

Classification and cladistics

Four one-hour lesson plans

This subtopic is higher level only, so there are four one-hour lessons and all of them are HL. They follow the chapters: why we classify and where the old ranks fail, clades and the molecular clock, building and reading cladograms with [the dry lab](#), then the figworts, the three domains and exam practice. The guide can be read for homework and the lesson used for the activities. Every figure plays on a projector: step through it with the arrow keys and stop on each caption.

LESSON	COVERS	FOCUS	CHAPTERS
1 Why sort life, and when the boxes fail HL	A3.2.1 to A3.2.3	Why classification is needed, why the traditional ranks do not always follow evolution, and what a classification by ancestry lets you predict	1, 2, 3
2 Clades, and a clock made of DNA HL	A3.2.4, A3.2.5	What a clade is, why sequences are the most objective evidence, and how the molecular clock estimates divergence times	4, 5
3 Building and reading cladograms HL	A3.2.6, A3.2.7	Choosing a tree by parsimony, reading nodes and clades, and what changes when you change the data	6, 7, 1ab
4 Figworts, three domains and putting it together HL	A3.2.8, A3.2.9	Cladistics testing an old classification, rRNA and the three domains, and an exam question on the whole subtopic	8, 9

The guide, for the class to read and play: biologybybradford.com/guides/ib-biology-a3-2-classification-and-cladistics

Why sort life, and when the boxes fail HL

60 minutes • A3.2.1 to A3.2.3 • Chapters 1, 2, 3

Why classification is needed, why the traditional ranks do not always follow evolution, and what a classification by ancestry lets you predict

BY THE END, STUDENTS CAN

- ☐ Explain why classification is needed, and what it makes possible A3.2.1
- ☐ Describe why the traditional hierarchy of taxa does not always match evolution, and why a fixed ranking is arbitrary A3.2.2
- ☐ Explain why a classification that follows evolutionary relationships lets you predict the features of its members A3.2.3

TIMING

0-8	8 min	Do now: sort it your way	
8-18	10 min	Why classify?	
18-30	12 min	When the boxes do not fit	
30-40	10 min	Questions on a paradigm shift	
40-52	12 min	What does ancestry let you predict?	
52-60	8 min	Exit: two groups	
	60 min	One lesson	

STARTER

- 8 min** **Do now: sort it your way**
- Each pair gets a set of organism cards (the card sort below) and two minutes to make groups with any rule. Pairs then say their rule, and the class notes how many different rules there were. Leave the rules on the board.

ON THE BOARD, FROM THE GUIDE

Open the guide on the projector at each chapter (the links work in this PDF). Every figure plays from its own buttons, and the lesson's slides have the same figures, step by step, in the order of this plan.

01 Why sort life at all?

CHAPTER 01 IN THE SLIDES

Step through the figure (3 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. Six organisms, to sort **any way you like**.
2. Rule one: **flies**. The bat, the bird and the butterfly go together.
3. Rule two: **has a backbone**. Now the bat sits with the fish and the frog, and the butterfly has left it. Same six, different groups.

Predict box: Which is the best reason for classifying organisms? Hands up or mini whiteboards first.

Answer B: There are too many species to study one by one, and a group lets what we know about one guide the rest

02 When the boxes do not fit

CHAPTER 02 IN THE SLIDES

Step through the figure (4 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. The traditional ranks: each one **nest**s inside the next, from kingdom down to species.
2. Now the branching tree of descent for four vertebrates, built from DNA (simplified).
3. The old classes. **Reptilia** holds the crocodile and the lizard, and **Aves** holds the bird on its own.
4. But the crocodile and the bird share an ancestor that the lizard does not. The old class **cuts that family in two**.

Step through the figure (4 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. **Normal science**: a framework everyone shares. For classification, the ranks.
2. Cases that **do not fit** build up, such as groups that split a family in two.
3. A **new idea** replaces the rule for grouping: use the branching tree, and group only whole clades.
4. The new idea becomes the new normal. A change in the basic ideas of a field is a **paradigm shift**.

