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Human Perspectives ATAR Units 3 & 4

Answers: Chapter 10 Biotechnology provides evidence of evolution

Questions 10.1

RECALL KNOWLEDGE

1 What does 'PCR' stand for?
Answer: Polymerase chain reaction

2 List the three steps in PCR.
Answer:

- Denature
- Anneal
- Extend

3 Explain the role of a primer in PCR.
Answer: The primers are complimentary to either rend of the section of DNA to be copied. They act as the starting point for elongation of the DNA strands.

4 What is the advantage of using Taq polymerase over other DNA polymerases?
Answer: Taq polymerase is a heat tolerant polymerase, its optimum temperature is 72°C, and will not denature at 96°C when the DNA is melted.

5 Explain the role of restriction enzymes in DNA profiling.
Answer: When restriction enzymes are added to DNA, it cuts the strand into different lengths depending on the base sequence of the specific DNA sample. The length of these pieces can be analysed and compared with other DNA samples.

6 Will the shorter or longer lengths of DNA travel the greatest distance during electrophoresis? Explain your answer.
Answer: The shorter lengths will travel further. They encounter less resistance from the agarose gel.

7 Name the instrument used to place the DNA in the wells for gel electrophoresis.
Answer: A micropipette.

8 Explain why a DNA ladder is useful in interpreting results from electrophoresis.
Answer: A DNA ladder contains fragments of DNA of a known length. The results from the unknown sample can be compared to the ladder to determine the length of the DNA strands in the sample.

9 List three methods of visualising DNA after electrophoresis.
Answer:

- Ethidium bromide is added and an ultraviolet light is shone over the gel to see the DNA fluoresce.
- Methylene blue binds to the DNA and stains it a deep blue.
- DNA probes with a radioactive or fluorescent molecule that binds to the DNA.

10 Draw a simplified structure of:
a deoxynucleotide triphosphate
Answer: Refer to Figure 10.9 on page 275 of the student book.

b dideoxyribonucleotide triphosphate.
Answer: Refer to Figure 10.11 on page 276 of the student book.

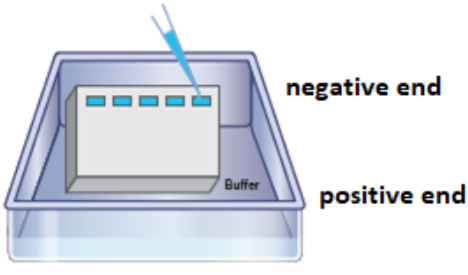
APPLY KNOWLEDGE

11 Explain why temperatures of approximately 96°C are sufficient to denature the DNA.
Answer: 96°C is hot enough to break the hydrogen bonds holding the two strands together without disrupting the individual strands.

12 Suggest what would happen if the temperature were too high during the annealing step of PCR.
Answer: Primers would not be able to attach, the lower temperature allows hydrogen bonds to form between the DNA strands and the primers.

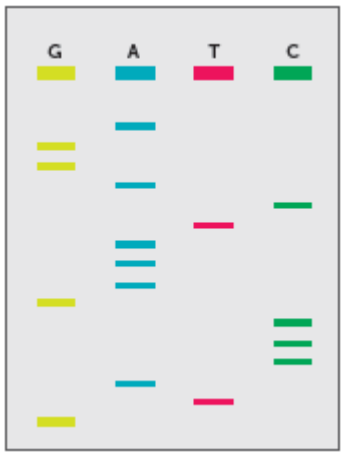
13 'DNA sequencing makes it possible for suitable primers to be chosen for PCR.' Discuss this statement.
Answer: DNA sequencing has allowed the determination of the precise order of nucleotides in a sample of DNA. Primers need to be specific to a sequence of DNA to allow the DNA segment to be copied. Knowing the precise order of nucleotides allows for the primers to be made so they can attach to the segment needed to be copied.

