

Chapter 5

How are species related over time?

Keywords and terms

Genetic changes in a population over time

- adaptation
- allopatric speciation
- antigenic drift
- conjugation
- fitness value
- gene pool
- genetic drift
- germ line cell
- homozygous
- natural selection
- point mutation
- population
- somatic cell
- translocation
- allele
- antigenic shift
- evolution
- bottleneck effect
- founder effect
- gene pool
- genetic variation
- heterozygous
- isolating mechanism
- non-disjunction
- polymorphic population
- selection pressure
- speciation
- allele frequency
- bacterial resistance
- biological evolution
- extinction
- gene flow
- genetic diversity
- genotype
- homologous chromosome
- mutation
- phenotype
- polyploidy
- selective breeding
- species

Changes in species over time

- absolute dating
- cast
- index fossil
- divergent evolution
- index fossil
- palaeontology
- transitional fossil
- allopatric speciation
- convergent evolution
- transitional fossil
- faunal succession
- isotope dating
- relative dating
- carbon dating
- fossil
- genetic divergence
- homologous structures
- mould
- sympatric speciation

Determining relatedness of species

- adaptive radiation
- mitochondrial DNA
- phylogeny
- common ancestor
- molecular homology
- phylogenetic tree
- DNA hybridisation
- molecular clock
- vestigial structures

Human change over time

- Australopithecus*
- foramen magnum
- Homo*
- Homo sapiens*
- mammal
- opposable thumb
- binocular vision
- hominin
- Homo erectus*
- Homo neanderthalensis*
- putative
- Cro Magnon
- hominoid
- Homo denisovana*
- mitochondrial DNA
- primate

Content review questions

Unit 2 revision

- 1 Why is meiosis significant to sexually reproducing organisms? You should be able to make several points.
- 2 What is the difference between an allele and a gene? Are they the same thing?
- 3 Distinguish between the terms 'homologous', 'homozygous' and 'heterozygous'.
- 4 What is the difference between the terms 'genotype' and 'phenotype'? What factors determine each?

Changes in the genetic makeup of a population

- 5 What is meant by variation when looking at members of a population?
- 6 List the major types of variation that exist between organisms.
- 7 List the various sources and processes that provide genetic variation in a population. Start with variation that arises during gamete production.
- 8 Point mutations are minor alterations to base sequences in genes. Describe the three major types of point mutation.
- 9 Explain why mutations are usually harmful. Which of the three types of point mutation are the least harmful? Why? Refer to frameshift in your answer.
- 10 What are block mutations?
- 11 Give an example of a condition that arises as a result of non-disjunction. Explain what must have happened during meiosis.
- 12 How do aneuploidy and polyploidy differ?
- 13 List some causes of mutation.
- 14 Distinguish between germline and somatic mutations.
- 15 Which sorts of mutation can be beneficial to a species' long-term survival? Explain.
- 16 Which is the more important source of variation – recombination during meiosis or mutation? Justify your opinion explaining the significance of each.
- 17 What is meant by the terms 'gene pool' and 'allele frequency'?
- 18 How is allele frequency calculated?
- 19 In terms of the gene pool and allele frequency, what is the difference between gene flow and genetic drift? When will the two processes have the greatest effect on allele frequency?
- 20 Complete the following table.

	Bottleneck	Founder effect
Definition		
Genetic diversity		

- 21 What is biological evolution? Is evolution a process or a result? Explain.
- 22 Is biological evolution a theory or fact?
- 23 How are 'Natural Selection' and 'Biological Evolution' related?
- 24 If natural selection is to occur, what must exist in a population?
- 25 Is selection at the phenotypic or genotypic level? Explain what sorts of individuals are most likely to survive in a particular environment.

Molecular homology		
- Universal genetic code		
- similar DNA sequences		
- similar amino acid sequences		

- 64 What is molecular homology and how can it be used to determine the relatedness between species?
- 65 Draw a phylogenetic tree based on the following hybridisation results.
Human and chimpanzee: 97.7%
Human and gibbon: 94.7%

Human change over time

- 66 List the major characteristics that distinguish mammals from other animals.
- 67 Humans are primates. Describe the major features that distinguish primates from other mammals.
- 68 Why are opposable digits important to primates? In particular, how is an opposable digit important to humans?
- 69 Why do netballers and footballers require good stereoscopic vision?
- 70 What features distinguish hominins from other primates?
- 71 Distinguish between the terms 'hominoid' and 'hominin'.
- 72 Describe the location changes of the foramen magnum.
- 73 What changes in jaw and tooth structure have occurred during human evolution? How might behaviour have changed during this evolution?
- 74 Skull shape and size have changed during human evolution. Describe their changes and their significance.
- 75 What has been the limiting factor to a further increase in skull size?
- 76 What selective pressures might have led to increased brain size?
- 77 Is it true to say that man has evolved from chimps and gorillas? If not, rephrase the statement.
- 78 Complete the following table.

	<i>Homo neanderthalensis</i>
When did they live?	
Where did they live?	
Features of their skull	
Brain size	
Culture	
Disappeared from the fossil record	

- 79 How is mitochondrial DNA different from nuclear DNA?
- 80 Why is mitochondrial DNA useful for tracking human evolution?

- 81 What does the comparison of mitochondrial DNA indicate about *Homo sapiens*, *Homo neanderthalensis* and *Homo denisovan*?
- 82 Complete the following table summarising two theories of human migration.

Hypothesis	Description	Evidence
Out of Africa		
Multi-Regional		

- 83 There is debate about when humans first arrived in Australia. What is the evidence that arrival was at least 65 000 years ago?

Multiple-choice questions

Use the following information to answer Questions 84 and 85.

		Second letter					
		U	C	A	G		
First letter	U	UUU } phe UUC UUA } leu UUG	UCU } UCC } ser UCA UCG	UAU } tyr UAC UAA STOP UAG STOP	UGU } cys UGC UGA STOP UGG trp	U C A G	
	C	CUU } CUC } leu CUA CUG	CCU } CCC } pro CCA CCG	CAU } his CAC CAA } gln CAG	CGU } CGC } arg CGA CGG	U C A G	
	A	AUU } AUC } ile AUA AUG met	ACU } ACC } thr ACA ACG	AAU } asn AAC AAA } lys AAG	AGU } ser AGC AGA } arg AGG	U C A G	
	G	GUU } GUC } val GUA GUG	GCU } GCC } ala GCA GCG	GAU } asp GAC GAA } glu GAG	GGU } GGC } gly GGA GGG	U C A G	

Consider the following sequence of six amino acids that make up part of a polypeptide.

--- phe --- leu --- pro --- val --- tyr --- ala ---

A mutation within the gene coding for this sequence of six amino acids resulted in the following six amino acids in the same position.

--- phe --- leu --- ala --- val --- tyr --- ala ---

84 [VCAA 2018 SA Q20]

This change in the sequence of amino acids was caused by

- A a deletion of a nucleotide.
- B an insertion of a nucleotide.
- C a substitution of a nucleotide.
- D an inversion of adjacent nucleotides.

85 [VCAA 2018 SA Q21]

Another mutation within the original gene resulted in a shortened protein. The protein was truncated (cut short) after the amino acid valine, as shown below.



This truncated protein resulted from the codon

- A UAU changing to UAA.
- B UAC changing to UGC.
- C GUA changing to UGA.
- D GUG changing to UGG.

86 [VCAA 2018 SA Q22]

In humans, Duchenne muscular dystrophy (DMD) is caused by mutations in the dystrophin encoding DMD gene. The DMD gene contains 79 exons. In some patients, duplication of one exon occurs.

If the number of nucleotides in the duplicated exon is divisible by three, the

- A transcribed mRNA will contain many stop codons.
- B length of each of the 79 exons will increase by three nucleotides.
- C translated protein will be longer than the dystrophin protein found in a person without DMD.
- D dystrophin of these patients will show one amino acid change in the sequence compared to normal dystrophin.

87 [VCAA 2014 SA Q23]

In populations of fruit flies, there are individuals that are resistant to the effects of insecticides. Insecticide-resistant fruit flies arose as a result of a mutation. In normal insecticide-susceptible fruit flies, a specific section of mRNA has the sequence GCU, whereas in the insecticide-resistant fruit flies, the sequence is UCU.

This mutation is an example of a

- A chromosomal deletion during the formation of a gamete.
- B nucleotide substitution during the formation of a gamete.
- C chromosomal deletion during the formation of a somatic cell.
- D nucleotide substitution during the formation of a somatic cell.

Use the following information to answer Questions 88 and 89.

The codon table below can be used to determine the sequence of amino acids coded for by a nucleotide sequence.

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	STOP	STOP	A
	Leu	Ser	STOP	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

The following nucleotide sequence occurs on the template strand of a DNA molecule.

AAA GCT ACC TAT CGG TTA

88 [VCAA 2017 SA Q27]

In a mutation, the eighth nucleotide in this sequence was changed from C to T.

What would be the result of this mutation?

- A The peptide chain would be shortened.
- B The third amino acid would change from Thr to Ile.
- C The fourth amino acid would change from Ile to Tyr.
- D There would be no change in the amino acid sequence.

89 [VCAA 2017 SA Q28]

In a different mutation, a T was inserted after the fourth nucleotide on the given template strand.

The result of this mutation would be that

- A all amino acids in this entire sequence would change.
- B only the first amino acid in the sequence would change.
- C only the second amino acid in the sequence would change.
- D all amino acids after the first in the sequence would change.

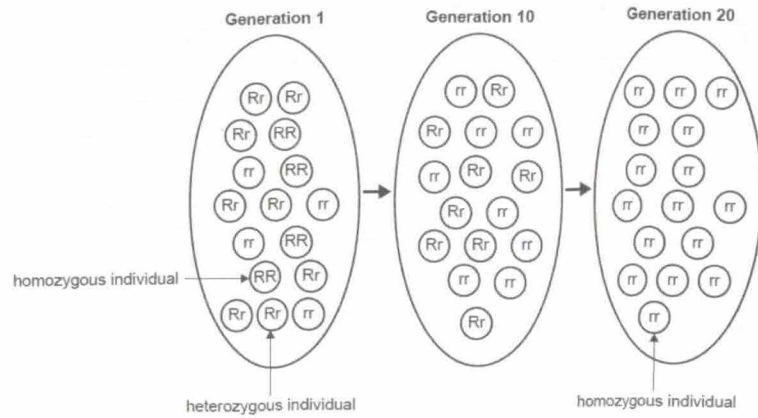
90 [VCAA 2012 E2 SA Q25]

Biological evolution

- A includes changes in the learnt behaviour of individuals in a population.
- B involves inherited change in a population over many generations.
- C occurs faster than technological evolution.
- D is defined as simply change over time.

91 [VCAA 2019 SA Q26]

Consider the diagram below showing the gene pool of a population over 20 generations.



It would be correct to conclude that, over the 20 generations

- A genetic diversity is increasing in this population.
- B individuals with the genotype RR had a selective advantage in this population.
- C the frequency of each allele is equal in Generation 1 but not in other generations.
- D new advantageous alleles for this gene were introduced as individuals joined this population.

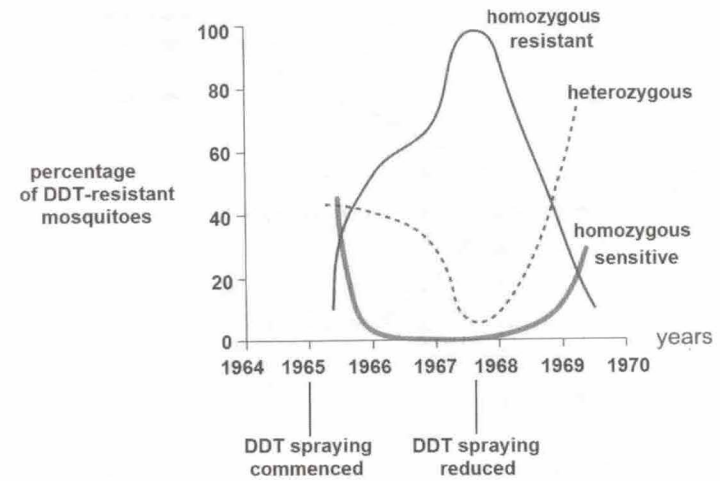
92 [VCAA 2010 E2 SA Q23]

In the mid-1960s, DDT was widely used as an insecticide against mosquitoes. The sensitivity to insecticide in mosquitoes is determined by a single gene that has two alleles.

allele 1 : resistant to DDT

allele 2 : sensitive to DDT

Over several years genotypic frequencies were measured in a population of mosquito larvae. The graph below shows the results.

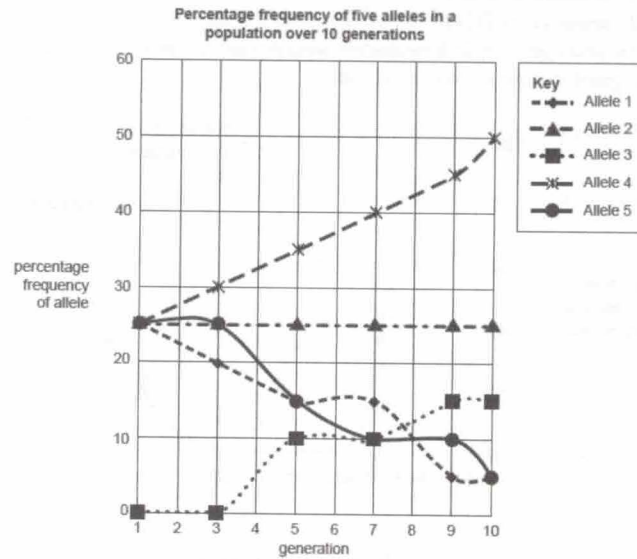


Analysis of the graph reveals that in the population

- A when spraying levels declined, heterozygous advantage occurred.
- B there were no alleles for sensitivity present in the population in 1967.
- C the number of alleles for resistance was equal to the number for sensitivity in 1966.
- D the homozygous resistant genotype was unable to produce offspring at low spraying levels.

93 [VCAA 2020 SA Q28]

The graph on the following page shows the frequency of five alleles in a population over 10 generations. The change in allele frequency is represented as a percentage of the frequency of the five alleles.



Based on the information in the graph, which one of the following is most likely?

- A The founder effect can explain the change in allele frequency in the first three generations.
- B Genetic diversity within the population remains unchanged over the 10 generations.
- C The appearance of Allele 3 after Generation 3 may be explained by gene flow.
- D A bottleneck event occurred between Generation 7 and Generation 9.

