

	<i>Homo neanderthalensis</i>
When did they live?	200 000 to 30 000 years ago
Where did they live?	Western Europe Central and Northern Asia
Features of their skull	low sloping foreheads heavy brow ridges rounded chins large eye sockets projecting faces larger jaw with a gap between the last molar and back of the jaw
Brain size	1400 mL (large)
Culture	stone tools ornaments buried their dead clothing
Disappeared from the fossil record	30 000 years ago

5-79 Comparison of mitochondrial DNA and nuclear DNA.

	Mitochondrial DNA	Nuclear DNA
Shape	Circular	Linear
Location	Within the mitochondria	Within the nucleus
Inherited from	Mother	Mother and Father
Number of alleles per gene per cell	Many	Two alleles per gene. The alleles maybe the same or different.

5-80 When a sperm fertilises an ovum, the sperm's nucleus passes into the ovum. This forms the first cell of the new individual and therefore the mitochondrial DNA present, comes from the mother not the father. This makes mitochondrial DNA very useful in the study of evolution as changes in mitochondrial DNA are due to mutation and not recombination during meiosis. Evolutionary change can be measured by comparing the mitochondrial DNA from two different species. The longer the time passed since their divergence, the longer the time for the accumulation of different mutations.

5-81 The mitochondrial DNA of *Homo sapiens*, *Homo neanderthalensis* and *Homo denisovan* are different enough to classify them as separate species but there are similarities, and these indicate that at times they have interbred. *Homo neanderthalensis* and *Homo denisovan* are more closely related to each other.

Hypothesis	Description	Evidence
Out of Africa	Early <i>Homo sapiens</i> lived in Africa and spread out from Africa to the rest of the world. There has been more than one migration out of Africa. The most recent resulted in the modern <i>H. sapiens</i> ancestral population.	-most older hominin fossils are found in Africa. - <i>Homo neanderthal</i> in Eurasia interbred with European and Asian <i>H. sapiens</i> but not African <i>H. sapiens</i> . -African populations have the greatest genetic diversity.
Multi-Regional	<i>Homo erectus</i> migrated from Africa into a variety of different regions. As the spread was gradual and did not result in isolated populations, interbreeding occurred, increasing the gene pool but maintaining one species. Change to <i>Homo Sapiens</i> were worldwide.	-low genetic diversity in modern human populations -physical differences between human populations indicate a long time has passed since a common ancestor.

5-83 Fossil evidence, for example, the skeletons at Lake Mungo are dated at over 40 000 years old. DNA evidence suggests that indigenous Australians have been present in Australia for at least 50 000 years.

Chapter 5: Multiple-choice questions

5-84 [VCAA 2018 SA Q20]

This change in the sequence of amino acids was caused by

C a substitution of a nucleotide. (The third amino acid, pro is coded for a codon that starts with C – a change to G would result in a codon coding for ala.)

5-85 [VCAA 2018 SA Q21]

This truncated protein resulted from the codon

A UAU changing to UAA. (This change causes a codon that codon for tyr to result in a STOP codon.)

5-86 [VCAA 2018 SA Q22]

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

C translated protein will be longer than the dystrophin protein found in a person without DMD. (From the information given the only thing that can be said is that the transcribed protein will be longer. If an exon is duplicated many stop codons will not be created. The exon will code for an amino acid, so the protein will be longer.)

5-87 [VCAA 2014 SA Q23]

This mutation is an example of a

B nucleotide substitution during the formation of a gamete. (All cells of the fruit fly carry the mutation therefore the mutation must occur during the formation of a gamete and not during the formation of a somatic cell. The sequence found in normal insecticide-susceptible fruit flies differs by one base from the sequence found in insecticide resistant fruit flies and both sequences are the same length therefore the mutation is a substitution.)

5-88 [VCAA 2017 SA Q27]

What would be the result of this mutation?

A The peptide chain would be shortened. (The mutation in the DNA sequence results in triplet ATC. This is transcribed into mRNA codon UAG. UAG is a stop codon therefore the rest of the DNA sequence will not be transcribed, the mRNA sequence will be shorter and when this is translated, a shorter polypeptide chain will be produced.)

5-89 [VCAA 2017 SA Q28]

The result of this mutation would be that

D all amino acids after the first in the sequence would change. (This mutation results in a frameshift where all amino acids after the first would change.)

5-90 [VCAA 2012 E2 SA Q25]

Biological evolution

B involves inherited change in a population over many generations. (Changes in learnt behaviour are classed as cultural evolution. Technological evolution occurs faster than biological evolution.)

5-91 [VCAA 2019 SA Q26]

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

C the frequency of each allele is equal in Generation 1 but not in other generations. (From the information provided alternative C is correct. Diversity is decreasing in the population – not increasing. The frequency of R is decreasing therefore it must be of selective disadvantage and there is no evidence that individuals joined the population.)

5-92 [VCAA 2010 E2 SA Q23]

Analysis of the graph reveals that in the population

A when spraying levels declined, heterozygous advantage occurred. (B is an incorrect statement. Alleles for sensitivity were present in heterozygous individuals. With respect to alternative C, it is more likely that there will be a greater number of alleles for resistance in 1966 as the frequency of homozygous resistant individuals is increasing and each resistant individual is homozygous. The presence or absence of DDT is a selective pressure and heterozygous individuals were at an advantage when DDT levels were reduced.)

5-93 [VCAA 2020 SA Q28]

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

C The appearance of Allele 3 after Generation 3 may be explained by gene flow. (Allele 3 appears after generation 3 – supported by the graph. A is incorrect as a new allele has been introduced – not in the founding population. Genetic diversity has changed with a new allele appearing. There is no evidence to support alternative D.)

5-94 [VCAA 2016 SA Q37]

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

B This population has less genetic variation than the Arizona populations and is an example of the founder effect. (The 20 introduced sheep represent a relatively small gene pool that will contain less variation than the original mainland populations – so in 1999 the variation on the island would be less than that in Arizona. Speciation may occur eventually, but the time involved is short.)

5-95 [VCAA 2015 SA Q40]

Based on this information, it is true to say that

B northern elephant seals would show less genetic variation than southern elephant seals. (Very few northern elephant seals were left and hence there was a

limited gene pool from which the recovered population have come from. The southern elephant seals are descended from a more diverse gene pool and would show greater genetic variation.)

5-96 [VCAA 2014 SA Q33]

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

A migration. (The diagram is of the founder effect. This is when a population that is unrepresentative of the original population settles in a new area.)

5-97 [VCAA 2012 E2 SA Q21]

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

5-98 [VCAA 2010 E2 SA Q13]

In populations

A genetic drift will have less effect in a large population compared to a small population. (Genetic drift – random changes in allele frequency in a population – is only significant in small populations.)