14 The image below shows DNA being put into the wells of an agarose gel prior to electrophoresis. Label the positive and negative sides and explain why it must be placed this way.
Answer:



DNA is negatively charged, so is placed at the negative end so that when the current is applied, the DNA will be attracted to the positive end of the agarose gel.

15 The diagram below shows the bands produced from electrophoresis during DNA sequencing using Sanger's method. Write the base sequence for the section of DNA.



Answer:
C A T G G G C T T T A G T C C T

16 Identify two situations when it may be unethical to use genetic information. For each situation, discuss the reasons for and against its use.
Answer: Students responses will vary. Possible suggestions include:
Applying for a job. It is unethical to access genetic information to determine if applicants have any genetic disease that may make one person more suited than another. This does not allow everyone equity to the job. The employer may want to know if their desired candidate will have good health.
Insurance. It is unethical for insurance companies to access genetic information prior to approving health insurance of life insurance. The insurance companies may want to access this information to increase premium rates, but this breaches confidentiality.

Questions 10.2

RECALL KNOWLEDGE

1 Where do scientists gain information from when comparing DNA?
Answer: Information is gained form DNA profiles and DAN sequencing.

2 Define 'genome'. Describe how sequencing the genome can be used to provide evidence for evolution.
Answer: The complete set of DNA in each cell of an organism is called the genome. Sequencing the genome and comparing sequences of human genome with the genome of other organisms, researchers are able to identify regions of similarity and difference. This provides evidence for evolution because the more similar the sequences, the organisms are more closely related.

3 Define 'endogenous retrovirus' and 'non-coding DNA'.
Answer: Endogenous retroviruses are viral sequences that have become part of an organism's genome. Non-coding DNA are sequences of nucleotides that have no apparent function and appear to serve no purpose.

4 Describe how endogenous retroviruses are used as evidence for evolution.
Answer: Endogenous retroviruses appear in the non-coding sections of DNA. As they are inherited, they will appear in the same location of DNA in different species that share a common ancestor. The more aligned the location of the ERVs are, the more similar the two species are.

5 What do the genes on mtDNA code for?
Answer: Mitochondrial DNA contains 37 genes. 24 genes contain the code for making transfer RNA molecules and 13 genes have instructions for making some enzymes needed for the reactions of cellular respiration.

6 Why do we only inherit mitochondrial DNA from our mothers?
Answer: The mitochondrial DNA in the sperm is destroyed after fertilisation.

APPLY KNOWLEDGE

7 The DNA of dogs is 85% similar to that of humans, while the DNA of chimpanzees is 98% similar to that of humans. Explain how this information supports the idea that we have a more recent common ancestor with chimpanzees than with dogs.
Answer: When speciation occurs, the new species will have very similar DNA; however as the new species gradually change through mutations, natural selection and genetic drift, they accumulate more differences in their DNA. Species that are more closely related share a greater portion of their DNA. Sharing 98% of our DNA with chimpanzees compared to 85% of DNA with dogs indicates we had a more recent common ancestor with chimpanzees.

8 Explain why not all retroviruses are endogenous retroviruses, and why only endogenous retroviruses are useful in providing evidence for evolution.
Answer: Retroviruses copy their DNA or RNA into the host cell through reverse transcription. The retroviruses will only become endogenous when the DNA or RNA is reverse transcribed into the gametes. When retroviruses become endogenous, the viral sequence will be passed on to the offspring from the common ancestor, so when comparing different species that share a common ancestor, the ERV would be found at the same location in the chromosome of both species.

9 Explain why comparison of structures such as endogenous retroviruses and mitochondrial DNA was not available prior to the development of techniques such as electrophoresis and DNA sequencing.
Answer: Endogenous retroviruses are viral genome sequences inserted into another organism's genome. Mitochondrial DNA is small, circular molecules of DNA found within the mitochondria of a cell. DNA sequencing has allowed scientists to locate and determine the nucleotide sequence of the ERVs and mtDNA. Due to the molecular structure of DNA, it would not have been possible to just 'see' the sequence in an organism's cell. ERVs are also found in the non-coding sections of DNA so do not produce functional proteins that could affect the phenotype of an individual. Electrophoresis allows for a DNA profile to be generated, which allows for comparison of DNA bands.

