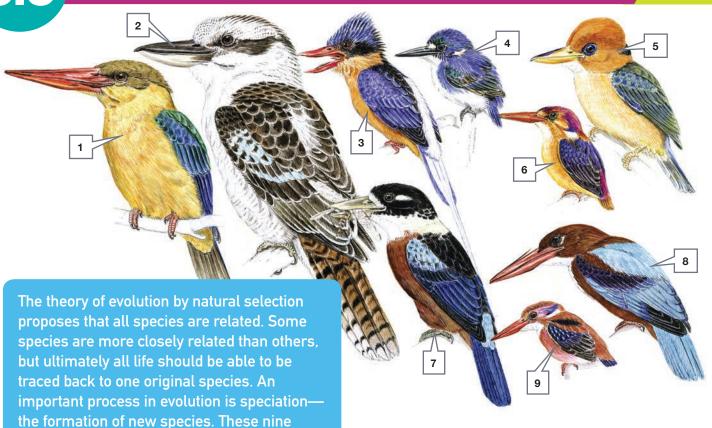
Speciation and evolution



Evolution

ancestral kingfisher.

Charles Darwin proposed that natural selection could result in the formation of new species. In his book On the Origin of Species, he called this 'modification by descent' rather than evolution. The term evolution was applied to his work by other scientists.

species from the kingfisher family show that

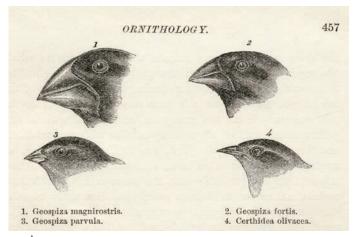
some are more closely related than others.

All these species descended from a single

The theory of evolution states that similar species must be closely related to each other. For example, the kingfishers labelled 6 and 9 above are in the same genus Ceyx and so they are closely related to each other. Kingfisher 4 is from another genus (*Alcedo*) but is classified in the same sub-family as kingfishers 6 and 9. So kingfisher 4 is related to kingfishers 6 and 9 too. These three species are commonly called river kingfishers and their similarities suggest that they had a common ancestor at some time in the past. The other six species of kingfishers are more distantly related to the river kingfishers. This suggests that these six species separated into a different breeding line at a different time.

The earliest hints of Darwin's theory can be found in his first book The Voyage of the Beagle, written in 1845. This book

describes his epic journey around the world between 1831 and 1836. On this voyage, Darwin studied many different species in many different environments, including the Andes Mountains, the coast of Australia and the Galapagos Islands. It was on these islands that he studied differences in the beak shapes of finches. Some of his results are shown in Figure 3.3.1. Each of the fifteen finch species seemed to have come from a common ancestor but had beaks that were different. It was as if the different beaks had been selected for the different food sources (such as seeds, honey and insects) found on the different islands.



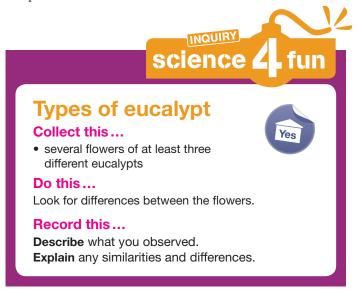


This illustration from Darwin's book The Voyage of the Beagle shows the finch beaks that started him thinking about species being able to change.

What is a species?

It is impossible to determine whether two organisms are the same species from their anatomy. In the past, the test for a **species** was to see if two organisms could interbreed to produce fertile offspring under natural conditions. They were only considered to be the same species if they could produce fertile offspring. An example is the mule. A mule is produced by crossing a horse and a donkey. The mule produced is always sterile and so the horse and donkey are different species.

This interbreeding test can still be used to classify living organisms at the species level. However, these days biologists study DNA and also identify the similarities in the amino acid arrangement in the proteins they make. Since proteins are made by genes, identical proteins must mean identical genes (or at least genes that are very similar). Fossil DNA and proteins are also being analysed to help define relationships. There are now laboratories that specialise in analysing DNA samples from ancient bones.



Speciation

Speciation is the process by which one species splits into two or more separate species. Speciation is responsible for the formation of any new species that appear in the fossil record.

Speciation has resulted in the high level of biodiversity on Earth. **Biodiversity** refers to the number and range of different species that exist, either on the whole Earth or in any of Earth's ecosystems.

The process of speciation occurs in three basic steps:

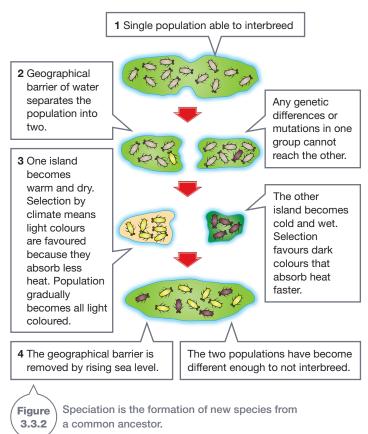
- variation
- · isolation
- selection.

Step 1. Variation

There must be variation in the population or speciation cannot occur. This is because natural selection is involved, and selection can only act on variation that is already present in the population.

Step 2. Isolation

The formation of new species requires **isolation**. This means that different groups of the population are prevented by some mechanism from interbreeding. Isolation prevents gene flow throughout the population, stopping any differences in one population from reaching the other population. For example, any new genes that arise by mutation in one isolated population cannot spread to the other isolated population. An example of one way in which speciation can occur is shown in Figure 3.3.2.



Isolation into separate populations occurs in several ways, for example by a geographical or climatic barrier. Geographical barriers are oceans, rivers, mountain ranges and gorges. Climatic barriers include rainfall, temperature, salinity, ocean currents and sunlight.

Step 3. Selection

Once isolated by barriers, natural selection affects the genotype and causes changes that prevent the groups breeding even if they came back together again at some time in the future. There are many possible changes. A few examples are:

- courtship behaviour—animals may develop different breeding songs, displays and rituals
- breeding seasons—animals may breed at a different time of year
- sterility— animals may breed but the offspring are sterile (like mules)
- chemical barriers—sperm may be killed by the chemistry of the female.