Predict box: A taxonomist finds that a group in the old system leaves out one species that descends from the same common ancestor as the rest. What does that show? Hands up or mini whiteboards first.

Answer C: The group does not follow the pattern of divergence

Remember it: King Philip Came Over For Good Soup (Kingdom, Phylum, Class, Order, Family, Genus, Species).

03 Groups that are family trees

CHAPTER 03 IN THE SLIDES

Step through the figure (3 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. Hair and milk appeared once, on the branch leading to the **mammals**. Every descendant of that ancestor inherits them, unless a line loses them.
2. A newly found animal. Its DNA says it is the mouse's closest relative: it **joins the tree** there (a made-up animal).
3. It sits inside the mammal clade, so you can **predict** its features before you have studied it.

Predict box: A newly found frog falls inside a clade whose other members all make a toxin in their skin. Which statement is best? Hands up or mini whiteboards first.

Answer C: It probably makes the toxin, but a feature can be lost, so the prediction needs testing

THE LESSON

10 Why classify?

Chapter 1's figure on the board, step by step. Pairs answer "Why do scientists classify organisms?" and "What could a biologist do with a group that she could not do with a heap?" Collect two answers and write the key ideas: too many species, and a broad range of further study. Then the predict box.

12 When the boxes do not fit

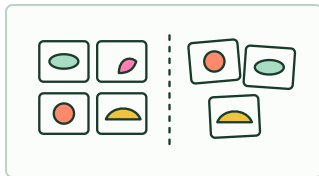
Chapter 2's first figure, stopping on each caption. Students sketch the tree of the bird, crocodile, lizard and mouse, then draw the old class Reptilia round the lizard and crocodile and say what is wrong with it. Add "arbitrary": ask whether a family of beetles and a family of mammals are the same kind of thing. Turn over the mnemonic tiles for the seven ranks.

10 Questions on a paradigm shift

The paradigm shift questions below, in pairs, using chapter 2's second figure. Take one answer to each question, and land on the nature of science point: cladistics replaced fixed ranks with unranked clades, which is a paradigm shift.

12 What does ancestry let you predict?

Chapter 3's figure: follow hair and milk down the tree, then add the new species. Students write one prediction they could make about a member of a clade and one way it could fail (a feature lost along a branch). Then the chapter's predict box.



CARD SORT

Sort it your way

Pairs get twelve cards, each with a picture and name of an organism: for example a bat, a bird, a butterfly, a fish, a frog, a lizard, a crocodile, a mushroom, an oak leaf, a bacterium, a mouse and a spider. They sort the cards into groups by any rule, write the rule, then sort again by a different rule. Pairs compare rules around the room. Ask which rule told them the most about each organism, and which would still work if a new species turned up.

Needs: printed cards, one set per pair (or the six organisms in [chapter 1](#)'s figure on a screen).

DISCUSSION

Questions on a paradigm shift

Four questions to answer from [chapter 2](#): (a) Outline why it is hard to classify flying animals, such as birds and insects, by the features that make traditional groups. (b) Why does the traditional hierarchy not always match the pattern of divergence in evolution? (c) What does it mean to say that a fixed ranking of taxa is arbitrary? (d) Suggest why a classification that follows evolutionary relationships has an advantage over the ranks. Then ask which of the four stages of the cycle in [chapter 2](#)'s second figure each answer belongs to.

Needs: [chapter 2](#)'s figures on screen; the four questions on the board.

PLENARY

8

min

Exit: two groups

On a slip: "A group of look-alike animals has members from two different clades. Give one reason this group is less useful than a clade for predicting."

WHAT STUDENTS GET WRONG

"Classification is just naming." A name is a label. A group tells you what to expect from an organism, which is why it is useful.