5-99 [VCAA 2012 E2 SA Q23]

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

D do not produce fertile offspring with members of known species.

(Definition.)

5-100 [VCAA 2011 E2 SA Q19]

From this information, it would be reasonable to conclude that

C the diameter of the golden rain tree fruit acted as a selection pressure on beak length. (There is not enough evidence to conclude when the golden rain tree was introduced but it was probably earlier than 1970. There would have always been some long-beaked bugs in the population, but they would have become more common with a new selective pressure – the fleshy golden rain tree fruit.)

5-101 [VCAA 2011 E2 SA Q20]

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. (If the bugs tend to stay with particular trees, then if fruiting seasons do not overlap populations in the different trees may become genetically isolated.)

5-102 [VCAA 2020 SA Q27]

The conservation program for Tasmanian devils is an example of

C selective breeding. (The scientists have chosen Tasmanian devils with particular characteristics and allowed them to breed – the basis of selective breeding.)

5-103 [VCAA 2019 SA Q27]

One way this could be achieved is by

C selective breeding. (The farmer would only use seeds from plants that produced green beans – that is selective breeding. Over time, it would be expected that the vast majority of beans produced would be green.)

5-104 [VCAA 2017 SA Q30]

This is an example of

C selective breeding. (Definition.)

5-105 [VCAA 2014 SA Q38]

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

D human intervention through artificial selection. (Humans have decided which dogs to breed.)

5-106 [VCAA 2011 E2 SA Q22]

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

D result from the restriction of breeding to chosen animals in the herd.

(Farmers will only allow those animals with the desired characteristics to breed. Over time, the number of offspring with the characteristics required will increase. In dairy cattle, farmers might look to breed from cows that produce more milk than the average.)

5-107 [VCAA 2010 E2 SA Q20]

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

B plant height. (Plant height is lower in the cultivated sunflowers, supporting the idea that humans have selected against taller plants. All the other characteristics are greater in the cultivated sunflowers.)

5-108 [VCAA 2013 SA Q39]

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

D antibiotic-resistant phenotypes being favoured through natural selection.

(Antibiotics do not induce mutations. There would have originally been genetic and phenotypic variation in the bacteria in terms of resistance to antibiotics. When the antibiotic was used, those bacteria that were resistant survived, reproduced and their offspring inherited resistance. Over time, more resistant bacteria would be present.)

5-109 [VCAA 2013 SA Q40]

These therapies could include

C preventing biofilm bacteria from detecting others of their own species.

(Bacteria divide by binary fission not mitosis, promoting flagella development would encourage spreading and alternative D would encourage the use of antibiotics. Preventing bacteria from detecting others of their own species would mean that the bacteria could not sense that their numbers were large enough to invade a new area successfully and therefore the area would not be invaded.)

5-110 [VCAA 2019 SA Q28]

This type of fossil is best described as

C a trace fossil. (A footprint is not preserved remains or a petrified fossil. A cast is produced when remains are surrounded by something like mud or ash. Over time, the remains disappear. Footprints are trace fossils rather than casts because there were never organic remains involved.)

5-111 [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. (Younger fossils will generally be found nearer the surface unless there has been dramatic land movement. They would also contain larger amounts of carbon-14 rather than small amounts.)

5-112 [VCAA 2018 SA Q26]

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. (These continents were once joined in one large landmass – Gondwanaland. The common ancestor was widely distributed before the continents separated.)

5-113 [VCAA 2016 SA Q38]

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

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. (As G. major is less deeply buried than G. obliqua this indicates G. major is younger. The carbon-14 data do not reflect a difference in age.)

5-114 [VCAA 2015 SA Q35]

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

C 1.25 billion years. (After 1.25 billion years you would expect that half the Potassium-40 to have broken down – therefore ratio between Potassium-40 and Argon-40 would be 1:1.)

5-115 [VCAA 2014 SA Q34]

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

C Q. (Q is the fossil of the only organism that existed 328–359 million years ago.)

5-116 [VCAA 2014 SA Q35]

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

D potassium-argon dating. (Transition fossils and index fossils are forms of relative dating. The fossils are too old to use carbon dating.)

5-117 [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. (Each time period is characterised by the organisms that existed at the time. Mass extinctions result in major change of organisms present and signify a new time period.)

5-118 [VCAA 2014 SA Q37]

The chance of a trilobite becoming fossilised is increased by

C the presence of hard body parts. (Hard body parts fossilise best.)

5-119 [VCAA 2013 SA Q31]

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

C measuring the proportion of carbon-14 atoms in the carcass. (Potassium-argon is used for older fossils and comparing teeth will not give an actual age.)

5-120 [VCAA 2012 E2 SA Q16]

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

D its hard-plated mouth and spiny appendages. (Hard parts of organisms are more easily fossilised.)

5-121 [VCAA 2012 E2 SA Q17]

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

A index fossils. (The fossil is older than 50 000 years therefore carbon-14 dating, DNA hybridisation and a molecular clock cannot be used.)

5-122 [VCAA 2012 E2 SA Q18]

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

D selection pressures changed dramatically due to rapid climate change.

(High genetic diversity reduces the chance of extinction when the environment changes as there is a greater chance that one variant will be suited to the environment.)

5-123 [VCAA 2011 E2 SA Q12]

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

D 40 000 years. (Fact. Carbon dating is only useful for relatively young fossils – less than 50 000 years old.)

5-124 [VCAA 2015 SA Q36]

This increased diversity of species can be explained by

D the extinction of many species providing many unoccupied niches.

(After the extinction event, there would be opportunities for divergent evolution in the remaining species to fill the unoccupied niches. Consider an example such as the Galapagos' finch – an ancestral population diversified to fill many slightly different niches on neighbouring islands.)

5-125 [VCAA 2019 SA Q29]

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

D five. (Looking along the extinction rate of 10 families per million years on the graph there are 5 peaks near or above the line – therefore 5 extinction events.)

5-126 [VCAA 2017 SA Q33]

Mass extinctions

C are followed by a period of rapid divergent evolution. (Mass extinctions result in an increase in availability of unoccupied niches and therefore more opportunity for divergent evolution.)

5-127 [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

D consist of all the genetic sequences within the haploid cells of individuals of the species. (Definition.)

5-128 [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 (The *Drosophila* shares 5 of the 6 amino acids tested. Not that the pig also does but is not an alternative.)

5-129 [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?

D human and yeast (These two organisms have the least amino acids in common with wheat at the sites analysed.)

5-130 [VCAA 2013 SA Q37]

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

B a molecular clock. (Definition. Stratigraphy and relative dating refer to the dating of rock according to the position of the layer in which it is found. Radiometric dating refers to dating rock according to the ration of radioactive isotopes present.)