Evidence for evolution

The theory of evolution by natural selection is supported by a great deal of evidence.

Fossils

Early fossils are of fairly simple organisms and later ones are increasingly complex. This makes sense in terms of genetics because new alleles and genes develop from existing genes by mutation. It seems unlikely that complex organisms (with many different genes) would develop first and become simpler (with fewer genes).

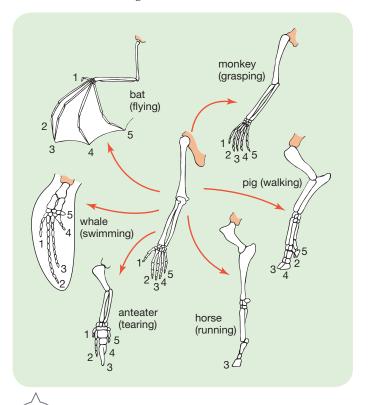
The fossil record also shows that there is an increasing number of species that have lived on Earth. Many of these species became extinct along the way, such as the dinosaurs, the diprotodons and marsupial lions. The increasing number of species (increased biodiversity) supports the theory of evolution because that is what you would expect if species continually split into two or more other species over time.

Fossils showing transitional forms have also been found. For example, there are transitional forms that show that a group of small dinosaurs had feathers. Archaeopteryx and Anchiornis (Figure 3.3.3) are examples. Their fossils suggest that one group was in the process of changing from dinosaurs to birds. Transitional forms are hard to classify because they have features of two different groups. In the case of feathered dinosaurs, they have the features of both reptiles (class Reptilia) and birds (class Aves).

Lobe-finned fish are another transitional fossil group that are part fish and part amphibian. They suggest a way in which life moved from the sea and onto the land.

Comparative anatomy

Comparative anatomy compares the structures of organisms of both living species and fossils. Homologous structures fit into this category. Homologous structures such as pentadactyl limbs provide strong evidence for evolution from a single vertebrate ancestor (Figure 3.3.4).



The pentadactyl limb of vertebrates is a homologous **Figure** 3.3.4 structure that provides evidence for evolution.



DNA and protein structure

All living cells have the same basic DNA structure and use the same genetic code. Proteins produced from genes all come from the same set of amino acids.

Comparing sections of DNA in different species has shown that even organisms that seem to be very different, such as bacteria and humans, have large sections of identical DNA. For example, one of our genes for cell energy release, makes the enzyme cytochrome c. This gene has over 50% of its code identical to the gene in some fungi, and 70% identical to the gene in moths.

Organisms that seem to be fairly similar, on the basis of comparative anatomy, show more genes in common than organisms that are less alike. For example, 96% of the genes in humans and chimpanzees are identical. This is strong evidence supporting evolution: you would expect that two species and their common ancestor would have much of their DNA the same. Fossil DNA can also be compared with that of living species.

Protein amino acid sequences can also be used to compare how closely related species are. This is mostly done with living species, but proteins from fossils can be analysed as well.

Proteins are made out of amino acids like beads on a chain. The sequence of these amino acids is controlled by genes. Cytochrome c is a protein found in all living organisms. Comparing how many of the amino acids are in the same positions on the protein chain can provide some idea of how closely related two species are. For example, humans and monkeys only have one position on the chain where they differ in the amino acid. Humans and moths have 31 positions where they are different. However, studying only one protein like this is unlikely to give a definite answer about how closely two species are related. Many more proteins need to be studied to make such judgements. You can see some of these comparisons in Figure 3.3.5 and Table 3.3.1.

Table 3.3.1 Number of positions with differences in the amino acid present in cytochrome c protein

	Human	Monkey	Kangaroo	Chicken	Turtle	Tuna	Moth
Human	0	1	10	13	15	21	31
Monkey	1	0	11	12	14	21	30
Kangaroo	10	11	0	12	11	18	28
Chicken	13	12	12	0	8	17	28
Turtle	15	14	11	8	0	18	28
Tuna	21	21	18	17	18	0	32
Moth	31	30	28	28	28	32	0

Distribution of current species

Scientists call a map of all the places where a species occurs the **distribution** of the species. When studying distributions, it is very obvious that many unique species occur on isolated islands. With evolution, you would expect to find unusual species on particular islands because isolation is necessary before speciation can occur.

The surface of the Earth is made of tectonic plates. These tectonic plates slowly and continually move. On these tectonic plates are the continents, such as Australia, Africa and Antarctica. As the tectonic plates move, so do the continents. One of the pieces of evidence that convinced scientists that continents moved was the distribution of fossils of particular species.

Moving continents helps explain why Australia has most of the world's marsupial mammals and the only two monotremes. These are the platypus and echidna (Figure 3.3.6). Evidence from plate tectonics shows Australia has been isolated from all other landmasses from about 40 million years ago, providing plenty of time for the evolution of these major groups of mammals.

Cytochrome c comparisons (104 amino acids)

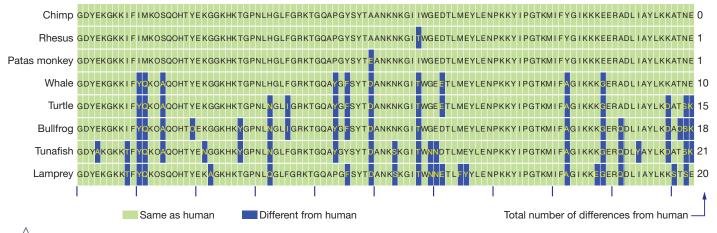


Figure 3.3.5

The amino acid sequences in cytochrome c are shown here for eight different vertebrates. The letters stand for different amino acids.



Figure 3.3.6

The platypus and echidna are the only living monotremes. They evolved in Australia at about the time when it separated from Antarctica and became an isolated continent.

Embryology

Embryology is the study of the development, structure, and function of embryos (Figure 3.3.7). Comparisons of vertebrate embryos show striking similarities in the early stages of their development. For example, there is a time during the embryonic development of fish, lizards and humans when there are branchial arches. These are arch-shaped structures in the throat region. Many other similar structures are also present, such as a 'tail'.

