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A3.2 Teacher view

Classification and cladistics (HL)



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A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

The big picture (HL)

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Higher level (HL)

? Guiding question(s)

- What tools are used to classify organisms into taxonomic groups?
- How do cladistic methods differ from traditional taxonomic methods?

Keep the guiding questions in mind as you learn the science in this subtopic. You will be ready to answer them at the end of this subtopic. The guiding questions require you to pull together your knowledge and skills from different sections, to see the bigger picture and to build your conceptual understanding.

How might you organise a collection of hundreds or even thousands of different items? Consider how a library is organised (**Figure 1**). For your own book collection you might choose to sort books alphabetically by author or by genre. You might even choose to arrange them by colour. However, if you are managing a library with many thousands of books and need to keep an accurate record of borrowing, as well as having a system in place for finding specific books on the many shelves, you would need a detailed classification system. Around the world libraries use a variety of different systems, but they all have one thing in common: they facilitate the organisation and use of extremely large collections of books.



Figure 1. A child finding some books at the library.

Credit: Klaus Vedfelt, Getty.Images. (<https://www.gettyimages.ae/detail/photo/cute-schoolgirl-smiling-balancing-stack-of->



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[books-on-royalty-free-image/1049281412\)](#)

What if the collection you were trying to organise consisted of millions of different things, scattered across the world? That is the case when studying living organisms. There are millions of known species, millions of species that have gone extinct and also millions yet to be discovered. In this subtopic, we discuss how we go about classifying life and how we can also use data to determine the evolutionary relationships between different groups of living things.

Prior learning

Before you study this subtopic make sure that you understand the following:

- Evidence for a last universal common ancestor (see [section A 2.1.7—9](#) (/study/app/bio/sid-422-cid-755105/book/the-last-universal-common-ancestor-hl-id-44284/)).
- Conservation of the genetic code across all life forms as evidence of universal common ancestry (see [section A1.2.10](#) (/study/app/bio/sid-422-cid-755105/book/summary-and-key-terms-id-43582/)).
- DNA as the genetic material of all living organisms (see [section A1.2.1](#) (/study/app/bio/sid-422-cid-755105/book/nucleic-acids-and-their-structure-id-43580/)).

A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Classification (HL)

A3.2.1: Need for classification of organisms (HL) A3.2.2: Difficulties with traditional hierarchy of taxa (HL) A3.2.3: Classification using evolutionary relationships (HL)

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Learning outcomes

By the end of this section you should be able to:

- Explain why a classification system is needed.
- Describe difficulties with the traditional hierarchy of taxa.
- Describe the advantages of basing classification on evolutionary relationships.

Imagine discovering a new species never described before. What kind of organism is it? How would you decide? Would you compare it with other creatures? What other species might it be related to? We will consider the answers to these questions in the following section.

Need for classification of organisms

Classification is the sorting and organising of things or ideas into groups or categories based on a set of criteria. It is a valuable tool for a number of reasons:

- It allows us to better organise and understand the world around us by grouping similar things or ideas.
- It allows for better communication by providing a common language to discuss or refer to certain groups of things.



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- It allows us to be more efficient by being able to quickly and easily find and categorise things and information.
- It allows for further research and analysis to identify patterns and trends to better understand the things we have classified and the systems and phenomena that are a part of them.

The vast diversity of organisms that exist or have existed makes a classification system necessary. Without a way to organise and categorise living things, it would be extremely difficult to study them and their interconnections in a meaningful way.

While Carl Linnaeus developed much of the system of classification and nomenclature in use today, he did not invent the idea of classification. He merely developed a system that worked very well with the information and knowledge of the time and one that could be used internationally.

🌐 International Mindedness

Carl Linnaeus' work on classification and nomenclature allowed scientists from around the world, working in many different languages, to communicate clearly and effectively. For example, if you wanted to research the biology of a robin, information from North American scientists would be focused on one species, while information from European scientists would be focused on a different species. Both are known as robins locally. Linnaeus' system of naming and classification gives each species a unique and universally accepted species name so that there is no confusion.

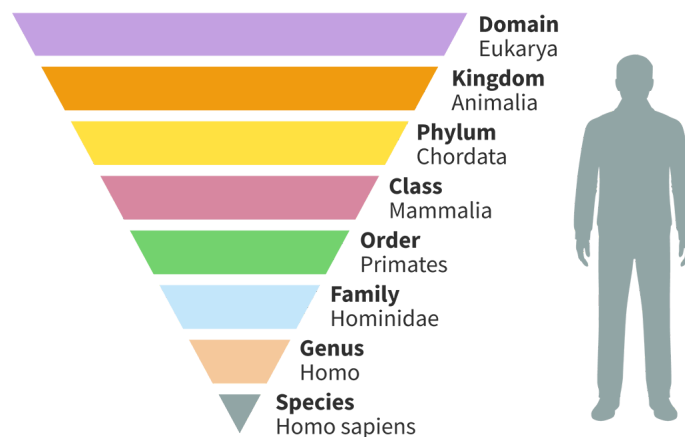


Figure 1. The hierarchy of taxa including the classification of humans.

More information for figure 1

The image is a colorful diagram showing the hierarchy of human classification. The diagram is composed of stacked horizontal bands, each representing a different taxonomic level. Starting from the bottom, the levels are: Species (in grey), Genus (beige), Family (light blue), Order (green), Class (pink), Phylum (yellow), Kingdom (orange), and Domain (purple). These bands are visually aligned to represent the classification path, with each broader category encompassing the ones below it, illustrating how humans are classified in the biological taxonomy.

[Generated by AI]

His initial hierarchy of taxonomy, which has been added to and adjusted since his time, still forms the basis of modern taxonomy and was based on shared characteristics. The current hierarchy of taxa (**Figure 1**) includes the main taxa:

- domain
- kingdom
- phylum
- class
- order



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- family
- genus
- species.

There are also many intermediate taxa, such as subfamilies and superorders, that have been added to account for the complexities in relationships between different groups. The shared characteristics used to place species into taxa were mostly morphological. In other words, organisms that looked most alike were most closely related.