10 Compare and contrast mitochondrial DNA and nuclear DNA.
Answer:
Compare: Both are composed of nucleotides and hold the code to build proteins (genes).
Contrast: Mitochondrial DNA is inherited maternally whereas nuclear DNA is inherited from both parents. Nuclear DNA contains tens of thousands of genes, whereas mitochondrial DNA contains only 37 genes.

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Questions 10.3

RECALL KNOWLEDGE

1 State the relationship between DNA, RNA, amino acids and proteins.
Answer: DNA contains the code for building proteins. The DNA is transcribed into mRNA and tRNA is used to translate the code into a sequence of amino acids at the ribosome. Amino acids are the building blocks of proteins. Determining the sequence of amino acids can allow for the determination of the sequence of nucleotides in a DNA molecule.

2 How many different amino acids make up proteins?
Answer: There are 20 amino acids used to build proteins.

3 When comparing amino acid sequences, scientists use a single letter rather than the three letters that are usually used to identify them. Why do scientists do this?
Answer: Coding the amino acids makes it easier for a comparison to be made when determining amino acid sequences in common proteins in different species.

4 Ubiquitous proteins are important when comparing proteins.
a Define 'ubiquitous protein'.
Answer: A ubiquitous protein is one of a group of proteins that appears to be in all species. It performs the same function in each species it is found in.

b Give an example of a ubiquitous protein.
Answer: Cytochrome C.

5 What is bioinformatics?
Answer: Bioinformatics is the use of computers to describe the molecular components of living things. It uses biochemical analysis to gain information about DNA and proteins and computer software to store and analyse it.

6 What is annotation, and why is it part of bioinformatics?
Answer: Annotation is the identification of genes in a DNA sequence. The process needs to be computerised because genome sequences are too large to be annotated by hand.

APPLY KNOWLEDGE

7 Evolution results from changes in DNA. Given this fact, explain why a comparison of the sequence of amino acids in a particular protein can provide evidence for evolution.
Answer: Amino acids are the building blocks of proteins; their order and number in a protein is determined by the sequence of nucleotides in a gene on the DNA molecule. Comparing the sequences of amino acids is by proxy, comparing the DNA sequence. The more similar the amino acid sequences, the more closely related the two species are.

8 Table 10.5 sets out an amino acid sequence from alpha haemoglobin of five different species of animals. Compare each of the amino acid sequences to the one from humans.

TABLE 10.5 The amino acid sequence for alpha haemoglobin of different species

SPECIES	AMINO ACID SEQUENCE FROM ALPHA HAEMOGLOBIN
Human	VLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTK TYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNAL SALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVH ASLDKFLASVSTVLTSKYR
Whale	VLSPTDKSNVKATWAKIGNHGAEYGAEALERMFMNFPSTKT YFPHFDLGHDSAQVKGHGKKVADALTKAVGHMDNLLDALS DLSDLHAHKLRVDPANFKLLSHCLLVTLALHLPAEFTPSVHA SLDKFLASVSTVLTSKYR
Macaw	VLSGSDKTNVKGIFSKIGGQAEDYGAEALERMFATFPQTKTY FPHFDVSPGSAQVKAHGKKVAAALVEAANHIDDIATALSKLS DLHAQKLRVDPVNFKLLGQCFLVVVAIHNPSALTPEVHASLD KFLCAVGNVLTAKYR
Baboon	VLSPDDKKHVKAAWGKVGEHAGEYGAEALERMFLSFPTTKT YFPHFDLSHGSDQVNKHGKKVADALTLAVGHVDDMPQALSK LSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASL DKFLASVSTVLTSKYR
Frog	HLTADDKKHIKAIWPSVAAHGDKYGGEALHRMFMCAPKTKT YFPDFDFSEHSKHILAHGKKVSDALNEACNHLDNIAGCLSKLS DLHAYDLRVDPGNFPLLAHQILVVVAIHFPKQFDPATHKALD KFLVSVSNVLTSKYR

a Which species' sequence is the most similar?
Answer: Baboon is most similar with 11 differences in amino acid sequence compared to humans.