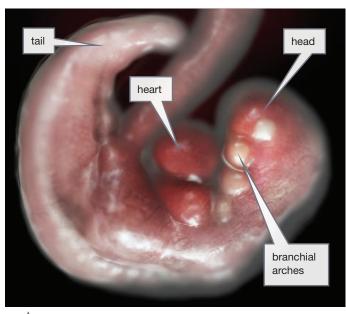


Figure 3.3.7

Human embryo at 4 weeks, showing the branchial arches typical of vertebrate embryos

In humans, the parathyroid glands (endocrine glands in your neck) develop from the branchial arches. Two of the arches grow into the bones in your middle ear. In reptiles, their lower jaws grow from one of the arches. In fish, a gene called

Gcm-2 controls the development of the branchial arches into gills. If the gene mutates (or if scientists prevent it working) in embryonic development, the gills fail to develop. In chick embryos, the Gcm-2 gene turns two of the arches into the parathyroid gland. If scientists prevent the gene from working, the parathyroid gland fails to develop. So vertebrate embryos have structures that appear to be homologous on the basis of anatomy, and studying genes shows the same gene has produced different effects in two different species. Somehow the Gcm-2 gene has changed in its effect on the branchial arches from one species to another.

So the development of mammals, reptiles, birds and fish are linked to the branchial arteries. Biologists long ago proposed that fish evolved into amphibians, which evolved into reptiles, which evolved into birds. Evidence from studying embryos including branchial arches supports this idea.

The evidence in brief

In summary, the evidence for evolution is:

- fossils—there is increasing complexity in species, changes over geological time in a lineage and transitional forms
- comparative anatomy—homologous structures can be identified at many different levels of classification, such as the limb bones in classes of vertebrates
- DNA—species that have similar anatomy have been shown to have many common genes
- protein structure—closely related species have more similarities in amino acid sequences in particular proteins
- distribution of species—isolated islands have unusually high proportions of unique species; continents now separated by oceans and containing identical fossil species were once connected in the past
- embryology—embryos with similar anatomy share some of the same genes for development of the embryo. These same genes can exert different effects in different species.

SCIENCE AS A HUMAN ENDEAVOUR

Nature and development of science

DNA profiling and evolution

Figure 3.3.8 Part of an autoradiogram

The genome of a species is the entire genetic information of that species. It is only in the last decade or so that scientists have been able to determine the genome of a species.

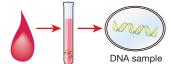
Genomics is the study of the genome structure and function. Comparing the genomes of different species has given biologists a better understanding of evolution and the classification of organisms.

Genomics uses many techniques, one of which is DNA profiling, also known as DNA fingerprinting. The process of DNA fingerprinting is very complex, but a simplified version is shown in Figure 3.3.9.

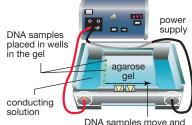
In evolutionary studies, DNA profiling enables scientists to obtain a DNA fingerprint showing fragments of DNA that have been cut at the same place. Then the DNA fingerprints of different species are compared. From the results, common sequences of DNA including genes can be isolated and compared and evolutionary relationships between species can be tested. These evolutionary studies are in their early stages, but genomics has already shown the following.

- Different species possess similar genes associated with the same traits.
- Similar species must be closely related to each other because they share many similar genes.
- Genes are not the whole story in inheritance; other factors such as gene regulators (DNA sections that control genes) are also important and these affect evolution.
- Distantly related species often share stretches of DNA that do not appear to code for any protein.
 The function of these DNA sections is currently being studied.
- DNA is not the only evidence that is needed to decide evolutionary relationships; studies of anatomy, behaviour and development are also helpful.

1 The process begins with a blood or cell sample from which the DNA is extracted.



2 The DNA is cut into fragments using a restriction enzyme. The fragments are then separated into bands using a technique called electrophoresis.

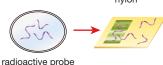


DNA samples move and separate in electric current

3 The DNA band pattern is transferred to a nylon membrane.



4 A radioactive DNA probe is introduced. The DNA probe binds to specific DNA sequences on the nylon membrane.



5 The excess probe material is washed away, leaving the unique DNA band pattern.



6 The radioactive DNA pattern is transferred to X-ray film. When developed, the resultant visible pattern is the DNA fingerprint known as an autoradiogram (Figure 3.3.8).



Figure 3.3.9

The steps involved in DNA fingerprinting

3.3 Unit review

Remembering

- 1 Name the term now used for the process that Charles Darwin called 'modification by descent'.
- **2** List three ways of determining if two organisms are the same species.
- **3 List** the three main steps in the process of speciation.
- 4 List four reasons why two very similar animals might not be able to mate.
- Specify homologous structures in fish and bird embryos that have been shown to be affected by the gene called Gcm-2.

Understanding

- **6** Explain three methods used to determine if two organisms are in the same species or not.
- **Explain** what is meant by genetic isolation.
- 8 It has long been known that horses and donkeys are different species. Explain the evidence that shows this.
- **9 Discuss** how fossils support the theory of evolution.
- **10** Explain why a barrier is necessary before speciation can
- 11 Explain how the Gcm-2 gene observed in fish and bird embryos supports the theory that birds are related to fish.

Applying

- 12 Use the model of speciation to explain why isolated islands often have a high proportion of species not found elsewhere, even on neighbouring islands.
- 13 Some early lobe-finned fish are difficult to classify into fish or amphibians, because they have features of both. **Demonstrate** how such difficulties support the theory of evolution,
- **14** Use the concept of speciation to demonstrate how biodiversity developed on Earth.

Analysing

- **15 Distinguish** between:
 - evolution and natural selection
 - speciation and natural selection
 - evolution and speciation.

Evaluating

16 There is no difference in the sequence of amino acids on the cytochrome c molecules of humans and apes. However, monkeys and humans have one difference, while humans and kangaroos have ten differences.