"Look-alikes are close relatives." Convergent evolution gives unrelated lines similar structures: wings, and the flowers of the figworts.

"A higher rank means older, or more different." Ranks have no fixed meaning, which is why a fixed ranking is arbitrary.

STRETCH AND SUPPORT

Support: give the captions of each figure as a cut-up storyboard to put in order, and use the key terms (tap the dotted words) as a glossary.

Support: the two mnemonics (King Philip Came Over For Good Soup; Rabbits Nibble Tasty Carrots Slowly) as a starter, with the tiles turned over for the answers.

IN THE GUIDE

- 1** [Why sort life at all?](#)
- 2** [When the boxes do not fit](#)
- 3** [Groups that are family trees](#)
- A11** [The whole guide, with the figures that play](#)
- PPTX** [This lesson's slides, in the order of this plan](#)

PRACTISE AND REVISE

BUILD FOR YOUR CLASS

- [Tarsia puzzle, dominoes and picture reveal](#) on A3.2, built from its key terms and ready to print
- A [pub quiz](#) with rounds on A3.2, to present or run with no projector
- An [escape room built from the question bank](#) on A3.2

ALREADY ON THE SITE FOR A3.2

- [Quiz: Cladistics \(HL\)](#)
- Revision map: [A3.2 Classification and cladistics](#), to fill in
- Exam questions: [A3.2 in the exam maker](#), a paper with its markscheme

CARD SETS ON SPLYCR

Open a set to host it as a class game, or make a copy to edit.

- [A3.2 Classification and Cladistics \(HL\)](#)

EXAM PRACTICE

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biologybybradford.com/exam-maker/sit?topics=A3.2&level=HL&paper=quiz&marks=15&src=ep



Clades, and a clock made of DNA HL

60 minutes • A3.2.4, A3.2.5 • Chapters 4, 5

What a clade is, why sequences are the most objective evidence, and how the molecular clock estimates divergence times

BY THE END, STUDENTS CAN

- ☐ Define a clade, and say what evidence best places organisms in one A3.2.4
- ☐ Explain how the molecular clock estimates when clades diverged, and why it only gives estimates A3.2.5

TIMING

0-6	6 min	Do now: clade or not?	
6-20	14 min	Ring the clades	
20-30	10 min	Which evidence would you trust?	
30-46	16 min	Plot the clock	
46-54	8 min	Why only an estimate?	
54-60	6 min	Exit	
60 min		One lesson	

STARTER

- 6 min** **Do now: clade or not?**
- On the board: an ancestor X with four descendants P, Q, R and S, and the group P, Q, R. Is it a clade? Students vote, then defend their vote in pairs. Do not reveal the answer: [chapter 4's](#) predict box does that.

ON THE BOARD, FROM THE GUIDE

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04 A clade is an ancestor and all its descendants

CHAPTER 04 IN THE SLIDES

Tap the parts of the figure in turn: Node E, the root, Node D, Node C, Node B, Node A and The old reptiles.

Predict box: A tree shows an ancestor X with four descendants, P, Q, R and S. Someone proposes the group P, Q and R. Is it a clade? Hands up or mini whiteboards first.

Answer A: No, because S also descends from X and is left out

05 Differences that count the years

CHAPTER 05 IN THE SLIDES

Step through the figure (4 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

- Two pairs of species whose split is **dated from fossils**: 5 differences at 10 million years and 15 at 30 million (made-up numbers).
- The differences grow steadily with time, so a straight line through the points is the **molecular clock**.
- A pair with **no fossil date** differs at 6 places. Read across to the clock, then down: about 12 million years.
- If this pair's lines collected changes **twice as fast**, the same 6 differences would mean about 6 million years. The clock gives an estimate, not a date.

Play the animation, Watch it happen: two lines collect changes. It loops; pause it on each moment below and ask what is happening (in the lesson slides it is a video).

