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Overview
(/study/app/
422-
cid-
755105/o

Teacher view

Table of
contents

Notebook

Glossary A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

The big picture

Reading
assistance

Index

- The big picture
- What is a species?
- What chromosomes tell us
- Comparing genomes
- Exceptions to the rule (HL)
- Identifying species (HL)
- Summary and key terms
- Checklist
- Investigation
- Reflection

? Guiding question(s)

- What is a species?
- What patterns are seen in the diversity of genomes within and between species?

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.

We are not the only human species to have lived on Earth. We had cousins; closely related species that evolved alongside us in various parts of the world. Modern humans, *Homo sapiens*, are the only surviving human species but other members of the genus *Homo* include the Neanderthals (*Homo neanderthalensis*) (**Interactive 1**) and *Homo floresiensis* (**Figure 1**), a small species of humans who lived on the island of Flores, Indonesia until around 50 000 years ago. Recently, skeletal remains and other archaeological discoveries from a cave in Siberia provided evidence for the existence of a further unique group, referred to as the Denisovans. However, we do not have sufficient genetic or fossil evidence to classify the Denisovans as a separate species.

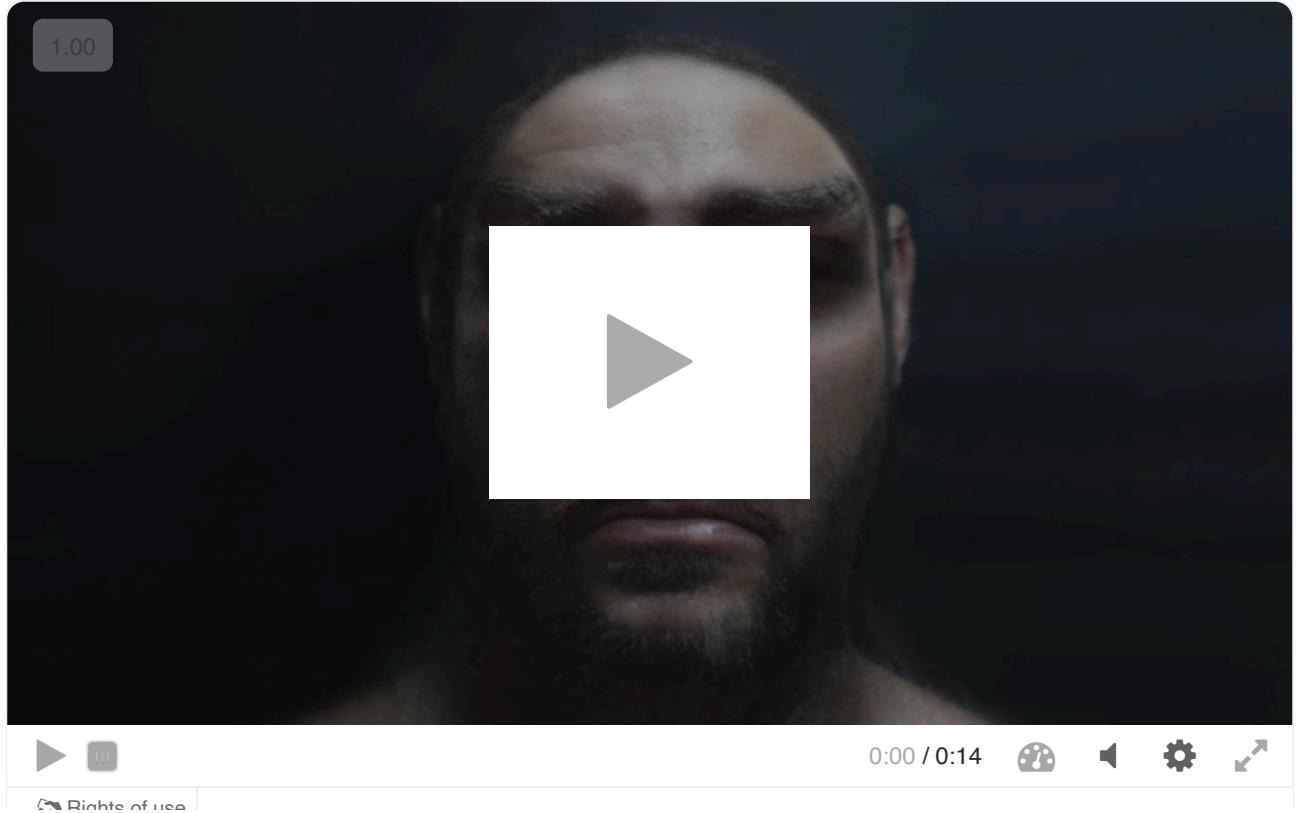


Student
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Overview
(/study/app/
422-
cid-
755105/o



Interactive 1. A Comparison of a Reconstruction of a Neanderthal's Face With a Modern Human's Face.

More information for interactive 1

An interactive video displays a reconstruction of a Neanderthal's face with a modern human face. The Neanderthal's face features thick brows, wrinkled skin on the nasal bone just below the eyebrows, a wide nose, a small forehead, and a prominent jaw, giving a rugged appearance.

As the video progresses, the Neanderthal's face gradually transforms into that of a modern human face. The forehead becomes larger, the thick brows become thinner, the wide nose changes to a smaller one, the wrinkles on the nasal bone disappear, and the prominent jaw softens into a more typical human jawline.

This video helps users understand the facial differences between Neanderthals and modern humans, highlighting the evolutionary changes in the facial structure over time.



Student
view



Overview
(/study/app/
422-
cid-
755105/o



Figure 1. Reconstruction of the facial features of *Homo floresiensis* based on skeletal remains.

Source: "Homo floresiensis v 2-0 (https://commons.wikimedia.org/wiki/File:Homo_floresiensis_v_2-0.jpg)" by Cicero Moraes et alii is licensed under CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/deed.en>)

In another cave in Siberia, the fossilised remains of a group of Neanderthals were discovered from which scientists were able to extract DNA. This provided evidence that there was a father and daughter among the group. Additional conclusions were drawn from this evidence, providing a clearer understanding of Neanderthal societies. For example, it is now thought that Neanderthals lived in small groups, showing low genetic diversity, and that it was females who moved to other groups upon finding a mate, while the males tended to remain with their own family groups.

Imagine similar finds in future – what other mysteries could we uncover and answer? What else can the past tell us about ourselves?

Although we are aware of the variety of life around us, our knowledge of extinct species is much more variable. Our understanding of how organisms differ is still developing, but DNA has opened new pathways for inquiry. Through genetic analysis we can see how closely we

Overview
(/study/app/
422-
cid-
755105/o

are related to other groups, such as the Neanderthals, and even find evidence for interbreeding and the remnants of Neanderthal DNA in populations of humans today. We can also develop a clearer understanding of how other organisms are related.

Prior learning

Before you study this subtopic, keep in mind your understanding of the following areas of biology:

- 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/)).
- diversity of possible DNA base sequences and the limitless capacity of DNA for storing information (see [section A1.2.9](#) (/study/app/bio/sid-422-cid-755105/book/hershey-and-chase-and-chargaff%E2%80%99s-data-hl-id-43581/)).
- 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/)).

Refer to [subtopic A1.2](#) (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43236/) for more information.

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

What is a species?

A3.1.1: Variation between organisms A3.1.2: Species A3.1.3: Binomial system A3.1.4: Biological species concept

Learning outcomes

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

- Identify variation as a defining characteristic of life.
- State that a species is a group of organisms with shared morphological traits.
- Name species using binomial nomenclature.
- Explain the biological species concept.