5-131 [VCAA 2013 SA Q38]

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

D process and remember more complex information than chimpanzees. (The presence of: the LCT sequence means that humans can digest milk as an adult, The HAR2 sequence that humans have a more opposable thumb than chimpanzees and there is not information about walking on two feet.)

5-132 [VCAA 2012 E2 SA Q20]

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

C mitochondria. (Plasmids are not found in plant cells and ribosomes are made of RNA not DNA.)

5-133 [VCAA 2019 SA Q24]

O. latipes is most closely related to

C P. chilotes. (*O. latipes* and *P. chilotes* have a most recent common ancestor. The other 3 alternatives are members of the Tetraodontiformes whose common ancestor is older than that of *O. latipes* and *P. chilotes*.)

5-134 [VCAA 2019 SA Q25]

Which one of the following statements is correct?

D T. flavidus and T. lineatus diverged to form two distinct species 25 million years ago. (Drawing a line from 25 million years ago up intersects with the branch *T. flavidus* and *T. lineatus* - point where the divergence occurred.)

5-135 [VCAA 2017 SA Q32]

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

B R – bacteria, S – protists, T – plants, U – animals (Bacteria diverge first and B is the only alternative stating this.)

5-136 [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 Fabrenholzja pinnata. (Look for the branching patterns. *Pedicinus badii* and *Pthirus gorilla* share a more recent branch than *Fabrenholzja pinnata* so the statement is true.)

5-137 [VCAA 2012 E2 SA Q19]

It would be reasonable to conclude that

B speciation in Eucalyptus was assisted by different selecting pressures. (*Eucalyptosis* and *Stockwellia* are on the same branch and therefore will be the most similar. Their point of divergence is the most recent, so they have been the most recent to evolve.)

5-138 [VCAA 2011 E2 SA Q23]

One similarity between the alternatives is

C Amborella and Nymphaeales diverged first from Angiospermae. (This can be seen as *Amborella* and Nymphaeales are the first branch – see the top of each diagram. Monocots and Chloranthales diverged at similar times. Looking at the first diagram *Ceratophyllum* and eudicots are on different branch to monocots. Magnoliids in the first diagram diverge after monocots and the Chloranthales.)

5-139 [VCAA 2019 SA Q40]

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

D the absence of a tail. (An opposable thumb, presence of hair and claws are not unique to hominoids.)

5-140 [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
B	binocular vision	opposable thumbs	Fully rotating shoulder joints

(Primates do not have tails, so **C** is incorrect. Arms longer than legs is not a characteristic of all primates, so **D** is incorrect. In **A** the sloping forehead is not a

characteristic of all primates – consider humans. Alternative **B** features are present in all primates.)

5-141 [VCAA 2019 SA Q32]

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?

D *H. floresiensis* (The information in the graph shows that *H. floresiensis* had on average the smallest inferred average brain size. The general trend is one of increased brain size in hominin evolution.)

5-142 [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
D	decreasing size of canines, decreasing size of zygomatic arch, increasingly bowl-shaped pelvis, increasing arch of feet

(C can be eliminated on basis of increasing jaw size. A is eliminated on increasing brow size and B on a more-opposable big toe.)

5-143 [VCAA 2018 SA Q38]

Consider the evolution of hominins.

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

C *Homo erectus* was a bipedal primate. (*Homo erectus* was named for its upright stance and hence bipedal – walking on two feet.)

5-144 [VCAA 2018 SA Q39]

Which general trend is shown by hominin fossils?

B The older the fossil, the smaller the braincase that surrounds the cerebral cortex. (Earlier hominins had smaller brains and therefore smaller brain cases. Jaw bones have over time decreased in size and the pelvis has become more bowl-shaped.)

5-145 [VCAA 2018 SA Q40]

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

C the free use of hands to manipulate objects. (Free use of hands allowed more elaborate tool making which accelerated cultural evolution.)

5-146 [VCAA 2015 SA Q37]

Which sequence best shows the order from the most ancient fossil skull to the most modern fossil skull?

A Skull 3, Skull 1, Skull 2. (Skull 2 has the flattest face therefore is the most recent. Skull 3 has the largest jaw and brow ridge therefore is the oldest.)

5-147 [VCAA. 2015 SA Q38]

These fossil remains

C show early evidence that hominins were bipedal. (*Homo erectus* evolved after *Australopithecus* and older fossils of primates and apes – part of the hominoid super-family have been found.)

5-148 [VCAA 2011 E2 SA Q25]

The order of oldest to youngest hominin species is

B P O M N. (The genus *Homo* is more recent than *Australopithecus* therefore alternative having M and N last must be correct.)

5-149 [VCAA 2017 SA Q35]

From this new discovery, it would be reasonable to conclude that

B there was an early migration of *H. sapiens* out of Africa before 100 000 years ago. (Modern Africans did not breed with Neanderthals therefore they are not directly related and Neanderthals were not present in Africa. If Neanderthals were not present in Africa but were able to interbreed with *H. sapiens* 100 000 years ago, *H. sapiens* must have migrated before 100 000 years ago.)

5-150 [VCAA 2013 SA Q22]

You have the same mitochondrial DNA as your

D maternal grandmother. (Mitochondrial DNA is inherited through ova, i.e. from the mother, grandmother and so on.)

5-151 [VCAA 2014 SA Q39]

The above evidence and current theories of hominin evolution indicate that

B *H. floresiensis* was a species that showed considerable social cooperation and methods for passing on knowledge. (The presence of tools, evidence of fire and the ability to catch prey much larger than themselves suggests that *H. floresiensis* hunted and this requires considerable social cooperation.)

5-152 [VCAA 2014 SA Q40]

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

C was an important anatomical development that assisted tool making in hominins. (Apes have an opposable thumb and arm-to-leg ratio relates to bipedalism not the ability to manipulate tools.)

Chapter 5: Short-answer questions

5-153 [VCAA 2020 SB Q7]

- a Substitution point mutation
- b i In Europe where milk was an important component of the diet, those individuals without the mutation that allowed them to digest milk throughout their life obtained less food. They were less healthy, mated less frequently and produced fewer offspring. Fewer alleles for digesting milk were passed on to their offspring. Those with the mutation were able to digest milk obtained more food, were healthier, survived to mate and produced more offspring that inherited the alleles for digesting milk. Over many generations, the allele frequency and phenotype for digesting milk increased.
- ii Any two of:
- The mutation had not occurred in an isolated population with no gene flow. The population did not rely on milk as a major component of the diet, therefore, there was no selective advantage to be able to digest milk.
 - The population was founded by a group of individuals that did not have the mutation.
- c Through selective breeding where the farmer allows only high milk-producing cows to breed with bulls whose mother was high milk-producing.