Organisms that look alike share a similar characteristics traits. However, organisms that do not look alike can also exhibit similar features, for example, insects and bats both use wings to fly (**Figure 2**). This is covered in more detail in [subtopic A4.1 \(/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43246/\)](#).

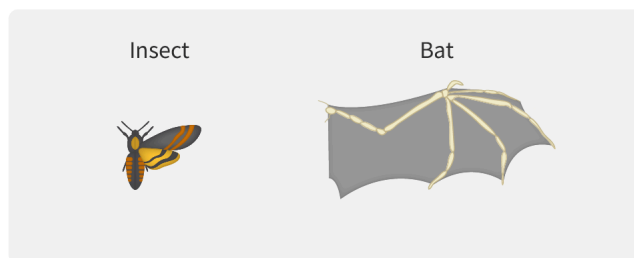


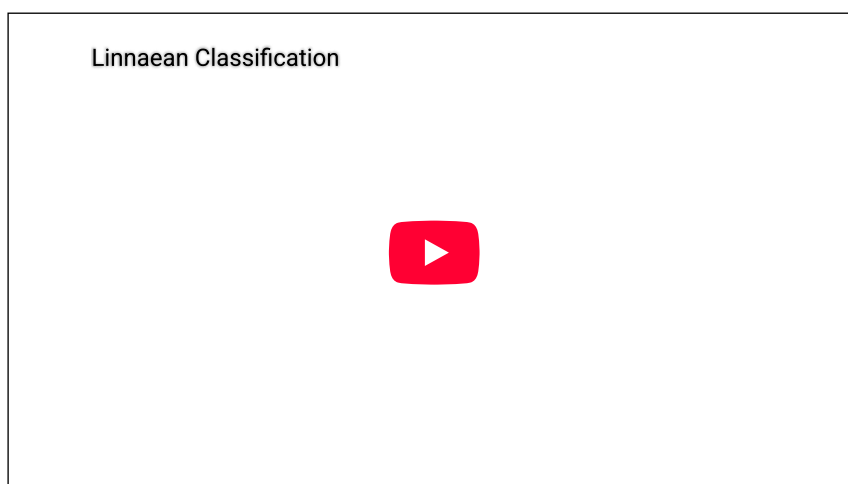
Figure 2. Wings in bats and insects

More information for figure 2

The image shows a comparison between an insect and a bat. On the left side, an illustration of an insect with a pair of wings is labeled 'Insect.' The wings are depicted with a pattern of orange and black stripes. On the right side, there is an illustration of a bat's wing labeled 'Bat.' The bat wing is shown as a membranous structure with bones extended through the membrane, resembling a stretched hand with webbing between the fingers. This visual illustrates the differences in wing structure between insects and bats, despite both being used for flight.

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Video 1 discusses the current system of classification further.



Video 1. Taxonomy and classification.

Difficulties classifying organisms into the traditional hierarchy of taxa

The traditional hierarchy of taxa poses some problems, however. These taxa are arbitrary and do not reflect the complex evolution that has occurred over billions of years. The traditional way of grouping organisms does not always correspond to the patterns of divergence generated by evolution.



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Classification was initially based on shared characteristics. This worked for many groups of organisms and was a very good place to start, given the knowledge and understanding available at the time. However, more recent developments in our understanding of genetics have forced us to rethink our approach to classification. We have even reclassified and reorganised different species based on this new evidence. For example, the giant panda (*Ailuropoda melanoleuca*) and red panda (*Ailurus fulgens*) were initially thought to be closely related due to having similar features, diet and habitat. However, upon genetic analysis, scientists determined that giant pandas are members of the bear family, whereas red pandas are more closely related to other mammals such as raccoons, weasels and skunks. We will explore this in more detail in [section A3.2.7-9 \(/study/app/bio/sid-422-cid-755105/book/applying-cladistics-hl-id-44215/\)](#).

Nature of Science

Aspect: Theories

A fixed ranking of taxa (kingdom, phylum and so on) is arbitrary because it does not reflect the gradation of variation. Cladistics offers an alternative approach to classification using unranked clades.

This is an example of the paradigm shift that sometimes occurs in scientific theories where the accepted way of viewing or doing things is fundamentally changed by the discovery of new information. Another example would be how the thinking and work around evolution was changed by Darwin's ideas on natural selection.

Advantages of classification corresponding to evolutionary relationships


We have shifted our perspective of the classification of life. From a system based on similarities in appearance and behaviour, to a more precise and detailed one. The latter is based on the use of genetic analysis to determine evolutionary relationships, specifically nucleic acid or amino acid sequences. This system has many advantages, including:

- It reflects the evolutionary relationships among different organisms, providing a natural and biologically meaningful way to group them in clades based on common ancestry.
- It reflects the process of evolution, such as the branching patterns of speciation shown through cladistics and the emergence of new features.
- It can be used to make predictions about the characteristics of organisms, such as their biochemistry or ecology, based on their evolutionary relationships.
- It helps us to understand the diversity of life on Earth by providing a context for the evolution and distribution of different organisms.

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Being curious about the natural world
- **Time required to complete activity:** 20 minutes
- **Activity type:** Individual activity

Use the information provided in the downloadable table to answer the following questions.

Classification table  (https://d3vrb2m3yrmyfi.cloudfront.net/media/edusys_2/content_uploads/Biology_A3.2.1-3_ACTIVITY.f8c739f910f5a9a5dfce.pdf)

1. Which two species are most closely related?



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2. A new species of creature has been discovered and its genus is *Varanus*. Which order would this species belong to?
3. What would be the complete classification of lions (*Panthera leo*)?
4. Humans are members of the class Mammalia. What phylum do we belong to?
5. Suggest the smallest level that contains all butterflies. What is the name of the group?
6. Suggest the name of the smallest group that includes all cats.
7. Wolves belong to the order Carnivora and the family Canidae. Hyenas are more closely related to the Felidae family than to the Canidae family. Explain why this system of classification is unable to explain this evolutionary relationship.

5 section questions ▾

A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Cladistics (HL)

A3.2.4: Clades (HL)

A3.2.5: Estimates of when clades diverged (HL)

A3.2.6: Construction of cladograms (HL)

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Higher level (HL)



Learning outcomes

By the end of this section you should be able to:

- Define a clade.
- Explain how the gradual accumulation of sequence changes can be used to determine the time since a common ancestor diverged into extant species.
- Describe how base or amino acid sequences can be used in the construction of cladograms.