94 [VCAA 2016 SA Q37]

Tiburon is an isolated island off the coast of Mexico. Desert bighorn sheep became extinct on this island hundreds of years ago. In 1975, 20 desert bighorn sheep were taken from a population in the American state of Arizona (shown on the map below) and were re-introduced to Tiburon Island. By 1999, the population of desert bighorn sheep on Tiburon Island had risen to 650.



Which one of the following statements about this 1999 population of desert bighorn sheep on Tiburon Island is correct?

- A The gene pool of this population will be identical to the gene pool of the Arizona populations.
- B This population has less genetic variation than the Arizona populations and is an example of the founder effect.
- C This population will have become a new species because the mutation rate on Tiburon Island will be much higher than in Arizona.
- D Having been through a population bottleneck, the current population will now show increased genetic variation compared to the Arizona populations.

95 [VCAA 2015 SA Q40]

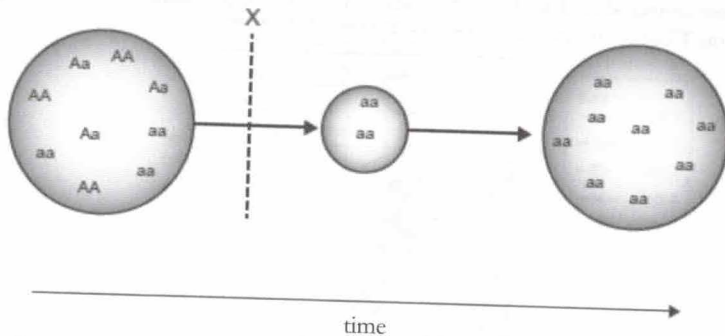
Northern elephant seals, *Mirounga angustirostris*, were nearly hunted to extinction in the 1890s, with only about 20 individuals left at the end of the century. The population has now grown to more than 120 000. In the 1890s, southern elephant seals, *Mirounga leonina*, were not as severely hunted and currently there are estimated to be 600 000 southern elephant seals.

Based on this information, it is true to say that

- A northern elephant seals have evolved as a result of the 'founder effect'.
- B northern elephant seals would show less genetic variation than southern elephant seals.
- C southern elephant seals would have experienced greater genetic drift than northern elephant seals.
- D the mutation rate in northern elephant seals would have been greater than in southern elephant seals.

96 [VCAA 2014 SA Q33]

Consider the diagram below that models the changes in allele frequencies for one trait in a population over two generations. The original population is shown on the left.



If the diagram above models the founder effect, then event X is

- A migration.
- B a natural disaster.
- C random mating.
- D a random assortment of alleles.

97 [VCAA 2012 E2 SA Q21]

Retinitis pigmentosa (RP) is an autosomal recessive trait that results in progressive blindness in humans. On the island of Tristan da Cunha in the Atlantic Ocean, the frequency of the allele causing RP is four times greater in its population of a few hundred individuals than in the original British population from which it was colonised in the early 1800s. No natural disasters have occurred on the island since it was colonised.

The process that is most likely responsible for this observation related to allele frequency is

- A genetic drift.
- B founder effect.
- C bottleneck effect.
- D natural selection.

98 [VCAA 2010 E2 SA Q13]

In populations

- A genetic drift will have less effect in a large population compared to a small population.
- B bottlenecks enable a population to become better equipped for future changes in the environment.
- C some organisms develop mutations in order to better suit them to their environment compared to other members of the population.
- D allele frequencies remain constant if the number of individuals leaving the population equals the number of individuals entering it.

99 [VCAA 2012 E2 SA Q23]

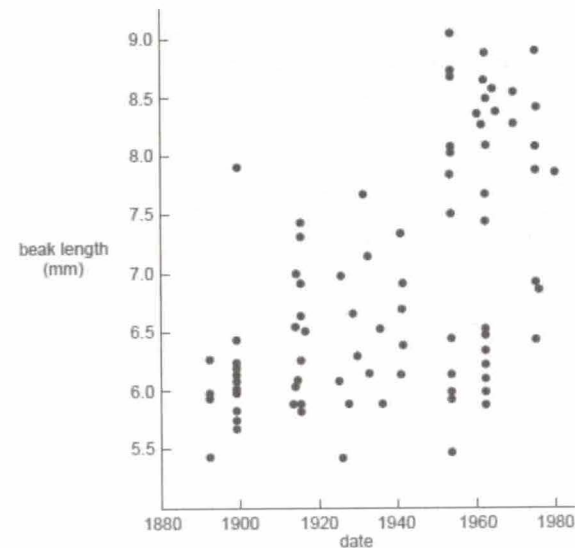
Early in 2012, biologists announced the discovery of a new lizard species.

To claim that the lizards belong to a new species, the biologists must show that the lizards

- A look different from one another.
- B look different from known species.
- C have similar genetic sequences to known species.
- D do not produce fertile offspring with members of known species.

Use the following information to answer Questions 100 and 101.

The soapberry bug (*Jadera haematoloma*) uses its long beak to penetrate the fleshy fruit of plants to feed on the seeds at the centre. The bug feeds on the native soapberry tree. The bug also feeds on the fruit of the introduced golden rain tree. Investigators measured the average beak length of the soapberry bug over eighty years. The results are shown on the next page.



100 [VCAA 2011 E2 SA Q19]

From this information it would be reasonable to conclude that

- A the golden rain tree was introduced around 1970.
- B no long-beaked bugs existed prior to the introduction of the golden rain tree.
- C the diameter of the golden rain tree fruit acted as a selection pressure on beak length.
- D the response of an individual golden rain tree to predation by soapberry bugs would be to grow larger fruit.

101 [VCAA 2011 E2 SA Q20]

In neighbouring regions, the fruits of other introduced plants have also been used by the soapberry bug. Male and female soapberry bugs from different regions can interbreed. Evidence indicates that genetic isolation of some of these populations is gradually occurring.

The situation that would lead to an increase in genetic isolation would be if

- A different types of host plants have fruiting seasons which do not overlap.
- B pheromones of female soapberry bugs attract soapberry males from neighbouring populations.
- C the soapberry tree is common throughout the distribution and each tree produces large amounts of fruit.
- D male soapberry bugs new to a region are reproductively active, whereas female bugs need to feed before becoming reproductively active.

102 [VCAA 2020 SA Q27]

Tasmanian devils (*Sarcophilus harrisi*) were originally broadly distributed across Australia. When sea levels rose 12 000 years ago, an island, now referred to as Tasmania, was formed. The small number of Tasmanian devils on Tasmania was cut off from the Australian mainland populations. The population in Tasmania showed less genetic variation than the mainland populations. Mainland populations became extinct approximately 3000 years ago.

Over the last 20 years, the total Tasmanian devil population on Tasmania has halved. Many of the deaths have been the result of Tasmanian devil facial tumour disease (DFTD). Scientists have taken some Tasmanian devils that do not have DFTD to mainland Australia to set up a conservation program. The scientists have shown that greater genetic diversity among offspring in this program is observed when the Tasmanian devils are kept in isolated male–female pairs rather than in larger groups.

The conservation program for Tasmanian devils is an example of

- A a population bottleneck.
- B allopatric speciation.
- C selective breeding.
- D natural selection.

103 [VCAA 2019 SA Q27]

Farmers and supermarkets agree that green beans are bought more frequently than yellow beans. A supermarket has asked a farmer to produce only green beans.

One way this could be achieved is by

- A condensation polymerisation.
- B DNA hybridisation.
- C selective breeding.
- D adaptive radiation.

104 [VCAA 2017 SA Q30]

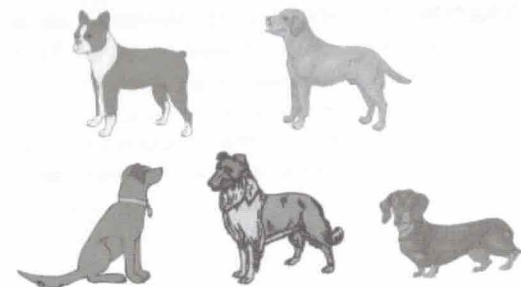
In the 18th century, farmer Robert Bakewell separated large, fine-boned sheep with long, shiny wool from his native stock to interbreed for future sheep flocks.

This is an example of

- A genetic fitness.
- B natural selection.
- C selective breeding.
- D allopatric speciation.

105 [VCAA 2014 SA Q38]

The diagram below shows five different breeds of dog that now exist within the *Canis lupus familiaris* species.



The development of variant breeds within *Canis lupus familiaris* is an example of

- A natural selection occurring in geographically isolated populations.
- B gene-transfer technology transforming the genotype of a species.
- C convergent evolution occurring in a range of similar habitats.
- D human intervention through artificial selection.

106 [VCAA 2011 E2 SA Q22]

Selective breeding over many generations has produced gradual changes in farm animals.

It is reasonable to state that such gradual changes in a herd of cattle

- A result from random mating in the herd in each generation.
- B are due to the occurrence of gene mutations in each generation.
- C will improve traits that enhance survival of the animals in the wild.
- D result from the restriction of breeding to chosen animals in the herd.

107 [VCAA 2010 E2 SA Q20]

The wild sunflower plant has been cultivated by humans over several generations. During that time, selection for or against particular sunflower traits has been carried out.

A comparison of some of the traits in wild and cultivated sunflowers is given the diagram that follows.

	Wild sunflower	Cultivated sunflower
fruit weight	9–10 mg	55–65 mg
plant height	153–170 cm	120–136 cm
flower diameter	3–5 cm	9–11 cm
number of branches	12–16	0
leaf area	180–270 cm ²	300–315 cm ²

From the information above, we can assume that humans have selected against large

- A leaf area.
- B plant height.
- C fruit weight.
- D flower diameter.

Use the following information to answer Questions 108 and 109.

Health professionals are concerned about the over-prescription of antibiotics. Many antibiotics have become ineffective against certain species of bacteria.

108 [VCAA 2013 SA Q39]

Any rise in incidence of antibiotic-resistant bacteria is due to

- A these bacteria having acquired immunity to antibiotics.
- B the overuse of antibiotics causing mutations in bacteria.
- C the introduction of selectively-bred, antibiotic-resistant bacteria.
- D antibiotic-resistant phenotypes being favoured through natural selection.

Up to 80 per cent of bacterial diseases are caused by bacteria living in biofilms. Biofilms are large communities of bacteria encased in extra-cellular coverings that attach to slippery surfaces, such as teeth and contact lenses. Special features of biofilms include the following.

- Some regions of cells form spores for reproduction and dispersal.
- Other regions of cells grow flagella for movement.
- Cells can detect others of their own species through cell-to-cell signalling (so they can sense when sufficient numbers are present to invade new areas successfully).

109 [VCAA 2013 SA Q40]

Researchers are trying to develop therapies that avoid the use of antibiotics. These therapies could include

- A using drugs that stop spindle fibres forming during mitosis.
- B providing amino acid supplements to promote flagella development.
- C preventing biofilm bacteria from detecting others of their own species.
- D targeting the biofilm's covering to make it more permeable to antibiotics.

110 [VCAA 2019 SA Q28]

Consider the close-up image that follows of a dinosaur footprint discovered by scientists.



Due to copyright restrictions, this image has been replaced with an equivalent likeness. To view the original image, please visit the VCAA website.

This type of fossil is best described as

- A preserved remains.
- B a petrified fossil.
- C a trace fossil.
- D a cast.

111 [VCAA 2018 SA Q25]

It is most probable that the two stratigraphically younger fossils would have been found in a layer of rock that

- A was closer to the present-day ground surface than the rock surrounding the *D. pickeringi* fossil.
- B contained a smaller quantity of carbon-14 than the rock surrounding the *D. pickeringi* fossil.
- C was located at a depth of 2.3 m below the ancient riverbed.
- D was formed from extremely hot, volcanic lava flow.

112 [VCAA 2018 SA Q26]

Palaeontologists believe that the Victorian ornithopods shared a close common ancestor with several ornithopod fossils found in Antarctica, South America and Africa.

Which one of the following is the most likely explanation for the distribution of these fossils?

- A Antarctica, South America and Africa were joined to Australia in the distant past.
- B The strong tails of the ornithopods enabled them to swim for sustained periods of time.
- C The small forelimbs of the ornithopods suggest that they were evolving wings for flight.
- D Seagoing, scavenger birds carried the fossil bones of the ornithopods to other continents.

113 [VCAA 2016 SA Q38]

In India, a group of scientists was studying fossils from a coal deposit formed during the Permian period (290–245 million years ago). They found three fossil species from the same genus in different levels (strata) of the coal. When radiocarbon dating on these fossils was performed, it showed exactly the same levels of carbon-14 in all three fossil species.

The data is summarised in the table below.

Fossil species	Depth at which fossil was found in the coal deposit (m)	Proportion of carbon-14 (%)
<i>Gangamopteris major</i>	6.2	0.0001
<i>Gangamopteris obliqua</i>	8.1	0.0001
<i>Gangamopteris clarkeana</i>	4.7	0.0001

Which one of the following is the correct conclusion to draw from these findings?

- A There is no evolutionary relationship between these three fossil species.
- B *G. clarkeana* is the common evolutionary ancestor of *G. major* and *G. obliqua*.
- C As carbon dating is a more reliable dating technique than analysis of strata in coal deposits, the fossils of *G. major*, *G. obliqua* and *G. clarkeana* are all of the same age.
- D An analysis of strata in coal deposits is a more reliable dating technique than carbon dating for Permian fossils; the fossil of *G. major* is younger than the fossil of *G. obliqua*.

114 [VCAA 2015 SA Q35]

Potassium-40 has a half-life of 1.25 billion years. In igneous rocks closely associated with a fossil layer, the ratio of potassium-40 to its radioactive breakdown product, argon-40, is approximately 1:1.