- Based on this, identify the more recent common ancestor of humans: apes, monkeys or kangaroos.
- Justify your answer.
- 17 Scientists studying vertebrates in the 1800s and 1900s proposed that they had a common fish ancestor. They proposed that lobe-finned fish evolved into amphibians, which evolved into reptiles, while mammals and birds both evolved from separate branches of the reptiles. Refer to Table 3.3.1 on page 88 and evaluate whether this more recent evidence supports the proposal of the early biologists.

Creating

- **18** Construct a series of steps by which two different species of mice could develop from one species after the formation of a deep canyon.
- 19 Construct a diagram showing a series of steps by which two different species of frogs could develop after the formation of the desert of the Nullarbor Plain. Both species came from one species that was originally spread from Western Australia to Victoria (Figure 3.3.10).



Inquiring

- 1 Research the story of the giant Galapagos tortoise and what it tells us about evolution.
- 2 Research how flowering plants evolved at a time when Gondwana was breaking up and how this affected which plant families ended up in different countries.

of a frog species (in blue) into two groups.

3 Research the FOXP2 gene in mammals (including early humans) and what it can tell scientists about evolutionary relationships.

3.3

Practical activities

1 Family relationships

Purpose

To compare the structure of flowers from different genera in the family Myrtaceae.

Materials

- specimens from genera in the family key shown right
- · hand lens or stereomicroscope
- Stanley trimmer for cutting through fruits
- forceps
- · Petri dish
- books with illustrations or photos of members of the Myrtaceae family
- · access to the internet

SAFETY

Be careful handling blades. Wash your hands after handling plant material.

Procedure

- 1 Your task is to use the key shown right to identify the name of the genus to which each of the plants belongs. This will involve cutting into some flowers and fruits. Your teacher will show you how to do this, or will display cut sections for you to observe. You will be using the hand lens or microscope to observe flower parts. You will need to know the names of the parts of a flower to do this activity.
- 2 Collect one specimen from the selection at the front of the room. Note down its number. You must write down each of the choices you make for the specimen as you proceed through the key. Finally, write down the name of the genus for the sample.
- 3 Use the books or internet to see if your specimen looks like the images shown for that genus. If you appear to be incorrect, go back over your choices to see if you made an error.
- 4 Repeat steps 2 and 3 for as many other specimens as you can in the time you have.

Discussion

- **1** Explain what is meant by a family, genus and species.
- **2 Propose** some characteristics of flower structure that members of this family share.
- **3 Assess** whether any of these genera seem to have more in common with some genera than with others.

- **4 Explain** why classifying a plant into this family on the basis of its flower structure also suggests that it is related to the other members of this group through inheritance.
- **5 Explain** why the genera in this family would have some genes the same.

Key to some genera in family Myrtaceae						
1a	Ovary with between 3 and 10 sections.	Go to 2.				
1b	Ovary with 1 section.	Go to 8.				
2a	Stamens separate.	Go to 3.				
2b	Stamens in 3–5 bundles, joined for part of length of stamen.	Go to 7.				
3a	Flowers with no stalk. Stamens no longer than petals.	Go to 4.				
3b	Stamens longer than petals, in two rows.	Go to 5.				
3c	Stamens longer than petals, in single row	v. Kunzea				
4a	Leaves in pairs and opposite each other.	Baeckea				
4b	Leaves alternating. Le	ptospermum				
5a	Flowers with no stalk, in a cylindrical column. Fruit woody. Shrubs.	Callistemon				
5b	Trees with flowers at ends of branches and each with a stalk.	Go to 6.				
6a	Flower with petals. Trees.	Angophora				
6b	Flower bud covered by a cap which falls off when flower opens. Trees.	Eucalyptus				
7a	Flowers with no stalk and in cylindrical heads or ball shaped heads. Stamens in five bundles joined at the base for less than ¼ length of the stamen.	Melaleuca				
7b	Flowers with stalks growing from leaf base. Trees.	Tristania				
7c	Stamens joined over ¾ length. 3–4 stamens per bundle. Small shrubs.	Beaufortia				
8a	Flowers waxy and in open groups of 2–4 each with stalks at tip of branches. Shrubs less than 2 m. Ch	amelaucium				
8b	Flowers in terminal heads often covered by petal-like coloured bracts.	Darwinia				

Human evolution



The name of our species, Homo sapiens, means 'wise man'. According to the fossils so far discovered, we have been around for about 200 000 years. Fossils indicate that other species of human-like animals have existed too. Biologists and palaeontologists have a good idea about how humans came to be here, but more fossil evidence is needed to trace our origins.

Figure 3.4.1

A lemur shows the typical primate features of forwardfacing eyes, nails and grasping hands.

Primates

Humans are classified into the class Mammalia, order Primates, family Hominidae, genus *Homo*. **Primates** include the lemurs, tarsiers, monkeys, apes, gibbons and humans. There is no one specific feature that puts an animal into this order. However, most of them have 'grasping' hands, nails rather than claws and forward-facing eyes. You can see a typical primate in Figure 3.4.1.



Mammals

Do this...

- If you have a cat or dog at home, carefully observe its face and describe where its eyes are.
- Observe the paws and describe where the toes are and what is on the toes.
- Compare these with your own features.

Record this...

Describe what you observed.

Explain why these features might be similar or different.

The living animals most like humans are gorillas and chimpanzees, which live only in Africa. On the basis of our similar anatomy, Charles Darwin predicted that the best place to find fossils of human origins would be in Africa, because the ancestors of apes and humans should be found there. Darwin's prediction was supported when many fossils were found in Africa that were classified into the family Hominidae.

Dud genes

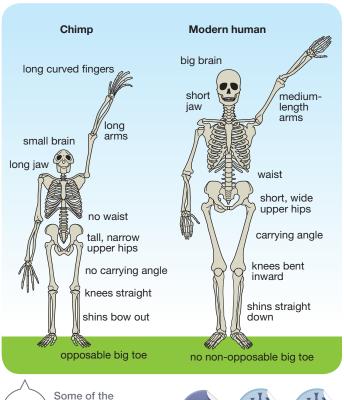
Not all genes you inherit actually function. For example, all humans inherit the GULOP gene, which would allow us to make vitamin C if it functioned. But it is defective and has many mutations within it. Some distant cousins of humans, the more 'primitive' primates such as lorises, galagos and pottos, still have a working GULOP gene. No higher primates have a GULOP gene that works.