So think again of that new species you found, and have now classified. To see the evolutionary relationships between your species and others of the same group you would use cladistics.

Clades as groups of organisms with common ancestry and shared characteristics

A clade is a group of species with a single common ancestor and a set of common traits or characteristics. Cladistics is a way to work out the evolutionary relationships between species based on shared traits, and genetic evidence. Scientists compare the molecular sequences or the physical traits of a group of organisms to work out the evolutionary history of different species.

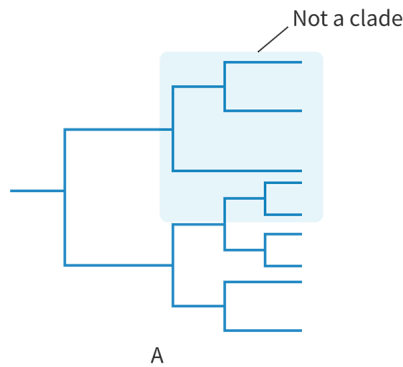
Molecular sequences provide the most unbiased evidence that two species belong to the same clade. For instance, chimpanzees (*Pan troglodytes*) are more closely related to humans (*Homo sapiens*) than to gorillas (*Gorilla gorilla*). We can test this by comparing the base sequences of the cytochrome c gene. Although physical traits can be used to classify species into clades, they are less reliable than molecular evidence. Phenomena such as convergent evolution and mimicry may lead to incorrect classifications (see section A4.1.2–5 (</study/app/bio/sid-422-cid-755105/book/evidence-from-sequence-data-id-43791/>)).



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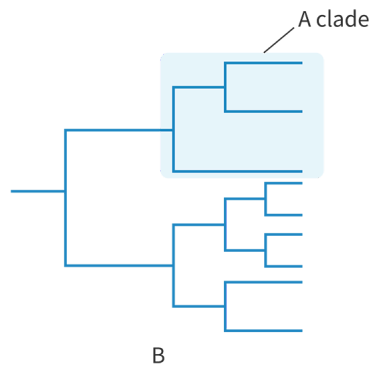
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More information

The image is a blue and light blue diagram illustrating a mind map. At the center of the map, labeled as 'My Blue Thoughts,' there are branches extending in multiple directions, each leading to nodes labeled respectively as 'Rights' (three branches connected upwards), 'Note' (two branches connected slightly below the center), 'Chat' (three branches connected rightwards), 'Doc' (one branch connected downward), and 'Search'. Each node represents a different category, showing a visual organization of various thoughts or topics stemming from the central idea, 'My Blue Thoughts.' The flow demonstrates how each category interrelates as a part of the larger mind map structure.

[Generated by AI]



More information

This is a flowchart diagram illustrating the sequence of steps in a process. It includes labeled nodes and decision points connected by paths. The nodes have text inside, depicting different stages or actions in the process. Arrows indicate the flow direction from one node to the next, showing pathways and connections between them.

[Generated by AI]

Figure 1. Both images show the same cladogram. In image A the highlighted section does not make up a single clade as it does not include all organisms from a single highlighted common ancestor. Image B's highlighted area is a clade as all members share a highlighted common ancestor.

Clades are hierarchical, which means that they can be subdivided into smaller groupings. This is a significant feature of clades. The clade of mammals, for example, is made up of subclass Prototheria (monotremes) and subclass Theria (live-bearing mammals) which is further divided into infraclass Metatheria (marsupials) and Eutheria. Cladistic analysis is a technique in evolutionary biology. It is based on the idea that shared genetics or traits that have been passed down from a common ancestor are what identify a clade (**Figure 1**). With this approach, scientists compare the base sequences, amino acid sequences or traits of several organisms to determine which traits are most likely to have originated from a common ancestor.



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Gradual accumulation of sequence differences as the basis for estimates of when clades diverged from a common ancestor

Genetic and molecular differences between organisms slowly increase over time as a result of evolution. The ‘molecular clock’ is the name given to this technique of measuring the time since there was a common ancestor. The molecular clock can only provide estimates because mutation rates depend on a range of things. These include the size of a population, the selection pressures, the genome size as well as a degree of randomness. For example, using the molecular clock approach, we have calculated that the separation between humans and chimpanzees occurred approximately 6 million years ago. The event could have occurred at any time within a range of 1–2 million years around that point. We have not yet discovered a fossil of the most recent common ancestor, and until we do, this will remain an estimate only.

Worked example 1 shows how the idea of the molecular clock can be used to determine the length of time since two species shared a common ancestor.

Worked example 1

If a particular mitochondrial gene accumulates base sequence mutations at a rate of 3 every 5 million years, about how long ago would two species have shared a common ancestor if their gene base sequence differs by 13 bases?

If you know that 3 mutations occur per 5 million years, then 1 mutation occurs per $5/3$ million years (or 1 mutation every 1.67 million years).

So, 13 mutations occur over $13 \times 5/3$ million years = 21.7 million years.

The two species would have shared a common ancestor around 21.7 million years ago.

The need for a calibration point in molecular clock analysis is an essential component. A calibration point is a period of time in which the precise moment at which two species diverged is known. As an example, the oldest fossil of a specific species that is known to exist can be used as a calibration point. The molecular clock can be used to calculate the divergence times of other species in reference to a calibration point once it has been established.

Base sequences of genes or amino acid sequences of proteins as the basis for constructing cladograms

Cladograms are used to compare the traits of various organisms and explore evolutionary links. The first step in creating a cladogram is to identify the group of organisms and choose the traits that will be compared and used to determine the evolutionary relationships. Traditionally these traits might be morphological, such as the shape of a bone or the number of fingers on a hand. However, the best information is molecular, such as base sequences in DNA or amino acid sequences in proteins. The information about these traits is gathered and used to build a matrix. The matrix is then used to create the cladogram, which can then be used to visualise and infer the evolutionary relationships among the organisms.

