DP Biology – A3.2 (HL only)

Classification and cladistics

- Which tools help us sort organisms into taxonomic groups?
- How does cladistics differ from traditional classification?

HL statements A3.2.1–9. Textbook pp. 125–137.
Image: a stoat. Steve Hillebrand, USFWS, public domain.



Objectives for each class

Class	Statements	By the end of the class, you can...
1	A3.2.1–3	Explain why we classify, the problems with ranked taxa, and the value of classifying by ancestry
2	A3.2.4–5	Explain clades, and how sequence differences act as a molecular clock
3	A3.2.6–7	Build a cladogram from sequence data and analyse cladograms
4	A3.2.8–9	Use cladistics to test classifications, and explain the three domains

Why classify?

A3.2.1



Arum maculatum: one species, dozens of common names. H. Zell, CC BY-SA 3.0.

- There are millions of species: grouping them makes the diversity manageable
- Each species has one **binomial** name, the same in every language
- Classification helps us identify organisms and find information about them
- It lets us **predict** features of a newly found species from its group

Try it

This plant is called lords-and-ladies, cuckoo-pint and many other names. Why is one scientific name better?

The traditional hierarchy of taxa

A3.2.2

Rank	Grey wolf	Common daisy
Kingdom	Animalia	Plantae
Phylum	Chordata	Angiospermophyta
Class	Mammalia	Magnoliopsida
Order	Carnivora	Asterales
Family	Canidae	Asteraceae
Genus	Canis	Bellis
Species	Canis lupus	Bellis perennis

- Seven main ranks, with domains above
- Each rank is nested inside the one above
- Genus and species give the binomial name

Problems with ranked taxa

A3.2.2

- Evolution produces a branching tree, not neat levels: there is no natural rule for what counts as a family or an order
- Ranks are not equal: one genus may hold one species, another hundreds
- Similar features can evolve separately (**convergent evolution**), so groups based on appearance can mix unrelated organisms
- Traditional groups such as reptiles leave out descendants (birds) of their common ancestor
- Hybrids and species that are still diverging do not fit clear boundaries

Key idea

The traditional hierarchy does not always match the pattern of divergence that evolution actually produced.

Classifying by evolutionary relationships

A3.2.3

- Every member of a group has evolved from one **common ancestor**
- So the group shares features inherited from that ancestor
- We can **predict** features of a member that has not been studied
- Classification shows evolutionary history, not just appearance

Example

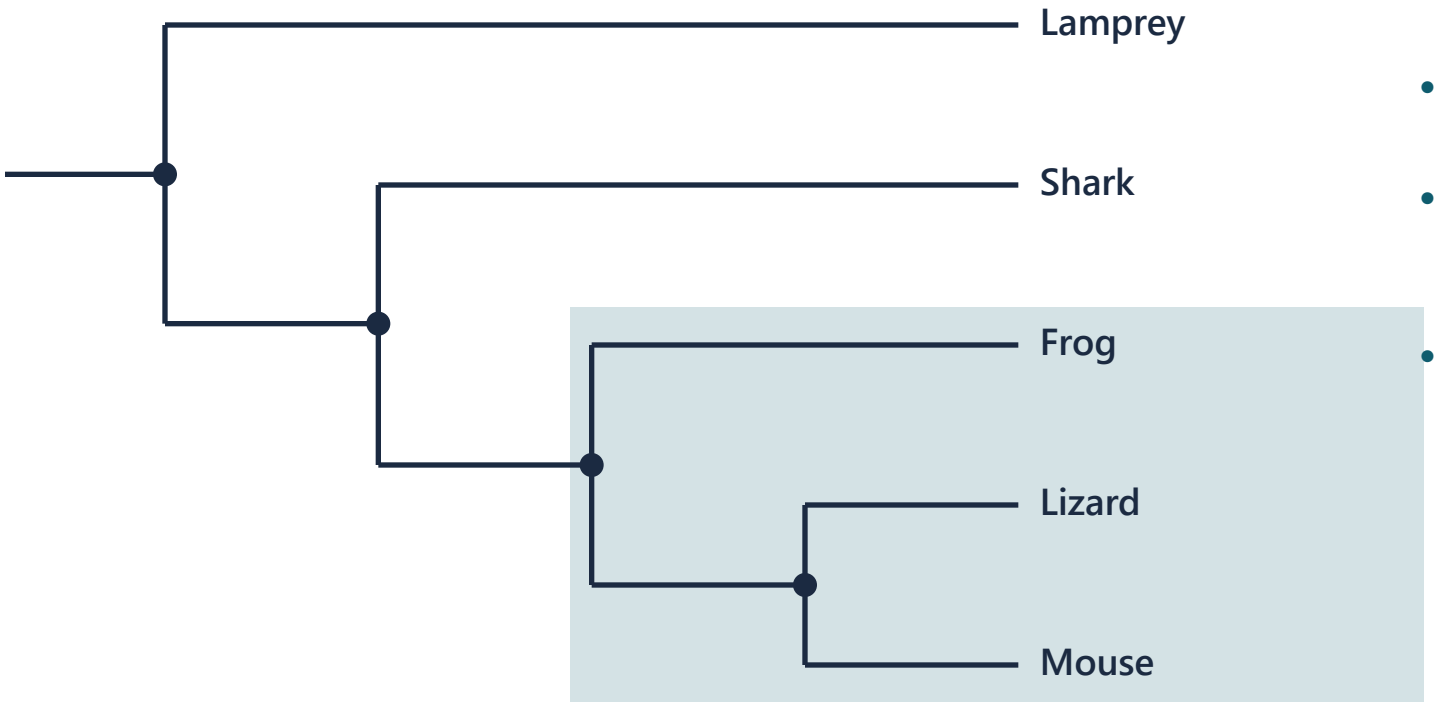
Bats fly like birds, but share hair, milk and a three-bone middle ear with other mammals. Grouping them with mammals lets us predict that a new bat species will also produce milk.