5-154 [VCAA 2019 SB Q6]

- a i Aneuploidy refers to cells with too many or too few chromosomes (abnormal number) due to non-disjunction during cell division.
- ii The number of chromosomes in foetal cells.

- b Any two of the following:
- Deletion where a large section of a chromosome is missing
 - Inversion where a large section of a chromosome is cut and rejoined upside down
 - Duplication where a large section of chromosome is copied and added to the chromosome
 - Translocation where a section of one chromosome becomes attached to another

c

5'	AUG	CUC	CAC	CUG	ACU	CCU	GAG	GAG	3'
	met	leu	his	leu	thr	pro	glu	glu	

d i

5'	AUG	CUC	CAC	CUG	ACU	CCU	GUG	GAG	3'
	met	leu	his	leu	thr	pro	val	glu	

The 7th amino acid will change from glu in the person without the mutation to val in the person with the mutation.

ii

5'	AUG	CUC	CAC	CUG	ACU	CCU	GGG	AG	3'
	met	leu	his	leu	thr	pro	gly		

This would result in a frameshift where all amino acids after the 6th amino acid would be different. This would affect the primary, secondary and tertiary structure of the resulting protein therefore the proteins would have a different shape and would not function effectively.

5-155 [VCAA 2018 SB Q7]

- a An individual's phenotype is determined by the expression of genes found on chromosomes. Genes are made of DNA and the order of bases determines the proteins produced by the organisms. New forms of genes are introduced into a population by mutation. Mutagens include certain chemicals and radiation. Additionally, errors in cell division may result in changes in chromosome number and size (chromosomal mutations). Lizards reproduce sexually. They inherit half their chromosomes from each parent via sperm and ova. Crossing over during prophase I of meiosis shuffles the alleles within a homologous pair of chromosomes and random assortment of chromosomes during meiosis results in new combinations of alleles again increasing variation in the lizard population.
- b Offspring inherit their characteristics from their parents. The new populations are descended from only two individuals therefore the founding gene pool was smaller than the gene pool on the large island. As there is no gene flow between the islands the gene pool will only include the alleles found in the founders of the population.
- c There was original variation in length of hind legs of lizards living on the smaller islands. There were different selection pressures on the small islands compared with the large island. Shorter hind limbs were an advantage on smaller islands so lizards with short hind limbs were more likely to survive, reproduce and pass on the alleles for short hind limbs to their offspring. Over time the population would have an increased number of lizards with short hind limbs.

5-156 [VCAA 2017 SB Q5]

- a Gene flow is the exchange of alleles between different populations or gene pools. Gene flow is unlikely to occur between these populations as the birds are poor flyers and the populations are 200 km apart therefore, they are unlikely to interbreed.
- b Small populations will have low genetic diversity. If the environment changes and one individual is adversely affected, then there is a high probability that all individuals will be adversely affected, and the population will be wiped out.

5-157 [VCAA 2017 SB Q10]

- a The rapid extinction model suggests that a dramatic change in the environment may lead to widespread death of organisms. When the First Australians arrived in Australia, they dramatically changed the environment through burning and hunting. This drastically reduced the amount of food available to the megafauna and hunting further reduced their numbers, causing their extinction.

b

Evidence	Justification
1. No record of fire-sensitive plants undergoing a bottleneck as a result of significant burning events	If the rapid extension model occurred then significant burning events would result in most of the populations of fire-sensitive plants dying. The plants remaining would be similar as they are descended from the small surviving population. There is no evidence of this.
2. For tens of thousands of years, aboriginal populations were not that large.	If the population was not large then the people would have little effect on the immediate environment therefore, there would be no significant habitat change and no rapid extinction.
3. Many of the megafauna species became extinct before the First Australians arrived.	If the extinction of the species occurred before the First Australians arrived, the First Australians could not have caused the extinction.

5-158 [VCAA 2013 SB Q9]

- a Extinction means that individuals of a particular species no longer exist.
- b i Gene pool refers to all the alleles, of all the genes, of all the individuals, in a population. (Note: all the genes)
- ii Natural selection relies on genetic diversity in a population. Genetic diversity results in phenotypic variation. If all individuals are similar and the environment changes to the detriment of one individual, all individuals will be selected against, and extinction may result. If the gene pool is diverse, there is a chance that some individuals may have characteristics that are selected for, and the population will survive.

Term	Explanation
Genetic drift	Unpredictable changes in allele frequencies from one generation to the next due to the action of chance events. More likely to occur in small populations.
Bottleneck effect	Chance effects on allele frequencies in a population as a result of a major reduction in population for example disease or loss of habitat. The descendants from the small, reduced population will be genetically similar as they are descended from the same ancestors.

d Any one of the following:

- Wildlife officers could continue to introduce brush-tailed rock wallabies from other areas.
- Fencing to remove foxes or other introduced species.
- Restore the habitat through reduced grazing/control of hikers to walking paths
- Reduce the number of predators.

5-159 [VCAA 2011 E2 SA Q6]

- a Genetic drift: changes, unpredictable in direction, in allele frequencies from one generation to the next owing to the action of chance events. More likely to occur in small populations.
- b i The Illinois birds have a lower average number of alleles per gene locus (3.67) compared to prairie chickens from the other states (5.33–5.83). They show less genetic variation than the birds from the other three states. This is because they are descended from less than 50 individuals. They are closely related. The other groups are descended from larger populations of genetically different birds.
- ii Kansas birds and the Nebraskan birds are similar (5.83 average number of alleles per gene locus) to each other as there is probably gene flow or interbreeding occurring between the two adjacent populations.
- c i If individuals in a population are genetically similar then they will also be phenotypically similar. If the environment changes to the detriment of one individual then all individuals will be similarly affected and the population could die out. For example, if they were exposed to a new disease, if one individual is susceptible they will all be susceptible and all may die.
- ii The Illinois prairie chickens could be interbred with prairie chickens from the other states. This would increase genetic variation and thus phenotypic variation. If the environment changes to the detriment of some, there may be some variants that will not die out.