The age of the fossils in the fossil layer will be close to

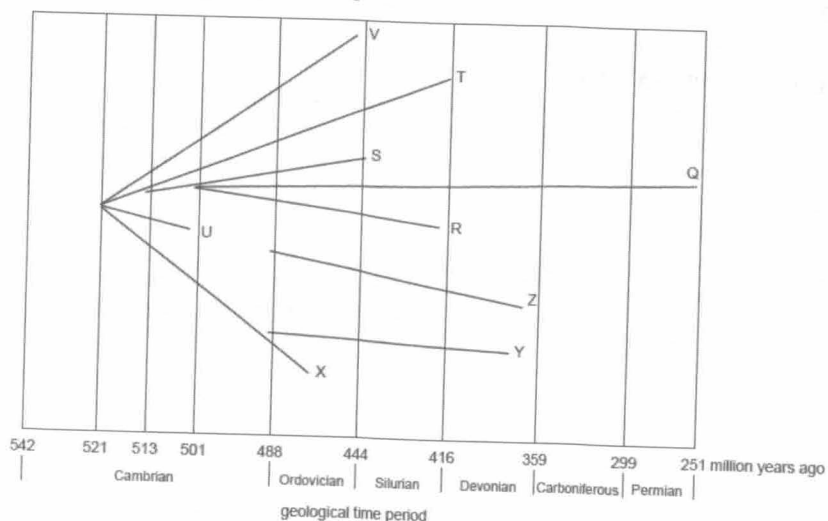
- A 125 million years.
- B 310 million years.
- C 1.25 billion years.
- D 2.5 billion years.

Use the following information to answer Questions 115–118.

Trilobites existed from the Early Cambrian period (521 million years ago) until the end of the Permian period (251 million years ago). The chart below, based on fossil evidence, shows the phylogeny of some trilobite orders present in Earth's oceans over this time.



A trilobite fossil
order: Ptychoparida



115 [VCAA 2014 SA Q34]

Trilobite fossils in a particular layer of rock were used to date a fossil shell in the same layer. A palaeontologist dated the fossil shell to 328–359 million years old.

It is most likely that the trilobite fossils present were of the order

- A Y.
- B U.
- C Q.
- D T.

116 [VCAA 2014 SA Q35]

The absolute age of the trilobite fossils was most likely determined by using

- A carbon dating.
- B transition fossils.
- C index fossils.
- D potassium-argon dating.

117 [VCAA 2014 SA Q36]

The geological time periods shown on the chart differ in duration because the time periods reflect

- A the diversity of fossils and mass extinction events.
- B the absence of trilobite fossils in the Late Cambrian period.
- C different rates of radioactive decay.
- D different rates of fossilisation.

118 [VCAA 2014 SA Q37]

The chance of a trilobite becoming fossilised is increased by

- A slow burial of its remains in dry sediment.
- B large temperature variations in the sediment containing its remains.
- C the presence of hard body parts.
- D the presence of scavengers at the time of its death.

119 [VCAA 2013 SA Q31]

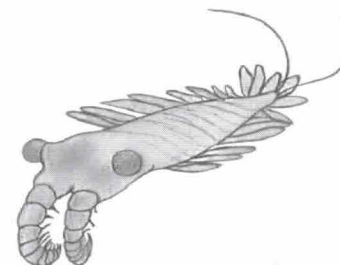
The thylacine (*Thylacinus cynocephalus*) was a large, dog-like marsupial that was declared extinct in 1986. A mummified carcass of a thylacine was found in a cave on the Nullarbor Plain. The carcass was dated about 5000 years old.

The most likely method used to date the mummified carcass would involve

- A dating the layers of rocks within the cave.
- B potassium-argon dating of the mummified remains.
- C measuring the proportion of carbon-14 atoms in the carcass.
- D comparing the teeth in the mummified carcass to the teeth of other dog-like marsupials.

Use the following information to answer Questions 120–122.

Anomalocaris fossils have been found at Emu Bay in South Australia. *Anomalocaris* was a predatory, shrimp-like invertebrate measuring 60 cm in length. It had long, spiny, frontal appendages and a powerful, disc-shaped mouth made of overlapping, hard plates. The Emu Bay fossils were found in layers of shale and dated back to about 520 million years ago. *Anomalocaris* fossils that have been found around the world suggest that this genus existed for at least 50 million years.



120 [VCAA 2012 E2 SA Q16]

Factors that would have contributed to the fossilisation of this animal include

- A its predatory way of life.
- B the action of waves and currents.
- C the salt content of the water in which it lived.
- D its hard-plated mouth and spiny appendages.

121 [VCAA 2012 E2 SA Q17]

In order to estimate the age of *Anomalocaris* fossils, paleontologists would have most likely used

- A index fossils.
- B carbon-14 dating.
- C a molecular clock.
- D DNA hybridisation.

122 [VCAA 2012 E2 SA Q18]

A likely explanation for the extinction of *Anomalocaris* is that

- A its populations had high genetic diversity.
- B its disc-shaped mouth was unsuitable for ingesting prey.
- C it produced offspring that were suited to their environment.
- D selection pressures changed dramatically due to rapid climate change.

123 [VCAA 2011 E2 SA Q12]

The technique of carbon dating would be most suitable for dating organic remains that are aged

- A 4 000 000 000 years and beyond.
- B 4 000 000 years.
- C 400 000 years.
- D 40 000 years.

124 [VCAA 2015 SA Q36]

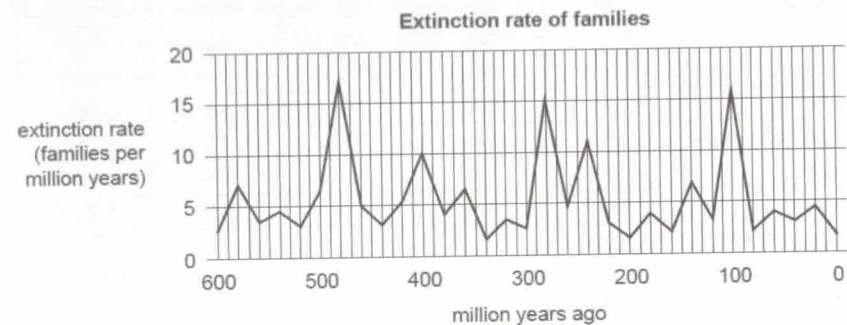
Biologists have found evidence for mass extinction events in Earth's history at approximately 65 million years ago (mya) and at approximately 200 mya. The fossil record indicates a rapid increase in diversity of species after these mass extinction events.

This increased diversity of species can be explained by

- A decreased mutation rates associated with the extinction event.
- B increased numbers of fossils produced by the extinction event.
- C populations of species returning to their pre-extinction event size.
- D the extinction of many species providing many unoccupied niches.

125 [VCAA 2019 SA Q29]

Refer to the following graph that shows the extinction rate of families.



A scientist stated that a mass extinction occurred when the extinction rate was eight families per million years or greater.

The number of mass extinction events recorded on the graph above is

- A eight.
- B seven.
- C six.
- D five.

126 [VCAA 2017 SA Q33]

Mass extinctions

- A kill all but the most primitive species.
- B are caused by the introduction of competing species.
- C are followed by a period of rapid divergent evolution.
- D have been caused by continental drift and earthquakes.

127 [VCAA 2015 SA Q24]

The genome of the northern white-cheeked gibbon, *Nomascus leucogenys*, has been sequenced and compared to other primate species.

The *N. leucogenys* genome would

- A include only the non-coding DNA sequences.
- B be an uninterrupted, circular sequence of DNA base pairs.
- C be identical to the genome of the black-crested gibbon, *Nomascus concolor*.
- D consist of all the genetic sequences within the haploid cells of individuals of the species.

Use the following information to answer Questions 128 and 129.

Cytochrome c is a protein that consists of 104 amino acids. Many of these 104 sites on cytochrome c contain exactly the same amino acid across a large range of organisms. There are, however, some differences at certain sites. It is hypothesised that different organisms, all containing cytochrome c proteins, descended from a primitive microbe that lived over 2 billion years ago.

The table on the following page uses the three-letter codes for various amino acids found at specific sites for each organism.

Molecular homology of cytochrome c

Organism	Site 1	Site 4	Site 11	Site 15	Site 22
human	Gly	Glu	Ile	Ser	Lys
pig	Gly	Glu	Val	Ala	Lys
dogfish	Gly	Glu	Val	Ala	Asn
chicken	Gly	Glu	Val	Ser	Lys
<i>Drosophila</i>	Gly	Glu	Val	Ala	Ala
yeast	Gly	Lys	Val	Glu	Lys
wheat	Gly	Asp	Lys	Ala	Ala

128 [VCAA 2016 SA Q39]

Using only the data for the molecular homology of cytochrome c, which one of the following organisms is most closely related to the dogfish?

- A *Drosophila*
- B chicken
- C human
- D yeast

129 [VCAA 2016 SA Q40]

Using only the data for the molecular homology of cytochrome c, which pair of organisms is most distantly related to wheat?

- A dogfish and *Drosophila*
- B *Drosophila* and yeast
- C *Drosophila* and pig
- D human and yeast

Use the following information to answer Questions 130 and 131.

Chimpanzees are the closest living relatives of humans. Less than 1 per cent of our DNA has changed in the 6 million years or so since the human and chimpanzee lineages diverged.

130 [VCAA 2013 SA Q37]

The measurement of the rate of accumulation of random genetic changes in the genomes of chimpanzees and humans is called

- A stratigraphy.
- B a molecular clock.
- C radiometric dating.
- D relative dating.

131 [VCAA 2013 SA Q38]

Research has shown that in a number of genes the sequence of nucleotides is unique to humans and is not found in chimpanzees.

Gene with sequence unique to humans	Functional role of gene with sequence unique to humans
HAR1	active in the brain necessary for development of the cerebral cortex
FOXP2	facilitates formation of words by the mouth
AMY1	facilitates digestion of starch
ASPM	controls brain size
LCT	permits digestion of milk sugar in adulthood
HAR2	drives gene activity in the wrist and thumb during development

Using the information in the table, it is reasonable to conclude that humans

- A can digest milk sugar only in infancy.
- B have less-opposable thumbs than chimpanzees.
- C are able to walk on two feet in an upright position.
- D process and remember more complex information than chimpanzees.

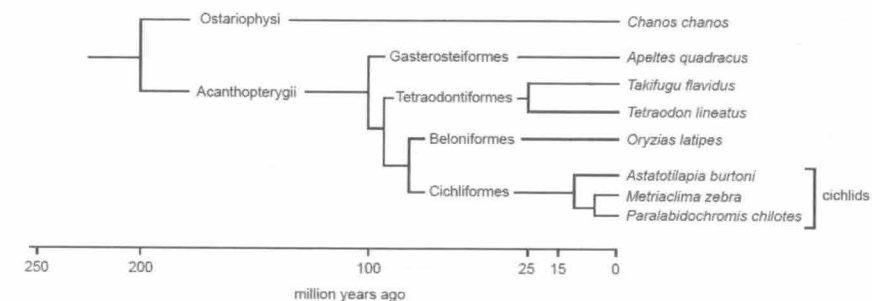
132 [VCAA 2012 E2 SA Q20]

Another source of DNA that could be used to determine evolutionary relationships among eucalypts would be

- A plasmids.
- B ribosomes.
- C mitochondria.
- D reverse copy DNA.

Use the following information to answer Questions 133 and 134.

Consider the following phylogenetic tree, which summarises the evolutionary relationships between certain fish species.



133 [VCAA 2019 SA Q24]

O. latipes is most closely related to

- A *A. quadracus*.
- B *T. lineatus*
- C *P. chilotes*.
- D *T. flavidus*.

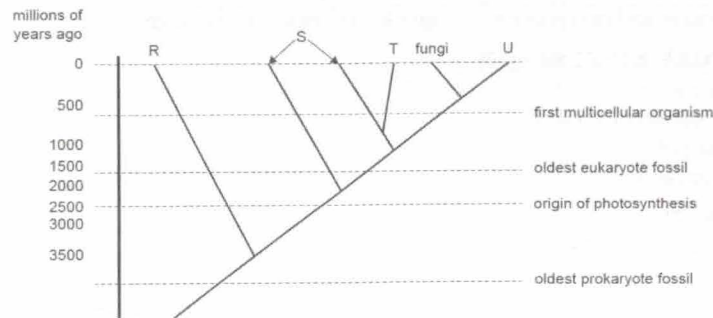
134 [VCAA 2019 SA Q25]

Which one of the following statements is correct?

- A Cichlids diverged to form three distinct species 100 million years ago.
- B *C. chanos* was the last species to diverge from the most distant common ancestor.
- C Gasterosteiformes, Beloniformes and Cichliformes do not share a common ancestor.
- D *T. flavidus* and *T. lineatus* diverged to form two distinct species 25 million years ago.

135 [VCAA 2017 SA Q32]

The phylogenetic tree below represents one model of the order and approximate time of appearance of the major groups of living organisms, and includes four groups represented by the letters R, S, T and U.

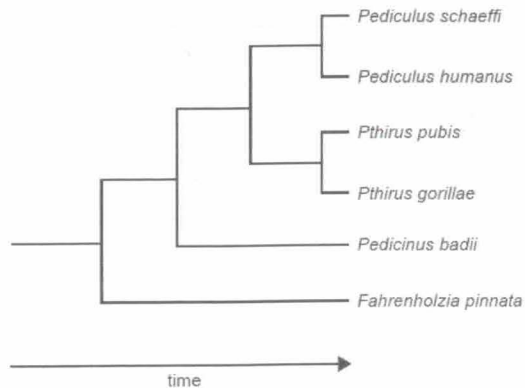


Which of the following shows the correct placement of the organisms on the phylogenetic tree?

- A R – animals, S – plants, T – bacteria, U – protists
- B R – bacteria, S – protists, T – plants, U – animals
- C R – protists, S – animals, T – bacteria, U – plants
- D R – plants, S – animals, T – bacteria, U – protists

136 [VCAA 2016 SA Q29]

Consider the following phylogenetic tree for different species of lice. The tree has been constructed based on molecular and morphological data.

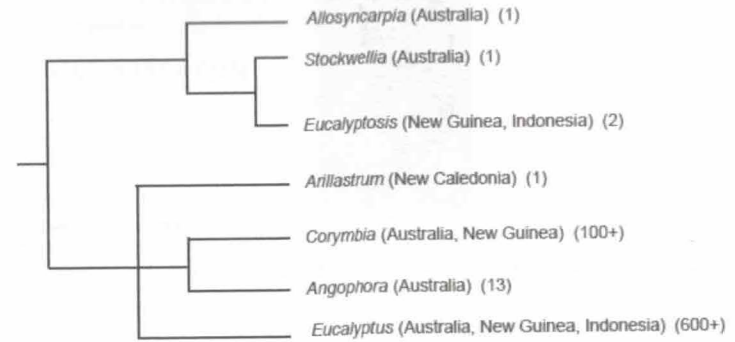


This information suggests that

- A *Pedicinus badii* shares a more recent common ancestor with *Pthirus gorillae* than with *Fahrenholzia pinnata*.
- B *Pediculus humanus* is more closely related to *Pedicinus badii* than it is to *Pthirus pubis*.
- C the six species of lice would have evolved by convergent evolution.
- D *Pediculus schaeffi* is the ancestor of *Pediculus humanus*.