Link

Evidence for evolution and the origin of species (A4.1).

Clades

A3.2.4



Shaded: one clade, a common ancestor and all its descendants.

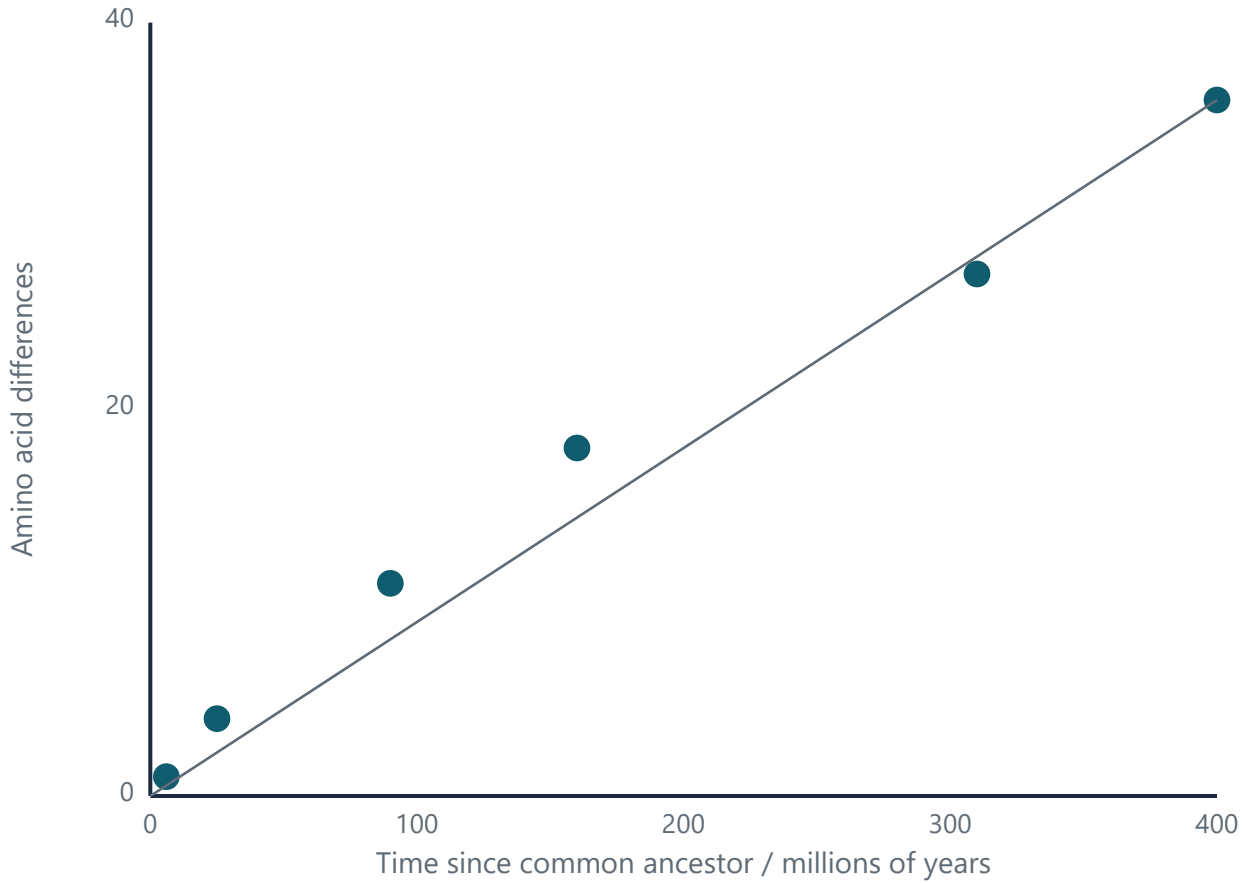
- A **clade** is a group made of one common ancestor and **all** of its descendants
- Members share characteristics inherited from that ancestor
- The most objective evidence comes from **base sequences of genes** and **amino acid sequences of proteins**
- Morphology can also be used, with care