Student
view

Home
Overview
(/study/app/
422-
cid-
755105/o

The relationship between ourselves and our closest living relatives, the chimpanzees (*Pan troglodytes*) is fairly clear. We have distinct morphological (physical) characteristics and you wouldn't confuse a human with a chimp. But what about our extinct closer relatives? If a human male and female stood beside a Neanderthal male and female, could you tell them apart? Could you pick Neanderthals out of a group of humans? Just how different would we be?

Variation between organisms as a defining feature of life

All living organisms show variation. No two individuals are identical in all of their traits. This variation is one of the defining features of life (**Figure 1**). The significance of variation to life and its evolution is explored in subtopic D4.1 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43238/).



Figure 1. In a crowd of commuters variation is apparent.

Credit: JohnnyGreig, Getty Images (<https://www.gettyimages.co.uk/detail/photo/people-commuting-royalty-free-image/523536219>)

Because of the large amount of variation between organisms, we have developed systems of classification to group and organise our knowledge about them. These systems structure our understanding and allow for clearer communication between people studying organisms around the world. The 'modern' system for classifying living organisms was published in 1735 by Carl Linnaeus, a Swedish naturalist.

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Species as groups of organisms with shared traits

Overview

(/study/app

422-

cid-

755105/o

Linnaeus classified organisms into species based on shared morphological characteristics.

Individuals of the same species tend to look more similar to each other than to members of other species. This is the original morphological concept of a species. Take lions (*Panthera leo*) and tigers (*Panthera tigris*) as an example (**Figure 2**). These two species of large cats are closely related but separate species, with recognisable, distinct characteristics. Once you recognise what those characteristics are, you wouldn't confuse a tiger and a lion.



Figure 2a. A lion (*Panthera leo*)

Credit: Neale Howarth / 500px, Getty Images (<https://www.gettyimages.co.uk/detail/photo/studio-portrait-of-lion-royalty-free-image/1068195910>)



Figure 2b. A tiger (*Panthera tigris*)

Credit: Steve Wilson, Getty Images (<https://www.gettyimages.co.uk/detail/photo/isolated-profile-of-a-tiger-royalty-free-image/567871241>)

Figure 2. Lions and tigers, two closely related species, have unique physical characteristics which define them as separate species according to the morphological species concept.

Student
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Binomial system for naming organisms

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As part of his work, Linnaeus developed a naming convention for species. Today, this is known as binomial nomenclature. Species are named using both their genus and species names. The genus name comes first and the first letter is capitalised, followed by the species name in lowercase. This is put in italics within text or underlined when handwritten. For example, *Homo sapiens*, *Homo neanderthalensis*, *Panthera leo* and *Panthera tigris*.

Species sharing a genus share common characteristics. The names themselves are based on Latin and have varying origins, from descriptions of specific defining features to the names of the people who first discovered or described the species. For example, the humpback whale is *Megaptera novaeangliae* (**Figure 3**), meaning big-winged New Englander referring to their extremely long pectoral fins and one of the locations in which they were first encountered by whalers. Dall's porpoise, *Phocoenoides dalli* (**Figure 4**), is named after the American naturalist William Healey Dall, who collected the first specimen of the species.



Figure 3. Humpback whale, *Megaptera novaeangliae*, named for its appearance and where it was first encountered (note the long pectoral fins).

Credit: George Karbus Photography, [Getty Images](https://www.gettyimages.co.uk/detail/photo/humpback-whales-underwater-view-tonga-western-fiji-royalty-free-image/1016327824) (<https://www.gettyimages.co.uk/detail/photo/humpback-whales-underwater-view-tonga-western-fiji-royalty-free-image/1016327824>)



Figure 4. Dall's porpoise, *Phocoenoides dalli*, named after the naturalist who collected the first specimen.



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Credit: Gerald Corsi, [Getty Images](https://www.gettyimages.co.uk/detail/photo/dalls-porpoise-is-a-species-of-porpoise-found-only-royalty-free-image/1283797058) (<https://www.gettyimages.co.uk/detail/photo/dalls-porpoise-is-a-species-of-porpoise-found-only-royalty-free-image/1283797058>)

Nature of Science

Aspect: Science as a shared endeavour

Scientists from all over the world need to communicate and collaborate. Agreed conventions and common terminology facilitate clear communication.

The system of binomial nomenclature for naming species allows scientists speaking different languages to communicate effectively about these species.

Biological species concept

So, we can classify organisms into species based on shared morphological characteristics. But how do we then define species that look so similar they can't be easily distinguished from each other (**Figure 5**)? How do we classify when there is sexual dimorphism within a species and males and females have very different characteristics (**Figure 6**)? To deal with these issues, among others, the biological species concept was developed. This describes an alternate method for defining species with a basis not on morphology but rather on the ability to interbreed and produce fertile offspring. A species thus is a group of organisms that can potentially interbreed and produce fertile offspring.



Figure 5a. Red grouse (*Lagopus lagopus scotica*)

Credit: David and Louise Gibbon, [Getty Images](https://www.gettyimages.co.uk/detail/photo/red-grouse-north-pennine-moors-county-durham-royalty-free-image/685030507) (<https://www.gettyimages.co.uk/detail/photo/red-grouse-north-pennine-moors-county-durham-royalty-free-image/685030507>)



Overview
(/study/app/
422-
cid-
755105/o



Figure 5b. Black grouse (*Lyrurus tetrix*)

Credit: Peter Orr Photography, Getty Images (<https://www.gettyimages.co.uk/detail/photo/black-grouse-hen-royalty-free-image/1128242466>)

Figure 5. Two morphologically similar species, the red grouse (*Lagopus lagopus scotica*) and black grouse (*Lyrurus tetrix*).



Figure 6. The Mandarin duck (*Aix galericulata*) is sexually dimorphic, with the male (left) and female (right) of the species being quite distinct in appearance.

Credit: Mark L Stanley, Getty Images

(<https://www.gettyimages.co.uk/detail/photo/mandarin-duck-aix-galericulata-royalty-free-image/546289571>)

According to this concept, if members of two different species do interbreed, any offspring produced will be infertile and unable to produce their own offspring. These (infertile) offspring between two different species are known as hybrids. One such example is the

Student view

☞ mule, which is produced by breeding a horse with a donkey. Two mules are unable to breed to produce more mules. This can only be done by breeding more horses with donkeys.

Overview
(/study/app)

422-
cid-
755105/o



Figure 7. A mule, the hybrid result of breeding a horse and donkey.

Credit: Jose A. Bernat Bacete, [Getty Images](#)

(<https://www.gettyimages.co.uk/detail/photo/mule-in-a-field-of-pasture-to-half-a-day-royalty-free-image/529645758>)

The biological species concept, however, is not a strict biological rule. There have been cases of two different species producing fertile offspring. One such example is a liger, produced when a lion and a tiger interbreed. Ligers are hybrids that challenge the biological species concept as

- They are fertile
- They can interbreed with other lions, tigers or ligers leading to a blurring of species boundaries

Also, the biological species concept cannot be applied to organisms that reproduce asexually. Both the morphological and biological species concepts attempt to provide criteria for determining how to identify a group of organisms as a species. Both concepts have challenges and neither are universally applicable. As biological systems are incredibly complex, determination of just how things work is a very challenging task for biologists. As

Overview
(/study/app/
422-
cid-
755105/o

such, there are competing definitions of what a species is, and scientists may use these based on their context of study. In summary, there is no one-size-fits-all definition of a species and it remains fluid and debatable.

Check your understanding of the meanings of some shark and cat species names in this activity.

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Communication skills — Presenting data appropriately
- **Time required to complete activity:** 30 minutes
- **Activity type:** Pair activity

Round A

Take a look at the images of five different shark species (**Interactive 1**). Would you group any together based on their morphology? If you knew that three belonged to the same genus, which three would you place together and why? Discuss with your partner.