137 [VCAA 2012 E2 SA Q19]

A proposed phylogeny for the seven genera is shown in the diagram below, along with the countries in which they are found.



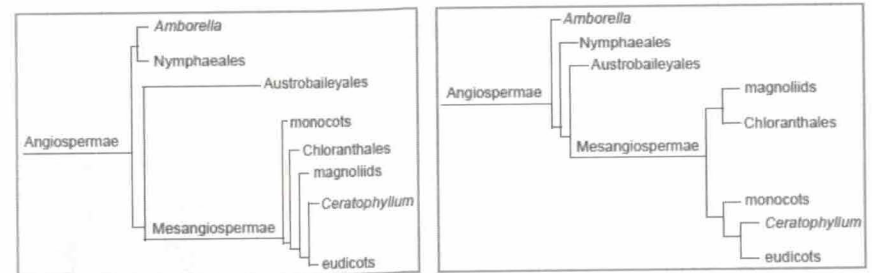
Key Numbers in brackets () refer to the numbers of species in the genus.

It would be reasonable to conclude that

- A DNA sequences in *Eucalyptosis* would be more similar to those in *Allosyncarpia* than to those in *Stockwellia*.
- B speciation in *Eucalyptus* was assisted by different selecting pressures.
- C the greater the number of species in a genus, the younger the genus.
- D the genus that evolved most recently was *Angophora*.

138 [VCAA 2011 E2 SA Q23]

Two possible phylogenetic relationships between eight groups of flowering plants are shown in the following diagrams.



One similarity between the alternatives is

- A monocots diverged before Chloranthales.
- B *Ceratophyllum* and eudicots diverged from monocots.
- C *Amborella* and Nymphaeales diverged first from Angiospermae.
- D magnoliids were the first group to diverge from Mesangiospermae.



Due to copyright restrictions, this image has been replaced with an equivalent likeness. To view the original image, please visit the VCAA website.

What evidence in the image above enables the primate shown to be classified as a hominoid?

- A the presence of an opposable thumb
- B the absence of claws on the toes
- C the presence of hair
- D the absence of a tail

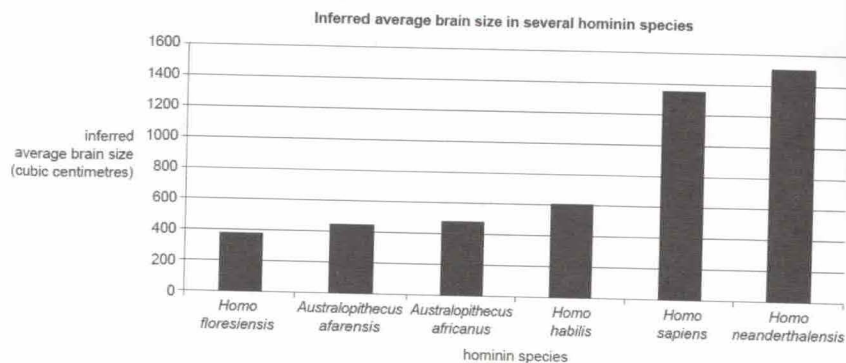
140 [VCAA 2018 SA Q37]

Members of the order Primates are mammals.

Which combination of features is common to all primates and distinguishes them from other mammals?

	Feature 1	Feature 2	Feature 3
A	forward-facing eyes	sloping forehead	fur or hair
B	binocular vision	opposable thumbs	fully rotating shoulder joints
C	parabolic jaw	tail	nails instead of claws
D	even-sized teeth	arms longer than legs	bipedal stance

141 [VCAA 2019 SA Q32]



The graph above shows the inferred average brain size of a number of hominin species.

Based on your knowledge and using the information in the graph, which one of the following species does not follow the general trend in inferred brain size seen in hominin evolution?

- A *H. habilis*.
- B *H. sapiens*.
- C *A. afarensis*
- D *H. floresiensis*

142 [VCAA 2019 SA Q33]

Which row shows the group of characteristics that best reflects the trends in hominin evolution from the *Australopithecus* species to the *Homo* species?

	Characteristics
A	decreasing tooth size, increasing size of brow ridges, increasingly bowl-shaped pelvis, increasing size of zygomatic arch
B	decreasing tooth size, decreasing size of brow ridges, decreasing arch of feet, more-opposable big toe
C	increasing jaw size, decreasing size of zygomatic arch, increasing arch of feet, decreasing tooth size
D	decreasing size of canines, decreasing size of zygomatic arch, increasingly bowl-shaped pelvis, increasing arch of feet

143 [VCAA 2018 SA Q38]

Consider the evolution of hominins.

Which one of the following statements about hominin evolution is correct?

- A *Homo sapiens* and *Homo neanderthalensis* are the only present-day hominin species.
- B Members of the *Australopithecus* genus are not classified as hominins.
- C *Homo erectus* was a bipedal primate.
- D All hominoids are also hominins.

144 [VCAA 2018 SA Q39]

Which general trend is shown by hominin fossils?

- A The older the fossil, the more central the position of the foramen magnum in the skull.
- B The older the fossil, the smaller the braincase that surrounds the cerebral cortex.
- C The more recent the fossil, the less bowl-shaped the pelvis.
- D The more recent the fossil, the larger the jaw bones.

145 [VCAA 2018 SA Q40]

Biologists have suggested that the development of bipedalism was a factor contributing to cultural evolution in hominins.

The advantage of bipedalism that had the greatest impact on cultural evolution was that it allowed

- A improved teamwork and social bonding during ritual dances.
- B food sources to be seen from long distances.
- C the free use of hands to manipulate objects.
- D fast escape from predators.

114 [VCAA 2015 SA Q35]

Potassium-40 has a half-life of 1.25 billion years. In igneous rocks closely associated with a fossil layer, the ratio of potassium-40 to its radioactive breakdown product, argon-40, is approximately 1:1.

The age of the fossils in the fossil layer will be close to

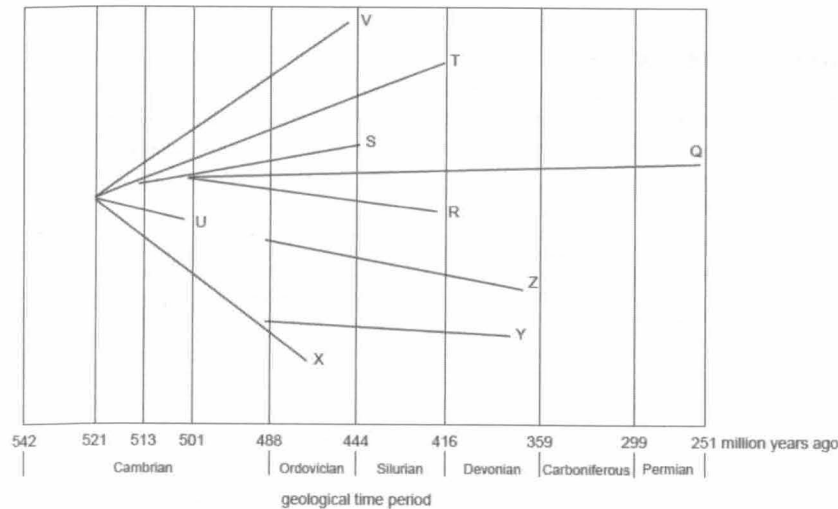
- A 125 million years.
- B 310 million years.
- C 1.25 billion years.
- D 2.5 billion years.

Use the following information to answer Questions 115–118.

Trilobites existed from the Early Cambrian period (521 million years ago) until the end of the Permian period (251 million years ago). The chart below, based on fossil evidence, shows the phylogeny of some trilobite orders present in Earth's oceans over this time.



A trilobite fossil
order: Ptychopariida



115 [VCAA 2014 SA Q34]

Trilobite fossils in a particular layer of rock were used to date a fossil shell in the same layer. A palaeontologist dated the fossil shell to 328–359 million years old.

It is most likely that the trilobite fossils present were of the order

- A Y.
- B U.
- C Q.
- D T.

116 [VCAA 2014 SA Q35]

The absolute age of the trilobite fossils was most likely determined by using

- A carbon dating.
- B transition fossils.
- C index fossils.
- D potassium-argon dating.

117 [VCAA 2014 SA Q36]

The geological time periods shown on the chart differ in duration because the time periods reflect

- A the diversity of fossils and mass extinction events.
- B the absence of trilobite fossils in the Late Cambrian period.
- C different rates of radioactive decay.
- D different rates of fossilisation.

118 [VCAA 2014 SA Q37]

The chance of a trilobite becoming fossilised is increased by

- A slow burial of its remains in dry sediment.
- B large temperature variations in the sediment containing its remains.
- C the presence of hard body parts.
- D the presence of scavengers at the time of its death.

119 [VCAA 2013 SA Q31]

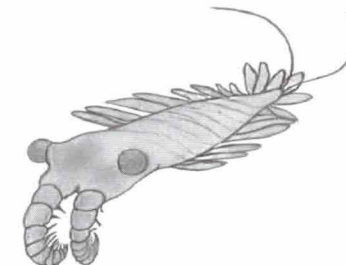
The thylacine (*Thylacinus cynocephalus*) was a large, dog-like marsupial that was declared extinct in 1986. A mummified carcass of a thylacine was found in a cave on the Nullarbor Plain. The carcass was dated about 5000 years old.

The most likely method used to date the mummified carcass would involve

- A dating the layers of rocks within the cave.
- B potassium-argon dating of the mummified remains.
- C measuring the proportion of carbon-14 atoms in the carcass.
- D comparing the teeth in the mummified carcass to the teeth of other dog-like marsupials.

Use the following information to answer Questions 120–122.

Anomalocaris fossils have been found at Emu Bay in South Australia. *Anomalocaris* was a predatory, shrimp-like invertebrate measuring 60 cm in length. It had long, spiny, frontal appendages and a powerful, disc-shaped mouth made of overlapping, hard plates. The Emu Bay fossils were found in layers of shale and dated back to about 520 million years ago. *Anomalocaris* fossils that have been found around the world suggest that this genus existed for at least 50 million years.



152 [VCAA 2014 SA Q40]

The fossils of *H. floresiensis* showed that they had opposable thumbs. The development of an opposable thumb in primate evolution

- A is used to distinguish members of the genus *Homo* from the other great apes.
- B was a necessary step in the development of bipedalism in hominins.
- C was an important anatomical development that assisted tool-making in hominins.
- D is a significant factor in determining the arm-to-leg ratio of modern humans.

Short-answer questions

153 [VCAA 2020 SB Q7]

Only 35% of the world's adult human population can digest lactose, which is found in milk. These people continue to produce the enzyme lactase throughout their lives. Most people who can digest lactose have European ancestry. There is evidence that people kept animals for milk in Europe 10 500 years ago. About 7500 years ago in central Europe, a gene mutation occurred in the lactase gene, where cytosine was replaced by thymine. The allele produced by this mutation allows individuals to produce lactase and to digest lactose throughout their lives.

Researchers have estimated that populations in Europe with this mutation produced more offspring than populations who did not have this mutation.

- a Name the type of mutation that occurred 7500 years ago in central Europe. [1 mark]
- b i The increase in frequency of the allele for lactase persistence happened relatively quickly in some populations. Explain why the frequency of this allele increased relatively quickly. [3 marks]
- ii In some present-day populations there are no individuals with the mutation. Give **two** reasons for the absence of the mutation in these populations. [2 marks]
- c Cows are the main source of milk in Europe. Modern dairy cow breeds can produce 25 L of milk each day – much more than their wild ancestors. Describe how an increase in production of cow's milk could be achieved by farmers over many generations of cows. [2 marks]

[Total 8 marks]

154 [VCAA 2019 SB Q6]

From 10 weeks into pregnancy, a woman can decide to have a non-invasive prenatal test that detects fetal aneuploidies. A blood sample is taken from the woman for the test.

- a i What does aneuploidy refer to? [1 mark]
- ii What would scientists examine in the woman's blood sample? [1 mark]

If there is a requirement to look for other genetic abnormalities, such as block mutations, different procedures can be conducted.

- b Describe **two** different types of block mutations. [2 marks]

Some procedures can detect single gene mutations. Sickle-cell anaemia is produced by a single gene mutation that affects the production of the beta chain of the haemoglobin protein (the oxygen-carrying protein that makes blood cells red). Beta haemoglobin is a single chain consisting of 147 amino acids.

Shown below is a small section of the mRNA nucleotide sequence found in an individual without the mutation.

5'	AUG	GUG	CAC	CUG	ACU	CCU	GAG	GAG	3'
----	-----	-----	-----	-----	-----	-----	-----	-----	----

The codon table below can be used to determine amino acids coded for by a nucleotide sequence.

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
U	phe	ser	tyr	cys	U
	phe	ser	tyr	cys	C
	leu	ser	STOP	STOP	A
	leu	ser	STOP	trp	G
C	leu	pro	his	arg	U
	leu	pro	his	arg	C
	leu	pro	gln	arg	A
	leu	pro	gln	arg	G
A	ile	thr	asn	ser	U
	ile	thr	asn	ser	C
	ile	thr	lys	arg	A
	met	thr	lys	arg	G
G	val	ala	asp	gly	U
	val	ala	asp	gly	C
	val	ala	glu	gly	A
	val	ala	glu	gly	G

- c Use the section of mRNA provided on the previous page and the codon table above to complete the table below. [2 marks]

Translated sequence	
---------------------	--

- d i The gene for sickle-cell anaemia produces misshapen red blood cells that do not carry oxygen efficiently. In an individual with sickle-cell anaemia, the twentieth nucleotide has changed to uracil in the transcribed mRNA provided after part b.

How would this alter the amino acids coded for in this sequence? [1 mark]

- ii If this twentieth nucleotide was deleted, how could this mutation alter the structure and function of the haemoglobin protein produced? [2 marks]

[Total 9 marks]

155 [VCAA 2018 SB Q7]

Populations of the lizard species *Anolis sagrei* are found on the many islands of the Bahamas. There is natural variation between the phenotypes of individuals within each population.