Try it

Is "Shark, Frog and Lizard" a clade? Explain using the diagram.

The molecular clock

A3.2.5



Schematic: differences in one protein between pairs of species.

- Mutations build up in a gene at a roughly steady rate
- So the number of differences between two species estimates how long ago they diverged
- Calibrated with fossils of known age

Only an estimate

Mutation rates vary with generation time, population size, strength of selection and the gene studied.

Building a cladogram from sequences

A3.2.6

Species	Base sequence (12 bases)
W	ATGCCTAGGTCA
X	ATGCCTAGCTCA
Y	ATGACTAGCTGA
Z	TTGACAAGCAGA

	W	X	Y	Z
W	–	1	3	6
X		–	2	5
Y			–	3

Number of differences between each pair.

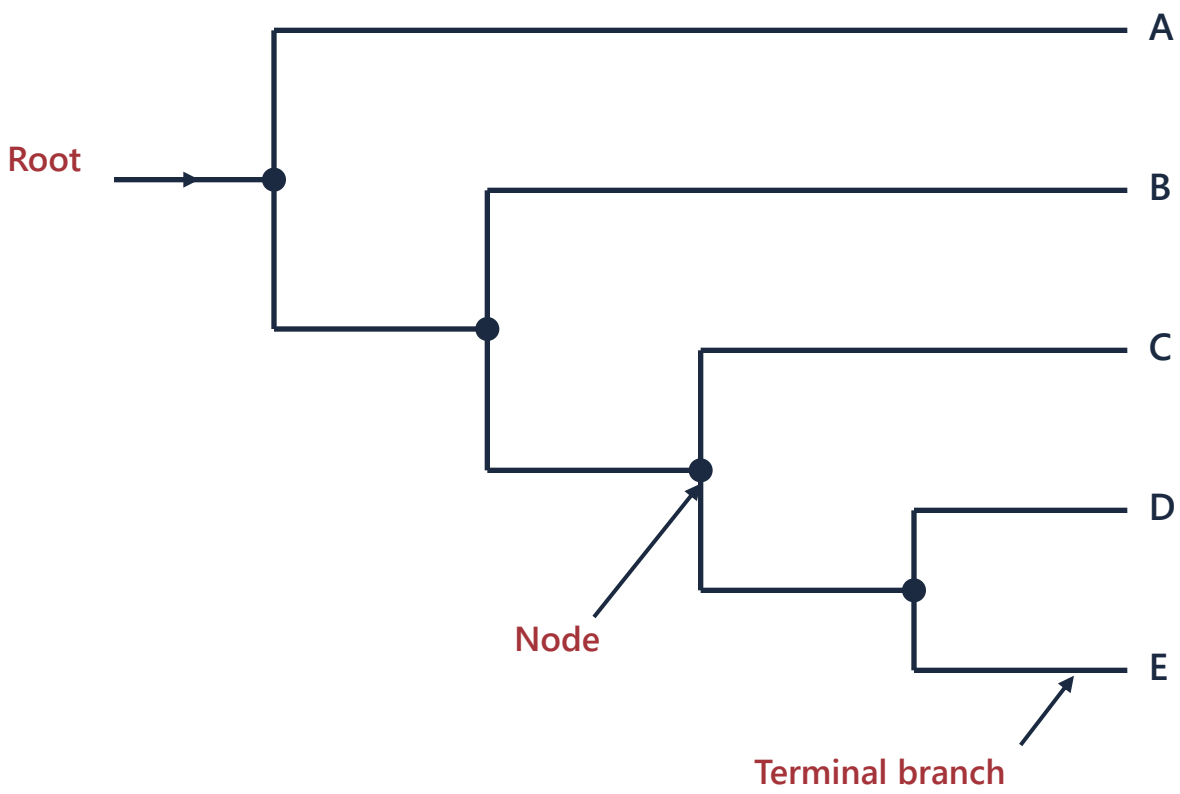
- 1. Count the differences between every pair
- 2. Join the two most similar first (W and X), then add the next closest (Y), then the least similar (Z)
- Fewest differences = most recent common ancestor