Using what you have discussed with your partner and the meanings of each species name below, attempt to match the species names with each image.

- *longimanus* — long hand
- *obesus* — fat or stout (in this context refers to a blunt snout)
- *melanopterus* — black fin
- *carcharias* — jagged-toothed
- *leucas* — white



Student
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Overview
(/study/app/
422-
cid-
755105/o



Great White Shark



Bull Shark



Oceanic Whitetip Shark



Blacktip Reef Shark



Whitetip Reef Shark

Carcharhinus longimanus

Carcharhinus melanopterus

Carcharodon carcharias

Carcharhinus leucas

Triaenodon obesus

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422-
cid-
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Interactive 1. Shark species.

Round B

Now try this a second time with five different species of cat (**Interactive 2**). Again, three belong to the same genus. Which would you place together and why? Discuss with your partner.

Using what you have discussed with your partner and the meanings of each species name below, attempt to match the species names with each image.

- *pardus* — leopard
- *nebulosa* — obscure
- *pardalis* — mottled
- *jacobita* — heel-grabber
- *tigrinus* — striped like a tiger



Student
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Overview
(/study/app/
422-
cid-
755105/o



Andean cat



Leopard



Clouded leopard



Ocelot



Northern Oncilla

Panthera pardus

Neofelis nebulosa

Leopardus pardalis

Leopardus tigrinus

Leopardus jacobita

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(/study/app/
422-
cid-
755105/o

Interactive 2. Cat Species.

5 section questions ▾

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

What chromosomes tell us

A3.1.5: Speciation A3.1.6: Chromosome numbers of plant and animal species A3.1.7: Karyotyping and karyograms

Learning outcomes

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

- Describe speciation and the difficulties in distinguishing between populations and species.
- Outline that there is diversity of chromosome number between species.
- Explain karyotyping and be able to classify chromosomes in a karyogram by banding patterns, length and centromere position.

Originally, thinking in terms of morphology, scientists believed hippos were most closely related to pigs as they have similar ridges on their molars. More recently, however, DNA analysis has shown that hippos are more closely related to the fully aquatic cetaceans, such as dolphins. Does appearance or DNA provide a better guide to evolutionary relationships? In the following, we consider how DNA can highlight diversity.



Student
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Overview
(/study/app/
422-
cid-
755105/o



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Figure 1. Humans and Some of Our Closest and Most Recognisable Relatives, Chimpanzees (*Pan troglodytes*), Orangutans (*Pongo sp.*) and Gorillas (*Gorilla sp.*).

Diversity in chromosome numbers of plant and animal species

The DNA of eukaryotes ([section A2.2.4 \(/study/app/bio/sid-422-cid-755105/book/prokaryotic-and-eukaryotic-cells-id-43583/\)](#)) is organised into chromosomes within the nucleus of cells. Each species has a set number of chromosomes that is common to all members of that species. For example, humans (*Homo sapiens*) have 22 pairs of autosomes (numbered 1 to 22 based on length) and 2 sex chromosomes (either X or Y). Each individual has 46 chromosomes in total in each of their diploid cells. Chimpanzees (*Pan troglodytes*), our closest living relatives (**Figure 1**) with whom we share over 98% of our DNA, have 23 pairs of autosomes and 2 sex chromosomes. Each individual has 48 chromosomes in total in each of their diploid cells ([see subtopic D3.2 \(/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43244/\)](#)). As diploid cells contain pairs of chromosomes, they will always contain an even number.



Student
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Difficulties distinguishing between populations and species due to divergence of non-interbreeding populations during speciation

Speciation describes formation of a new species from the splitting of one pre-existing species into two or more new species. The mechanisms of this process are covered in [subtopic A4.1 \(/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43246/\)](#). There are a number of possible causes for species splitting. Reproductive barriers could prevent or limit interbreeding between two populations. A physical barrier might exist between two populations preventing interbreeding, or there might be a change in behaviour or timing around reproductive cycles. Occasionally, a sudden event that changes the chromosome number can occur and this sometimes results in the creation of a new species. This is often due to an error occurring during cell division where chromosomes do not separate as they should, producing cells with twice as many chromosomes than they should have. Speciation events often take a very long time after the physical splitting of a population.

Karyotyping and karyograms

It is possible to visibly compare the chromosomes of two individuals. In fact it is a diagnostic technique used to identify sex and chromosomal abnormalities. [Karyotyping](#), which involves isolating condensed chromosomes taken from actively dividing cells, allows for this comparison. The individual chromosomes are stained to highlight banding patterns and the images can be arranged to create the matching pairs as seen in the [karyogram](#) in **Figure 2**. If the chromosomes are isolated at the correct point in cell division, the chromosomes have replicated and can be seen as sister chromatids joined at their [centromere](#), the location of which also helps distinguish between them.

Practical skills

Tool 1: Experimental techniques — Applying techniques

You should be able to classify chromosomes by banding patterns, length and centromere position. **Figure 2** and the activity detailed below will give you an opportunity to practise this skill.

Overview
(/study/app/
422-
cid-
755105/o

Figure 2 shows a karyogram of a human male with 22 pairs of autosomal chromosomes and 1 pair of sex chromosomes. Chromosomes are paired and ordered based on size/length, centromere location and banding patterns. The sex chromosomes in this case are unmatched in length as they are X and Y making this individual a male. The X chromosome contains more genes and is therefore longer than the Y chromosome that only has a small number of male-specific genes. If this individual was female the sex chromosomes would match as they would be XX.

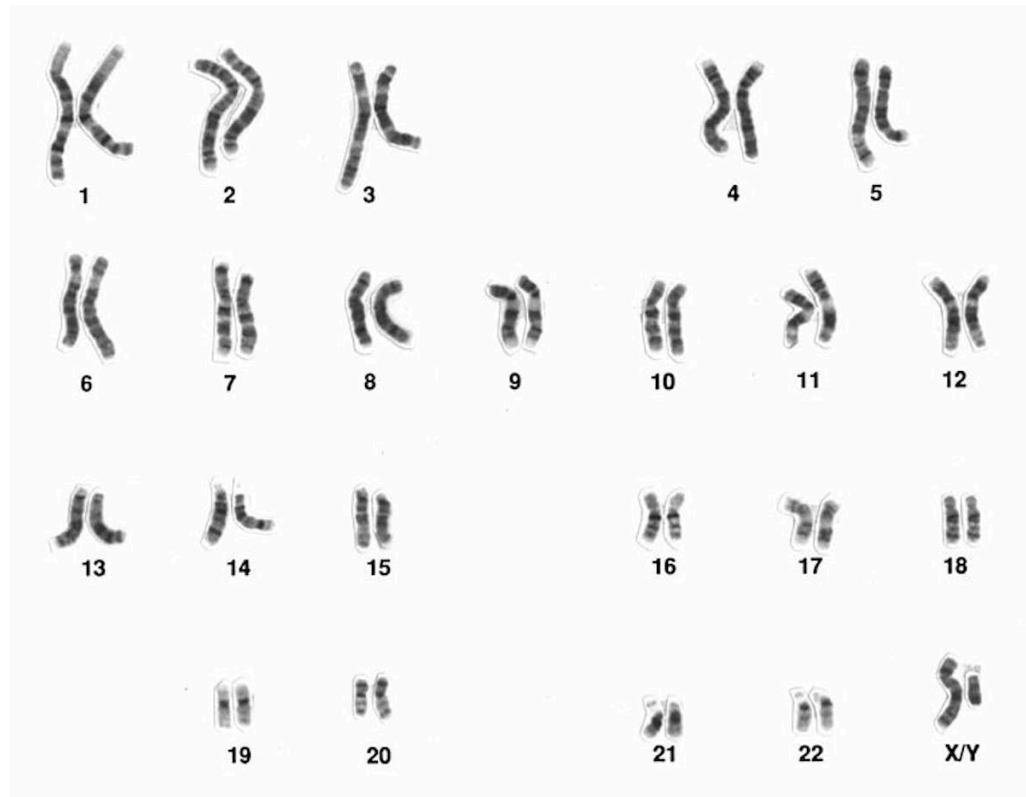


Figure 2. A karyogram of a human male showing 22 pairs of autosomal chromosomes and 1 pair of sex chromosomes.