1. One ancestor species, and one of its genes: a stretch of 30 bases, drawn as boxes.
2. Its descendants split into new species. In every line, mutations build up in the gene at a fairly steady rate: **the ticks of a clock**.
3. Today there are four species, A to D. Each gene now differs from the ancestor's, in its own places.
4. A dated fossil shows that A and B split **30 million years** ago. Their genes differ at **15** bases.
5. So this clock runs at $15 \div 30 = \mathbf{0.5 \text{ differences per million years}}$.
6. C and D differ at **6** bases: $6 \div 0.5 = \text{about } \mathbf{12 \text{ million years}}$ since they split.
7. Only an **estimate**: generation time, population size and selection all change how fast differences build up. Try the settings.

Predict box: A clock is calibrated on mammals that breed every few years. It is then used to date a split between two lines of insects that breed several times a year. What will the estimate probably be? Hands up or mini whiteboards first.

Answer C: Too old, because the insects probably collected changes faster each year

Remember it: Gerbils Play Sports (Generation time, Population size, Selection pressure).

THE LESSON

14

min

Ring the clades

Chapter 4's figure: tap each lettered node and say the clade it rings, then tap the old reptiles and say why the ring is not a clade. Students write the two-question test for a clade. Then the predict box.

10

min

Which evidence would you trust?

The clade or not card sort below. Pairs decide for each card which evidence would place the organism, and where morphology could mislead. Land on: base and amino acid sequences are the most objective evidence, and morphological traits can also be used.

16

min

Plot the clock

The data task below on graph paper: plot the fossil-dated pairs, draw the clock, and read the undated pair. Then chapter 5's figure and its last step on a faster clock, and the film for the changes building up along two lines.

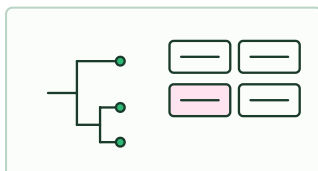
8

min

Why only an estimate?

Students link each of the three factors (generation time, population size, selection pressure) to what it does to the number of changes, using the mnemonic tiles. Then the chapter's predict box on calibrating a clock on mammals and using it on insects.

ACTIVITIES

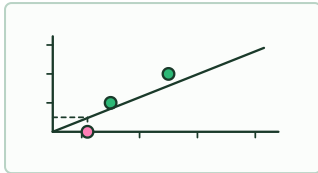


CARD SORT

Clade or not?

A printed tree of six or seven organisms and a set of cards, each naming a group of tips. Pairs sort the cards into "a clade" and "not a clade", and for each one that is not, name the descendant that is missing or the member that does not belong. Include the old reptiles. Then say for each clade which evidence (sequences or structure) you would use to check it.

Needs: the tree from chapter 4 printed, one per pair; cards cut from a sheet.



DATA TASK

Plot the clock

Students plot three pairs of species with fossil-dated splits against the number of differences in one gene (the teacher gives made-up numbers that fall on a straight line, such as 5, 10 and 15 differences at 10, 20 and 30 million years), draw the line through the origin, then read off the age of an undated pair. A second part gives one line a faster rate and asks how the answer changes. Ask what the gradient measures.

Needs: graph paper, rulers, a table of made-up data on the board or printed.

PLENARY

6

min

Exit

Two sentences: what a molecular clock measures, and one reason its estimate could be wrong.

WHAT STUDENTS GET WRONG

"Any group of relatives is a clade." A clade is an ancestor and all its descendants. Leave one out, as the old reptiles do with birds, and it is not a clade.

"The molecular clock gives dates." It gives estimates, calibrated from fossils, which shift with generation time, population size and selection pressure.

STRETCH AND SUPPORT

Support: give the captions of each figure as a cut-up storyboard to put in order, and use the key terms (tap the dotted words) as a glossary.

Stretch: why might the same gene tick at different rates in different lines? Give an example for each of the three factors.