b Which species' sequence is the most different?
Answer: Frog is the least similar with 58 differences in amino acid sequence compared to humans.

c Does this correlate with our current understanding of evolution and common ancestors?
Answer: Yes, this correlates as the baboon is a primate and belongs in the same family as humans. Frogs are amphibians and phenotypically very different from humans.

Chapter 10 Activities

Activity 10.1 Investigating electrophoresis simulation

Go to the weblink and work through the electrophoresis simulation. As you go, or after you have finished, answer the following questions.

1 What ingredients are used to make the gel?
Answer: The gel ingredients consist of powdered agarose (agarose is one of the main constituents of agar) and buffer (a salt solution).

2 Describe how the gel is made using the ingredients that you have listed.
Answer: Powdered agarose and buffer solution are mixed together in a flask and then heated (in a microwave) so that the agarose melts into the buffer solution.

3 DNA samples are placed in wells in the gel. Explain how the wells are made.
Answer: A device like a comb is placed into the melted solution. It is left in place until the gel solidifies. When the comb is removed, wells are left in the gel.

4 What is the purpose of the DNA size standard?
Answer: The DNA size standard contains DNA fragments of known length which can then be used as reference points against which the length of the unknown DNA fragments can be estimated.

5 What electrical charge does a DNA molecule have?
Answer: DNA has a negative charge.

6 Which electrical charge is applied to the well end of the gel?
Answer: The negative charge

7 Is it possible to tell whether an electric current is running through the gel?
Answer: When the current is running, air bubbles appear on the electrodes at each end of the electrophoresis box.

8 What makes the DNA migrate through the gel?
Answer: The negatively charged DNA fragments are repelled by the negative charge at the well end of the electrophoresis box.

9 Describe the technique that is used to make the DNA visible in the gel.
Answer: The gel is taken out of its mould and placed in a solution that stains the DNA so that it can be seen.

10 Why do shorter DNA strands move further through the gel than longer strands?
Answer: The gel acts as a filter and smaller molecules move through the filter more rapidly than larger molecules.

ACTIVITY 10.2 Investigating the effect of restriction digestion enzymes on lambda DNA

Discussion

1 Why was 1 µL of nuclease-free water to be added to microtube labelled 'C'?
Answer: The nuclease-free water was added to the microtube labelled 'C' to act as the control for the experiment. This microtube does not contain any DNA.

2 Why do we incubate the restriction digests at 37°C?
Answer: Restriction enzymes are taken from bacteria. Typically, the environment of the bacteria is approximately 37°C. Thus, the enzymes evolved to function optimally at a temperature of 37°C.

3 What is the purpose of the dye?
Answer: The function of the loading dye is to visualise the electrophoresis through the separation of the dyes into two distinct bands because the DNA is not observable in this procedure if a blueGel apparatus is not used. It also provides colour to make it visible when loading into the gel.

4 What would occur if the gel electrophoresis chamber were filled with distilled water instead of TBE buffer?
Answer: Buffer keeps the pH stable to avoid deionisation of the DNA molecules. If they were to lose their charge, they would not be attracted to the positive electrode in the apparatus, and therefore would not move. The buffer also provides ions to transmit the charge through the gel. If distilled water were used, the electrophoresis would not work.

5 Explain why DNA samples must be loaded at the negative end of a gel electrophoresis chamber.
Answer: DNA samples are loaded at the end with the negatively charged electrode because DNA is negatively charged, and therefore will migrate the positive electrode. By loading it at the negative end, students provide the DNA with space to travel.