Table 1 is a matrix showing the number of differences in an amino acid sequence for a gene found in the mitochondria of all species. This is just a representation of data and is not accurate. A matrix like this could be used to construct a cladogram (**Figure 2**) of the evolutionary relationships among these species.

Table 1. Number of differences in amino acid sequences for same gene found in Species U–Z.



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	Species U	Species V	Species W	Species X	Species Y	Species Z
Species U	0	8	15	16	18	54
Species V		0	16	17	18	55
Species W			0	2	21	60
Species X				0	20	59
Species Y					0	52
Species Z						0

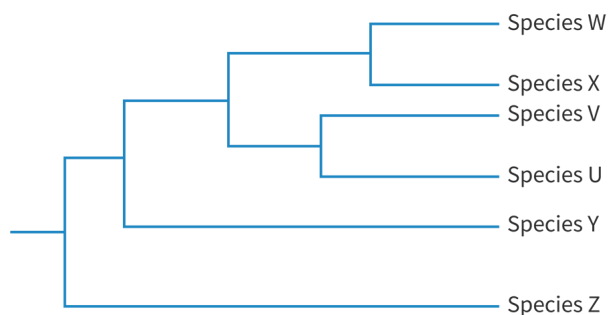


Figure 2. A possible cladogram to show the relationships between the species in Table 1.

More information for figure 2

This is a diagram representing a cladogram with branching lines that connect different groups, indicative of evolutionary relationships. Each node represents a common ancestor, and the lines branching from the nodes indicate the divergence of species. The sequence of branching is based on morphological and genetic data, aiming to illustrate the most probable evolutionary paths taken by different species. The diagram highlights various clades including mammals, reptiles, birds, and others, with examples such as monotremes placed in the mammal clade due to fewer required evolutionary changes compared to other placement options.

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Consider further, a cladogram of vertebrates as an example. Scientists might collect morphological information such as number of limbs, skin covering, limb type and reproductive characteristics. They can then create a matrix that compares these traits among the various vertebrates using this information. From the matrix they create the cladogram that illustrates the evolutionary links between the organisms. The cladogram might show, for example, that all organisms with fur are more closely related to each other than to other vertebrates. An important part of building cladograms is that organisms are placed, and relationships determined, based on the most probable evolutionary relationships. The most probable relationship will be the one that required the fewest overall number of sequence changes or developments of new characteristics. For example, placing egg-laying monotremes, such as the echidna and platypus, in the mammal clade makes most sense. This is because it would require fewer sequence changes or developments of new characteristics than if they were a separate clade or placed into another clade such as birds or reptiles that also lay eggs.

Nature of Science

Aspect: Hypotheses



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You should recognise that different criteria for judgement can lead to different hypotheses. Here, we use parsimony analysis to select the most probable cladogram. This is the cladogram in which observed sequence variation between clades is accounted for with the smallest number of sequence changes. Now let's try this out in this next activity.



Activity

- **Learner profile attribute:** Knowledgeable
- **Approaches to learning:** Thinking skills — Applying key ideas and facts in new contexts
- **Time required to complete activity:** 15—20 minutes
- **Activity type:** Individual activity

Consider the following organisms and a sequence of bases taken from a section of their mitochondrial DNA. Mutations have occurred three times within this section of DNA over time. The sections that have mutated are in red, blue and green.

Species V: TAGTAGGATGATGATTCATCCTCCTCACACATCAT

Species X: TAGTAGGACGACGACTCATCATCATCACATCATCAT

Species Y: TAGTAGGACGACGACTCATCCTCTCACATCATCAT

Species Z: TAGTAGGATGATGATTCATCCTCCTCACATCATCAT

More information

On the cladogram in **Interactive 1**, drag the species names to the correct location. Apply parsimony and place the species based on the simplest sequence of mutations.

1 2 3 4

Species V Species X Species Y Species Z

Check

Interactive 1. Cladogram for Species V—Z.



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Now consider the matrix in **Table 2**, and use the information to arrange the species on **Interactive 2**. Also, indicate where the traits emerged.

Table 2. Matrix of species and their characteristics.

Species	Traits				
	Placenta	Opposable thumbs	Mammary glands	Jaws	Bony skeleton
Human (<i>Homo sapiens</i>)	x	x	x	x	x
Lion (<i>Panthera leo</i>)	x		x	x	x
Hagfish (<i>Myxine glutinosa</i>)					
Koala (<i>Phascolarctos cinereus</i>)			x	x	x
Whale shark (<i>Rhincodon typus</i>)				x	
Clownfish (<i>Amphiprion percula</i>)				x	x

1 2 3 4 5 6

A B C D E

Koala Human Whale shark Hagfish Clownfish Lion

Bony skeleton Opposable thumbs Jaws Mammary glands Placenta

✓ Check

Interactive 2. Cladogram for Species and Their Characteristics.

More information for interactive 2

This drag-and-drop activity presents a cladogram depicting the evolutionary relationships between six animals. There are 6 gaps at the top of the cladogram. There are 5 gaps at the bottom of the cladogram. The cladogram branches to show when certain key characteristics arose in their evolutionary history.

The first branching point, labeled 'A' slightly above the root, sends a line straight upwards to a box labeled '1' at the top.

Further up the main line, at point 'B', another branch extends upwards to a box labeled '2' at the top.



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Continuing along the main line to point 'C', a third branch goes upwards to a box labeled '3' at the top.

The main line continues to point 'D', where a fourth branch extends upwards to a box labeled '4' at the top.

Further along the main line, at point 'E', a fifth branch goes upwards to a box labeled '5' at the top.

Finally, the main line continues to the top right, ending at a box labeled '6'.

The options given are Koala, Human, Whale shark, Hagfish, Clownfish, Lion, Bony skeletons, Opposable thumbs, Jaws, Mammary glands, and Placenta.

Read below for solution:

To complete the activity, users need to drag each characteristic to the point on the cladogram where it first appeared, indicating which groups possess that trait and their shared ancestry. At the top, the animals from left to right are Hagfish, Whale shark, Clownfish, Koala, Lion, and Human. At the bottom, the suitable characteristics from left to right are Jaws, Bony skeletons, Mammary glands, Placenta, and Opposable thumbs.