Source: ["Human male karyotype"](#)

(https://commons.wikimedia.org/wiki/File:Human_male_karyotype_high_resolution.jpg) by National Human Genome Research Institute is in the public domain

[More information for figure 2](#)

The image is a karyogram displaying 22 pairs of autosomal chromosomes and 1 pair of sex chromosomes for a human male. Each chromosome pair is arranged in an ordered sequence from 1 to 22, with an additional pair labeled as X/Y. The autosomal chromosomes are organized by decreasing size, and each pair is visually distinct, with dark and light banding patterns visible on them. The male's sex chromosomes are mismatched, consisting of one longer X chromosome and one shorter Y chromosome. These chromosomes have been extracted from a cell, arranged, and photographed to appear as two vertical lines of varying angles, mimicking a standard human karyotype arrangement.

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Overview
(/study/app/
422-
cid-
755105/o

Try the activity below to examine matching chromosomes to form a karyotype.

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Being curious about the natural world
- **Time required to complete activity:** 10—15 minutes
- **Activity type:** Individual/class activity

Visit the following page from the University of Utah's Learn.Genetics website and try to match up the chromosomes using size and banding patterns to form a complete karyotype.

[Learn.Genetics - Make a Karyotype ↗](https://learn.genetics.utah.edu/content/basics/karyotype)
(<https://learn.genetics.utah.edu/content/basics/karyotype>)

Then, have a class discussion about the medical benefits of knowing the karyotype of a person.

Speciation events, including changes to DNA and chromosome number, occur slowly over time. How is it that humans and our closest living relatives, the great apes, have different chromosome numbers? If we compare a human karyogram with that of a chimpanzee (**Figure 3**), we might spot a clue.



Student
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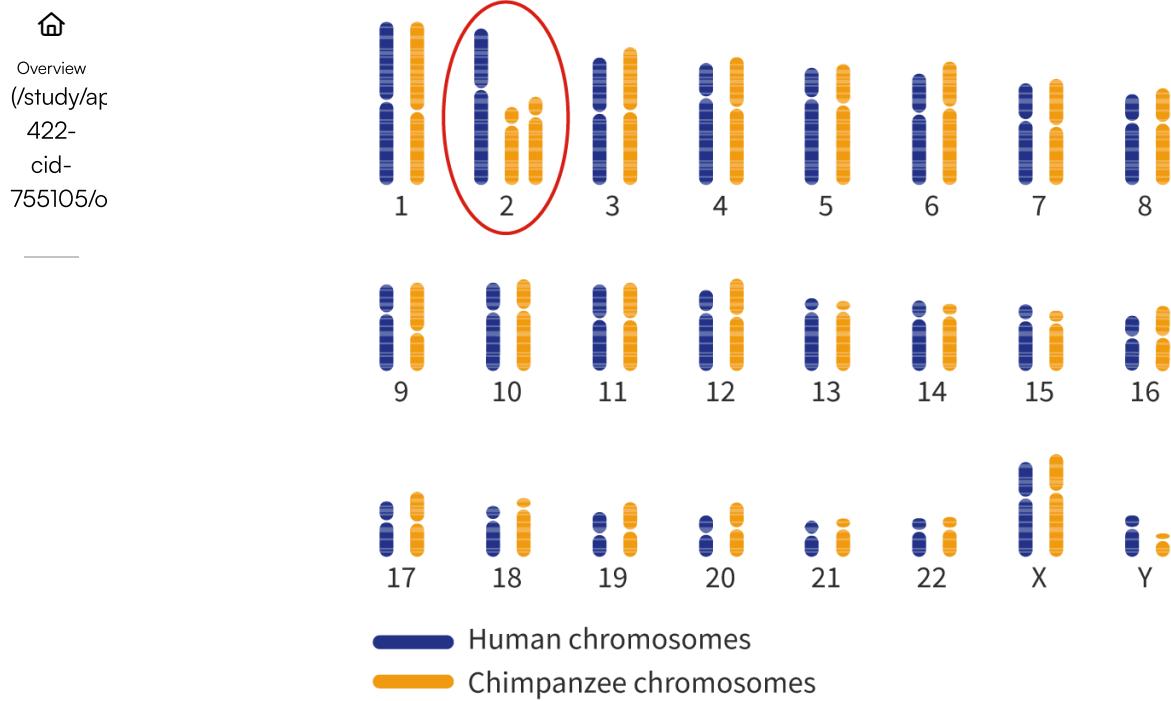


Figure 3. Human and chimpanzee chromosomes side by side.

[More information for figure 3](#)

The image shows karyograms of humans and chimpanzees. The chromosomes are presented in pairs, side by side, with human chromosomes in blue and chimpanzee chromosomes in orange. Most pairs look similar, though there are minor differences in the heights of some chromosomes. Chromosome 2 in humans is highlighted with a red circle because it corresponds to two separate chromosomes in chimpanzees, suggesting a fusion event. This feature is notable as it may explain the change in chromosome number between the two species. Each chromosome pair is labeled from 1 to 22, and X and Y for sex chromosomes. This description highlights the observed similarity and the notable difference regarding chromosome 2.

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Looking at the karyograms for both humans and chimpanzees, it was suggested that at some point chromosomes 12 and 13 of the great ape karyotype fused, creating what is now chromosome 2 in the human karyotype. On further investigation, there are several pieces of evidence supporting this hypothesis:

- The genes of chromosome 2 closely match those of the two suspected fusion chromosomes in chimpanzees.

- Telomeric DNA, repetitive sequences found at the ends of chromosomes where they help protect the ends of the chromosome from damage, were found at the suggested fusion region of chromosome 2.
- There is a second centromere region, the site where the cell's cytoskeleton attaches to the chromosome during cell division, but this one has mutated and does not function.

⚠ Practical skills

Inquiry 3: Concluding and evaluating — Evaluating

You should be able to evaluate the evidence for the hypothesis that chromosome 2 in humans arose from the fusion of chromosomes 12 and 13 in a shared ancestor.

🔗 Nature of Science

Aspect: Hypotheses

When investigating new ideas and trying to answer questions, scientists will come up with testable hypotheses. These are tentative or proposed answers to questions that can be tested and shown to be true or false.

Section Student... (0/0)   Print (/study/app/bio/sid-422-cid-755105/book/what-is-a-species-id-43227/print/)

In contrast, a non-testable statement is one that cannot be shown to be true or false through experimentation. For example, the statement 'dogs make better pets than cats' is non-testable as it is based on an opinion and there is no clear definition of what 'better' means in this context.

Assign

Interestingly, genome sequencing of samples of Neanderthal and Denisovan DNA extracted from fossil evidence shows that they also had 46 chromosomes like modern humans. This suggests that the fusion of chromosomes 12 and 13 occurred prior to the separation of our species and others from our common ancestor.

❖ Theory of Knowledge

How do we distinguish claims that are contestable from claims that are not?

In the natural sciences, hypotheses should allow testable predictions, for example the origin of human chromosome 2 from the fusion of two smaller chromosomes. However, even when certain results or outcomes are not contestable, the hypotheses they support may be.

The theory of evolution for example, is based on non-contestable observations and results including more recent genetic evidence. Yet the overall theory of evolution and its implications are still widely contested.