5-160 [VCAA 2012 E2 SB Q6]

- a i The X should be placed exactly on the curve at the 2 time units (half-lives) point.
- ii 12 000 years (2×6000 years)
- b i C_{14} has a short half-life. If the fossil is very old, very little C_{14} will be present.
- ii Any one of the following:
- Potassium–Argon dating
 - Uranium-238 dating
 - Thermoluminescence
 - Electron spin resonance

5-161 [VCAA 2010 E2 SB Q7]

- a It is assumed that the oldest layer is at the bottom (deepest) and the youngest layer is near the surface.

b i and ii Any one of the following and its associated evidence:

i Hypothesis	ii Evidence
The disappearance of bird species is due to hunting by humans.	The number of bird fossils decreases at the same time pottery appears in the fossil record. Pottery indicates the presence of humans.
The disappearance of bird species is due to predation by dogs.	The number of bird fossils decreases at the same time dog bones appear in the fossil record.
The disappearance of bird species is due to habitat destruction by humans.	The number of bird fossils decreases at the same time pottery and charred plant remains appear in the fossil record. Pottery and charred plants indicate human settlement and associated habitat destruction.
The disappearance of bird species is due to volcanic eruptions.	The number of bird fossils decreases at the same time charred plant remains appear in the fossil record. The plants were destroyed by volcanic eruptions.

c i Founders.

- ii The new and old colonies were separated by a geographical barrier (the sea) that resulted in no gene flow. Each population was subject to different selection pressures and, as a result of this and the accumulation of new mutations, the populations became progressively different. The two populations eventually became so different that when brought back together they could no longer reproduce to produce vigorous, fertile offspring.

5-162 [VCAA 2015 SB Q10]

- a i The salinity of the lake has changed over time.
- ii The top and lower sediment layers contain fossils that have small pelvis and small or absent spines. These fossilised bones are similar to bones of modern-day fish found in fresh water. This suggests that the lake was fresh when the top and lower sediments were formed. The middle layer contains fossilised bones similar to bones of modern-day fish found in the ocean. This suggests that the lake was salty when the middle sediments were formed.
- b Size of pelvis is genetically determined in fish. There was original variation in size of pelvis in the population of fish in the lake. When the water in the lake was fresh, those fish that had small pelvises grew more quickly and were able to escape predators better than those with large pelvises. Those with large pelvises died early and left behind less offspring. Those with small pelvises survived and left behind more offspring that inherited the alleles for small pelvis. Over time, the alleles for small pelvis increased in frequency in the population's gene pool.

5-163 [VCAA 2016 SB Q8]

- a Originally there was one population of sea stars that differed genetically and phenotypically. The population became separated with little gene flow between the two new populations. Those sea stars in the south were exposed to lower water temperatures and predation by cold water predators. Those sea stars that had adaptations that allowed them to survive in cold water or cold-water predators, survived, reproduced and their offspring inherited their favourable adaptations. In the north, those sea stars that had adaptations that allowed them to survive in warmer water survived, reproduced and their offspring inherited

their favourable adaptations. As a result of these different selection pressures, over time the populations would become progressively phenotypically different.

- b *Cryptasterina pentagona* would have the highest diversity of alleles as offspring result from the gametes produced by different individuals whereas *C. hystera* offspring result from gametes produced by one individual.

5-164 [VCAA 2016 SB Q9]

- a Yes. Populations B and A have different skull sizes. For example, the difference between B and A for measurement position 1 is 20 mm. The difference between the other 3 species ranges from 4 to 8 mm which is smaller than between B and A.
- b Comparison of karyotypes. Different number of chromosomes in the karyotypes of the two populations would suggest that the two populations belong to different species. To belong to one species, individuals must be able to produce vigorous fertile offspring. If individuals of each population have a different number of chromosomes in their karyotypes, they will produce gametes with a different number of chromosomes. The cells of individuals formed from the fertilisation of these gametes will contain non-homologous chromosomes and will therefore not be able to undergo meiosis and the individual will be infertile.

Or

Comparison of DNA sequences. Different DNA sequences in the DNA of the two populations. The greater the difference in DNA sequences the longer the time since divergence from a common ancestor and the more likely the two populations are different species.

Or

Comparison of mitochondrial DNA. Different mitochondrial DNA sequences in the DNA of the two populations. The greater the difference in DNA sequences the longer the time since divergence from a common ancestor and the more likely the two populations are different species.

- c i Any one of: mountain, large river, canyon, lake
- ii This feature would stop gene flow between the two populations of tortoise. Different selection pressures on each population would lead to different phenotypes being selected for and the populations would become increasingly different until, when the populations were brought back together, they could no longer produce vigorous, fertile offspring.

5-165 [VCAA 2019 SB Q7]

- a Type of evolution: Divergent
- Divergent evolution occurs when populations of organisms that have a recent common ancestor are exposed to different selection pressures and therefore appear different. These animals are all mammals, therefore they are closely related and have a recent common ancestor. They have been exposed to different selection pressures – hyrax living in rocky outcrops, the elephant savannah and the dugong the sea.
- b Any one of the following:
- the bison were hunted by humans
 - the bison had gone through a bottleneck and were genetically similar. When the environment, e.g. a new disease, changed to the detriment of one, it was to the detriment of all, so they died out.
 - the bison were descended from a small group that moved to the area. They were genetically similar. When the environment, e.g. a new disease, changed to the detriment of one, it was to the detriment of all so they died out.

- c The animal died and quickly was covered by snow (snow meant that liquid water/oxygen was not available to decomposers therefore the body did not decompose. The area was permanently cold, so the body did not thaw out.

5-166 [VCAA 2020 SB Q8]

- a *Amatitlania siquia* and *Hypsophrys nematopus*. The shortest time has passed since their divergence; therefore, they have the most recent common ancestor, so there has been less time for mutations that code for different amino acids to accumulate.
- b Fossilisation occurs when organisms are protected by decay from decomposers. When an organism dies in water, it is more quickly covered by sediments than on land. This reduces disturbance from scavengers and the low oxygen environment does not allow decomposers to survive.
- c Carbon-14 Dating
Carbon-14 is radioactive and along with carbon-12 is incorporated into the bodies of organisms at a rate that stays constant while the organism is alive. When an organism dies, it is no longer eating or breathing in carbon and as the carbon-14 decays the ratio of ^{14}C to ^{12}C changes. By comparing the ratio of ^{14}C to ^{12}C in a fossil with the known half-life, it is possible to calculate how much time has passed.

5-167 [VCAA 2012 E2 SB Q5]

- a Availability of prey/food (Not just diet, predators or feeding location)
- b i Velvety free-tailed bat (*Molossus molossus*)
- ii Velvety free-tailed bats feed above the trees in open spaces. There are few objects to bounce signals off therefore if the closest object is far away there may be long delay before the pulse is bounced back to the bat. If many short signals were sent, it would be difficult to establish which signal is returning. Longer signals travel better over larger distances, increasing the chance of velvety free-tailed bats finding food.
- c Divergent evolution (adaptive radiation)
- d Velvety free-tailed bats and Mexican long-tongued bats would have fewer differences in their DNA than between themselves and the black myotis bat. The approximate number of differences between the velvety free-tailed bat and the myotis bat would be the same as the number of differences between the Mexican long-tongued bat and the black myotis bat.
- e Disagree. Allopatric speciation occurs when one population is split into smaller populations separated by a geographical barrier. These bats are all living in the same forest/island, therefore are not separated by a geographical barrier.

