

Diversity of organisms Why is variation a defining feature of life?	Diversity of organisms What was Linnaeus's species concept?
Diversity of organisms Binomial system: what do the two parts of the name show?	Diversity of organisms Biological species concept
Diversity of organisms Give two challenges to the biological species concept.	Diversity of organisms Speciation
Diversity of organisms Chromosome numbers of humans and chimpanzees	Diversity of organisms Why do diploid cells have an even number of chromosomes?

Morphological: a species is a group of organisms with shared traits.

No two individuals are identical in all their traits, and patterns of variation are the basis for naming and classifying organisms.

A species is a group of organisms that can breed and produce fertile offspring.

First part: genus (capital letter). Second part: species (lowercase). Written in italics, e.g. *Homo sapiens*.

The splitting of one species into two or more, usually gradually, so the point where populations become separate species can be arbitrary.

Any two: fossils cannot be tested; separated populations never meet; asexual reproduction; some species form fertile hybrids.

Chromosomes are in homologous pairs, one of each pair from each parent.

Humans 46, chimpanzees 48.

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Karyogram

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Three features used to classify chromosomes in a karyogram

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Evidence that human chromosome 2 formed by fusion

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Genome

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Single-nucleotide polymorphism (SNP)

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Two ways eukaryote genomes vary

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Does genome size correlate with complexity?

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How has whole genome sequencing changed since the first human genome?

Length, centromere position and banding pattern.

An image of a cell's chromosomes arranged in homologous pairs in order of decreasing length.

All the genetic information of an organism.

Banding matches chimpanzee chromosomes 12 and 13 (2A and 2B) end to end; telomere sequences near its middle; remains of a second centromere.

Overall size (total amount of DNA) and base sequence. Variation between species is much larger than within a species.

A position in the base sequence where individuals of a species differ in a single base; a source of diversity within a species.

Much faster and cheaper: about 13 years then, around a day now.

Not closely. Some plants, e.g. *Paris japonica*, have genomes far larger than the human genome.

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A current and a potential future use of whole genome sequencing

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Why does the biological species concept not work for bacteria?

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Horizontal gene transfer

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Why is a mule infertile?

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Dichotomous key

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Good features to use in a dichotomous key

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Environmental DNA (eDNA)

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Steps in identifying species from eDNA

They reproduce asexually, and horizontal gene transfer moves genes between species, blurring species boundaries.

Current: research into evolutionary relationships. Future: personalised medicine.

Horse (64) and donkey (62) chromosome numbers differ; the mule's 63 chromosomes cannot all pair in meiosis, so viable gametes are not made.

Transfer of genes between organisms other than from parent to offspring, e.g. plasmids passed between bacteria, even of different species.

Easily observed features that do not vary within a species, e.g. leg number, not size or colour.

A series of numbered steps, each with two contrasting descriptions, leading to the name of an organism.

Sample habitat; extract DNA; copy barcode region by PCR; sequence; match to a reference barcode database.

DNA shed by organisms into their surroundings, such as water or soil.

Classification and cladistics **HL only**

Why is classification needed?

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Traditional hierarchy of taxa

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Why is the traditional hierarchy a problem?

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Advantage of classification by evolutionary relationships

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Clade

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Most objective evidence for placing organisms in a clade

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Molecular clock

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Why does a molecular clock give only estimates?

Kingdom, phylum, class, order, family, genus, species.

Because of the immense diversity of species; once classified, a broad range of further study is facilitated.

All members share a common ancestor, so characteristics can be predicted because they are shared within a clade.

Fixed ranks are arbitrary and do not always correspond to the patterns of divergence generated by evolution.

Base sequences of genes or amino acid sequences of proteins.

A group of organisms with common ancestry and shared characteristics: an ancestor and all its descendants.

Mutation rates are affected by generation time, population size, intensity of selective pressure and other factors.

Estimating when clades diverged from a common ancestor using the number of accumulated sequence differences.

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Parsimony analysis

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Root, node and terminal branch

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How do you find the closest relative of a species on a cladogram?

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What did cladistics show about the figwort family (Scrophulariaceae)?

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The three domains

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Why is rRNA useful for comparing all organisms?

Root: common ancestor of all. Node: branching point, a hypothetical common ancestor. Terminal branch: ends at a species compared.

Selecting the most probable cladogram: the one that accounts for observed sequence variation with the fewest sequence changes.

It was not a single clade; similar morphology was due to convergent evolution, so many species were moved to other families.

Find the species sharing the most recent node (common ancestor) with it, not simply the neighbour at the tips.

It is present in all cells and its base sequence changes slowly, so distantly related organisms can be compared.

Bacteria, Archaea and Eukarya, proposed in 1977 from rRNA base sequences as a level above kingdoms.