The following activity will give you an opportunity to explore and evaluate further.

Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:**
 - Research skills — Evaluating information sources for accuracy, bias, credibility and relevance
 - Thinking skills — Providing a reasoned argument to support conclusions
- **Time required to complete activity:** 15–20 minutes
- **Activity type:** Pair/group activity

With a partner, discuss the evidence presented for the fusion of two smaller chromosomes found in chimpanzee DNA into chromosome 2 in humans. Carry out an online search for any evidence that may conflict with this hypothesis, making sure to consider sources for accuracy, bias, credibility and relevance. You can use the TRAAP model to ensure this. Watch this video to learn more about the TRAAP model.

Evaluating Information Sources





Video 1. The TRAAP model.

Then, have a class discussion, sharing what you have found in your research and whether you believe there is sufficient evidence for the hypothesis.

5 section questions ▾

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Comparing genomes

A3.1.8: Unity and diversity of genomes within species A3.1.9: Diversity of eukaryote genomes A3.1.10: Comparison of genome sizes
A3.1.11: Uses of whole genome sequencing

☰ Learning outcomes

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

- Describe what a genome is and that members of a species share most of their genome.
- Describe the variation of genomes between species on the basis of size and base sequence.
- Extract genome size data from online databases for comparison.
- Describe the potential future uses of genome sequencing technologies.

We know that our closest living relatives are the great apes but just how closely are we related to them? What about other human species? Genetic comparisons show that all humans share on average 99.9% of their DNA with other humans. We also share about 98.8% of our DNA with chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*). We share an incredible amount of our DNA with the other great apes, giving us strong evidence of our close evolutionary relationships with them.





Unity and diversity of genomes within species

Overview

(/study/app/422-cid-755105/o)

A genome is all of the genetic information of an organism. Within most species the genome is very much the same, usually with only single-nucleotide polymorphisms (SNPs) to contribute to variation and diversity. An SNP occurs when a single nucleotide is replaced with another (**Figure 1**). Much of what makes each person genetically different to every other person is due to these SNPs. For more about DNA and the potential significance of changes in nucleotide sequence, see subtopic D1.3 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43250/).

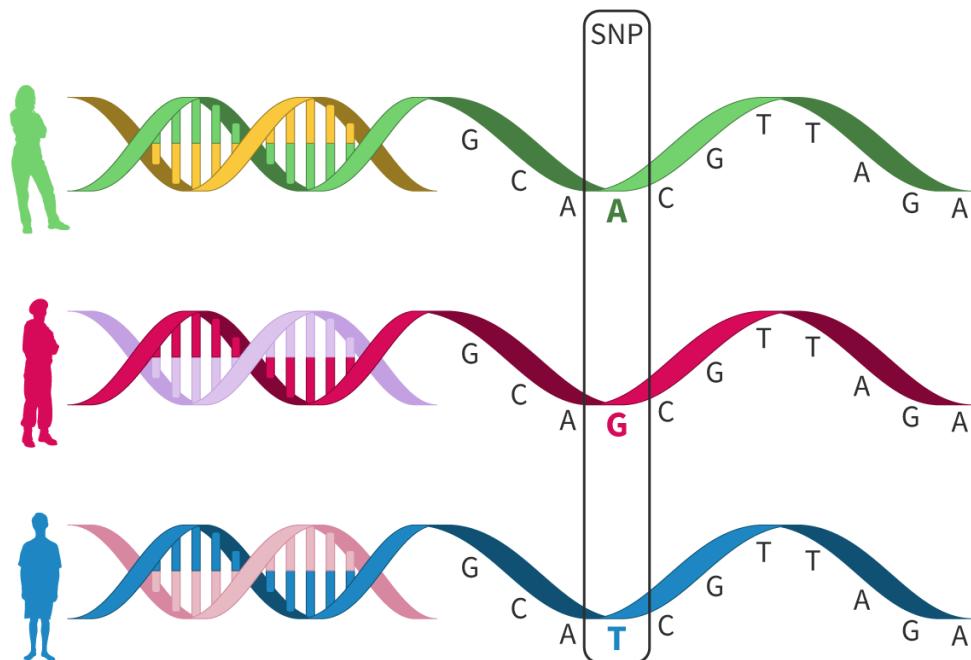


Figure 1. Single-nucleotide polymorphisms increase genetic diversity through the replacement of single nucleotides, often in non-coding regions of DNA.

More information for figure 1

The image displays three colored DNA strands, each with a labeled SNP (single-nucleotide polymorphism). The SNPs are highlighted as follows:

- **Top DNA Strand:** A green DNA strand with a SNP indicated by the letter "A" highlighted in green. This strand features alternating colors in the helix.
- **Middle DNA Strand:** A red DNA strand with a SNP labeled "G" highlighted in red. This strand also shows color variation, representing the genetic diversity.
- **Bottom DNA Strand:** A blue DNA strand with the SNP represented by the letter "T" highlighted in blue. Similar color alternation is presented.



Student view

Home
Overview
(/study/app/
422-
cid-
755105/o

To the left of each DNA strand is the silhouette of a person in the corresponding color to signify individual genetic differences due to SNPs. The image visually communicates the concept of genetic diversity resulting from single nucleotide changes, often occurring in non-coding regions of DNA.

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Diversity of eukaryote genomes

There can be very large differences in genomes between different species. There are two main ways in which genomes differ: size and base sequences. The size of a genome is the actual amount of genetic material, as determined by the number of base pairs (**Table 1**). For example, the blue whale (*Balaenoptera musculus*) has a genome size of 2374.87 million base pairs while the humpback whale has a genome size of 2265.79 million base pairs. The base sequences of a genome largely determines how the DNA is expressed and what genetic characteristics the species will have.

Table 1. Examples of species and genome size.

Species	Genome size (millions of base pairs)
Hippopotamus (<i>Hippopotamus amphibius</i>)	2424.26
Grizzly bear (<i>Ursus arctos horribilis</i>)	2328.64
English oak (<i>Quercus robur</i>)	789.35
Strawberry (<i>Fragaria × ananassa</i>) (× indicates a hybrid combining the characteristics of two different species)	805.68

Comparison of genome sizes

We can compare genome sizes using online databases, which store the genetic information for all species whose genomes have been sequenced to date. The activity below will give you an opportunity to try this.



Student view

 Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:** Thinking skills — Being curious about the natural world
- **Time required to complete activity:** 30 minutes
- **Activity type:** Individual activity

You are going to compare the genomes of several species as well as a virus. Below is a list of 10 of these that you should recognise.

1. Human - *Homo sapiens*
 2. White/button mushroom — *Agaricus bisporus*
 3. African elephant — *Loxodonta africana*
 4. Common octopus — *Octopus vulgaris*
 5. Goldfish — *Carassius auratus*
 6. Platypus — *Ornithorhynchus anatinus*
 7. Apple — *Malus domestica*
 8. Carrot — *Daucus carota*
 9. Honey bee — *Apis mellifera*
 10. Ebola virus
- Add 5–10 of your own local species to this list. Try to select a variety of different types.
 - Order them based on what you think their genome sizes will be. What factors might influence genome size? Organism size? Organism complexity?
 - Go to the National Library of Medicine's National Center for Biotechnology Information website  (<https://www.ncbi.nlm.nih.gov/genome/browse#!/overview/>) and search for these species. This can be done with either their common name or scientific name. Only those species that have had their genomes sequenced can be found here so you may have to change some of the local species you selected.
 - Record the genome size of each species and reorder them based on these.
 - Discuss with your class what you have discovered. Did size or complexity of organisms influence genome size? Which species had the largest genomes? Which had the smallest? Did anything surprise you?