5 section questions ▾

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Applying cladistics (HL)

A3.2.7: Analysing cladograms (HL)

A3.2.8: Using cladistics (HL)

A3.2.9: Classification using rRNA base sequences evidence (HL)

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Learning outcomes

By the end of this section you should be able to:

- Deduce evolutionary relationships from cladograms.
- Describe how cladistics can be used to assess whether classifications correspond to evolutionary relationships.
- Describe how the analysis of rRNA base sequences led to the introduction of the domain taxa.

Your new species has been classified and placed in a cladogram with other related species. How do you interpret the cladogram to determine the evolutionary relationships between your species and the others? Find out in the following section.

Analysing cladograms

A cladogram is a diagram that shows the relationships between a group of organisms in terms of evolution. Hypothetical ancestors and their descendants are shown in a branching diagram. Cladograms are visual representations of evolutionary relationships, common ancestors between groups and the grouping of related organisms into clades.

In a cladogram you need to be familiar with several features to correctly interpret the relationships presented. These include:

- the root, which represents the most ancient common ancestor
- a node, which represents a hypothetical common ancestor



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- a terminal branch, which represents an extant species.

Interactive 1 shows two cladograms to illustrate these terms.

Species A Species B Species C Species D Species E Species F

Terminal branch Root Node

✓ Check

Interactive 1. Generalised Cladograms to Identify the Locations of the Root, Nodes and Terminal Branches.

More information for interactive 1

This interactive has two slides illustrating two cladograms.

The first slide illustrates a cladogram used to represent evolutionary relationships—featuring six species labeled Species A through Species F. The diagram starts at a single root on the lower left, representing the most recent common ancestor of all the species. From the root, the blue lines branch out, forming a tree-like structure. Each split or branching point, called a node, signifies a divergence where a common ancestor gave rise to two or more descendant species. Terminal branches extend from the last node to each species, showing that they are the final species in each lineage. Species B and C are shown to share a more recent common ancestor with each other than with the other species, as do Species E and F.

The three drag-and-drop options given below the cladogram are: Terminal branch, Root, and Node.

Read below for the solution:

From bottom to the top,

Blank 1: Root

Blank 2: Node

Blank 3: Terminal branch

The second slide displays a phylogenetic tree (cladogram) illustrating the evolutionary relationships among five species labeled Species A through Species E. The diagram consists of blue branching lines, where each tip represents a different species. The tree begins at the left with a single common ancestor (the root) and branches out toward the right. Points where the branches split represent nodes, indicating common ancestors shared by the species beyond that point. The outermost branches leading to each labeled species are called terminal branches.

The three drag-and-drop options given below the cladogram are: Terminal branch, Root, and Node.

Read below for the solution:

From bottom to the top,

Blank 1: Root

Blank 2: Node

Blank 3: Terminal branch



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The analysis of a cladogram relies on a number of assumptions and definitions.

- The branching pattern is assumed to represent the evolutionary relationship between species.
- If extinct species are included, information must be given on whether the cladogram is based on morphology only. This would be because DNA generally is not available for the analysis, although there are some exceptions to this.
- The more nodes there are between species, the more distant their relationship.
- Mutations at the DNA and protein level are assumed to occur at a constant rate. For example, one base change per 10^9 years. This may seem like a long time, but remember there are billions of bases in genomes.
- Some cladograms are drawn to scale. That is, the length of the branches is proportional to the time since divergence.

From the information provided in **Figure 1**, it appears that humans and chimps are more closely related to each other than any other combination. The lemurs are the least related to any other animal on this cladogram.

The cladogram can also be used to estimate when species diverged as well as when the common ancestor existed. We can set speciation to a timeline after analysing molecular differences and comparing them to fossil records. For instance, we can deduce from the cladogram that humans and chimpanzees last shared a common ancestor some 6–7 million years ago.

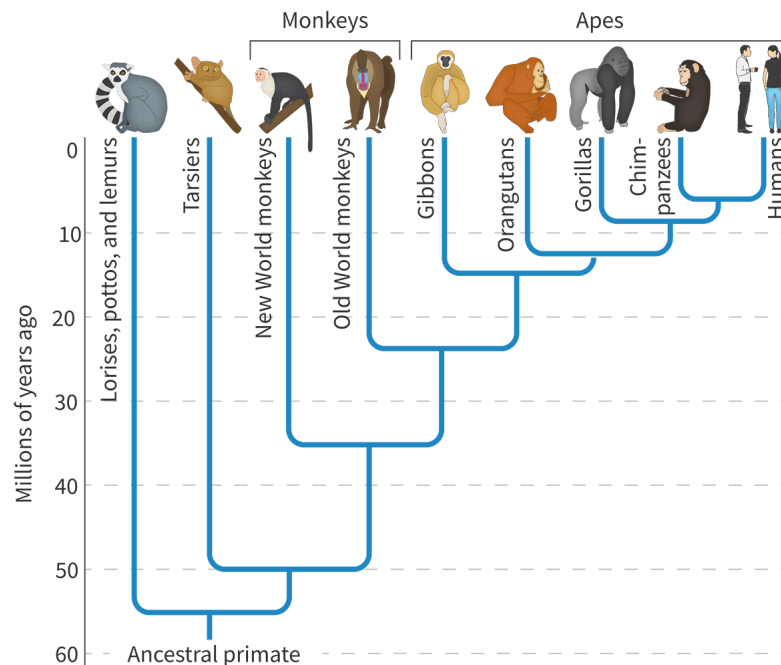


Figure 1. A cladogram of primates.

More information for figure 1

The image is a cladogram depicting the evolutionary relationships among various primate species. At the top, there are illustrations of different primates, including lemurs, tarsiers, monkeys, apes, and humans, each represented by a unique drawing above a branching timeline. The branches of the cladogram indicate the points at which species diverged from common ancestors, highlighted by connecting lines. Each split in the branches shows a different evolutionary divergence, illustrating how the species are related. The diagram includes text labels for each species and the estimated time of these divergences, with colored lines indicating the connections. The layout suggests a timeline format, offering a visual representation of speciation events over time.