IN THE GUIDE

- 4** [A clade is an ancestor and all its descendants](#)
- 5** [Differences that count the years](#)
- A11** [The whole guide, with the figures that play](#)
- PPTX** [This lesson's slides, in the order of this plan](#)

PRACTISE AND REVISE

BUILD FOR YOUR CLASS

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ALREADY ON THE SITE FOR A3.2

- [Quiz: Cladistics \(HL\)](#)
- Revision map: [A3.2 Classification and cladistics](#), to fill in
- Exam questions: [A3.2 in the exam maker](#), a paper with its markscheme

CARD SETS ON SPLYCR

Open a set to host it as a class game, or make a copy to edit.

- [A3.2 Classification and Cladistics \(HL\)](#)

EXAM PRACTICE

Check yourself

Set it for homework: a fresh paper of exam-bank questions on A3.2 at higher level each time, marked as students go and saved to their Exam practice when they are signed in.

biologybybradford.com/exam-maker/sit?topics=A3.2&level=HL&paper=quiz&marks=15&src=ep



Building and reading cladograms HL

60 minutes • A3.2.6, A3.2.7 • Chapters 6, 7 • The dry lab

Choosing a tree by parsimony, reading nodes and clades, and what changes when you change the data

BY THE END, STUDENTS CAN

- ☐ Build a cladogram from sequence data using parsimony, and say why different criteria can give different trees A3.2.6
- ☐ Read a cladogram: its root, nodes and terminal branches, its clades and common ancestors A3.2.7

TIMING

0–6	6 min	Do now: who goes with whom?	
6–20	14 min	Parsimony by hand	
20–32	12 min	Cladogram cards	
32–42	10 min	Reading a cladogram	
42–54	12 min	Grow a tree	
54–60	6 min	Exit	
	60 min	One lesson	

STARTER

- 6 min** **Do now: who goes with whom?**
- Four short sequences on the board with a fifth as the outgroup. Pairs mark the sites where two species share a difference from the outgroup and say which two species they would put together. Do not reveal the tree yet.

ON THE BOARD, FROM THE GUIDE

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06 The tree with the fewest changes

CHAPTER 06 IN THE SLIDES

Step through the figure (4 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

- A made-up stretch of six sites in one gene. Pink marks where a species **differs from the orangutan**, the outgroup.
- Three trees could join the human, chimpanzee and gorilla. Sites 4 and 6 differ in only **one species**, so they cost one change on every tree and cannot choose between them.
- Count the changes each tree needs to explain all six sites. Tree 1 needs 7, tree 2 needs 10 and tree 3 needs 9.
- Parsimony** picks the tree that explains the data with the fewest changes: tree 1, with the human and chimpanzee as closest relatives.

Step through the figure (2 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

- The table gives each beetle's traits (made up for teaching). Moss is the outgroup: its states are taken as the ancestral ones.
- One tree, with a bar on each branch where a trait changes: 7 changes. Can you find a tree that needs fewer?

Step through the figure (2 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. The table gives each beetle's traits (made up for teaching). Moss is the outgroup: its states are taken as the ancestral ones.
2. One tree, with a bar on each branch where a trait changes: 16 changes. Can you find a tree that needs fewer?

Predict box: Three possible trees need 14, 11 and 11 changes. What does parsimony tell you? Hands up or mini whiteboards first.

Answer A: The two trees that need 11 are tied, so more data is needed to choose between them

07 Reading a cladogram

CHAPTER 07 IN THE SLIDES

Switch the figure through Parts and Spin it, and have the class say what will change before each.

Show the figure: Answer questions about a cladogram: common ancestors, clades and which pairs are closest relatives.

Predict box: In a cladogram, species X and Y branch from node 1, and node 1 and species Z branch from node 2. Which statement is correct? Hands up or mini whiteboards first.