SciFile

Humans and apes

Our species is classified into the family **Hominidae**, along with chimpanzees and gorillas. However, humans and these two apes have differences mainly in the way they stand and walk. Humans are placed in a level of classification called a sub-tribe.

The key features that place a species in the human sub-tribe involve walking upright on two legs. These features are in the skull, vertebral column, pelvis, femur, knees and feet. There are other characteristic features as well, such as the shape of the jaw and the hand structure. Figure 3.4.2 shows these comparisons.



3,6





Australopithecines

One early group that most anthropologists are fairly sure is ancestral to our genus *Homo* is the genus *Australopithecus*. This group contains at least six species, who are often referred to as 'ape-men'. Species belonging to *Australopithecines* lived in Africa about 3.7 million to 1.8 million years ago. Among them is probably the group that were ancestors to our genus *Homo*, but more fossils are needed of early *Homo* to better identify this link. The most likely candidate for the ancestor of the genus *Homo* is *Australopithecus afarensis* (see Figure 3.4.3).



Figure 3.4.3

Australopithecus afarensis is the earliest known likely ancestor of humans. The fossilised footprints shown here are about 3.7 million years old.

Australopithecus afarensis lived in East Africa between about 3.7 million and 2.5 million years ago. They were about 1.3 metres tall and weighed about 30 kg. Their brain, at 410 cm³, was about the size of a chimpanzee's, but they had a much smaller body weight. Australopithecus afarensis walked upright on two legs as shown by the shape of their pelvis and the carrying angle of the femurs. The carrying angle is the inward slope of each femur towards the knee. A carrying angle means that the knees are closer together than the hips, making upright walking more efficient. This upright walking on two legs placed them on the path towards being human. At present, scientists are searching for more fossils of species that existed around this time to help decide which Australopithecus, if any, may have given rise to genus Homo.

Early genus Homo

The earliest known member of our genus *Homo* dates from about 2.4 million to 1.4 million years ago. This is a species called *Homo habilis* (Figure 3.4.4). A comparison of *Homo habilis* with *Homo ergaster* and modern *Homo sapiens* suggests that *Homo ergaster* is a much more likely candidate as an ancestor of our species than *Homo habilis*. If both these species lived at the same time, they cannot both be ancestral to our species.

Figure

3.4.2

distinguishing features

of humans and apes



Figure 3.4.4

Homo habilis may be ancestral to our species, but more fossils are needed to test this view.

A skull labelled KNM 1470 and given the name Homo rudolfensis is a possible candidate to have been on the line from Australopithecines to humans. However, there is only one skull and no other bones. This makes classification of it difficult.

By about 1.9 million years ago, a new species of human had evolved in Africa. It has been called Homo ergaster (also known as *Homo erectus*). An example of this species is the amazing specimen labelled KNM WT 15000, and referred to as the Turkana Boy (Figure 3.4.5). This specimen is about 1.5 million years old. Turkana Boy was about 9-12 years of age when he died. He was 1.6 metres tall and may have reached 1.85 metres as an adult. Almost 90% of his skeleton was recovered. The Turkana Boy had a tall, slender body adapted for walking long distances. He had a more human-like face than Homo habilis, with a nose that projected outwards and a larger space for the brain at 880 cm³. His brain would have probably reached around 910 cm³ when he reached adulthood.



Figure 3.4.5

Homo ergaster migrated out of Africa around 1.9 million years ago. This is the Turkana Boy fossil. Most scientists call the fossils of this species found outside Africa Homo erectus.

Another fossil group that may be part of the line to modern humans is *Homo heidelbergensis* (Figure 3.4.6). This group may have evolved from Homo ergaster and also migrated

out of Africa into Europe. There it seems to have evolved into Homo neanderthalensis. Homo heidelbergensis may have evolved in Africa into Homo sapiens. Homo sapiens migrated out of Africa and around the whole Earth, replacing all other forms of *Homo* that existed elsewhere. such as Homo neanderthalensis.

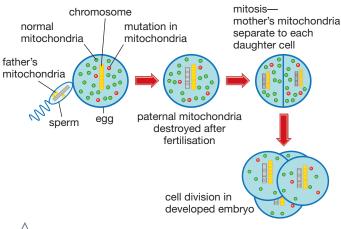


Homo heidelbergensis. European populations of this early human species were the ancestors of the Neanderthals. African populations probably gave rise to our own species.

Out of Africa

At the present time, the most widely accepted view among scientists of the origins of our species is the Recent African Origin model. This is also known as the **Out of Africa model**. This model proposes that a common ancestor of all modern humans evolved in East Africa between 200 000 and 100 000 years ago. Around 60 000 years ago, a small subgroup left Africa and ended up colonising the whole Earth. By about 15 000 years ago, all the continental landmasses (apart from Antarctica) were colonised by our species.

The Out of Africa model is supported by evidence from mitochondrial DNA testing and Y chromosome testing of modern humans. **Mitochondrial DNA (mtDNA)** is DNA contained within the cell mitochondria. This mtDNA is only passed from a mother to her children. As Figure 3.4.7 shows, mitochondria separate into each gamete (sex cell) during meiosis (division of the nuclear DNA) in the ovary. This mtDNA is not shuffled around between cells like the chromosomes are. The only changes that occur in mtDNA are mutations. These mutations are used to track the migration routes of our ancestors. Using mtDNA analysis and Y chromosome analysis, scientists have concluded that all human beings can trace their ancestry back to a small group who lived in Africa less than about 60 000 years ago (Figure 3.4.8).

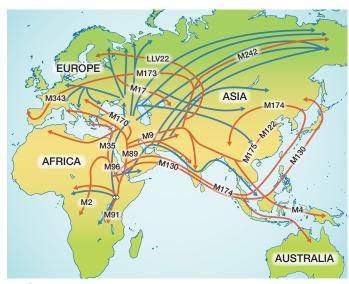




Mitochondrial DNA stays in the cytoplasm and generally does not affect the genes in the nucleus. The mtDNA is copied to each egg and to each cell when it divides in mitosis.

