as base sequence. Variations between species is much larger than variation within a species. While viruses and bacteria tend to possess smaller genomes, there is *no clear correlation* between organism complexity and genome size in species.

WHOLE GENOME SEQUENCING

Whole genome sequencing is the process of determining the DNA sequence of an entire genome at a single time. Technological advancements have allowed this process to occur with increasing speed and decreasing cost. For research purposes, this sequencing can allow for the determination of **evolutionary relationships**. For more personal uses, genome sequencing can be used to map individual pedigrees and also facilitate the development of individualised medicines (via **pharmacogenomics**) for the treatment of disease conditions.