 **Practical skills****Tool 2: Technology — Applying technology to collect data**

The ability to identify and extract data and information from online databases is an increasingly relevant skill as more and more biological data are stored and made accessible in this way.

Current and potential future uses of whole genome sequencing

Genome sequencing is a costly and slow process. The Human Genome Project that first successfully sequenced the human genome required the efforts of thousands of international researchers over 13 years (1990–2003) and cost approximately \$3 billion. Advances in technology, as well as the driving down of associated costs, are making genome sequencing more accessible and much easier to do.

 **International Mindedness**

International cooperation involving researchers from 20 universities and research centres in the United States, United Kingdom, France, Germany, Japan and China was required for completion of the Human Genome Project.

The ability to sequence the genomes of different species opens up a whole new world of investigation into the genetics and evolutionary relationships among all life on Earth. Provided we can extract enough DNA for the analysis, we can compare our genome with that of other great apes and that of any fossilised remains of other human species either already known or newly discovered.

Comparison of genomes has also allowed for revision of current classification systems to see whether any reorganisation is required. Take as an example, the red panda (*Ailurus fulgens*). Initially, it was thought to be closely related to the giant panda (*Ailuropoda melanoleuca*) and to raccoons and other similar mammals. Over time, comparisons were made suggesting

it could be included in either of these groups; however, recent genetic analysis has placed red pandas within the superfamily Musteloidea, which includes weasels, raccoons, skunks and the like.

Overview
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Figure 2. A red panda (*Ailurus fulgens*).

Credit: Freder, Getty Images (<https://www.gettyimages.co.uk/detail/photo/tired-red-panda-royalty-free-image/173899753>)

Current and proposed future genome sequencing technologies have created a range of new possibilities for medicine. In the near future, we may be able to create personalised medical treatments and interventions based on the sequencing of our own genomes or the genome of the microorganisms that live symbiotically within us. The potential here is vast and could lead to great advances in our health and wellbeing. However, we must also consider the potential negative outcomes of this technology. Could knowledge of your genome result in your ineligibility for medical insurance? Could such knowledge mean that employers consider you unsuitable for certain jobs?

Consider these issues and more in the following activity.

Activity

- **IB learner profile attribute:** Balanced
- **Approaches to learning:** Thinking skills — Evaluating and defending ethical positions

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Overview
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- **Time required to complete activity:** 15 minutes

- **Activity type:** Group activity

Beginning in pairs, discuss the potential advantages and disadvantages of genome sequencing technologies becoming cheaper and more widely available. Try to consider this from a variety of perspectives including medical, scientific, ethical, economical, etc. (7–8 minutes)

Next, join up with another pair and discuss your ideas and positions. (5–6 minutes)

Finally, come together as a class and share your thoughts and ideas. How do you think those who make decisions about the uses of such technologies should proceed?

5 section questions ▾

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Exceptions to the rule (HL)

A3.1.12: Difficulties in applying the biological species concept (HL) A3.1.13: Chromosome number (HL)

Higher level (HL)

Learning outcomes

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

- Describe exceptions to the biological species concept and why it is difficult to apply to certain species.
- State that chromosome number is a shared trait within a species.

Deciding when a species is a species is not straightforward. There is often debate within the scientific community when making this decision. There is some disagreement about the status of the different species of humans and whether they

should be separate. For example, there is evidence of interbreeding between modern humans and Neanderthals as some populations of humans have a small

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amount of Neanderthal DNA in their genomes. As we can see this residual DNA in certain populations of humans today, the offspring of these two species must have been fertile to then pass this DNA on.

Chromosome number as a shared trait

The biological species concept is based on the successful production of fertile offspring resulting from the sexual reproduction between two members of the same species. If individuals are of different species, any resulting offspring tend to be infertile hybrids. This is not however, without exception, as there have been recent reports of mules being fertile, for example, as mentioned in [section A3.1.1–4](#) ([\(/study/app/bio/sid-422-cid-755105/book/what-is-a-species-id-43227/\)](#)).

It is suspected that one of the reasons breeding between some closely related species does not usually result in a fertile offspring is due to a mismatch in chromosome number. When a donkey that has 62 chromosomes is bred with a horse that has 64, they each pass half to their offspring. This means that the offspring would end up with an uneven number of chromosomes, and this is thought to play a part in making it infertile (**Figure 1**).

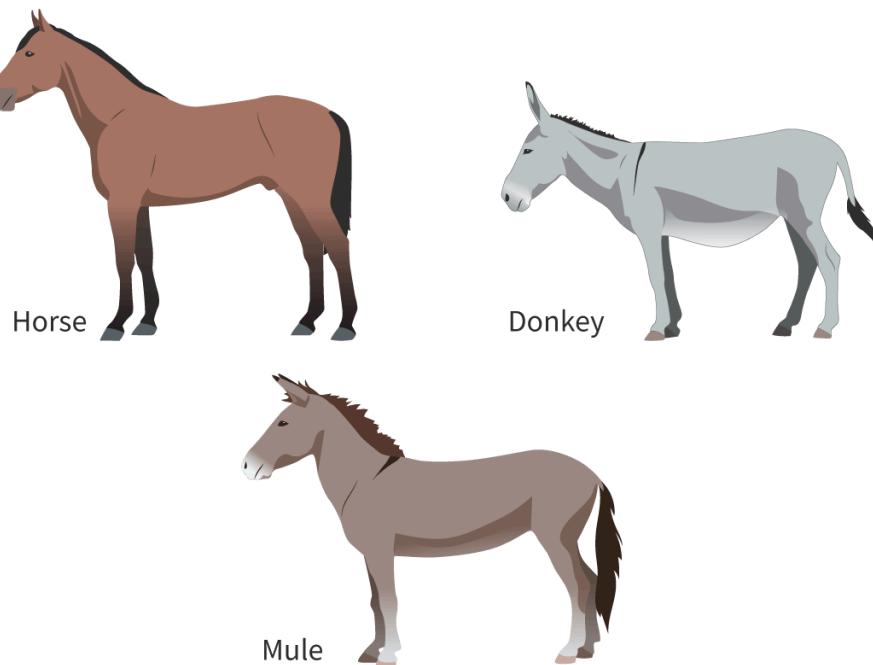


Figure 1. Horses (*Equus ferus caballus*) can be bred with donkeys (*Equus asinus*) to produce mules, which are hybrids and are infertile.



Asexually reproducing species and horizontal gene transfer

But what if a species reproduces exclusively asexually? Using this concept, those individuals would not be classified as a species as they are not capable of interbreeding and producing fertile offspring.

🔗 Making connections

The differences between asexual and sexual reproduction, as well as the advantages and disadvantages of each, are covered in greater detail in [subtopic D3.1 \(/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43252/\)](#).

Prokaryotes ([section A2.2.7 \(/study/app/bio/sid-422-cid-755105/book/processes-of-life-in-unicellular-organisms-id-44688/\)](#)) reproduce asexually in the process of binary fission. One bacterial cell grows and eventually splits into two identical cells. How can we classify bacteria as species if the biological species concept cannot be applied to these and other asexually reproducing organisms? Another example, the genus *Hydra*, a group of freshwater species related to jellyfish, anemones and coral, is shown in **Figure 2**. *Hydra* reproduce asexually through a process known as budding, where an offspring, genetically identical to the parent, is grown on the parent organism and buds off once large enough.





Overview
(/study/app/
422-
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Figure 2. The genus *Hydra* is a group of organisms that reproduce asexually by forming buds that are small clones of themselves.

Credit: Dr Paul Cook, Getty Images (<https://www.gettyimages.co.uk/detail/photo/hydra-viridis-royalty-free-image/523563548>)

Prokaryotes are also capable of horizontal gene transfer. This is a phenomenon where genetic material is exchanged between individuals rather than passed on from one generation to the next. This has led to a huge amount of genetic variation among prokaryotes that otherwise may have little due to their method of asexual reproduction. This further confuses our understanding of how species are defined and represents another major exception to the biological species concept.