Answer B: X is closer to Y than to Z, because X and Y share a more recent ancestor

Remember it: Rabbits Nibble Tasty Carrots Slowly (Root, Node, Terminal branch, Clade, Sister groups).

THE LESSON

14 min Parsimony by hand

Chapter 6's figure step by step. Students count the changes on the three trees from the table, and compare with the figure's counts of 7, 10 and 9. Then the cladogram tool: join the beetles, watch the count, and ask whether a tree with fewer changes exists. Run it again with the DNA column. Finish with the predict box on a tie.

12 min Cladogram cards

The sorting cards below: groups place five organisms on a tree from a table of features, then write one change on each branch. Compare trees across groups and ask why two groups could end with different trees.

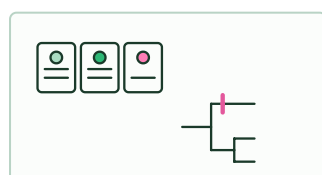
10 min Reading a cladogram

Chapter 7's figure: tap the root, a node, a terminal branch, a clade and sister groups, then spin the tree. Turn over the mnemonic tiles. Pairs use the read task in the tool.

12 min Grow a tree

The dry lab. Pairs run the tree lab on features, add one feature at a time, and record the winning tree and its score each time. Then they switch to sequence data and ask whether the winner changes.

ACTIVITIES



CARDS

Cladogram cards

Five cards, one for each of a lamprey, a shark, a frog, a lizard and a mouse, each with a strip of features (jaws, four limbs, an amnion around the embryo, hair). Groups arrange the cards into a tree so that each feature appears once, mark the branch where each feature first appears, and count the changes. Then give one group a card with a feature that fits nowhere neatly, and ask what they do. A rewrite of the classic sorting-cookies idea, with no food: the point is the counting.

Needs: printed cards and tape for the branches, one set per group; the cladogram tool for checking.

PRACTICE

Make your own sequences

Each pair writes four six-base sequences and an outgroup, then swaps with another pair. The other pair draws the three possible trees, counts the changes on each and says which tree is most parsimonious, and whether two trees tie. Pairs check each other's counts. Ask them to design a set with a tie.

Needs: squared paper; no devices needed.

DRY LAB

Grow a tree

The [dry lab](#) above, with the tasks and questions under it. It works on a phone as well as a laptop, and the results can be copied into a table for the class.

Needs: one device per pair.

PLENARY

6

min

Exit

A cladogram is a hypothesis. Give one thing that could make a scientist redraw it.

WHAT STUDENTS GET WRONG

"The tip at the top is the most advanced." Every node can be spun, so the order of the tips means nothing. Only the branching order carries meaning.

"A node is a real species we know of." A node is a hypothetical common ancestor. It need not be a known fossil.

"The most parsimonious tree is the true one." It is the most probable on the data, and it can change when more data is added.

STRETCH AND SUPPORT

Support: give the captions of each figure as a cut-up storyboard to put in order, and use the key terms (tap the dotted words) as a glossary.

Support: the two mnemonics (King Philip Came Over For Good Soup; Rabbits Nibble Tasty Carrots Slowly) as a starter, with the tiles turned over for the answers.

Support: for parsimony by hand, give a table with the three trees already drawn, so students only count.

Stretch: in the [dry lab](#), find a data set where adding one feature changes the winning tree, and explain what that feature does.

IN THE GUIDE

6 [The tree with the fewest changes](#)

7 [Reading a cladogram](#)

Lab [Dry lab: Grow a tree](#)

A11 [The whole guide, with the figures that play](#)

PPTX [This lesson's slides, in the order of this plan](#)

PRACTISE AND REVISE

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Figworts, three domains and putting it together

HL

60 minutes • A3.2.8, A3.2.9 • Chapters 8, 9

Cladistics testing an old classification, rRNA and the three domains, and an exam question on the whole subtopic