Neanderthal DNA

Mitochondrial DNA extracted from Neanderthal bones show that they were quite different from *Homo sapiens*, but more like us than chimpanzees. The scientists concluded that *Homo sapiens* and *Homo neanderthalensis* became separate species approximately 400 000 years ago. Recent studies of ancient nuclear DNA from a Neanderthal bone suggest that there was some interbreeding with *Homo sapiens*.





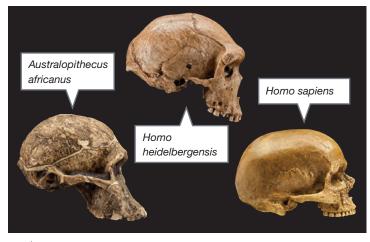
Migration routes out of Africa using Y chromosome analysis (red lines) and mtDNA analysis (blue lines) traced in the Genographic Project. The letters M and the numbers represent mutant genes. For example, M91 occurred about 60 000 years ago in Africa.

Signs in the skulls

When the skulls of all the different likely members of the human family are compared, there appear to be some striking changes that have occurred during their evolution. Figure 3.4.9 shows some of these changes clearly.

The apparent changes are as follows:

- The face becomes 'flatter', meaning more vertical.
- The lower jaw shortens and does not project out as much.
- A chin develops.
- The forehead becomes more vertical.
- The cranium (brain space) enlarges and becomes more rounded.
- The cranial capacity (brain size) increases.





A range of important fossil skulls in the human family

3.4 Unit review

Remembering

- 1 List terms used to classify modern humans from class to species.
- **2** Name ten primates other than humans.
- **3** List the characteristics of primates.
- **4** Name three species in the family Hominidae.
- Name the two living species most closely related to humans.

Understanding

- **6 Describe** the *Australopithecines*.
- **7 Outline** the Out of Africa model.
- **8** Explain how mitochondrial DNA (mtDNA) is passed on.

Applying

- **9 Identify** the person from whom you received your mtDNA.
- 10 In 2003, Australian scientists discovered fossils of nine individuals of a tiny species of human on the island of Flores in Indonesia. They classified it as a new species, Homo floresiensis. It had a brain volume about one-third the size of that of modern humans, and a height of about 109 cm. Apply the Out of Africa hypothesis to discuss the possible origins of this species.





Analysing

- **11 Compare** *Homo ergaster* with *Homo sapiens*.
- **12 Contrast** the origins of your nuclear DNA and mtDNA.

Evaluating

- **13 Justify** why at this time biologists should not make too many judgements about where Homo rudolfensis stands in the story of human evolution.
- **14 Justify** the Out of Africa model.
- 15 In 2001, some fascinating fossils were found in Georgia, between the Black Sea and the Caspian Sea. These fossils were classified as a new species named *Homo georgicus*. The almost-complete skull had a cranial capacity of about 600 cm³, and the body height was about 1.3 metres. The fossils were dated to 1.77 million years ago.
 - **Propose** a possible origin for this species
 - Justify your decision.





Homo georgicus

16 Deduce whether upright stance or increased brain size was the first feature that evolved in the lineage (line of descent) that led from apes to humans.

Creating

17 Construct an argument that could explain how *Homo* habilis evolved from Australopithecus afarensis.

Inquiring

- 1 Research the species commonly called Neanderthal man, discussing their characteristics and possible origins.
- 2 Research the mtDNA or Y chromosome evidence for the migration of humans out of Africa, including National Geographic's Genographic Project where you can trace your own ancestral journey out of Africa.
- 3 Research the DNA analysis of ancient Neanderthal bones and what this tells us about our relationship to Homo neanderthalensis.
- **4** Research the stone tools of the Oldowan, Acheulian, Mousterian and Magdalenian cultures and compare these with Australian Aboriginal stone tools.

3.4

Practical activities

1 Hand adaptations

Purpose

To identify some adaptations of the human hand.

Materials

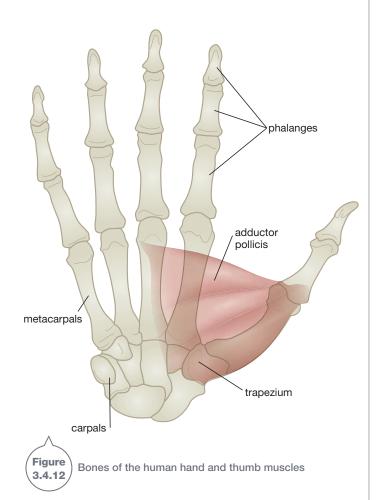
- · human skeleton
- hand X-rays
- ruler
- pencil

Procedure

- 1 Hold your left hand out in front of you palm face down and fingers spread out. Observe the position of the thumb compared with the fingers. Write a description of the differences.
- 2 Turn your left hand palm upwards. Touch each of the four fingertips on this hand with your left thumb. Observe carefully how the thumb can move. Describe how your thumb moves across the palm.
- **3** Grasp a ruler with your left hand the way you would hold a hammer. This is called the power grip. Describe how the thumb assists in holding the ruler.
- 4 Hold a pencil for writing. This is called the precision grip. Describe the difference in the position of the thumb and fingers in this grip compared with the power grip.
- 5 The trapezium bone enables you to move your thumb to touch your little finger. Hold your left hand palm upwards, with fingers together and thumb out to the side. Move your thumb across to touch your little finger. Describe which way the thumbnail points before and after moving your thumb.

Discussion

- 1 **Propose** the reasons for the names *power grip* and *precision grip*.
- **2** Look at Figure 3.4.12. Use it to locate the position of the trapezium on your own hand. Show your partner where you think this bone is.



- **3** Using Figure 3.4.12, **identify** the muscles involved in moving the thumb, and what role each has in moving the thumb.
- **4 Discuss** the adaptations of the human hand for object manipulation.
- **5 Propose** how the human hand may have evolved from the hand of an ape ancestor.