- a Explain how natural variation can exist between individuals within a lizard population. [3 marks]

In 2004 a hurricane killed all populations of *A. sagrei* lizards on seven of the smaller islands. Scientists randomly chose seven males and seven females from a remaining population on a large island. They introduced one male and one female to each of the seven smaller islands. Over the next three years, the scientists noted that the size of the populations increased on each of the seven smaller islands. The scientists measured the genetic diversity within each of the populations and found there was lower genetic diversity in each new population compared with the population on the large island.

b Explain the reasons for the lower genetic diversity of the new populations on the smaller islands compared with the population on the large island.

[2 marks]

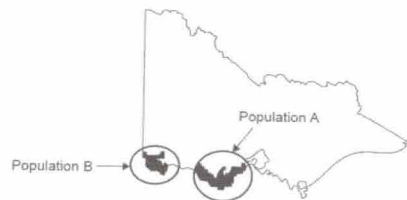
c The scientists noted that after three years there was a significant decrease in the average length of the hind legs of the lizards living on the smaller islands compared with those on the large island. Explain what may have happened on the smaller islands to produce this decrease in the average length of hind legs.

[2 marks]

[Total 7 marks]

156 [VCAA 2017 SB Q5]

The rufous bristlebird (*Dasyornis broadbenti*) is a ground-dwelling songbird. The rufous bristlebird is found in gardens near thick, natural vegetation and builds nests in shrubs close to the ground. The rufous bristlebird feeds on ground-dwelling invertebrates. It is a weak flyer and is slow to go back to areas from which it has been previously eliminated. Two distinct populations of rufous bristlebird exist in Victoria. The distribution of each population is shown on the map of Victoria below. The distance between Population A and Population B is over 200 km.



Source: *Flora & Fauna Guarantee Action Statement*, 1993, no. 49; © The State of Victoria, Department of Sustainability and Environment, 2003

a Define the term 'gene flow' and explain whether gene flow is likely to occur between these two populations.

[3 marks]

b Both of the rufous bristlebird populations in Victoria are small. Referring to the theory of natural selection, explain why the rufous bristlebird is at risk of extinction.

[3 marks]

[Total 6 marks]

157 [VCAA 2017 SB Q10]

Aboriginal Australians co-existed with the megafauna for at least 17 000 years

Australia was once home to giant reptiles, marsupials and birds known as megafauna. Many researchers have suggested a rapid extinction model to account for the extinction of megafauna thought to have occurred soon after the arrival of the First Australians¹.

The First Australians regularly burnt the landscape to encourage new growth for food and to attract prey for hunting. Perhaps this burning dramatically altered ancient Australia's ecology. One species, the giant flightless bird *Genyornis newtoni*, was shown to have succumbed to significant habitat change and excessive hunting.

In contrast, other evidence shows no record of fire-sensitive plants going through genetic bottlenecks as a result of significant burning events. Furthermore, evidence suggests that for tens of thousands of years, Aboriginal populations were not that large. Some researchers have argued that it is possible many of the 45 or so megafauna species thought to have become extinct may have in fact become extinct tens of thousands of years before the First Australians arrived.

If it can be shown that megafauna disappeared soon after the arrival of the First Australians, then there is support for the rapid extinction model. On the other hand, proof that megafauna and people co-existed suggests that other explanations for their extinction need to be proposed.

Recent dating of a specimen of *Zygomaturus trilobus*, a large wombat-like marsupial, showed that the specimen died around 33 000 years ago. This evidence suggests that people and megafauna co-existed for at least 17 000 years.

It is now possible that the rapid extinction model needs to be abandoned and researchers need to start to untangle how climate may have played a role or how changes in Aboriginal population numbers may have impacted on the ecology of the megafauna.

¹First Australians – the ancestors of Aboriginal Australians

Source: extract adapted from M Westaway (Griffith University), J Olley (Griffith University), R Grun (Griffith University), 'Aboriginal Australians co-existed with the megafauna for at least 17 000 years', The Conversation website, 12 January 2017, www.theconversation.com/au

a Using the information in the text, explain how the rapid extinction model may account for the extinction of Australia's megafauna.

[3 marks]

b Complete the following table by identifying three pieces of evidence in the text that cast doubt on the rapid extinction model. Justify how each piece of evidence can be used to reject the rapid extinction model.

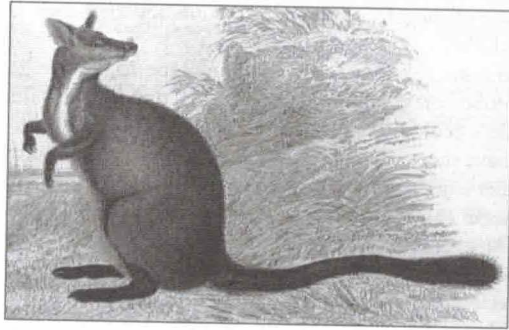
Evidence	Justification
1	
2	
3	

[6 marks]

[Total 9 marks]

158 [VCAA 2013 SB Q9]

The southern brush-tailed rock wallaby (*Petrogale penicillata*) is threatened with extinction in Victoria. Since European settlement, it has suffered from hunting for its fur, clearing of habitat and predation by foxes. Early in 2012, the population of brush-tailed rock wallabies in the Grampians National Park numbered only four individuals.



Source: Richard Lydekker, *A Hand-book to the Marsupialia and Monotremata*, R Bowdler Sharpe (ed.), WH Allen & Co. Limited, London, 1894

a What is meant by extinction? [1 mark]

Eighteen brush-tailed rock wallabies were released into the Grampians in late 2012. The wallabies had been bred in captivity in zoos and nature reserves in Victoria, South Australia, New South Wales and the Australian Capital Territory. Care was taken to ensure that the gene pool of the released wallabies was as diverse as possible.

b i What is a gene pool? [1 mark]
 ii Using your knowledge of natural selection, explain why it is an advantage to have a diverse gene pool among the released wallabies. [2 marks]

Wildlife officers are hoping that the Grampians population will increase to at least 50 wallabies in five years and that it will be maintained over time. A small population of wallabies could be affected by **genetic drift** and, possibly, a genetic **bottleneck effect**.

c Explain the meaning of each of these terms with reference to allele frequencies. [2 marks]

The Grampians wallabies will be closely monitored by surveillance cameras and radio collars after their release.

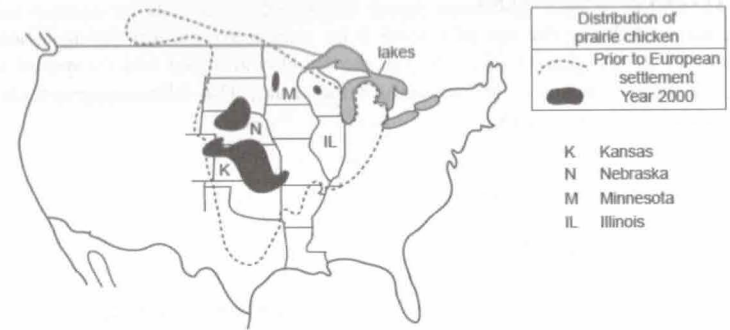
d Suggest one further measure that wildlife officers should carry out to help maintain the population over time. [1 mark]

[Total 7 marks]

159 [VCAA 2011 E2 SA Q6]

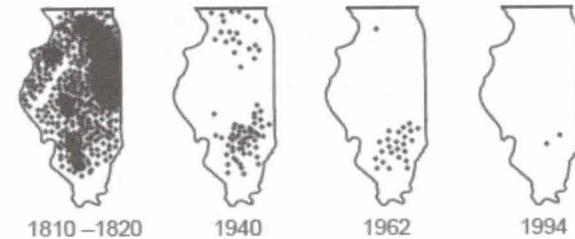
a Define 'genetic drift'. [1 mark]

The prairie chicken (*Tympanuchus cupido pinnatus*) is a grassland bird native to North America. A prairie chicken spends its entire life within several kilometres of its birthplace. Prior to European settlement, prairie chickens numbered in the millions across the Midwest of the United States of America. As a result of the grasslands being replaced by plant food crops, the distribution of prairie chickens has diminished, as shown in the diagram on the next page.

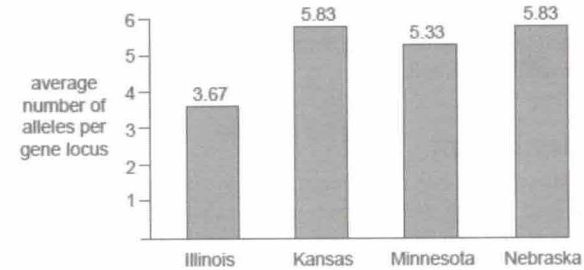


By 1994, Kansas, Nebraska and Minnesota still supported large and widespread populations; however, in the state of Illinois, the number of prairie chickens fell to less than fifty individuals isolated in two separate geographical areas.

Illinois – prairie chicken distribution



Representative samples of prairie chickens from the four states were selected for testing. Each prairie chicken had six gene loci tested. The average number of alleles at each gene locus for each prairie chicken group is shown in graph below.



b i Explain the significance of the results for the Illinois birds compared to the results of the birds from the three other states. [2 marks]

ii Explain why the results for the Kansan birds and Nebraskan birds are similar to each other. [1 mark]

Measures were taken in the 1990s to prevent the Illinois prairie chicken from dying out completely.

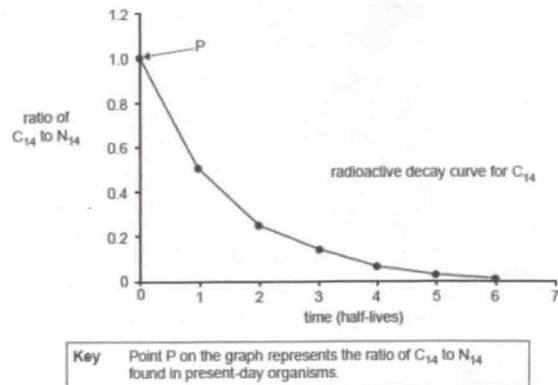
c i Explain why low genetic diversity in a population threatens the survival of the population. [2 marks]

ii Describe one measure that could be used to prevent the Illinois prairie chicken from dying out. [1 mark]

[Total 7 marks]

160 [VCAA 2012 E2 SB Q6]

One form of dating the age of a fossil is by radioactive carbon dating. The ratio of carbon-14 to nitrogen-14 ($C_{14} : N_{14}$) in the fossil is analysed and compared with the ratio of these elements in an organism living today. The following graph shows the rate of decay for carbon-14.



A fossil kangaroo skull was found in a limestone cave. The skull's $C_{14} : N_{14}$ ratio was analysed and found to contain one-quarter ($1/4$) of the carbon-14 of a kangaroo that died in 2012.

- a i Place an X on the curve to show the fossil's $C_{14} : N_{14}$ ratio. [1 mark]
 ii Given the half-life of carbon is approximately 6000 years, what is the approximate age, in years, of the kangaroo skull? [1 mark]

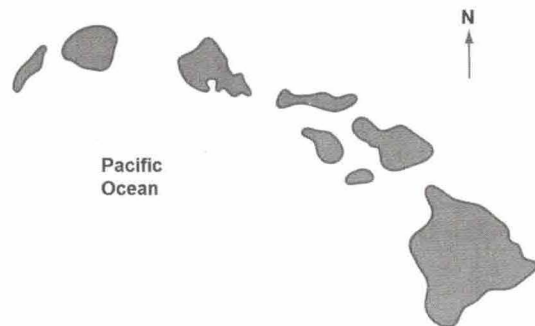
Carbon-dating analysis is not always possible and the age of the fossil can be estimated by dating the rock in which it is found.

- b i Why is carbon-dating analysis not always possible? [1 mark]
 ii Name another absolute dating technique that can determine the age of the rock surrounding a fossil. [1 mark]

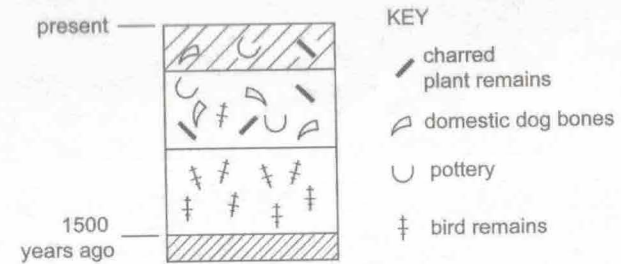
[Total 4 marks]

161 [VCAA 2010 E2 SB Q7]

The islands of Hawaii in the Pacific Ocean were formed as a result of volcanic action in which small land masses were thrown up by submarine volcanoes. The youngest of the islands lies to the east of the oldest.

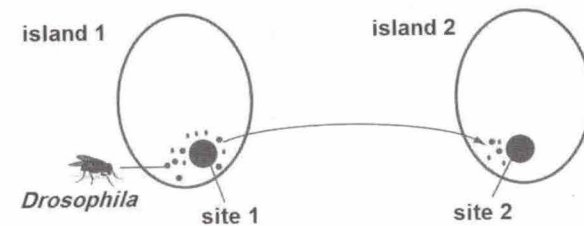


A similar pattern of deposition has been found across all islands, shown by the profile below.



- a What assumption is made about the formation of strata when interpreting profiles such as this? [1 mark]
 b i State a hypothesis to account for the disappearance of many of the bird species from the groups of islands. [1 mark]
 ii Provide evidence to support your hypothesis. [1 mark]

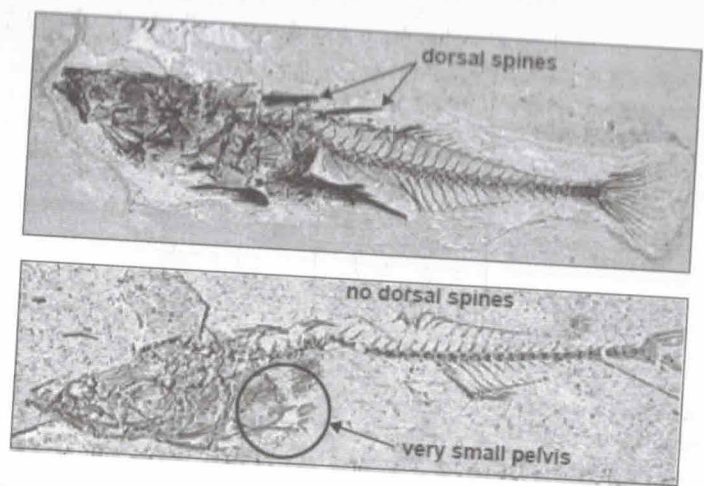
Biologists studied many species of the fruit fly, *Drosophila*, living on the Hawaiian islands. The species vary widely in appearance, behaviour and habitat. The diversity of *Drosophila* can be explained by the successive colonisation of newly formed islands by a small number of individuals 'island-hopping' from the neighbouring westerly island. This is represented in the diagram below.