BY THE END, STUDENTS CAN

- ☐ Use the figwort family to show how cladistics tests a classification, and why a claim can be falsified A3.2.8
- ☐ Explain how rRNA sequences led to the three domains, and what was new about them A3.2.9

TIMING

0-6	6 min	Do now: look-alikes	
6-20	14 min	Two trees for the figworts	
20-26	6 min	A hypothesis that failed	
26-40	14 min	Three domains	
40-54	14 min	Exam practice	
54-60	6 min	Plenary: back to the sort	
	60 min	One lesson	

STARTER

- 6 min** **Do now: look-alikes**
- Two plants with almost the same flowers, one DNA result that puts them in different clades. Students say which evidence they trust and why. Leave the answers up for the plenary.

ON THE BOARD, FROM THE GUIDE

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08 Testing the boxes

CHAPTER 08 IN THE SLIDES

Step through the figure (3 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

- Grouped by **flower structure**: six plants with similar flowers sit together as the figwort family (a simplified sketch).
- Grouped by **chloroplast DNA** instead. The same plants now fall into several different clades, with other plants between them.
- Only a small clade is still the figwort family. The flower resemblance was **convergence**, so the old family was not a real clade.

Predict box: Chloroplast DNA places two plants with almost identical flowers in different clades. What is the best explanation? Hands up or mini whiteboards first.

Answer C: Their flowers probably evolved separately, by convergent evolution

Step through the figure (3 steps, the arrow keys on a projector). Stop on each caption and ask what changed before you go on.

1. The tree from **rRNA sequences**: three main branches, the **domains** Bacteria, Archaea and Eukarya. Relationships inside each domain are not shown.
2. Archaea look like bacteria under a microscope, but their rRNA shows they share a more recent ancestor with **Eukarya**.
3. A new top level of classification, **above kingdom**, proposed in 1977.

Play the animation, Watch it happen: the tree of life from rRNA. It loops; pause it on each moment below and ask what is happening (in the lesson slides it is a video).

1. Before 1977, life was sorted by its cells: **prokaryotes**, with no nucleus, and **eukaryotes**, with one. All prokaryotes looked alike, so they were grouped together.
2. Carl Woese compared the base sequence of **ribosomal RNA**, which every cell has. Some prokaryotes, the archaea, differed from bacteria at many bases.
3. In this made-up stretch the archaeon differs from the bacterium at 9 bases but from the eukaryote at 7: **not a bacterium at all**, and a little nearer to us.
4. So the tree of life has three main branches, the **three domains**: Bacteria, Archaea and Eukarya. Archaea and eukaryotes share a more recent common ancestor.
5. So the tree of life has three main branches, the **three domains**: Bacteria, Archaea and Eukarya. Archaea and eukaryotes share a more recent common ancestor.
6. Woese and Fox proposed the three groups in 1977: a new level above kingdom. In 1990 they were named **domains**.
7. Every organism is now classed first by its **domain**, then kingdom, phylum, class, order, family, genus and species.

Predict box: Why was rRNA a good choice for comparing all of life? Hands up or mini whiteboards first.

Answer A: Every organism has ribosomes, so every organism has rRNA that can be compared

THE LESSON

14 min **Two trees for the figworts**

Chapter 8's figure, then the figwort cards below: students group the nine plants by flower structure, then regroup them from the DNA. Use the word convergent evolution, and the nature of science point that a claim can be falsified.

6 min **A hypothesis that failed**

Think, pair, share: "Is it a failure of science that the figwort family had to be broken up?" Land on: it was a prediction that was tested, which is science working.

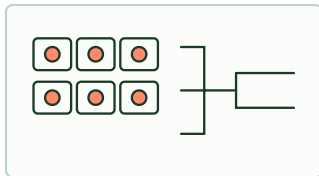
14 min **Three domains**

The rRNA table task below, then chapter 9's figure and the film. Students say which two groups the table joins first and why the result was a surprise. Then the predict box on why rRNA is a good molecule to compare.