Try it

Draw the cladogram for W, X, Y and Z.

Reading a cladogram

A3.2.7



- **Root**: the base, the common ancestor of all
- **Node**: a branch point, a hypothetical common ancestor
- **Terminal branch**: leads to one taxon
- Species sharing a more recent node are more closely related
- D and E are more closely related to each other than either is to C

Try it

Which taxa form the smallest clade that includes B and D? How many clades include C?

Testing a classification: the figworts

A3.2.8



Figwort, Scrophularia nodosa. H. Zell, CC BY-SA 3.0.



Greater plantain, Plantago major. Public domain.

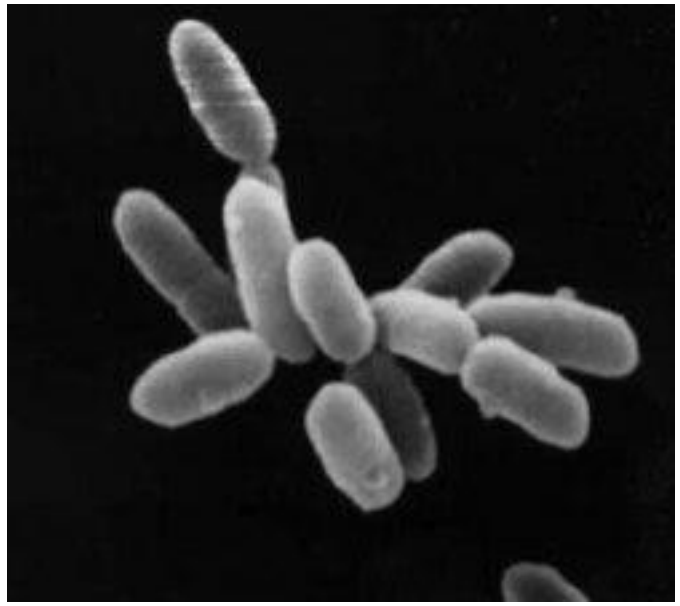
- The figwort family was based on flower shape
- DNA sequences of several genes were compared
- The family was not a clade
- Many genera, such as foxgloves and speedwells, moved to the plantain family

Key idea

Cladistics can show that a traditional group is not a single clade. The classification is then changed so that groups match evolutionary relationships. The figwort family lost over half its species.

Three domains

A3.2.9



Halobacterium, an archaean from salty water. NASA, public domain

	Bacteria	Archaea	Eukarya
Nucleus	No	No	Yes
Histones on DNA	No	Some	Yes
Introns	Rare	Some	Common
Membrane lipids	Ester-linked	Ether-linked	Ester-linked

The evidence

In 1977, comparisons of ribosomal RNA base sequences showed that prokaryotes form two groups as different from each other as either is from eukaryotes. A new rank, the domain, was added above kingdoms: Bacteria, Archaea and Eukarya.

Check that you can explain

1. Why organisms are classified
2. Why the traditional ranks do not always fit evolution
3. The advantages of classifying by common ancestry
4. What a clade is, and the best evidence for one
5. How the molecular clock works, and its limits
6. How to build a cladogram from sequences, and the terms root, node and terminal branch
7. How cladistics led to reclassifying the figworts
8. Why all life is placed in three domains

Exit activity: 5 minutes

On your own and without notes. Hand this in as you leave.

1. Define clade.
2. State why the molecular clock gives only an estimate.
3. Outline the evidence for the three-domain system.

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Scrophularia nodosa 001.JPG – H. Zell – CC BY-SA 3.0
Plantago major.jpg – Iorsh at English Wikipedia – Public domain
Halobacteria.jpg – NASA – Public domain

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