6 What would occur if the electrodes in the electrophoresis chamber were reversed?
Answer: If the electrodes in the electrophoresis chamber were reversed, the electrical field would be reversed as well. As a result, the DNA would not migrate to the bottom of the gel, and would instead run out of the top of the gel into the buffer solution and the sample would be lost.

ACTIVITY 10.3 Investigating biotechnological techniques

4 Present and explain your model to the other members of the class, or make a video of your model and add an explanation by a voice-over or annotations.
Answer: For the polymerase chain reaction, students should show:
• Denaturation: DNA fragments heated, the DNA double helix splits into single strands.
• The DNA is cooled down. Primers bind to complementary places on the DNA strands (this process may be called annealing).
• DNA polymerase brings about synthesis of a complementary strand of DNA so that a double helix is formed again.
• The process repeats over and over again, each time doubling the number of DNA molecules produced.
For DNA sequencing, students should show:
• Polymerase chain reaction (PCR) may be carried out to increase the amount of DNA for profiling.
• Enzymes are used to cut the DNA into short lengths. The cuts take place at specific points.
• The short pieces of DNA are used as a template to make many fragments.
• These fragments are separated by gel electrophoresis – the fragments migrate through a gel that is electrically charged; smaller fragments move faster than larger ones.

ACTIVITY 10.4 Investigating amino acid sequencing

What to do
2 Record your data in a table.
Answer:

Species comparison	Number of differences in the amino acid sequences of haemoglobin
Human and chimpanzee	0
Human and gorilla	1
Chimpanzee and gorilla	1

Human and rhesus monkey	2
Chimpanzee and rhesus monkey	2
Gorilla and rhesus monkey	1
Human and horse	5
Human and kangaroo	7

3 Using only the data from this section of the haemoglobin molecule, rank the species in order from the one closest to humans to the one most distant.
Answer: Chimpanzee → gorilla → rhesus monkey → horse → kangaroo

Studying your data
1 Based on this segment of the haemoglobin molecule, which species of mammal appears to be the most closely related to humans?
Answer: Chimpanzee

2 Which animal appears to be the least closely related to humans?
Answer: Kangaroo

3 Which of the other pairs of species show close relationships?
Answer: Chimpanzee and gorilla; gorilla and rhesus monkey

4 These sequences of amino acids are generally very similar but not identical. If these species were all descended from a common ancestor, how would the changes in the sequences of the different species have come about?
Answer: Mutation and then natural selection

5 Do you think the differences in the amino acid sequences between the species would affect the function of haemoglobin?
Answer: No. Although the sequence of amino acids in the haemoglobin molecule is different the basic structure of the whole molecule is the same and its function of binding the oxygen molecules is the same.

In summary
Using the information from this sequence of amino acids in haemoglobin, describe the evolutionary relationships between the species in terms of the evolution of humans.
Answer: Chimpanzees, gorillas, rhesus monkeys and humans are more closely related and have a more recent common ancestor. The kangaroo and horse would also have a common ancestor with chimpanzees, gorillas, rhesus monkeys and humans, but further back in time than the primate common ancestor.

Chapter 10 Review questions

Recall

1 a What is DNA sequencing and what is it used for?
Answer: DNA sequencing is the process of determining the order of bases (nucleotides), and thus genes, in a sample of DNA.

b Briefly outline the steps in building a DNA sequence.
Answer: Steps involved in building a DNA sequence include the following:
• DNA is extracted from cell nuclei.
• DNA is broken into pieces and the pieces copied many times.
• Double-stranded DNA separated into single strands.
• Primer added and binds to one strand.
• The second DNA strand is recreated by adding nucleotides in the correct sequence.
• A terminator nucleotide stops the nucleotide sequence.
• Strands can then be compared to determine the nucleotide sequence.