Watch **Video 1** for a further exploration of species and the exceptions to the biological species concept.



Student
view

What Makes a Species a Species?



Video 1. Exceptions to the biological species concept.

In this activity you will have a group debate on horizontal gene transfer in a species of bacteria.

Activity

- **IB learner profile attribute:**
 - Communicator
 - Open-minded
 - Thinker
- **Approaches to learning:**
 - Communication skills — Practising active listening skills
 - Social skills — Actively seeking and considering the perspective of others. Assigning and accepting specific roles during group activities
- **Time required to complete activity:** 20—30 minutes
- **Activity type:** Group activity

Split your class into groups of 4—8 people, splitting each into two small teams of 2—4 people. Each small group will spend 10—15 minutes researching and preparing to debate the opposing sides of the following statement:

- As *Escherichia coli*, a common species of bacteria, has acquired many genes from other bacteria via horizontal gene transfer, and reproduces asexually, it should not be considered a species.

In the first round, each group will prepare an opening statement in support of their position, laying out evidence and reasoning. The second round will involve direct questioning and rebuttal of any points made in the first round. The third and final round will be closing statements, summarising positions and arguments. All members of each group should have an assigned role and an opportunity to participate actively in the debate.

5 section questions ▾

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Identifying species (HL)

A3.1.14: Dichotomous keys (HL) A3.1.15: Barcodes, environmental DNA and biodiversity (HL)

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 Feedback



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Higher level (HL)

Learning outcomes

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

- Identify species using dichotomous keys as well as design your own.
- Explain the process and uses for DNA barcoding.

Identifying species

We are used to being able to identify species based on what they look like. We are exposed from a young age to other species and quickly learn to recognise those around us. But what do we do when we need to identify species we have not seen before? What if we want to know the identity of organisms we have only parts of, or have left only traces of themselves such as the other human species and the fossils we have discovered?

Section

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Overview
(/study/app/
422-
cid-
755105/o

Engagement with local plant or animal species to develop a dichotomous key

A dichotomous key is a tool used in fieldwork to aid in the identification of organisms. It is composed of a series of questions or statements based on the physical characteristics of the organisms concerned. Each question has only two possible answers – usually stating whether a feature or characteristic is present in the organism or not.

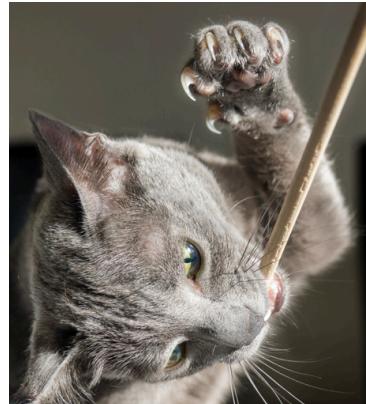
⚠ Practical skills

Tool 1: Experimental techniques — Applying techniques

Tool 3: Mathematics — Graphing

The ability to identify and classify local organisms and design your own dichotomous key for this purpose is a key skill. You will practise this in the activity below.

Here is a simple dichotomous key to identify six common farm animals (**Figure 1**).



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Overview
(/study/app/
422-
cid-
755105/o

Figure 1. Six Common Farm Animals.

More information for figure 1

A collage displays six farm animal photos in three columns based on foot adaptations: hooves, claws, and webbed or non-webbed toes.

Column 1: Hooves

Top: A horse standing in a paddock with a single hoof on each leg.

Bottom: A photograph of a cow standing on grassy land, displaying four legs. Each leg has a two-part hoof.

Column 2: Claws

Top: A cat biting a stick and raising its claw.

Bottom: A dog raising a paw, showing its claws.

Column 3: Webbed or non-webbed toes

Top: A chicken with two legs, with each foot having three forward-pointing toes and one backward-pointing toe.

Bottom: A duck with webbed toes.

This interactive collage helps users identify and classify common farm animals based on their foot adaptations.

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1.

- (a) Animal has two legs
- (b) Animal has four legs

[Go to 2](#)
[Go to 3](#)

2.

- (a) Animal has webbed feet
- (b) Animal does not have webbed feet

Duck
Chicken

3.

- (a) Animal has hooves
- (b) Animal has paws

Student
view

[Go to 4](#)[Go to 5](#)

Home
Overview
(/study/app/
422-
cid-
755105/o
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4.

- (a) Hooves are divided into two parts
(b) Hooves are in one piece

Cow

Horse

5.

- (a) Animal has retractable claws
(b) Animal has claws that do not retract

Cat

Dog

In the field, a dichotomous key of the local species being investigated will allow you to more easily identify any specimens collected or observed.

Now develop your own dichotomous key in this activity.

Activity

- **IB learner profile attribute:** Caring
- **Approaches to learning:**
 - Communication skills — Using terminology, symbols and communication conventions consistently and correctly, Using digital media for communicating information
 - Thinking skills — Designing procedures and models
- **Time required to complete activity:** 30 minutes
- **Activity type:** Pair activity

In pairs, and with your teacher's assistance, collect samples/photos of 8–10 local plant or animal species. This might involve the collection of leaves from each plant or use of a mobile device to take a photo of leaves and flowers of each species. If animals are chosen, an online search for

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Home
Overview
(/study/app/
422-
cid-
755105/o

high-quality photos of each species could be used. The important part of the specimen collection is to make sure the physical characteristics of each are clearly identifiable.

Design a dichotomous key to allow someone to identify these species. One possible approach to this is to begin by splitting the organisms into two groups based on a characteristic. The size of the groups does not matter. For example, if looking at local tree species, your first split might be between deciduous trees with broad leaves and coniferous trees with needles. Continue to split each group into two until you are able to split into separate species. These groupings should form the basis of your dichotomous key, composed of paired questions/statements that, if followed, will allow each species to be identified based on their distinguishing physical characteristics.

Share your keys with other pairs in the class. There are many ways to design a dichotomous key for any group of organisms.

Identification of species from environmental DNA using barcodes

Recently, developments in gene technologies have allowed for new techniques to be created to quickly and easily identify species and measure biodiversity. One of these methods is DNA barcoding where an unknown specimen or environmental sample, often water or soil, is collected and DNA is extracted (**Figure 2**). From this sample certain specific DNA sequences are identified, creating a unique ‘barcode’ for that specimen. The sequences used have been selected because they show much more variation between species than they do within species. The barcode of the specimen can then be compared with a catalogue of barcodes that allows for identification of the species.