14 min **Exam practice**

A written question on A3.2 from the exam maker (in Practise and revise, below), set at HL, in 10 minutes, then peer-marked against the markscheme. For homework, the Check step: a fresh paper on A3.2 from the exam bank, marked as students go.

ACTIVITIES

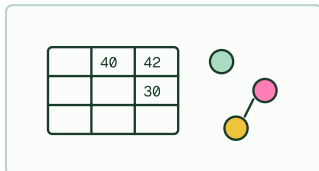


CARD SORT

Two trees for the figworts

Cards for nine plants (foxglove, snapdragon, monkeyflower, yellow rattle, mullein, figwort, plantain, broomrape and mint) with a note on their flowers. Round one: group them by flower structure. Round two: the teacher reveals which are in which clade from the chloroplast gene (use [chapter 8's](#) figure), and groups redraw. Ask what the flower resemblance turned out to be, and what that says about trusting structure alone.

Needs: printed cards, one set per group; [chapter 8's](#) figure hidden until round two.



DATA TASK

Three domains, from a table

A made-up table of rRNA differences (out of 100 compared sites) between a bacterium, a methane-making archaeon and a yeast: 40 between the bacterium and the archaeon, 42 between the bacterium and the yeast, and 30 between the archaeon and the yeast. Students say which two organisms the table joins first, draw the tree, and say why the result was a surprise to biologists who thought the archaeon was just a kind of bacterium. Make clear that the numbers are invented to show the method.

Needs: the table on the board or printed; no devices needed.

PLENARY

6
min

Plenary: back to the sort

Return to the rules on the board from lesson 1. Which of those rules would a cladist accept, and why? One sentence each.

WHAT STUDENTS GET WRONG

"Humans evolved from chimpanzees." Both descend from a shared ancestor, and are sister groups on the tree.

"Archaea are a kind of bacteria." Under a microscope they look alike, but their rRNA puts Archaea nearer to Eukarya. "Prokaryote" does not name a clade.

STRETCH AND SUPPORT

Support: give the captions of each figure as a cut-up storyboard to put in order, and use the key terms (tap the dotted words) as a glossary.

Stretch: bacteria can pass genes sideways to other cells. How would that make a tree of all life harder to draw?

Stretch: use a sequence database to compare one real gene across five species and build a tree by parsimony.

IN THE GUIDE

- 8** [Testing the boxes](#)
- 9** [A new level above kingdom](#)
- A11** [The whole guide, with the figures that play](#)
- PPTX** [This lesson's slides, in the order of this plan](#)

PRACTISE AND REVISE

BUILD FOR YOUR CLASS

- [Tarsia puzzle, dominoes and picture reveal](#) on A3.2, built from its key terms and ready to print
- A [pub quiz](#) with rounds on A3.2, to present or run with no projector
- An [escape room built from the question bank](#) on A3.2

ALREADY ON THE SITE FOR A3.2

- [Quiz: Cladistics \(HL\)](#)
- Revision map: [A3.2 Classification and cladistics](#), to fill in
- Exam questions: [A3.2 in the exam maker](#), a paper with its markscheme

CARD SETS ON SPLYCR

- Open a set to host it as a class game, or make a copy to edit.
- [A3.2 Classification and Cladistics \(HL\)](#)

How this was made. The course structure, the activities and the teaching choices come from my own classroom, my presentations and my years of teaching IB and AP Biology. I use Claude, an AI, to help write and build the interactive guides, lesson plans, slides and practice questions, and to draw the diagrams and code the interactives. I direct the work and review it against the IB and AP specifications before it goes live.

EXAM PRACTICE

Check yourself

Set it for homework: a fresh paper of exam-bank questions on A3.2 at higher level each time, marked as students go and saved to their Exam practice when they are signed in.

biologybybradford.com/exam-maker/sit?topics=A3.2&level=HL&paper=quiz&marks=15&src=ep