2 a What is a 'DNA profile'?
Answer: A sample of a person's DNA is cut at particular base sequences and placed on a bed of gel. Electrophoresis results in the pieces of DNA forming a banding pattern dependent on the size of the DNA fragment. This banded picture is the person's DNA profile or fingerprint.

b List two practical applications of DNA profiling.
Answer: DNA profiling can be used:
• in forensic science to match DNA found at a crime scene with that of a suspect
• in tracing ancestry to show relationships between related people
• to identify genes that cause inherited disease – often enabling early diagnosis of disease
• in families where there is a history of inherited disease to determine the chances of having a child with the disease.

3 a Outline the steps in the polymerase chain reaction.
Answer: The steps in the polymerase chain reaction include the following:
• DNA is heated to 96°C to separate the two strands of the molecule (denaturation).
• Primers are added and attach to each strand (annealing)
• Cooling occurs so that the new DNA strand is synthesised when the primer initiates the reaction with DNA polymerase (*Taq* polymerase)
• Heating occurs to separate the strands of the new DNA molecules and the process is repeated.

b Giving an example, explain what the term 'heat stable DNA polymerase' means.
Answer: Heat-stable DNA polymerase are forms of the DNA polymerase enzyme that are heat stable. They do not denature or break down at high temperatures. One example is *Taq* polymerase from the heat-loving bacterium *Taq aquaticus*.

c What are some of the practical applications of the polymerase chain reaction?
Answer: The polymerase chain reaction can be used to:
• reduce the time taken to identify hereditary disease in a person's genome
• detect viral infections, often before symptoms of disease occur
• amplify DNA from small samples left at crime scenes
• compare genomes of fossils where the fossils contain small amounts of DNA that can be extracted.

4 a Define 'endogenous retroviruses'.
Answer: Endogenous retroviruses are a viral sequence that has become part of an organism's genome.

b How do retroviruses become endogenous?
Answer: A retrovirus copies its RNA into the DNA of the host cell. The retrovirus only becomes endogenous if copies of its RNA are inserted into the DNA of a germ cell, which through meiosis becomes a sperm or an egg.

c What is the value of endogenous retroviruses in a study of evolution?
Answer: All offspring of the infected individual will have a copy of the ERV in the same place in the same number chromosome. Subsequent generations will all be affected in the same way. This makes the study of endogenous retroviruses important in determining evolution, because the ERVs will show relationships between species. Species with the same ERVs will be closely related.

5 a Define 'mitochondrial DNA (mtDNA)'.
Answer: Mitochondrial DNA (mtDNA) is DNA located in the mitochondria of cells.

b Describe how mtDNA has been used to provide evidence for evolutionary relationships between species.
Answer: mtDNA is inherited only from the mother. The mtDNA is a copy of that which was in the female parent's egg cell. mtDNA mutates more often than nuclear DNA, and the amount of mutation of mtDNA is roughly proportional to the amount of time that has passed. Similarities and differences in the mtDNA of species can thus show evolutionary relationships.

c Give an example of where mtDNA has provided information about such a relationship.
Answer: Studies of mtDNA have shown that most modern Europeans are descended from hunter-gathers who settled in Europe during the last Ice Age. mtDNA evidence has also shown that the last common ancestor of Neanderthals and modern humans lived approximately 600 000 years ago.

6 Describe how the sequence of amino acids in proteins can be used to determine the degree of similarity between species.
Answer: By comparing the type and sequence of amino acids in similar proteins from different species, the degree of similarity can be established. The greater the similarity between the sequence of amino acids in the proteins of species, the more closely related they are.

7 a Define 'ubiquitous proteins'.
Answer: Ubiquitous proteins are proteins that appear to be in all species. They carry out the same functions regardless of the species in which they are found.

b Why has cytochrome C been so valuable in providing evidence for evolution? Give examples of species that contain cytochrome C.
Answer: Cytochrome C is a ubiquitous protein that has changed very little over millions of years of evolution. It has common amino acid sequences among many species and provides evidence for evolution and relationships between species. The more similarity there is between the cytochrome C from different species, the more recently the species have evolved from a common ancestor. Cytochrome C is found in plants, animals and many unicellular organisms.

c Besides cytochrome C, what other proteins have been used to provide evidence about relationships between species?
Answer: Haemoglobin is another protein that can be used to show relationships between species.