Foot adaptations

Purpose

To compare the human hand and foot structure as adaptations of homologous structures.

Materials

- · human skeleton
- · X-rays of hands and feet
- ruler
- pencil

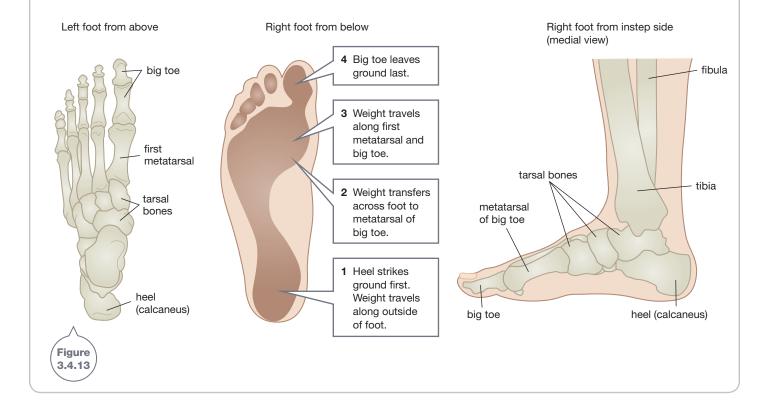
Procedure

- 1 Remove your shoe and sock from your left foot. Describe the position of the big toe and other toes.
- **2** Observe the instep of your foot (or someone else's foot). Describe the shape of the foot from the heel to the toes.

- **3** Observe a skeleton and X-rays of the foot. Describe how it looks from the side.
- **4** Observe the heel and the toes of the skeleton and X-rays. Compare the size of the toes and describe the heel.

Discussion

- **1 Compare** the position of the thumb with that of the big toe.
- **2** Using Figure 3.4.13, **propose** how the heel, first metatarsal and big toe could be considered adaptations of the foot for walking.
- **3 Discuss** how the same homologous structure could evolve into a hand and a foot.



Chapter review

Remembering

- **1 Name** the first person to propose the process of natural selection.
- **2 List** the steps involved in speciation.
- **3 List** the evidence that supports the theory of evolution.

Understanding

- 4 Modify the following statements to make them correct.
 - **a** Homologous structures have to perform the same function in different species.
 - **b** Any differences in the position of amino acids in a protein show that species are not related.
 - **c** Organisms that look similar must have the same genes causing the similarity.
 - d All variation in a species is caused by natural selection.
 - e Natural selection acts on the genes in an organism.
- **5 Explain** how fossils support the theory of evolution.
- 6 Natural selection has been demonstrated in organisms in recent times.
 - List two organisms in which these changes have been obvious.
 - **b** Explain how natural selection caused the change.
- **7 Explain** how domesticated animals and plants were altered through artificial (directed) selection.
- **8 Explain** the important role of genetic isolation in evolution.
- 9 Discuss some evidence supporting the Out of Africa model.

Applying

- 10 Demonstrate how an adaptive feature, such as coat colour in mice, can change when the 'selection pressure' (natural selection) changes.
- **11 Use** the fossil record of birds and dinosaurs to **demonstrate** that transitional forms occur between levels of classification.
- **12** Humans, lemurs, monkeys, gorillas, chimpanzees and tarsiers are classified into one group. **Identify** three structural features they all share that place them in this group.



Figure 3.5.1

Gorillas, lemurs and chimpanzees are primates.

Analysing

- **13 Compare** changes in the vertebrate pentadactyl limb over geological time.
- **14 Compare** the importance of variation in both artificial selection and natural selection.
- 15 Contrast homologous and analogous structures.
- 16 The flying possums of Australia are able to glide from tree to tree because of a thin webbing of skin between their front and back legs that catches the air like a parachute. Despite being very different animals, there are some flying lemurs and squirrels elsewhere in the world that have similar webbing. They too glide from tree to tree. Classify the webbing as a homologous or analogous structure.

Evaluating

- **17 Propose** a reason why natural selection is more likely to be visible in organisms such as bacteria and insects than in kangaroos and humans.
- **18 Justify** the conclusion that species with the same basic structure are related.
- **19** *Australopithecus* and *Homo* are both classified into the same sub-tribe. **Propose** what features placed *Australopithecus* in the same sub-tribe as us.
- **20** There is much more variation in domesticated species such as budgerigars than in the wild species. **Propose** why there is less variation in the wild.

Creating

primates

embryology

comparative anatomy

- **21 Construct** a story explaining how natural selection resulted in human beings becoming more intelligent over our geological history.
- 22 Use the following ten key terms to construct a visual summary of the information presented in this chapter. natural selection selective agent evolution homologous speciation fossils DNA



Thinking scientifically

Questions 1 and 2 refer to the following information.

A biologist was studying a population of mice that lived in an area with few trees and scattered low shrubs separated from each other by large areas of bare soil. He found that the mice had two genes that controlled their coat colour. One tended to give the coat a dark-brown colour, while the other produced a lighter yellowish brown colour.

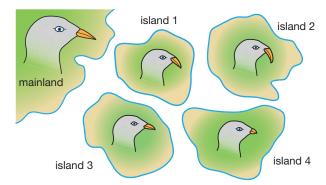
The area contained three different soil types: dark red clay, pale yellow sand and light grey sand. Studies of the proportion of mice with the different coat colour were done and are shown in the table. The area was a very dry semi-desert climate. The mice were preyed upon by hawks that hunted mainly in the morning and late afternoon.