5-168 [VCAA 2018 SB Q9]

- a The line does not continue to the present time therefore *Pakicetus* became extinct.
- b Any one of:
- the presence of even-toed hooves allowing *Ambulocetus* to walk on land
 - the presence of short legs allowing *Ambulocetus* to walk on mud
- And one of:
- a streamlined body shape allowing *Ambulocetus* to move easily through water
 - the presence of a blow hole on the top of the skull to allow *Ambulocetus* to breathe
 - the presence of a flat tail/fins to help *Ambulocetus* swim
- c i Any two mammals, e.g. hippopotamus and killer whale or any two fish, e.g. bronze whaler and blacktip reef shark, and as they have a recent common ancestor but have diverged as a result of different selection pressures.

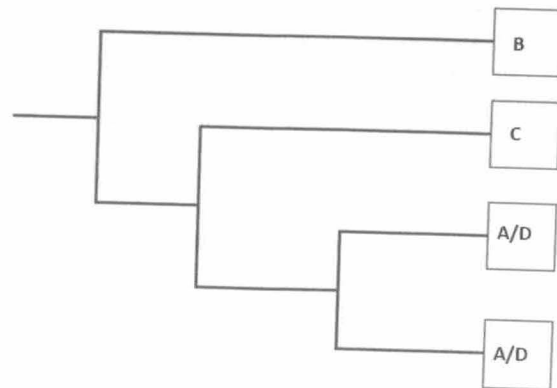
ii One mammal and one shark, e.g. whale shark and humpback whale and as they do not have a recent common ancestor but have been subject to similar selection pressure resulting in structures enabling them to filter feed.

- d Any two of the following:
- Interbreed the burrunan dolphin and common bottlenose dolphin. If they cannot produce vigorous, fertile offspring they are different species.
 - Use DNA hybridisation to compare the DNA sequences of burrunan dolphins and common bottlenose dolphins. Many differences would suggest they are different species.
 - Compare the sequence of amino acids in their proteins. Many differences would suggest they are different species.
 - Compare structural features of their skulls/bones. Many differences would suggest they are different species.

- e Any two of the following:
- The burrunan dolphin may become a separate species as there is no gene flow between the populations and there are different selection pressures acting on each population.
 - The burrunan dolphins may become extinct as a result of overfishing and/or pollution.
 - As there is no gene flow between the populations, the burrunan dolphins would have low genetic diversity. If the environment changes to the detriment of one individual, it will be to the detriment of all individuals, increasing the chance of extinction.

5-169 [VCAA 2015 SB Q9]

- a Divergent evolution
 b Comparative morphology/anatomy
 c i



ii Organism that share a more recent ancestor will be more similar as there is less time for mutations to accumulate. Whales and *L. major* have the most features (3) in common therefore, they are the closest together on the tree. Whales and *L. major* share two features with the hippopotamids and only one with the suids so are more closely related to the hippopotamids than the suids.

5-170 [VCAA 2010 E2 SB Q6]

a Any one of the following:

Name	Brief description
DNA hybridisation	Chromosomes from two species are isolated and mixed. They are heated so that they denature and separate. The mixture is allowed to cool and DNA to anneal so that pieces consist of one chain of DNA from the first species and one chain of DNA from the second species. The DNA is then reheated. The higher the temperature required for the DNA to denature, the more complementary the bonding and the more closely related the species.
mDNA sequencing	Mitochondrial DNA from two species is extracted and sequenced. The resulting sequences are compared. The more similar the sequences, the more closely related the species.

- b Most cells of the fish contain mitochondria. Therefore, mitochondrial analysis can be performed on any part of the fish including a portion of a fin. This can then be compared to the database and the identity of the fish determined. Any one of the following examples where humans would want to identify fish species:
- to identify endangered species.
 - to monitor fish population numbers.
 - to monitor fish movements.
 - to help identify fish wholesalers who are selling incorrectly labelled fish.
- (Note: The sequenced gene looks like a barcode. It is not attached to the fish as a barcode.)
- c Redundancy in the genetic code means more than one triplet/codon codes for the same amino acid.
- d Multiple samples from the same species ensures the accuracy of results as it allows the identification of any variations/mutations that may occur in the same species.

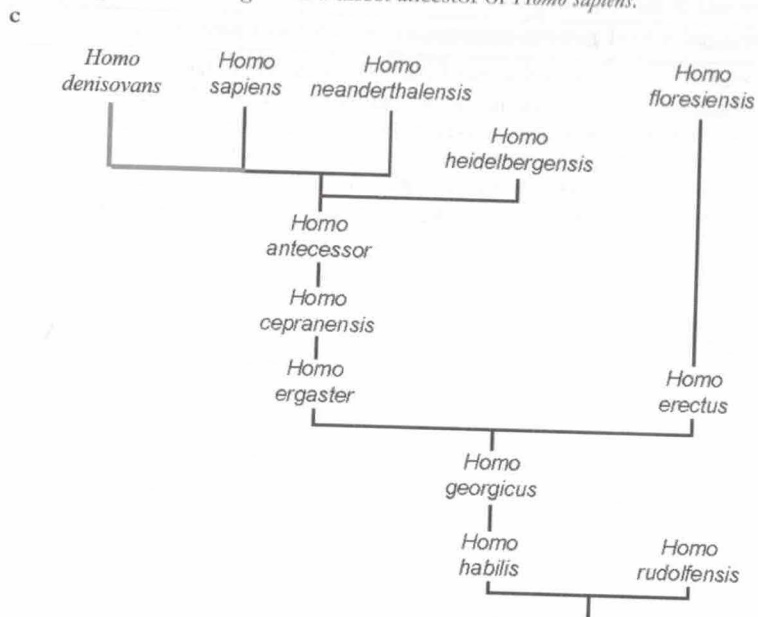
5-171 [VCAA 2013 SB Q10]

- a Sequencing the RNA would show the order of nucleotides present in the viral RNA or the order of amino acids in proteins coded for by the viral RNA.
- b Strains 2 and 3 are the most similar of the strains because they have the **most recent** common ancestor therefore there has been a shorter time to accumulate mutations/genetic differences.
- c The strain of virus that causes SARS in humans originated in bats and viral strains 5, 6 and 7 **share a recent common ancestor**.