8 a How has bioinformatics assisted biologists in refining evolutionary relationships?
Answer: Bioinformatics is the use of computers to describe the molecular components of living things and in doing so has allowed evolutionary biologists to trace the evolution of a large number of organisms by measuring their DNA. This has been a change to the more traditional approach of studying physical taxonomy or the use of physiological observations.

b What role has comparative genomics played in the study of evolutionary changes among organisms?
Answer: Comparative genomics compares the genomes of different species. Regions of similarity and difference between genomes can be identified. Using this technique, precise relationships between species can be determined.

9 List the key areas that need to be ethically considered when deciding whether to gain or use genetic information.
Answer:

- Confidentiality
- Autonomy
- Privacy
- Equity

Explain

10 One of the most frequently used ways to sequence DNA is to take advantage of the way it replicates. Explain how, if the sequence of bases on one side of a fragment of DNA is known, the sequence on the other side is known as well.
Answer: DNA is a double-stranded molecule that has complementary base pairs. So, if one strand's base sequence is known, then the other strand's sequence will be the complementary bases. Because adenine pairs with thymine, wherever adenine appears on one strand of the DNA molecule, thymine will be on the other strand and vice versa. Because cytosine pairs with guanine, wherever cytosine appears on one half of the DNA molecule, guanine will be on the other half and vice versa.

11 The polymerase chain reaction is a method of amplifying a small amount of DNA into a much larger amount. Explain the advantages of being able to do this.
Answer: The advantages are:
• decreased amount of time to detect hereditary disease
• detection of a hereditary disease before symptoms appear
• the targeting of the specific gene that causes hereditary disease (that is, you do not need to sequence all DNA)
• the use of DNA from a very small specimen, for example, a drop of blood or a strand of hair.

12 Using an example, explain how the study of DNA in different species has added to the evidence for evolution.
Answer: Comparing the nucleotide sequences in different species allows researchers to see similar sequences. As DNA is inherited, species that are closely related, or have a recent common ancestor, have

more overlapping sequences compared with species that have a least recent common ancestor.

13 Describe how each of the following has facilitated DNA sequencing:
a polymerase chain reaction
Answer: If only very small amounts of DNA are available, the polymerase chain reaction can be used to produce large amounts of the DNA so that it can be used in the sequencing of a genome.

b gel electrophoresis
Answer: Gel electrophoresis is used to establish a DNA profile, which can then be compared with other profiles to trace relationships between individuals and groups.

c bacterial enzymes.
Answer: Restriction enzymes derived from bacteria are used to cut the DNA molecule into smaller fragments, which can then be separated by gel electrophoresis. The DNA can then be sequenced.

Apply

14 When ancestral species evolve into two or more separate species, those new species would exhibit considerable similarity in their DNA. What causes the DNA to change over time? How has the information from DNA been used by scientists to speculate on the relationships between species?
Answer: DNA may change over time due to mutation. Mutant forms are then subject to natural selection or genetic drift or any other evolutionary process. Because the DNA would be the same in the ancestral species and, because only some of the DNA would change over time, the relationship between the new species can be determined by scientists by comparing the similarities in their DNA. Changes to the sequence of bases in a DNA molecule can also arise because of the insertion of endogenous retroviruses.

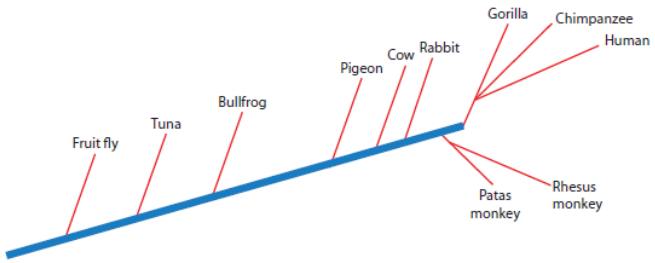
15 Modern technology has provided the means to compare DNA and protein sequences. How has this changed the traditional way of looking at the relationships between humans and apes?
Answer: Experimentation with the DNA strands from different primates suggests an increasing genetic distance between humans and the other primate groups as one progresses from chimpanzees, to gorillas, orangutans, gibbons and to Old World monkeys. This indicates that humans and chimpanzees are much more closely related than structure alone would appear to suggest. Therefore, modern classifications reflect this closer relationship.