- c i What name is given to this small group of colonising individuals? [1 mark]
 ii Explain how the new and old colonies became separate species. [3 marks]
 [Total 7 marks]

162 [VCAA 2015 SB Q10]

Scientists studying the fossils in an ancient lake bed have an almost perfect fossil record ranging more than 25 000 years. In this fossil record, there are two forms of a fish called a 'stickleback'. One form has large spines on the back of the fish (dorsal spines) and large pelvic bones. The other form has smaller or no spines and smaller pelvic bones. Modern-day stickleback fish with large dorsal spines are common in the ocean, while the stickleback fish with small spines are more common in fresh water.



The table below contains a summary of some structural features of the fossils found in different sediment layers in the ancient lake bed.

Sediment layer	Pelvis	Dorsal spines
top	small	small or absent
middle	large	large
lower	small	small or absent

- a i Suggest a hypothesis that could explain the change in the structural features seen in the different sediment layers. [1 mark]
 - ii Give evidence from the information provided to support your hypothesis. [2 marks]
 - b Scientists studying modern-day sticklebacks taken from freshwater lakes have discovered that young fish that grow to have small pelvises and small or no dorsal spines grow more quickly and move faster as young fish than those that grow into fish that have larger pelvises and dorsal spines. Outline how the sticklebacks with small pelvises have become more common over time in fresh water. [2 marks]
- [Total 5 marks]

163 [VCAA 2016 SB Q8]

Two species of *Cryptasterina* sea stars are found in coastal Queensland. *Cryptasterina pentagona* is found in warmer water further north, while *Cryptasterina hystera* is found further south in cooler water.



Researchers have concluded that these two species arose from a recent common ancestor via natural selection. They believe that, over thousands of years, the sea

environment has changed, with the boundary line between cold water and warm water moving further north. They have found that water temperature and predation of sea star larvae by cold-water predators are important selection pressures for these sea stars.

- a Using the information above, explain how natural selection can lead to differences in phenotypes between these two sea star species. [4 marks]
 - b One of the phenotypic differences between these two species of sea stars is their method of reproduction. *C. pentagona* reproduces sexually and its sperm and eggs are free-floating in the ocean. *C. hystera* self-fertilises and its fertilised eggs are kept within the sea star until maturity. The researchers found that one species of *Cryptasterina* has a significantly higher diversity of alleles in its gene pool than the other species. Using this information about reproduction strategies, which species of *Cryptasterina* would you expect to have the highest diversity of alleles? Explain your answer. [2 marks]
- [Total 6 marks]

164 [VCAA 2016 SB Q9]

Galápagos tortoises (*Chelonoidis* spp.) can be found on many of the islands that make up the Galápagos Islands. Originally, 14 different species were identified based on the islands on which they lived and on their morphology.

Santa Cruz, the second largest of the Galápagos Islands, has two isolated tortoise populations. Population A contains more than 2000 individuals covering an area of 156 square kilometres. Population B is a small population of 250 individuals covering an area of 40 square kilometres.

The position of the two populations on the island of Santa Cruz is shown below. The two populations are separated by a distance of 20 kilometres.



In 2015, scientists investigated whether the individuals of the two populations belong to the same species or whether they are two different species.

Average measurements of skull size were calculated for tortoises belonging to both populations A and B. The skulls were measured in six different places. The six measurements were also compared to average measurements taken from skulls of other Galápagos tortoise species. The results are shown in the table on the following page.




Comparisons have been made with three other Galápagos tortoise species.

Measurement position	Average skull measurement (mm)				
	Population B	Population A	<i>Chelonoidis vicina</i>	<i>Chelonoidis chathamensis</i>	<i>Chelonoidis ephippium</i>
1	118	98	86	80	74
2	40	37	28	27	25
3	21	18	16	14	12
4	26	23	21	18	17
5	10	9	8	7	6
6	19	17	16	14	13

- a Consider the data given.
Does the data support the hypothesis that individuals in Population A belong to a different species from individuals in Population B? Explain your answer. [2 marks]
- b Scientists have carried out genetic studies on the two populations.
Give an example of genetic evidence that may be produced by scientists to support the hypothesis that individuals of the two populations belong to different species. Explain your answer. [2 marks]
- c Some scientists thought that allopatric speciation may have occurred on the island of Santa Cruz.
i Name a feature that scientists would look for in the island environment to support the occurrence of allopatric speciation. [1 mark]
ii Explain how the feature named in part c.i. could contribute to allopatric speciation. [2 marks]
- [Total 7 marks]

165 [VCAA 2019 SB Q7]

Consider the information provided on the three species shown in the table that follows.

Species	rock hyrax	elephant	dugong
			
Size	small terrestrial mammal (2–5 kg)	large terrestrial mammal (4500–6000 kg)	mid-sized marine mammal (150–300 kg)

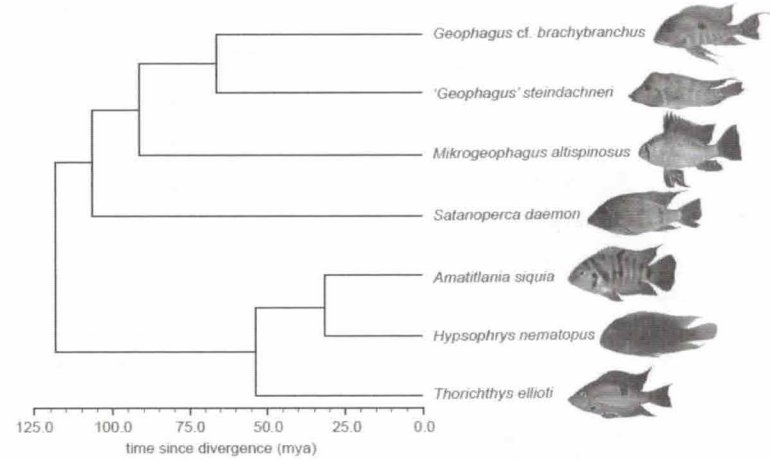
Due to copyright restrictions, these images have been replaced with equivalent likenesses. To view the original images, please visit the VCAA website.

- a These three species are closely related, sharing a relatively recent common ancestor, but have different features.
Identify the type of evolution involved. Justify your response. [2 marks]
- In 2014 palaeontologists discovered a frozen, well-preserved, complete specimen of an extinct species, the steppe bison, in Siberia. The intact specimen was dated at 9300 years old.

- b Scientists are debating the cause of the steppe bison's extinction.
Give **one** possible cause of its extinction. [1 mark]
- c Though steppe bison are extinct, palaeontologists know a lot about them as they have found several frozen, intact steppe bison bodies.
Describe what would have occurred to lead to the preservation of the animal from when the steppe bison died to when the frozen, well-preserved remains were discovered. [4 marks]
- [Total 7 marks]

166 [VCAA 2020 SB Q8]

The phylogenetic tree below shows the evolutionary relationship between seven species of cichlid fish.




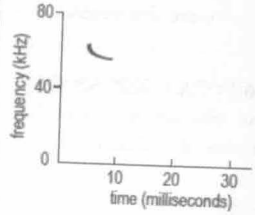

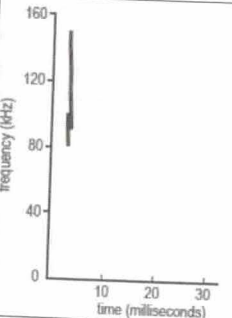

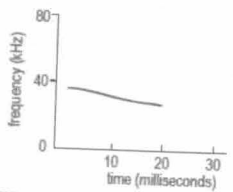
Source: H López-Fernández et al., 'Morphology and efficiency of a specialized foraging behavior, sediment sifting, in neotropical cichlid fishes', *PLoS ONE*, 9(3): e89832, 6 March 2014, <<https://doi.org/10.1371/journal.pone.0089832>>

- a Molecular homology can be used to construct a phylogenetic tree. Based on the information above, state which two species of cichlid fish would be expected to have the most similar amino acid sequences in their proteins. Justify your answer. [3 marks]
- b Fossils of species of fish are more likely to be found than fossils of land-dwelling animals. Explain why this is the case with reference to two conditions required for the fossilisation of an organism. [2 marks]
- c A group of scientists stated that a particular fossilised fish was 5000 years old. Outline a dating technique that could have been used by the scientists to determine the age of the fossil. [2 marks]
- [Total 7 marks]

167 [VCAA 2012 E2 SB Q5]

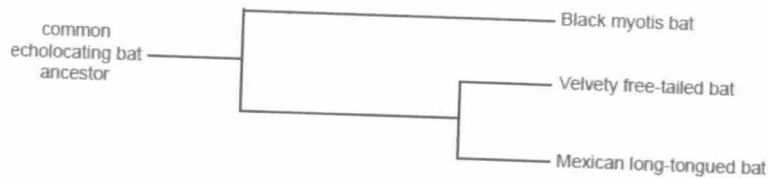
Barro Colorado Island is a small island covered by tropical forest in Central America. Seventy-four different species of bats live in the forest.
Bats are nocturnal, flying mammals. To find their way around in darkness, many bat species emit high-frequency sound pulses that bounce off obstacles and prey. These pulses enable them to judge the distance to an object. This behaviour is called echolocation.

Three of the Barro Colorado Island species are described in the table that follows.

Species name	Facial appearance of bat	Diet	Feeding location	Echolocation signal
Black myotis bat (<i>Myotis nigricaris</i>)		insects	around trees at forest's edge and in clearings	
Mexican long-tongued bat (<i>Choeronycteris mexicana</i>)		Nectar and pollen flowers that open at night, for example cactus, agave	narrow gaps and small spaces	
Velvety free-tailed bat (<i>Molossus molossus</i>)		Insects	above trees, in open spaces	

- a From the information provided, state one selection pressure operating on the bats of Barro Colorado Island. [1 mark]
- b i In terms of time, which of the three species emits the longest echolocation signal? [1 mark]
- ii Explain how this could be a selective advantage for this bat species. [1 mark]
- c A biologist suggested that the three species shown evolved from a recent common ancestor. What is this type of evolution called? [1 mark]

The biologist wanted to establish the order in which each species had evolved from the common ancestor. DNA hybridisation between the various species was carried out. After analysing the results, the scientist drew the following phylogenetic tree.

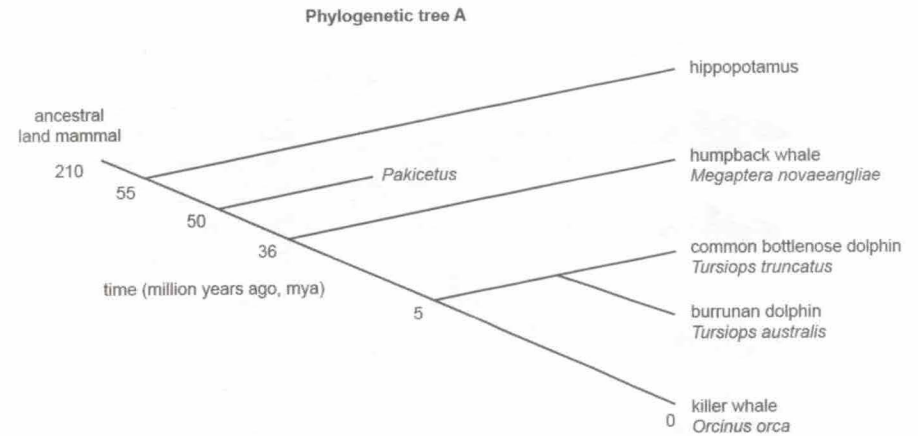


- d What results would have been obtained from the DNA hybridisation that led the biologist to construct this phylogeny? [2 marks]
- e A student suggested that the evolution of the three species was an example of allopatric speciation. Explain why you agree or disagree with the student. [2 marks]
- [Total 8 marks]

168 [VCAA 2018 SB Q9]

Cetaceans (whales, porpoises and dolphins) are marine mammals belonging to the order Artiodactyla (even-toed hoofed mammals). The closest living relatives of cetaceans are the hippopotamuses.

Phylogenetic tree A summarises the evolutionary relationships of four present-day cetacean species and the hippopotamus.

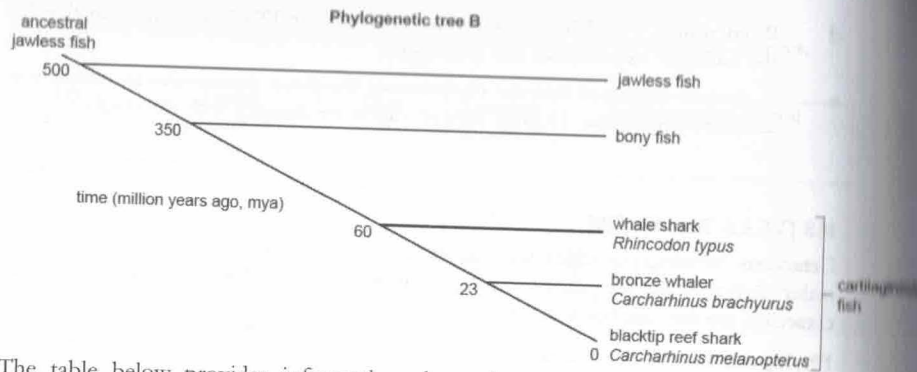


- a What does the length of the line that represents the evolution of *Pakicetus* suggest? [1 mark]
- b A fossil named *Ambulocetus* was found in 1992 and dated at 49 million years old. Some palaeontologists believe that it is a transitional fossil between the ancestral land mammal shown in Phylogenetic tree A and present-day cetaceans.








Predict **two** structural features of the *Ambulocetus* fossil that would provide evidence to support the hypothesis that it is a transitional fossil and suggest a survival advantage of each feature. [3 marks]

Sharks are marine fish of the order Chondrichthyes (cartilaginous fish).

Phylogenetic tree B on the following page summarises the evolutionary relationships of three present-day shark species and main fish classes.



The table below provides information about the present-day species shown in phylogenetic trees A and B.