5-172 [VCAA 2020 SB Q9]

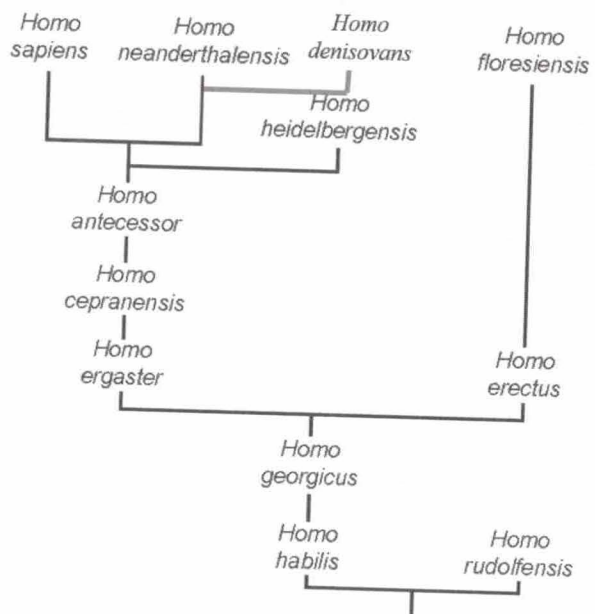
- a Any two of the following:
- *Homo erectus* would have a larger brow ridge than *Homo sapiens*
 - *Homo erectus* would have a small braincase than *Homo sapiens*
 - *Homo erectus* would have a more sloping forehead than *Homo sapiens*
 - *Homo erectus* would have a small braincase than *Homo sapiens*
 - *Homo erectus* would have a less parabolic jaw than *Homo sapiens*
 - *Homo erectus* would have a thicker jaw than *Homo sapiens*
 - *Homo erectus* would have less slender zygomatic arch than *Homo sapiens*.

b In Figure 1, *Homo ergaster* is not a direct ancestor of *Homo sapiens*, whereas, in Figure 2, *Homo ergaster* is a direct ancestor of *Homo sapiens*.



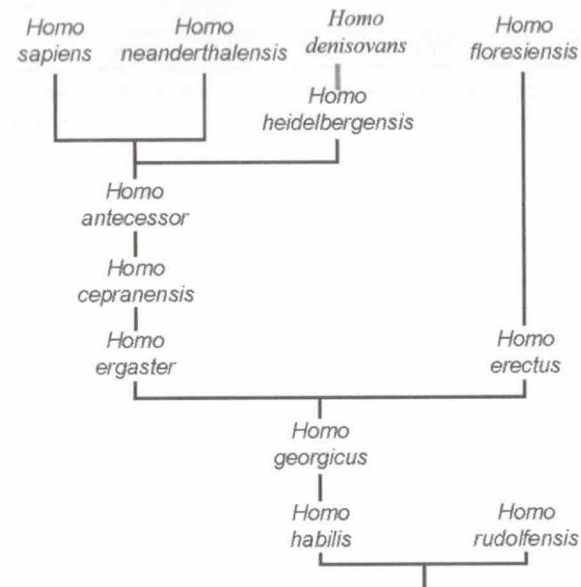
Reason: the DNA of *H. sapiens* and *H. neanderthalensis* is more similar to *H. denisovans* therefore, they are more closely related to *H. denisovans*, or they existed at the same time and are believed to have interbred.

OR



Reason: the DNA of *H. neanderthalensis* is more similar to *H. denisovans* therefore, they are most closely related.

OR



Reason: the DNA of *H. heidelbergensis* is more similar to *H. denisovans*; therefore, they are most closely related to *H. denisovans*, but as *H. heidelbergensis* existed before *H. denisovans*, *H. heidelbergensis* must be an ancestor of *H. denisovans*.

d Any two of the following:

- few *Homo* fossils have been found therefore the fossil record is incomplete
- *Homo* fossils continue to be found leading to new interpretations of the evidence
- *Homo* fossil evidence is based on small fragments; therefore, the evidence is open to interpretation

5-173 [VCAA 2017 SB Q7]

a Any two of the following:

- skull: a larger brain case
- skull: a more central foramen magnum
- skull: a flatter face
- jaw: more parabolic shape
- jaw: more uniform shaped teeth
- jaw: smaller canines
- skeleton: an S-shaped spine
- skeleton: a narrower pelvis
- skeleton: longer legs and shorter arms

b *Homo* fossils older than *H. naledi* (older than 900 000 years) are shown in the diagram therefore *H. naledi* cannot be the link.

5-174 [Adapted VCAA 2016 SB Q10]

a

Species	Environment	Condition
<i>H. erectus georgicus</i>	near the banks of the Black Sea	Any one of the following: - quick covering by sediments - low oxygen
<i>H. naledi</i>	cave South Africa	Any one of the following: - no scavengers - constant humidity - constant temperature - no wind/water/sunlight

b

- Any two of the following:
- sloping forehead whereas modern humans have a large vertical forehead
 - large brow ridges whereas modern humans have small brow ridges
 - large heavy lower jaw whereas modern humans have a small lower jaw
 - large canine teeth whereas modern humans have small canine teeth.

c

- Any one of the following:
- a narrower more bowl-shaped pelvis
 - an S-shaped spine
 - shorter arm : leg ratio.

d

- Any two of:
- presence of rock paintings
 - presence of musical instruments
 - presence of idols/totems
 - bodies positioned indicating burial
 - presence of bone or shell jewellery.

5-175 [Adapted VCAA 2012 E2 SB Q8]

a

- Any one of the following:
- presence of a tail
 - long arms for climbing and swinging between branches
 - presence of a prehensile toe.

b

Projecting nose: greater sense of smell. This makes it easier to find food or detect danger.
Precision grip: allows for greater manipulation of tools. This makes it easier to get food, defend against predators and to make shelters from environmental conditions.

c

Enlarged braincase/shape of the skull/large forehead: This allows for the development of a large cerebral cortex in the brain. The cerebral cortex is the area of the brain that is used for abstract thought and problem solving. Therefore, an increased ability to problem solve allows modern-day humans to use tools more effectively and adapt to changing new environments.