16 Explain why mtDNA is only of use when looking at the relationships within a species or between closely related species.
Answer: mtDNA has only 37 genes, so species that are not closely related may have so many mutations that relationships would be difficult to determine. Also, mtDNA has a higher rate of mutation than nuclear DNA, so that it is only possible to look at the relationships within a species or in groups that have only relatively recently become separate species.

17 Explain why scientists select ubiquitous proteins for their biochemical research on the relationships between species.
Answer: Ubiquitous proteins are used to determine relationships between species because:
• they are found in all organisms
• they are completely independent of an organism's specific function
• they are independent of the environment in which the organisms live

• they carry out the same function in all species.

18 Refer to Table 10.4, which indicates the degree of difference in the amino acids in cytochrome C between humans and some other species. Using this information, construct a family tree to illustrate a possible relationship between those species.
Answer: A possible family tree could be:



19 Why would scientists use a comparative study of haemoglobin in different species in a search for data to support their theories of primate evolution?
Answer: Haemoglobin is common to all primates. The idea that there is a common primate ancestor means all primates would have started with the same haemoglobin and, as they have formed separate species, there have been gradual changes in the haemoglobin. Comparing these differences will demonstrate the relationships. The more similar the haemoglobin, the more closely and recently related the species.

20 Imagine that you and your sister are identical twins. You have had genetic testing, and now know that you have a genetic predisposition to breast cancer. Discuss whether or not it is ethical to tell your twin about the testing results.
Answer: It is not ethical to tell your twin about the testing results. The right to autonomy respects the individual's right to be self-determining and to choose whether to be tested or not, and, if tested, to know and share the information.

Extend

21 Mitochondrial Eve is a name that has been given to the woman who, when traced through the female line, is the most recent common ancestor for all living humans. The mitochondrial DNA in all humans alive today is derived from her.
a How is the matrilineal line traced back to Mitochondrial Eve?
Answer: Mitochondrial DNA is inherited from the mother, with measurable mutations occurring at a rate of 1 nucleotide every 3500 years. Mitochondrial Eve is defined as the most recent woman from whom all living humans descended in an unbroken line.

b How long ago is Mitochondrial Eve believed to have lived?
Answer: The estimate is 150 000 years ago.

c In what part of the world did she live?
Answer: East Africa, Ethiopia, Kenya or Tanzania.

d Does the fact that the mitochondrial DNA of all humans is derived from Mitochondrial Eve mean that she was the only human female alive at the time?
Answer: No, nuclear DNA studies indicate that the size of ancient human populations never dropped below

tens of thousands of individuals. Other women living during Eve's time may have descendants alive today, but not in a direct female line.

e How is it possible that one woman could be the matrilineal ancestor of us all?
Answer: It is not possible. The species would have become extinct due to population bottleneck. Many women alive at the same time as Mitochondrial Eve have descendants alive today.

20 Haemoglobin and cytochrome C have been used to give support to the theory of evolution through natural selection. Scientists have similarly compared the biochemistry of universal blood proteins.
a Have such studies revealed evidence for the relationships between different species?
Answer: Yes. DNA holds the genetic code for proteins, and as DNA is inherited and conserved between species, similar nucleotide sequences occur in different species to enable them to produce ubiquitous proteins.

b Does such evidence imply that some species share a more recent common ancestor than other species?
Answer: Yes. The degree of similarity in amino acid sequence is correlated to the length of time passed since a common ancestor. The greater the degree of difference indicates more time has passed since the divergence.