[Generated by AI]

Using cladistics to investigate whether the classification of groups corresponds to evolutionary relationships

The addition of molecular data in the creation of cladograms and the analysis of evolutionary relationships has led to the reclassification of some groups of organisms. The figwort family (Scrophulariaceae) included more than 275 genera with around 5000 species, based on shared morphological features. The figwort family was the



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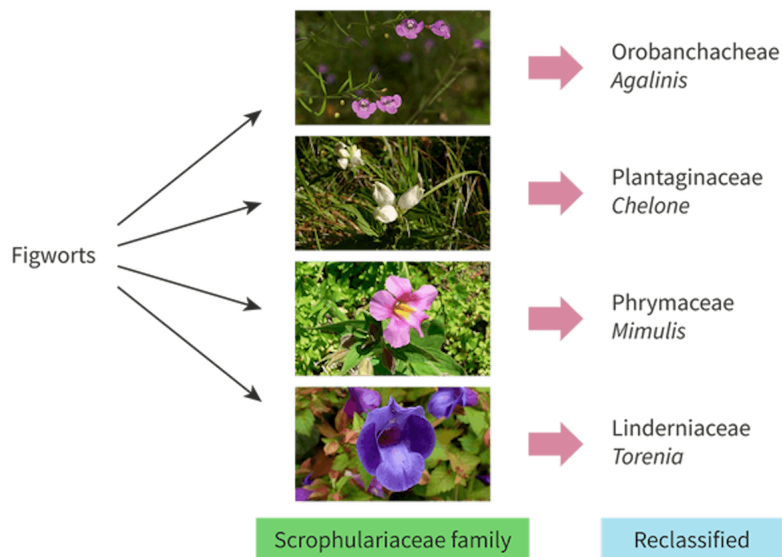
eighth largest of all of the angiosperm families. However, when scientists carried out genetic analysis on a gene from chloroplasts, they discovered that many of the species within this group were very different and should be reclassified into new families. Instead of these flowers all belonging to a single clade, they now make up five separate ones. Now the figwort family has around 200 species and is the 36th largest family of all of the angiosperms (**Figure 2**).



Figure 2. *Scrophularia nodosa*, a plant from the figwort family.

Credit: Picture Partners, Getty Images (<https://www.gettyimages.com/detail/photo/flowering-figwort-royalty-free-image/501513645>)

The five clades that contain the taxa traditionally assigned to Scrophulariaceae are: Calceolariaceae, Orobanchaceae, Scrophulariaceae, Stilbaceae and Veronicaceae. But, it should be noted that several figwort genera have also been moved to other families such as plantain and broomrape. In fact, less than half of plants classified as figworts still remain in the figwort family now that we know more about their DNA similarities and differences (**Figure 3**).



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Figure 3. The reclassification of the figwort family.

Sources (top to bottom): "Agalinis tenuifolia 2 (https://commons.wikimedia.org/wiki/File:Agalinis_tenuifolia_2.jpg)" by Eric Hunt is licensed under CC BY-SA 3.0 (<https://creativecommons.org/licenses/by-sa/3.0/>); "Chelone glabra 002 (https://commons.wikimedia.org/wiki/File:Chelone_glabra_002.JPG)" by SB Johnny is licensed under CC BY-SA 3.0 (<https://creativecommons.org/licenses/by-sa/3.0/>); "Mimulus lewisii p1080904 (https://commons.wikimedia.org/wiki/File:Mimulus_lewisii_p1080904.jpg)" by David Monniaux is licensed under CC BY-SA 3.0 (<https://creativecommons.org/licenses/by-sa/3.0/>); "Torenia 'Sunrenilabu' kz1 (https://commons.wikimedia.org/wiki/File:Torenia_%27Sunrenilabu%27_kz1.jpg)" by Krzysztof Ziarnik, Kenraizis licensed under CC BY-SA 3.0 (<https://creativecommons.org/licenses/by-sa/3.0/>).

🔍 More information for figure 3

Classification of all organisms into three domains using evidence from rRNA base sequences

In 1977, Carl Woese suggested a ground-breaking proposal to reclassify all living things by adding a new taxonomic level above kingdoms. This was based on the finding that ribosomal RNA (rRNA) sequences may be utilised to infer evolutionary relationships. Woese and his associates discovered that the rRNA sequences formed three distinct groups, which became the domains eubacteria, archaea and eukarya (**Figure 4**). This discovery fundamentally altered how creatures were categorised and demonstrated that molecular traits accurately represented evolutionary relationships.

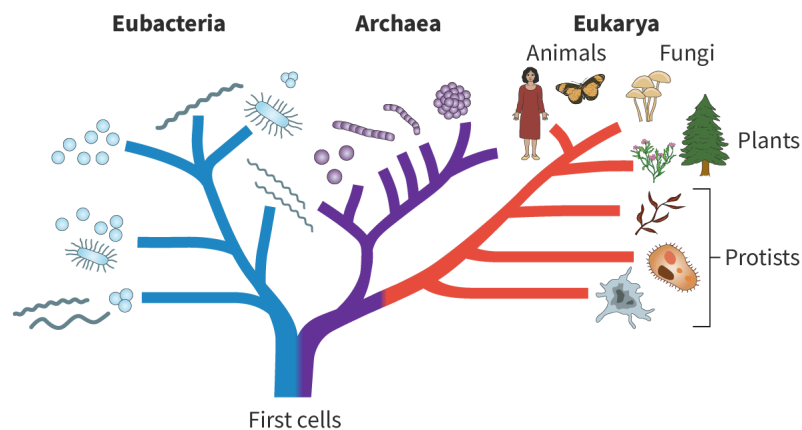


Figure 4. A diagram to show the domains and kingdoms of life as currently understood.

🔍 More information for figure 4

The diagram illustrates the domains and kingdoms of life, branching from a common origin labeled as "First cells." It shows three major branches or domains: Eubacteria, Archaea, and Eukarya.

The Eubacteria branch is colored blue and contains illustrations of various bacteria forms, like spherical and rod-shaped forms. The Archaea branch is colored purple and also displays different microbial shapes. The Eukarya branch is colored red and is further divided into several categories: Animals, displaying a human figure and a butterfly; Plants, showing a tree and some flowers; Fungi, depicted by mushrooms; and Protists, featuring microorganisms like algae. The branching structure represents evolutionary relationships as currently understood.