5-176 [VCAA 2019 SB Q10]

a

No. With no DNA evidence for the Denisovans and Neanderthals to be a separate group, they must be anatomically very similar. Only a finger bone was found of a Denisovans, and this is insufficient structural evidence. For organisms to belong to the same species they must be able to interbreed and

produce fertile offspring. As these groups are extinct, this is difficult to determine.

b

The more DNA that is analysed the more complete the DNA evidence. Mitochondrial DNA contains only a few genes, and these genes are inherited only from the mother whereas nuclear DNA contains DNA from both parents and all the genes except mitochondrial genes that code for that individual.

c

Site	Name of hominin group	Justification
1 Africa	<i>Homo heidelbergensis</i> Neanderthals <i>Homo sapiens</i>	There is no fossil evidence of the Neanderthals and Denisovans in Africa and there is no Neanderthal or Denisovan DNA present in modern Africans. Homo sapiens did not leave Africa until 60 000 years ago
2 SE Asia and PNG	Denisovan	3-5% Denisovan DNA is present in modern Asian and pacific islanders
3 Europe	Neanderthals	1-3% Neanderthal DNA ins present in most humans with European ancestry

5-177 [VCAA 2015 SB Q11]

a i

There was interbreeding between *H. neanderthalensis* and *H. sapiens* when they lived close to each other. Their offspring were fertile and would have inherited genetic information from both *H. neanderthalensis* and *H. sapiens* and they have passed this information onto their offspring in future generations.

ii

Organisms that belong to the same species are able to interbreed and produce fertile offspring. The presence of Neanderthal DNA in *H. sapiens* suggests that *H. sapiens* and *H. neanderthalensis* should be classified in the same species, as they were able to interbreed and produce fertile offspring.

b

Out of Africa theory.

This theory suggests that modern humans are descended from a population that originated in Africa where there were no Neanderthal populations. This is supported by the lack of Neanderthal DNA in African *H. sapiens*. The 'Out of Africa' theory suggests human populations moved out of North Africa encountering other *Homo* species. This is supported by the presence of Neanderthal DNA in European, East Asian and Australian Aboriginal *H. sapiens* but not in African *H. sapiens*.

c

Route: Migration occurred through northern Africa, through the Middle East, through East Asia to Australia.

Timing: After interbreeding with Neanderthals, i.e.: after 80 000 years ago.

- a Polymerase Chain Reaction
- DNA sample is heated to 95°C causing the strands to separate.
 - Primers, short sequences of DNA, that bind to either end of the DNA to be copied, are added to the DNA sample along with extra nucleotides.
 - Temperature is lowered to 50°C to allow primers to attach to the single stranded DNA.
 - The primers provide a 3' end to which DNA nucleotides can be added and joined together by Taq polymerase at 72°C.
 - The above steps are repeated many times.
- b i Sample 3
- ii The blood on Ötzi's clothes is from the three animals he hunted or from three people he had a fight with and all were injured.
- c Organisms that are closely related will have similar DNA sequences. DNA codes for amino acid chains therefore they will also have similar amino acid sequences. Mutations change the DNA sequence and may change the amino acid sequence. The greater the amino acid difference, the greater the time passed since divergence (last common ancestor) as there has been more opportunity for accumulation of mutations. Note: When referring to common ancestor you must include in your description recent or most distant.
- d Any one of the following:
- Bipedalism allowed early humans to live on open plains as they could stand up and see prey/predators more easily.
 - Bipedalism allowed humans to carry tools/more efficient hunting behaviours.
 - Bipedalism allowed more efficient long-distance locomotion, and this enabled humans to live a nomadic lifestyle. (Note: Must refer to a behaviour.)

5-179 [Adapted VCAA 2013 SB Q11]

Feature	Description of difference	Significance of difference
Pelvic structure	A narrow more bowl-shaped pelvis in <i>H. neanderthalensis</i> compared to <i>A. africanus</i>	This moves the centre of gravity so that it is easier to be bipedal Or gives greater support to organs when bipedal
Arm to leg length ratio	The arm to leg ratio of <i>A. africanus</i> is 1:1 whereas for <i>H. neanderthalensis</i> the ratio is 1:1.4. <i>H. neanderthalensis</i> had proportionally longer legs	This gives <i>H. neanderthalensis</i> a longer gait and makes it easier to be bipedal Or <i>A. africanus</i> were knuckle walkers Or <i>A. africanus</i> used arms to climb trees

- b Any one of the following:
- there was gene flow/interbreeding between modern humans and Neanderthals
 - modern humans and Neanderthals share a **recent** common ancestor
 - the DNA that is similar in modern humans and Neanderthals arose independently in each species.

5-180

- a i Two features of the skeleton that make it unique among the primates:
- broad and barrel-shaped pelvis
 - thighbone angles inwards

- ii Non-skeletal characteristic: lengthy gestation period and parental care. The long gestation period allows for greater brain development before birth leading to increased intelligence. The long period of parental care allows more time for the offspring to learn behaviours that help them live in a group and use tools. Living in a group provides protection from predators and increased chance of finding food.
- b i It can be inferred from the 2008 data that individuals within one fossil site are very closely related as the more similar the mtDNA, the closer the relationship. mtDNA is passed from mother to children. It can also be inferred that there was little gene flow/mating between populations as the sequences between fossil sites were different.
- ii It can be inferred from the lack of specific Neanderthal genes in modern sub-Saharan African humans that the Neanderthals evolved after early humans migrated out of Africa. The lack of specific modern human genes in nuclear DNA of Neanderthal fossils suggests that there was no interbreeding between modern humans and Neanderthals. The presence of specific Neanderthal genes in humans suggest that the Neanderthals interbred with at least one other early human group that in turn bred with early modern human populations. The Neanderthals were not direct modern human ancestors.

5-181

- a i Mitochondrial DNA is inherited from the mother only, whereas nuclear DNA is inherited from both the mother and the father.
- ii Mitochondrial DNA is more useful to evolutionary biology because:
- It is inherited from the mother only, whereas nuclear DNA is inherited from both the mother and the father. Therefore, any changes in base sequences can be tracked directly and are not due to recombination during meiosis.
 - There are many mitochondria in each cell each with the same mitochondrial DNA therefore there are many copies of each mitochondrial gene. There is only one copy of nuclear DNA in every cell. This means it is easier to extract mitochondrial DNA especially from fossils where there is little DNA.
 - Mitochondrial DNA is shorter and simpler than nuclear DNA therefore it is easier to track changes in sequence.
 - The high, known mutation rate can be used to estimate time of divergence for different species. The high rate means that mitochondrial DNA can be used to separate closely related species.
- b i Justification for the methods used to collect and present data:
- Data was used in the investigation that had been published in scientific journals. This data would be reasonably reliable as scientific journals are usually peer reviewed and follow a set format including citing of sources.
 - Each data point represents average cranial capacity of the adult skull. This means like skulls are compared as skulls may vary according to age, sex and health. Average also suggests that a number of measurements were used and averaged. This reduces the effect of individual variation on the results.
 - A large number of archaeological digs are represented. This reduces the effect of abnormal results on the overall results.
 - The use of a scatter graph to represent the results is a good way to show visually the trend of increasing cranial capacity and the spread of results at each point in time.
- ii A = *Australopithecus afarensis* from Ethiopia
B = *Homo erectus* from Asia