Site	Soil colour	Per cent of mice with brown coat	Per cent of mice with yellowish coat
1	Red	82.0	18.0
2	Light grey	52.0	48.0
3	Pale yellow	41.0	59.0

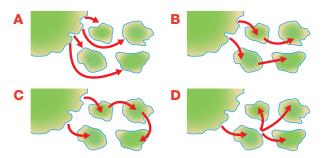
- Q1 Which of the following is a fair interpretation of the data?
 - A There are more brown-coated mice than yellow-coated mice in the population.
 - **B** Brown coats are more suited to red clay than they are to light-grey sand.
 - C Yellowish coats are more suited to the light-grey sand.
 - **D** Brown-coated mice are moving from pale-yellow sand and light-grey sand to the red clay.
- Q2 Considering the information in the table, which of the following conclusions is likely?
 - A Hawks always prefer to eat mice with a yellowish coat colour.
 - **B** The climate is selecting for lighter coloured mice because they will absorb less heat.
 - C The coat colour provides the mice with camouflage protection from the hawks.
 - Lighter colour soil selects for the yellowish coat colour.
- Q3 Domestic dogs were originally bred from ancestors of the wolf. There are now hundreds of different dog breeds with characteristics varying from tiny chihuahuas to the massive Irish wolfhounds. Natural selection acts to allow survival of offspring most suited to their environment. The environment of the wolf is forests of the Northern Hemisphere. The environment of domestic dogs is the homes of people around the world, where they are cared for and fed by their owners.

Consider the following suggestions. Which most likely explains why there are many different breeds of domestic dog and only one species of wolf, which is fairly alike over the whole Northern Hemisphere?

- A Not all variations would be suited for survival in the wolf's environment.
- **B** Wolves are artificially selected.
- C Domestic dogs are not being selected by the environment.
- Natural selection acting on the wolf made it evolve into many different types of dog.
- Q4 Consider the following diagram.



Which of the following is the most likely evolutionary pathway to form the four species of birds on the islands?



- Q5 Bacteria divide asexually approximately once every 20 minutes in ideal conditions. Fruit flies reproduce sexually in a life cycle of about 11 days. Why might an experimenter choose bacteria rather than fruit flies in an experiment on natural selection?
 - A Asexual reproduction cannot produce any genetic change so bacteria are useful as a control in experiments
 - **B** Variation, isolation and selection can not occur in bacteria so there will be no speciation
 - C There will not be any variation in the bacteria for natural selection to act on
 - A short generation time means any evolution in the species should occur faster

Glossary

Unit 3.1

Analogous: structures that appear similar or have the same function but are controlled by different genes

Artificial selection:

the process by which people choose to breed particular organisms with desirable features; also known as selective breeding or directed selection

Cross-breeding:

selective breeding by combining a desirable feature of one individual with another in the offspring



Evolution: change in the characteristics of a species over many generations

Generation: the time between the birth of an individual and when they produce their own offspring

Homologous: structures that are controlled by some of the same inherited genes

Inbreeding: selective breeding in which closely related individuals are allowed to breed

Unit 3.2

Antibiotics: chemicals made by organisms such as fungi to defend them against bacteria

Natural selection: the process where an environmental factor acts on a population and results in some organisms having more offspring than others

Resistance: inherited ability of a species to withstand chemicals such as pesticides

Selective agent: the environmental factor that acts on the population during natural selection

Sexual selection:

a special case of natural selection where the environmental factor is the selection of a mate

Variation: differences in characteristics due to different genes



Unit 3.3

Biodiversity: the number and range of different species that exist on Earth or in an ecosystem

Distribution: a map of all the places where a species occurs

Embryology: the study of the embryos of different species

Isolation: keeping interbreeding groups apart by some barrier or mechanism

Species: group of organisms that can interbreed to produce fertile offspring under natural conditions



Speciation: the process by which one species splits into two or more separate species

Transitional form: fossils that have features of two or more different groups

Unit 3.4

Australopithecus: a genus in the family Hominidae that is probably ancestral to our genus Homo

Hominidae: the family to which humans and the extinct genus Australopithecus belong

Homo: the genus to which human beings, and several other extinct species, belong

Mitochondrial DNA (mtDNA):

DNA contained within the cell mitochondria and passed from mother to sons and daughters

Out of Africa model: model (hypothesis) proposing a common ancestor of all modern humans evolved in Africa and then migrated out to colonise the whole Earth



Primates: order of animals with 'grasping' hands, nails rather than claws and forward-facing eyes

SCIENCE TAKES YOU PLACES

Look who is using science

AGRONOMIST

My name is Dugald Spenceley. I studied agricultural science and am now a business manager with Syngenta Crop Protection in Australia. The focus of our business is agronomy—the study of crop production.

I work with the company's sales and marketing teams and help to develop the strategies we use to sell our products. This requires me to have a good understanding of what is happening in the market and the suitability of our products for a variety of crops under different growing conditions.

Studying agricultural science has enabled me to work in different fields, such as land management, agronomy, marketing and business management. My science background has helped me to understand the relationships that exist in the farming environment and how my company can best use our products to increase crop production. Crop production is becoming more and more important to ensure that we are able to feed an ever-growing global population.



TECHNICAL OFFICER

I am Helen Gore and I work as a palaeontology technical officer in the Department of Earth and Planetary Sciences at a state museum.

Every day my work brings a new challenge. For example, I often prepare fossils for research. Some days I'll be picking tiny ancient sharks' teeth from sedimentary rock deposits so that the species can be identified and the geological age of the rock determined. Other days, I'll be stabilising (repairing) an extremely fragile fossil.

I also act as a curator (manager) of the museum's fossil collection, which now has more than a million

specimens. The collection gives us great insight into the Earth's evolutionary history over the last 3000 million years. We often lend fossil material to scientists throughout the world for research. An important part of the work is preparing fossils for safe transport, and tracking loans to ensure they are returned to the collection.

No two days at the museum are the same, and it's particularly exciting when a new fossil species, previously unknown to science, is discovered.





PLANT BREEDER

I am Dr Warwick Stiller, a plant breeder with CSIRO Plant Industry. My work involves developing new varieties of cotton that have higher yields, better disease resistance and higher fibre quality and use less water. I use conventional breeding methods as well as genetically modified technologies. Some of the more interesting work is identifying useful traits in some of Australia's native cotton species and other wild species that could be transferred into the cotton varieties that we grow.

Being a plant breeder means that I get to make a real impact on farmers' livelihood and the prosperity of rural Australia, as well as enjoying a diverse range of tasks from out in the field to the laboratory.