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Take *Escherichia coli* bacteria as an example. *E. coli* would have previously been categorised in the kingdom Monera, along with all other prokaryotes, prior to Woese's proposed reorganisation. However, according to its RNA sequence, *E. coli* belongs to the domain eubacteria. *Pyrolobus fumarii*, a prokaryote capable of surviving in



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temperatures up to 113 °C, is a member of the archaea domain. It is actually more closely related to eukaryotes than to members of the eubacteria domain like *E. coli*.



Creativity, activity, service

Strand: Service

Learning outcome: Demonstrate engagement with issues of global significance

Monitoring and surveying living organisms around the world is a huge task. There are potentially millions of species still to be identified, and classified, alongside monitoring of species we already know. Consider a project that helps a local wildlife organisation monitor and record various species of interest in your area. Who knows, perhaps you will help to discover a new species...

Try the activity below in pairs to analyse a cladogram of primates.



Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Providing a reasoned argument to support conclusions
- **Time required to complete activity:** 20 minutes
- **Activity type:** Pair activity

Using the cladogram in **Figure 5**, answer the following questions.

1. How many millions of years ago did tarsiers share a common ancestor with lemurs?
2. How many millions of years ago did new and old world monkeys share a common ancestor?
3. What are the members of the clade that shared a common ancestor with lesser apes?
4. Which primates are chimpanzees least closely related to?
5. How old would you expect the fossils of a common ancestor between humans and chimpanzees and bonobos to be?
6. How old would you expect the fossils of a common ancestor between gorillas and orangutans to be?
7. If the dating on this cladogram was based on base sequence analysis of one specific region of DNA that mutated at a rate of three mutations every 200 000 years, how many differences would you expect between bonobos and chimpanzees?
8. Would you expect more genetic differences between gorillas and orangutans or between humans and chimpanzees? Explain your reasoning.
9. Which current group of primates has existed the longest?
10. Which current group of primates evolved most recently?



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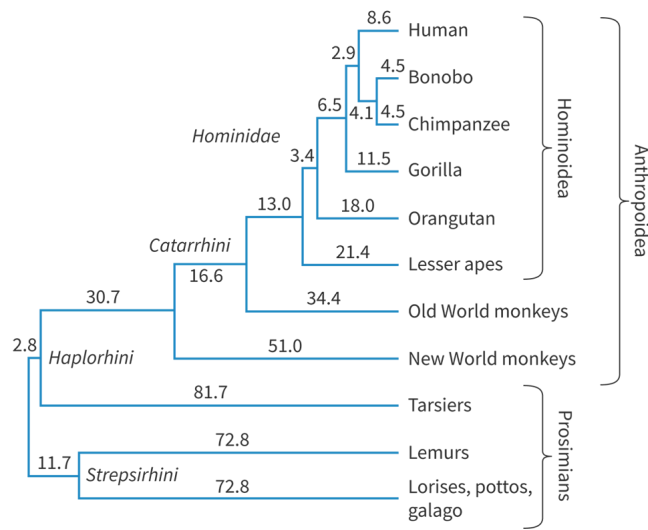


Figure 5. A cladogram of extant primates with branch lengths in millions of years.

© More information for figure 5

5 section questions ▾

A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Summary and key terms (HL)

Section

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Feedback



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Higher level (HL)

- The vast diversity of life makes a system of classification necessary. This classification then allows for further study, more effective scientific communication and a host of other benefits.
- The traditional method of classification, using the hierarchy of taxa has limitations as it does not accurately reflect the myriad patterns of divergence that have happened over the evolutionary history of life on Earth.
- A system that classifies based on evolutionary relationships is ideal. While the traditional methods of using morphology and other visible characteristics were successful given the knowledge of the time, the introduction of molecular analysis of both DNA and protein sequences has allowed for a more accurate and precise system to be created that more truly reflects evolutionary relationships and can be used to measure these relationships quantitatively.
- A clade is a group of organisms with a common ancestor and shared characteristics. Differences in DNA base sequence and protein amino acid sequence are accumulated over time and can be used to estimate how long ago groups diverged from common ancestors. This is known as the molecular clock.
- Base or amino acid sequence data can be used to construct cladograms. By using this as the basis for construction, evolutionary relationships can be deduced from the cladograms.
- Base sequence analysis has led to the reclassification of some groups such as the figwort family, which, upon analysis of chloroplast genes, was found to actually be a collection of five different families.
- Analysis of ribosomal RNA led to the development of a new level of taxa known as a domain. This is now the first level of classification and contains three domains: eubacteria, archaea and eukarya.



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Key terms

Review these key terms. Do you know them all? Fill in as many gaps as you can using the terms in this list.

1. The incredible _____ of life on Earth makes a system of _____ necessary.
2. _____ developed both a system of _____ or naming, as well as the _____ of taxa that we still use today.
3. _____ is an approach to classification that focuses on evolutionary relationships.
4. _____ are groups of organisms within a _____ that share a _____.
5. The idea of a _____ allows for the estimation of time since species diverged from common ancestors based on the accumulation of molecular change.
6. Molecular analysis led to the introduction of _____ as the highest level of classification for life.

common ancestor classification molecular clock Cladistics cladogram hierarchy
domains Clades Linnaeus nomenclature variation

✓ Check

Interactive 1. Classification and Cladistics (HL): Key Concepts and Terminology.

A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Checklist (HL)

Section

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Feedback



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Higher level (HL)



What you should know

After studying this subtopic you should be able to:

- Explain why a classification system is needed.
- Describe difficulties with the traditional hierarchy of taxa.
- Describe the advantages of basing classification on evolutionary relationships.
- Define a clade.
- Explain how the gradual accumulation of sequence changes can be used to determine the time since a common ancestor diverged into extant species.



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- Describe how base or amino acid sequences can be used in the construction of cladograms.
- Deduce evolutionary relationships from cladograms.
- Describe how cladistics can be used to assess whether classifications correspond to evolutionary relationships.
- Describe how the analysis of rRNA base sequences led to the introduction of the domain taxa.