Marine animal		Average length (m)	Diet
	Humpback whale <i>Megaptera novaeangliae</i>	16	filters plankton and krill by sucking water into mouth through baleen plates
	common bottlenose dolphin <i>Tursiops truncatus</i>	4	hunts fish, squid and crustaceans
	burrunan dolphin <i>Tursiops australis</i>	3	hunts fish and squid
	killer whale <i>Orcinus orca</i>	10	hunts sea birds, squid, seals, baleen whales, dolphins, fish, sharks and sea turtles depending on location
	whale shark <i>Rhincodon typus</i>	12	filters plankton, small squid and fish through filter pads and 300 rows of teeth
	bronze whaler <i>Carcharhinus brachyurus</i>	3	hunts squid, bony fish and other cartilaginous fish
	blacktip reef shark <i>Carcharhinus melanopterus</i>	2	hunts small bony fish, squid and shrimp

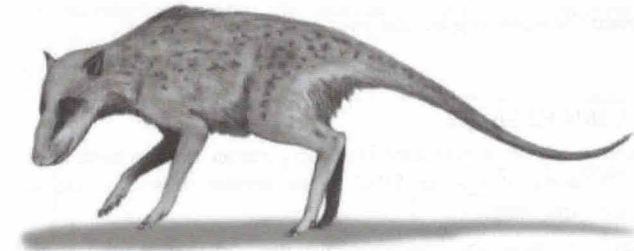
- c i Give a specific example of **divergent** evolution using two animals from the information provided in Phylogenetic trees A & B and the table above and justify your response. [2 marks]
- ii Give a specific example of **convergent** evolution using **two** animals from the information provided in Phylogenetic trees A & B and the table above and justify your response. [2 marks]

In 2011, Australian scientists identified the burrunan dolphin as a separate species from the common bottlenose dolphin. They gathered evidence from living dolphin populations as well as museum specimens.

- d Briefly describe **two** types of evidence that the scientists would have used to establish whether the burrunan dolphin is a separate species from the common bottlenose dolphin. [2 marks]
- e Burrunan dolphins are found only in Port Phillip Bay and the Gippsland Lakes in Victoria. There are only 150 burrunan dolphins alive today. The Port Phillip Bay population is very isolated and rarely mixes with dolphins outside the bay. Port Phillip Bay is impacted by the human population and industry of Melbourne and surrounding towns, and is used heavily for recreation, fishing and shipping. Suggest **two** possible future outcomes for the Port Phillip Bay population of burrunan dolphins. Justify each outcome. [2 marks]
- [Total 12 marks]

169 [VCAA 2015 SB Q9]

A fossil of an extinct species called *Indohyus major*, found in northern India, is thought to share a recent common ancestor with the group of living organisms called cetaceans. Cetaceans include dolphins and whales.



Indohyus major

- a Name the type of evolution that describes the relationship between *I. major* and cetaceans. [1 mark]
- For a long time, scientists have believed that cetaceans are related to the group of terrestrial mammals classified as artiodactyls, which includes pigs and hippopotami. The name artiodactyl refers to the shape of the feet or hooves of these animals. To work out the evolutionary relationships between *I. major* and living animals, scientists closely studied their bones and skeletal structures.
- b What name is given to the study of the similarities and differences between the bones and skeletal structures of animals, including fossils of extinct species? [1 mark]

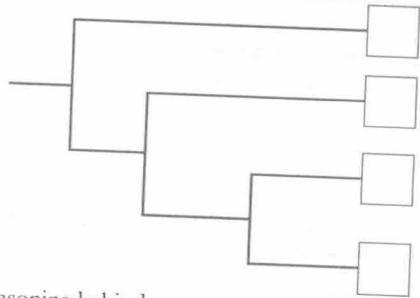
The table below shows a summary of the scientists' findings.

Animal	Feet	Limb bones	Inner-ear bones
cetaceans (e.g. whales)	artiodactyl	thick	thick
suids (e.g. pigs)	artiodactyl	thin	thin
hippopotamids (e.g. hippopotami)	artiodactyl	thick	thin
<i>I. major</i>	artiodactyl	thick	thick

c i Using all the information provided, complete the diagram on the following page to show the evolutionary relationships between the following animals:

A cetaceans (e.g. whales and dolphins)	B suids (e.g. pigs)
C hippopotamids (e.g. hippopotami)	D <i>I. major</i>

Write the corresponding letter of the animal (A.–D.) in the boxes provided. [2 marks]



ii Explain the reasoning behind your response to part c.i. [2 marks]
[Total 6 marks]

170 [VCAA 2010 E2 SB Q6]

DNA sequencing is often performed to help produce phylogenetic trees or to classify organisms. Sections of nuclear DNA from similar organisms are sequenced and compared for similarities.

a Name and describe another DNA method that is used to determine how closely related two species are. [2 marks]

Scientists use a specific mitochondrial gene called *cox1* in comparative studies in fish. The *cox1* gene lacks introns and is only 654 bp long, making it economical and easy to sequence. The sequenced gene appears like a 'barcode' found on grocery products, for example:



A worldwide database has over 45 000 *cox1* gene sequences obtained from different kinds of fish. Illegal fishing occurs in Australian waters. Often only a small portion, such as a fin, is kept by the fishermen and the remainder is thrown overboard.

b How would the barcode database be used to identify the fish species that had been caught by the fishermen? Provide an example of a situation (other than illegal fishing) when humans would want to identify the fish species. [2 marks]

Scientists using the *cox1* gene have seen that even within the same species of fish, differences within the DNA sequence can occur. The scientists believe this is often due to the redundancy in the genetic code.

c Explain what redundancy in the genetic code means. [1 mark]

As the database grows it is hoped that at least five samples for each species will be collected and analysed. The species samples will be taken from as many different locations as possible.

d Why is it important to sequence multiple samples from the same species? [1 mark]
[Total 6 marks]

171 [VCAA 2013 SB Q10]

In humans, severe acute respiratory syndrome (SARS) is a serious form of pneumonia. SARS is caused by a coronavirus that was first identified in 2003.

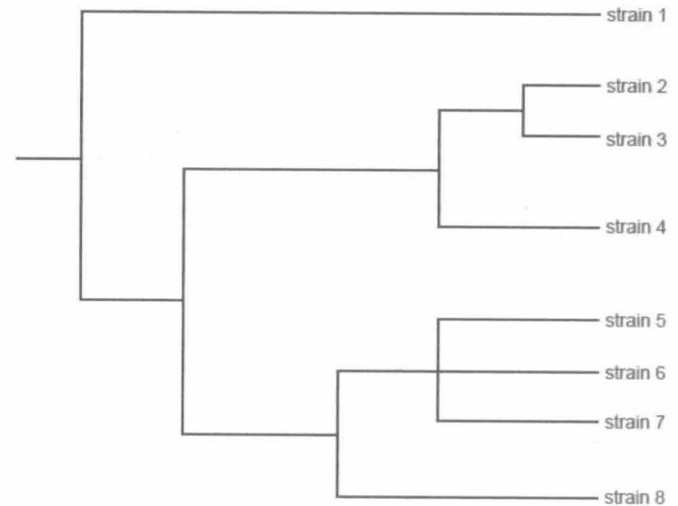
Scientists suspected that the virus had been transmitted to humans from some other animal. Testing was completed on several animal species. Strains of the coronavirus similar to those found in humans were identified in different species of horseshoe bats (genus *Rhinolophus*) and palm civets (*Paguma larvata*).

Samples were taken from the different sources and the virus's RNA from each sample was sequenced.

a What molecular information would the scientists obtain from sequencing RNA? [1 mark]

The molecular information enabled the scientists to draw an evolutionary tree for different strains of the coronavirus.

The following evolutionary tree was drawn.



b Coronavirus strains 2 and 3 are the most similar of the strains. Using your knowledge and the information given in the evolutionary tree, give two possible explanations as to why they are the most similar of the strains. [2 marks]

Strain 7 is found in palm civets, and strains 5 and 6 in humans. All other strains are found in different species of horseshoe bats.

c What conclusion can be drawn about the origin of the strain of virus that causes SARS in humans? [1 mark]
[Total 4 marks]

172 [VCAA 2020 SB Q9]

In 1931 a team of Dutch archaeologists unearthed 12 skulls and two leg bones at a site in Ngandong, Indonesia.

- a Describe two key structural features of these fossils that would suggest that the skulls were from *Homo erectus* rather than from *Homo sapiens*. [2 marks]

Figure 1 and Figure 2 below show *Homo* evolutionary trees that were created in 1997 and 2013 respectively.

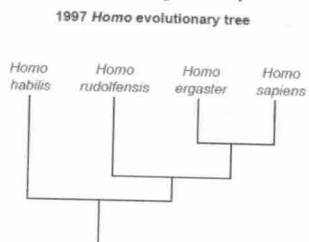


Figure 1

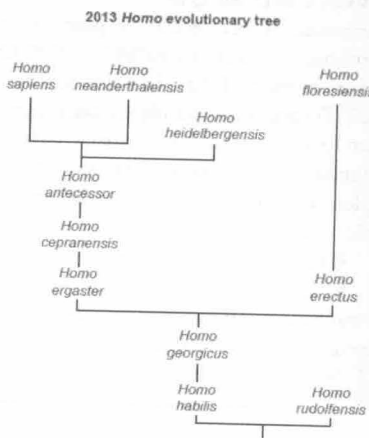


Figure 2

Sources (from left): adapted from DS Strait, FE Grine and MA Moniz, 'A reappraisal of early hominid phylogeny', *Journal of Human Evolution*, volume 32, issue 1, January 1997, pp. 17-82; C Schultz, 'Homo Sapiens' family tree may be less complicated than we thought', *Smithsonian Magazine*, 18 October 2013, <www.smithsonianmag.com>

- b State **one** difference between Figure 1 and Figure 2 with respect to the evolutionary relationships between *Homo ergaster* and *Homo sapiens*. [1 mark]

Homo denisovans is one species that is missing from both evolutionary trees shown in the previous figures.

- c Draw a branch on Figure 2, the 2013 *Homo* evolutionary tree, that represents where you think *Homo denisovans* should be placed. Justify why you have put the branch in that position. [2 marks]

- d Scientists do not always agree on the position of each *Homo* species on evolutionary trees. Explain why this is the case. [2 marks]

[Total 7 marks]

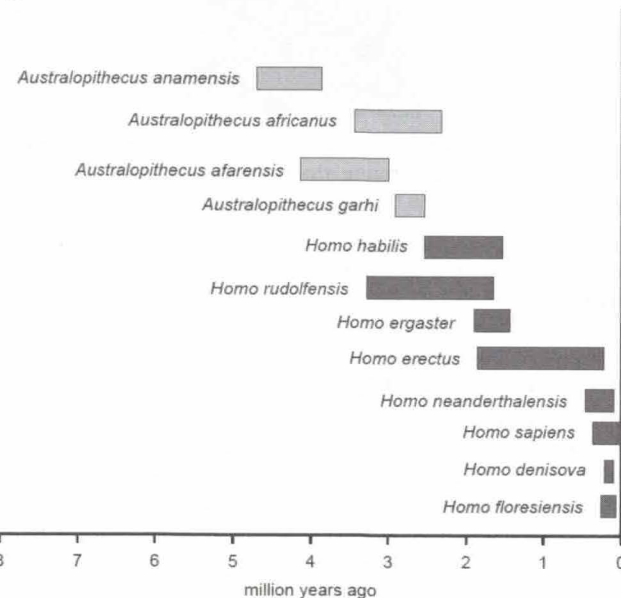
173 [VCAA 2017 SB Q7]

In 2013, about 1500 fossil bones of a hominin species were found in a cave in South Africa. From these bones, scientists have managed to construct an almost complete skeleton. The fossil bones have some features in common with those of the genus *Australopithecus*, however, they have enough similarities to the genus *Homo* that scientists have classified the fossil skeleton as belonging to a new species, *Homo naledi*.

- a What are **two** features that the fossil skeleton would need to have in order to be classified in the genus *Homo* and not in the genus *Australopithecus*? [2 marks]

Finding out the age of these *H. naledi* fossils has been both difficult and controversial. A group of scientists claims that the age of the fossils is more than 2 million years and suggests that *H. naledi* might be a 'link' between *Australopithecus* and *Homo*. A second group of scientists has calculated the age of the *H. naledi* fossils to be only about 900 000 years and claims that *H. naledi* cannot be the 'link' between *Australopithecus* and *Homo*.

The diagram that follows indicates the time periods for different *Australopithecus* and *Homo* species.



- b If the second group of scientists has correctly dated the *H. naledi* fossils, what evidence from the diagram above supports this group's claim that *H. naledi* cannot be the 'link' between *Australopithecus* and *Homo*? [1 mark]

[Total 3 marks]

174 [Adapted VCAA 2016 SB Q10]

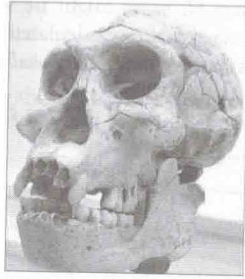
Over the past 20 years, a number of new hominin fossils have been discovered. *Homo erectus georgicus* was found near the banks of the Black Sea in Georgia and *Homo naledi* was found in a cave in South Africa.

- a Consider the conditions that may have led to the fossilisation of members of these species.

Complete the table below by identifying one condition in the environment of each species that will have made fossilisation possible. The same answer cannot be used for both species. [2 marks]

Species	Environment	Condition
<i>H. erectus georgicus</i>	Near the banks of the Black Sea	
<i>H. naledi</i>	Cave in South Africa	

Shown below is a photograph of a skull of *H. erectus georgicus*. Scientists compared this skull to that of modern humans (*Homo sapiens sapiens*).



- b Describe any two features of the skull shown in the photograph above that allowed scientists to determine that this was a much earlier species of the genus *Homo* than modern humans (*H. sapiens sapiens*). [2 marks]
- c Describe one structural feature (other than skull structure) of *H. naledi* that would indicate it is a more modern species than members of the genus *Australopithecus*. [1 mark]

[Total 5 marks]

175 [Adapted VCAA 2012 E2 SB Q8]

In 2008, two incomplete, fossilised skeletons were found in cave deposits in South Africa. The scientists compared the newly discovered bones with those of members of the genus *Australopithecus*, early *Homo*, modern humans and apes. The fossilised skeletons, named *Australopithecus sediba*, displayed an unusual mix of characteristics. They partly resembled primitive, ape-like animals.

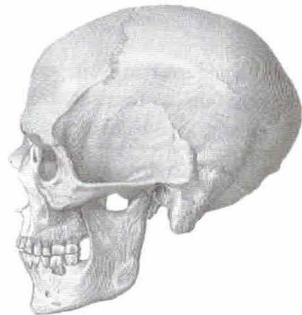
Like the apes, *A. sediba* was of small stature. Scientists determined that *A. sediba*, like apes, was suited to climbing in trees.