Home
Overview
(/study/app/
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Home
Overview
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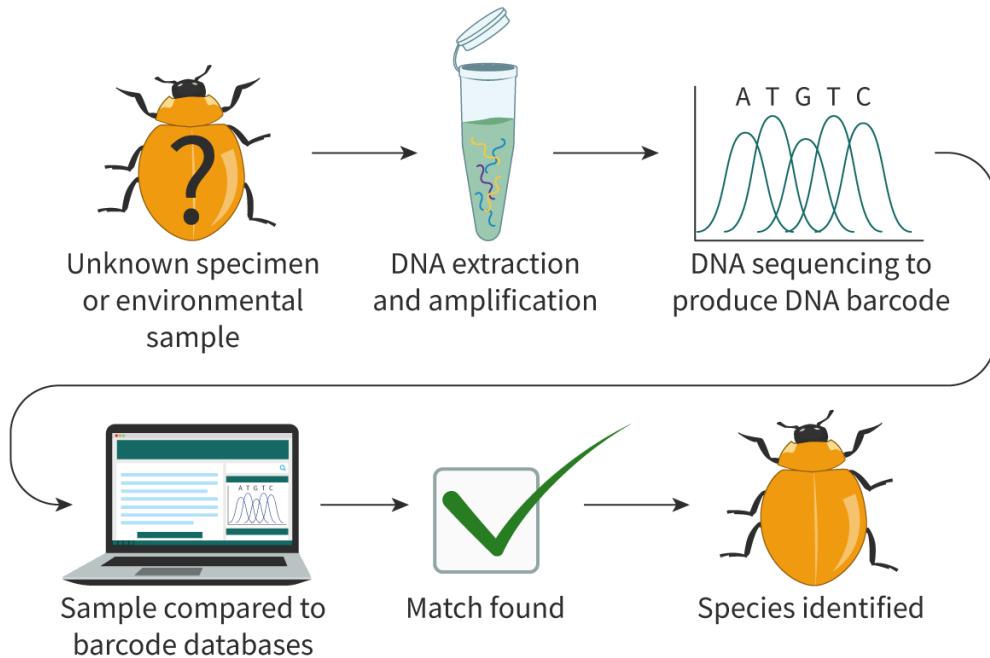


Figure 2. A simplified summary of the DNA barcoding process.

More information for figure 2

The diagram illustrates the DNA barcoding process in a series of sequential steps. It begins with an icon of a beetle labeled "Unknown specimen or environmental sample". An arrow points to a test tube labeled "DNA extraction and amplification", indicating the next step. This is followed by a graphic depicting DNA sequences, labeled "DNA sequencing to produce DNA barcode". The process continues as the sample is compared to barcode databases, depicted by a laptop icon. Then a checkmark icon signifies "Match found". Finally, it concludes with a beetle labeled "Species identified", completing the identification process through DNA barcoding.

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Using this method, environmental assessments which are concerned with particular species are able to determine whether that species is present without having to observe the organism itself. In the case of elusive, endangered species, this is quite significant. DNA barcoding can also assist in the measuring of biodiversity, a key environmental indicator of ecosystem health and sustainability. This technique has numerous other potential uses, including testing food for microorganism contamination, identifying species in different stages of their life cycle, identifying species from partial specimens and even analysing stomach contents to see what organisms have been consumed. **Video 1** describes the process of DNA barcoding in more detail.



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Home
Overview
(/study/app/
422-
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DNA Barcoding



Video 1. DNA barcoding and how it is carried out.

5 section questions ▾

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Summary and key terms

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- All living organisms show variation. The amount of variation between organisms allows the grouping or classification of organisms into species. How this is done varies depending on the concept used to decide on the groupings. The morphological species concept uses physical characteristics to group organisms into species. Organisms that look most alike will be of the same species. The biological species concept bases the decision on the ability to breed and produce fertile offspring.
- Chromosomes are strands of DNA and the number a species has is a characteristic of that species. All members of the species will have that number. Humans have 46, while chimpanzees have 48, for example. Images of chromosomes called karyograms pair up the chromosomes from a cell based on banding patterns, size and centromere location.
- Based on the evidence found, the fusion of two smaller chromosomes found in the DNA of chimpanzees and other great apes has formed human chromosome 2. It contains most of the same genes and has other signs of previously being two separate chromosomes.
- A genome is all of the genetic material of an organism. Genome sequencing allows us to compare the genomes of individuals and species. The genomes of individuals within a

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Overview
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422-
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755105/o

species tend to be more similar than the genomes of individuals of different species.

Genome sizes can be compared using online databases.

- Genome sequencing is becoming cheaper and faster, which may lead to better understanding of the evolutionary relationships between species as well as the possibilities of more personalised medical care based on your specific genome.
-

Higher level (HL)

- The biological species concept has many exceptions and cases where it cannot be applied successfully. This includes species that only reproduce asexually as well as species that can transfer genetic information horizontally between individuals outside of reproductive processes.
- Dichotomous keys are tools that can be created and used to aid in the identification of species in the field, from specimens or from photos. They are made of a series of questions with only two possible answers that when followed and answered allow for the correct identification of each species.
- DNA barcoding is a technique where environmental samples, such as water or soil, are analysed for DNA. Specific DNA markers are used to identify the species present in the environment. This is useful for determining and monitoring the biodiversity of an area, as well as identifying the presence of threatened or endangered species when carrying out environmental assessments.



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Overview
(/study/app/
422-
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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 difference shown between organisms is known as
2. According to the species concept organisms are grouped and assigned to a species based upon shared physical characteristics.
3. The species concept determines species based upon the ability to successfully breed and produce fertile offspring.
4. Species are named using nomenclature, naming each species using both its genus and species names.
5. Strands of DNA are known as and these can be arranged in a in order to determine certain characteristics of an organism.
6. All of the genetic information of an organism is known as its . Its size is different for different species.
7. [HL] The transfer of genetic material between individuals that does not involve reproduction is known as gene transfer.
8. [HL] are tools used in the identification of species using a series of paired questions.
9. [HL] Environmental samples can be analysed for DNA to identify the biodiversity of an area or the presence of an endangered species using

biological Dichotomous keys binomial variation horizontal
DNA barcoding chromosomes genome morphological
karyotype

Check

Interactive 1. Diversity of Organisms: Key Concepts and Terminology.



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A3. Unity and diversity: Organisms / A3.1 Diversity of organisms



Checklist

Overview

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422-

cid-

755105/o

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What you should know

After studying this subtopic you should be able to:

- Identify variation as a defining characteristic of life.
- State that a species is a group of organisms with shared morphological traits.
- Name species using binomial nomenclature.
- Explain the biological species concept.
- Describe speciation and the difficulties in distinguishing between populations and species.
- Outline that there is diversity of chromosome number between species.
- Explain karyotyping and be able to classify chromosomes in a karyogram by banding patterns, length and centromere position.
- Describe what a genome is and that members of a species share most of their genome.
- Describe the variation of genomes between species on the basis of size and base sequence.
- Extract genome size data from online databases for comparison.
- Describe the potential future uses of genome sequencing technologies.

Higher level (HL)

- Describe exceptions to the biological species concept and why it is difficult to apply to certain species.
- State that chromosome number is a shared trait within a species.
- Identify species using dichotomous keys as well as design their own.
- Explain the process and uses for DNA barcoding.

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Investigation



Student
view

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:**
 - Thinking skills – Being curious about the natural world, Asking questions and framing hypotheses based upon sensible scientific rationale
 - Research skills – Evaluating information sources for accuracy, bias, credibility and relevance, Using search engines and libraries effectively
- **Time required to complete activity:** 1.5 hours
- **Activity type:** Individual activity

So what is a species? In this subtopic, we have explored a variety of concepts and types of evidence relevant to this question and determined that the answer is not straightforward. We have also begun to examine our relationships with extinct humans such as the *Homo neanderthalensis*, the Denisovans and *Homo floresiensis*.

Your task

- Based on what you have learned in this subtopic, create your own definition of a species that could potentially be used in most if not all situations.
- Do some research into 3–4 other groups of archaic humans. Collect information about fossil evidence, skull shape, genetic information, proposed theories for why they became extinct and anything else that might be useful.
- Write a conclusion to the following question using your own definition of a species, with the evidence you collected as support: *Were other groups of archaic humans unique species separate from modern humans?*

A3. Unity and diversity: Organisms / A3.1 Diversity of organisms

Reflection



Overview
(/study/app/
422-
cid-
755105/o

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.



Reflection

Now that you've completed this subtopic, let's come back to the guiding question introduced in [The big picture \(/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43226/\)](#).

- What is a species?
- What patterns are seen in the diversity of genomes within and between species?

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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Overview
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Rate subtopic A3.1 Diversity of organisms

Help us improve the content and user experience.



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