A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Investigation (HL)

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Assign



Higher level (HL)

- **IB learner profile attribute:** Thinkers
- **Approaches to learning:** Thinking skills — Applying key ideas and facts in new contexts
- **Time required to complete activity:** 30 minutes
- **Activity type:** Individual activity

Your task

Cladistics is a valuable tool in analysing the evolutionary relationships between species. It also allows us to re-evaluate the current systems of classification to see what we got right and what we may need to change. In this investigation you will generate a cladogram from some molecular data and use this to analyse the evolutionary relationships of the species included.

Using the amino acid sequence data in **Table 1**, first generate a matrix of differences among all species listed. Then create a cladogram based on that matrix. The symbols for amino acids shown in **Table 2** are for information only.

Table 1. Amino acid sequence data for fictional species Alpha to Kappa.

Species	Amino acid sequence
Alpha	<u>G</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>I</u> <u>M</u> <u>K</u> <u>C</u> <u>S</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>T</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Beta	<u>G</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>V</u> <u>Q</u> <u>K</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>T</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Gamma	<u>G</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>V</u> <u>Q</u> <u>K</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>T</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>N</u> <u>G</u> <u>I</u> <u>E</u> <u>G</u>
Delta	<u>G</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>S</u> <u>M</u> <u>K</u> <u>C</u> <u>G</u> <u>T</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>E</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>T</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Epsilon	<u>G</u> <u>D</u> <u>V</u> <u>A</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>T</u> <u>E</u> <u>V</u> <u>Q</u> <u>K</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>N</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>V</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>W</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Zeta	<u>G</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>V</u> <u>Q</u> <u>R</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>A</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>V</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Eta	<u>G</u> <u>N</u> <u>A</u> <u>D</u> <u>N</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>E</u> <u>V</u> <u>Q</u> <u>R</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>I</u> <u>V</u> <u>E</u> <u>A</u> <u>G</u> <u>G</u> <u>K</u> <u>H</u> <u>K</u> <u>V</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>F</u> <u>E</u> <u>G</u>





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Species	Amino acid sequence
Theta	<u>G</u> <u>N</u> <u>P</u> <u>D</u> <u>A</u> <u>G</u> <u>A</u> <u>K</u> <u>I</u> <u>E</u> <u>K</u> <u>T</u> <u>K</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>T</u> <u>V</u> <u>D</u> <u>A</u> <u>G</u> <u>A</u> <u>G</u> <u>H</u> <u>K</u> <u>Q</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Iota	<u>G</u> <u>N</u> <u>P</u> <u>K</u> <u>A</u> <u>G</u> <u>E</u> <u>K</u> <u>I</u> <u>E</u> <u>K</u> <u>T</u> <u>K</u> <u>C</u> <u>A</u> <u>Q</u> <u>C</u> <u>H</u> <u>T</u> <u>V</u> <u>D</u> <u>K</u> <u>G</u> <u>A</u> <u>G</u> <u>H</u> <u>K</u> <u>Q</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>N</u> <u>G</u> <u>L</u> <u>E</u> <u>G</u>
Kappa	<u>G</u> <u>S</u> <u>A</u> <u>K</u> <u>K</u> <u>G</u> <u>A</u> <u>T</u> <u>L</u> <u>E</u> <u>K</u> <u>T</u> <u>R</u> <u>C</u> <u>E</u> <u>L</u> <u>C</u> <u>H</u> <u>T</u> <u>V</u> <u>E</u> <u>K</u> <u>G</u> <u>G</u> <u>P</u> <u>H</u> <u>K</u> <u>V</u> <u>G</u> <u>P</u> <u>N</u> <u>L</u> <u>H</u> <u>G</u> <u>I</u> <u>E</u> <u>G</u>
Note: amino acids in bold text are shared among all species.	

Table 2. Amino acid symbols.

Amino acids and their symbols			
A = Alanine C = Cysteine D = Aspartic acid E = Glutamic acid F = Phenylalanine	G = Glycine H = Histidine I = Isoleucine K = Lysine L = Leucine	M = Methionine N = Asparagine P = Proline Q = Glutamine R = Arginine	S = Serine T = Threonine V = Valine W = Tryptophan Y = Tyrosine

Figure 1. A matrix can be used to compare differences.

	Alpha	Beta	Gamma	Delta	Epsilon	Zeta	Eta	Theta	Iota	Kappa
Alpha	0									
Beta		0								
Gamma			0							
Delta				0						
Epsilon					0					
Zeta						0				
Eta							0			
Theta								0		
Iota									0	
Kappa										0

You can use a matrix like this to compare the differences between amino acid sequences among the species. Then, construct a cladogram to best represent the evolutionary relationships between the species based on these data.

Using your cladogram, try to answer the following questions.

1. Which species are most closely related?
2. Which species are least closely related?
3. Are there any species that could be grouped together into a clade?
4. What other information would be useful in constructing this cladogram accurately?



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A3. Unity and diversity: Organisms / A3.2 Classification and cladistics (HL)

Reflection (HL)

Section

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Feedback



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Teacher instructions

The goal of this section is to encourage students to reflect on their learning and conceptual understanding of the subject at the end of this subtopic. It asks them to go back to the guiding questions posed at the start of the subtopic and assess how confident they now are in answering them. What have they learned, and what outstanding questions do they have? Are they able to see the bigger picture and the connections between the different topics?

Students can submit their reflections to you by clicking on 'Submit'. You will then see their answers in the 'Insights' part of the Kognity platform.

Higher level (HL)



Reflection

Now that you've completed this subtopic, let's come back to the guiding questions introduced in [The big picture \(/study/app/bio/sid-422-cid-755105/book/big-picture-hl-id-43528/\)](/study/app/bio/sid-422-cid-755105/book/big-picture-hl-id-43528/):

- What tools are used to classify organisms into taxonomic groups?
- How do cladistic methods differ from traditional taxonomic methods?

With these questions in mind, take a moment to reflect on your learning so far and type your reflections into the space provided.

You can use the following questions to guide you:

- What main points have you learned from this subtopic?
- Is anything unclear? What questions do you still have?
- How confident do you feel in answering the guiding questions?
- What connections do you see between this subtopic and other parts of the course?

⚠ Once you submit your response, you won't be able to edit it.

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