- a What feature of the *A. sediba* skeleton allowed scientists to reach this conclusion? [1 mark]

A. sediba was found to have many characteristics in common both with the members of the genus *Australopithecus* and with the genus *Homo*. Two characteristics shared with the genus *Homo* included a projecting nose and hands with a precision grip.

- b Explain how each of these characteristics may have given *A. sediba* an advantage over other *Australopithecus* species. [2 marks]

Below is a drawing of the skull of a modern-day human.



- c Using the drawing, suggest one feature of modern-day humans that makes humans more advanced than other *Homo* species. Explain the significance of this feature to the evolution of modern humans. [2 marks]

[Total 7 marks]

176 [VCAA 2019 SB Q10]

Neanderthal or Denisovan?

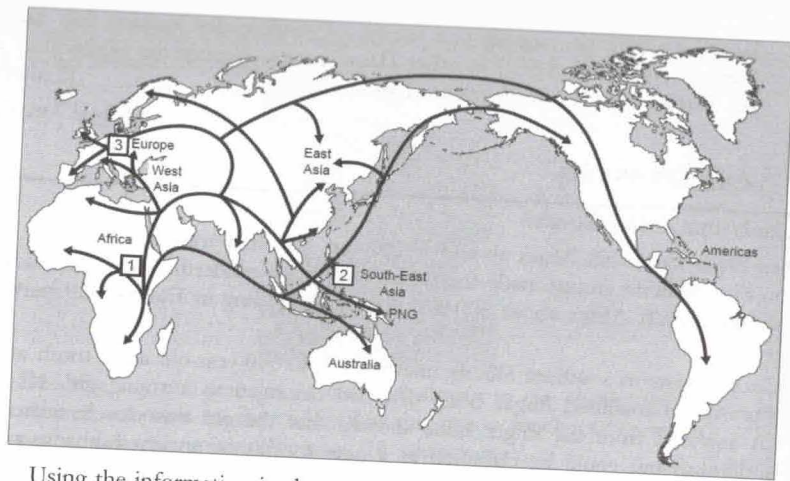
When *Homo sapiens* left Africa about 60 000 years ago, they were not alone. At least two other hominin groups made the same journey – Neanderthals and Denisovans. Neanderthals left Africa about 300 000 years ago, settling in Europe and parts of western Asia.

Anthropologists in southern Siberia unearthed a 40 000-year-old adult tooth and a well-preserved fossilised finger bone that had belonged to a young girl. Nuclear DNA analysed from the finger bone showed that the girl was closely related to Neanderthals but could be classified as a new species of ancient humans, which scientists named ‘Denisovan’.

The scientists found similarities between the Denisovan genome and that of some present-day Pacific Islanders living in Papua New Guinea (PNG), known as the Melanesians. It appears the Denisovans contributed between 3–5% of their genetic material to the genomes of the Melanesians. The scientists think the most likely explanation is that Denisovans living in eastern Eurasia interbred with the modern human ancestors of the Melanesians. When those humans crossed the ocean to reach PNG around 45 000 years ago, they brought their Denisovan DNA with them.

Studies of modern human DNA concluded that most humans with European ancestry have 1–3% Neanderthal DNA. According to one theory, Neanderthals, Denisovans and modern humans are all descended from the ancient human *Homo heidelbergensis*. Between 400 000 and 300 000 years ago, an ancestral group of *H. heidelbergensis* left Africa and then split shortly after. One branch ventured north-west into West Asia and Europe and became the Neanderthals. The other branch moved east, becoming the Denisovans. By 130 000 years ago, *H. heidelbergensis* in Africa gave rise to *H. sapiens*, who did not leave Africa until about 60 000 years ago.

- a Based on the information given in the article, would it be possible to classify Denisovans as a separate group from Neanderthals without using DNA analysis? Justify your response. [2 marks]
- b Scientists could have extracted mitochondrial DNA from the young girl’s finger bone sample but, instead, extracted and sequenced nuclear DNA. Explain why the scientists chose to sequence the nuclear DNA for this sample. [2 marks]



c Using the information in the article and by referring to the map above, name which hominin group would most likely have been found living at each site between 300 000 and 60 000 years ago. Justify your response.

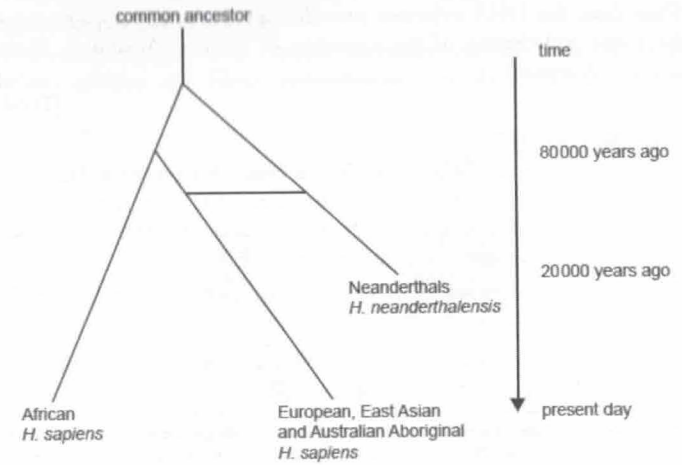
Site	Name of hominin group	Justification
1 – Africa		
2 – South-East Asia and Papua New Guinea		
3 – Europe		

[3 marks]
[Total 7 marks]

177 [VCAA 2015 SB Q11]

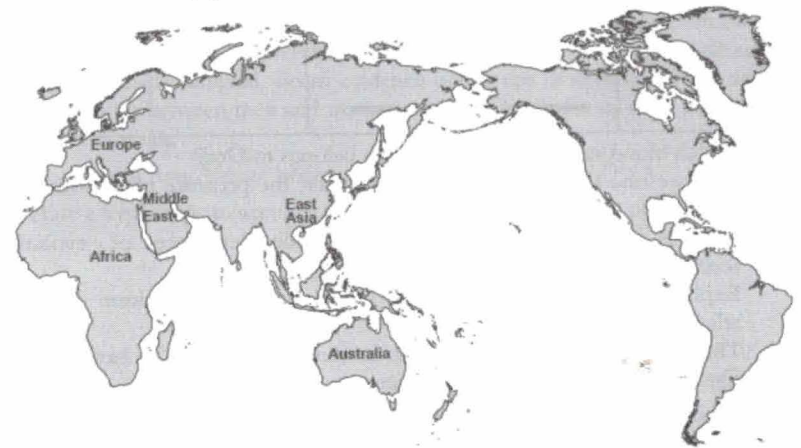
Fossil evidence indicates that between 30 000–80 000 years ago, populations of the two hominin species – modern humans (*Homo sapiens*) and the extinct Neanderthals (*Homo neanderthalensis*) – lived close to one another in parts of the Middle East, Europe and Asia.

Researchers have constructed a theory about the relationships between ancient populations. This is represented in the diagram on the next page.



Recent DNA evidence has shown that:

- the genome of living humans of African descent does not contain Neanderthal DNA
 - the genomes of living humans of European, East Asian and Australian Aboriginal descent all contain small amounts of Neanderthal DNA (1–4%).
- a i Suggest how DNA from *H. neanderthalensis* entered the genome of present-day European, East Asian and Australian Aboriginal *H. sapiens*, and continues to be found in modern populations. [2 marks]
- ii What implication does this DNA evidence have for the classification of the two hominin species, *H. sapiens* and *H. neanderthalensis*, according to the common definition of a species? [1 mark]
- b There are several theories about the geographical origins of *H. sapiens*. Scientists consider that the absence of Neanderthal DNA in present-day African *H. sapiens* lends support to one theory about the geographical origins of *H. sapiens*. Name this theory and explain how the recent DNA evidence provided above supports it. [3 marks]
- c Consider the map provided below.



What does the DNA evidence provided on the previous page suggest about the **route** and **timing** of the migration of the first Australian Aboriginals to arrive in Australia?

[2 marks]

[Total 8 marks]

178 [VCAA 2014 SB Q11]

In 1991, the body of a man was found frozen beneath a glacier in Italy. Researchers named him Ötzi. It was determined that Ötzi died 5300 years ago and that his body is the oldest mummified human body ever found. Scientists have successfully extracted DNA from the nucleus of his frozen cells.

- a Describe the process scientists would use on a small sample of Ötzi's DNA to obtain larger quantities of identical DNA. [3 marks]

Using gel electrophoresis, scientists discovered that there were four different types of blood on Ötzi's clothes. Their results were as follows.

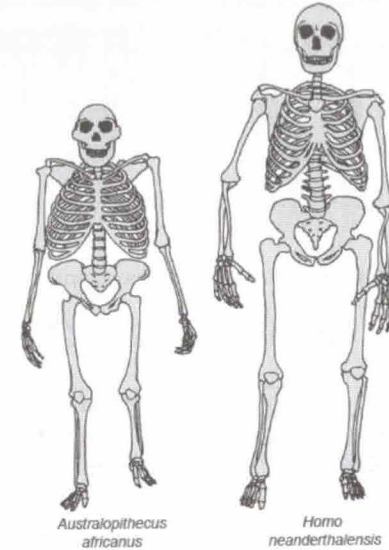
Ötzi's blood taken from his blood vessels	Blood sample 1 from Ötzi's clothes	Blood sample 2 from Ötzi's clothes	Blood sample 3 from Ötzi's clothes	Blood sample 4 from Ötzi's clothes
————		————	————	
	————			————
————	————		————	————
————			————	
		————		————
	————	————		

- b i Which blood sample on Ötzi's clothes belongs to Ötzi? [1 mark]
 ii Propose one hypothesis that would explain the presence of the other blood samples on Ötzi's clothes. [1 mark]
- c Analysis of mammalian proteins provides evidence of evolutionary relationships. Explain how amino acid differences in a protein can indicate evolutionary relationships. [2 marks]
- d The development of bipedalism in hominins is believed to have had a very significant effect on human evolution. Describe two effects of bipedalism on hominin behaviour. [2 marks]

[Total 9 marks]

179 [Adapted VCAA 2013 SB Q11]

The skeletal structures of two extinct members of the hominin family tree, *Australopithecus africanus* and *Homo neanderthalensis*, are shown in the diagram that follows.



- a Examine the skeletal structures. For each of the features listed in the table below, describe the difference between the two species and state the significance of the difference. [4 marks]

Feature	Description of difference	Significance of difference
Pelvic structure		
Arm to leg length ratio		

Neanderthals lived in the cold climate of Europe and Asia from 200 000 to 30 000 years ago. Modern humans and Neanderthals coexisted for around 10 000 years. Fossil evidence indicates Neanderthals shared much behaviour with modern humans. Scientists are undertaking research to find reasons why Neanderthals became extinct, but modern humans survived. Fossil evidence of the use of sewing needles and the division of labour between men and women was found only for modern humans, but not for Neanderthals.

People today with non-African heritage carry some Neanderthal DNA.

- b State a hypothesis to account for these findings. [1 mark]

[Total 5 marks]

- a i Using the diagram, name two features of the *Homo sapiens* skeleton, which make it unique among the primates. [2 marks]

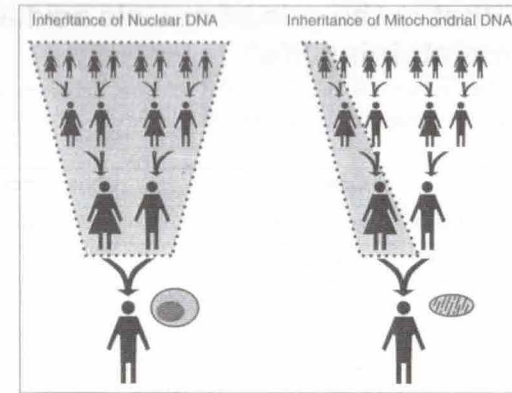


- ii Outline how one named non-skeletal characteristic has assisted primates in their evolution. [2 marks]
- b Examine the data collected on *Homo neanderthalensis* fossils found in recent years.

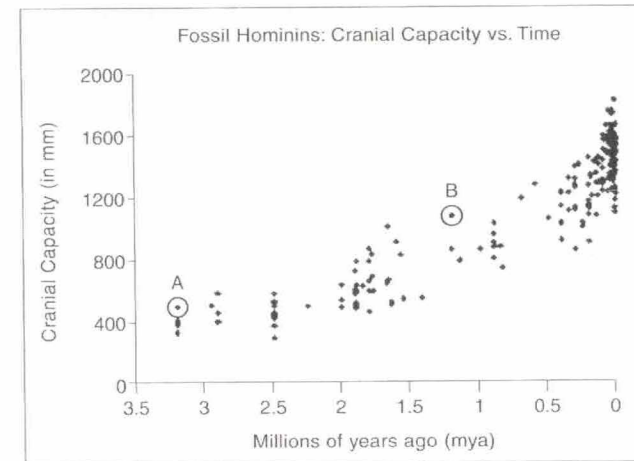
Date	Data
2008	<ul style="list-style-type: none"> • Full sequence of mitochondrial DNA of a range of Neanderthal fossils from within and between different fossil sites • The sequence is nearly identical within one fossil site • The sequence is very different between fossil sites
2010	<ul style="list-style-type: none"> • Full sequence of Neanderthal nuclear DNA • 1–4% of genes in European modern humans are specific Neanderthal genes • No identifiable specific Neanderthal genes in modern sub-Saharan African humans • No specific modern human genes in nuclear DNA of Neanderthal fossils

- i What inferences can be made about Neanderthal populations, based on the data collected in 2008? [3 marks]
- ii What inferences can be made about migration and breeding, based on the data collected in 2010? [3 marks]
- [Total 10 marks]

- a The diagram below compares the inheritance of nuclear DNA with mitochondrial DNA.



- i Compare the pattern of inheritance of nuclear DNA with mitochondrial DNA. [1 mark]
- ii Assess whether the analysis of nuclear DNA or mitochondrial DNA is more useful to evolutionary biology. [4 marks]
- b The graph below shows the results of an investigation into cranial capacity of fossil hominins.
- Data were obtained from measurements of hominin cranial capacity published in scientific journals.
 - Each data point on the graph represents the average cranial capacity of the adult skull at a single archaeological dig.
 - The results from 215 archaeological digs are represented.



- i Justify the methods used to collect and present the data. [4 marks]
- ii For either data point A or B, propose the name of the hominin species and its regional location. [2 marks]
- [Total 11 marks]