INSIGHT

Trial Exam Paper

2009

BIOLOGY

Written examination 2

Solutions book

This book presents:

- correct solutions
- explanatory notes
- mark allocations
- tips and guidelines

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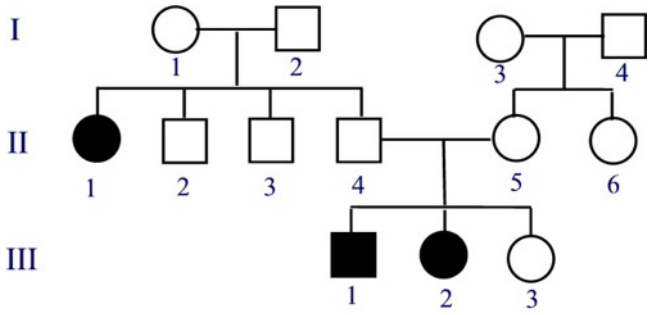
AREA OF STUDY 1 – Heredity

SECTION A – Multiple-choice questions

Question 1

In the following human pedigree the shaded individuals have the trait being investigated.



The mode of inheritance of the trait is

A. autosomal dominant.

B. **autosomal recessive.**

C. X-linked dominant.

D. X-linked recessive.

Answer is B

Explanatory notes

- A is incorrect – if I-1 and I-2 (or II-4 & II-5) are both autosomal recessive they will not be able to produce II-1 (or III-1 & III-2) with the dominant trait.
- B is correct – neither I1 and I2 (or II4 & II5) show the trait and yet they produce II1 (or III1 & III2) with the trait. This indicates that I1 and I2 (or II4 & II5) must carry the allele for the trait but it is not expressed in their phenotypes, therefore the trait must be recessive.
- C is incorrect – if trait was X-linked recessive, none of the daughters of II4 should have the trait, but II2 has the trait. This is not possible for an X-linked recessive trait if the father does not show the trait.
- D is incorrect – if trait was X-linked recessive, only the daughters of II4 should have the trait, but his son also has the trait, which is not possible for an X-linked recessive trait.

Question 2

For the trait shown in the pedigree, Individual III-3 can be

A. homozygous only.

B. hemizygous only.

C. heterozygous or hemizygous.

D. **homozygous or heterozygous.**

Answer is D

Explanatory notes

- A is incorrect – II-4 & II-5 produce offspring who are recessive therefore they BOTH must be heterozygous for the trait, III-3 could be homozygous OR heterozygous for the trait.
- B is incorrect – the trait is not sex linked and III-3 cannot be classified as hemizygous for the trait. (Hemizygous – describes a male who has only one X chromosome and therefore only one allele for traits that are X-linked. This means males cannot be homozygous or heterozygous for an X-linked trait).
- C is incorrect – trait could be heterozygous but not hemizygous.
- D is correct – II-4 & II-5 produce offspring who are recessive therefore they BOTH must be heterozygous for the trait, III-3 could be homozygous OR heterozygous for the trait.

The following information relates to Questions 3 and 4.

In the tomato plant, *Lycopersicon esculentum* (*L. esculentum*), smooth skin (S) is dominant to peach skin (s) and non-beaked fruit (Bk) is dominant to beaked fruit (bk).

Question 3

A heterozygous smooth, non-beaked plant was crossed with a peach, beaked plant. The gametes of the F1 would only include

A. SBk, sbk.

B. **SBk, sbk, Sbk, sBk.**

C. SS, BkBk, ss, bkbk.

D. SS, BkBk.

Answer is B

Explanatory notes

- Heterozygous smooth, non-beaked plant (SsBkbk) x peach, beaked plant (ssbkbk)
- Parental gametes: (SBk, sBk, Sbk, sbk) x sbk → F1 gametes: SBk, sbk, sBk, Sbk
- A is incorrect – SBk and sbk are two of the F1 gametes, however, there are two others, sBk & Sbk.
- B is correct – SBk, sbk, sBk & Sbk are the four gametes produced in the F1.
- C is incorrect – it is not possible for F1 to produce these gametes as gametes will contain one allele for each trait as homologous chromosomes separate during meiosis.
- D is incorrect – it is not possible to produce these gametes as gametes will contain one allele for each trait as homologous chromosomes separate during meiosis.
-

Question 4

The results of the cross between the heterozygous smooth, non-beaked plant and the peach, beaked plant are shown in the table.

	smooth, non-beaked tomato plant x peach, beaked plant			
Phenotype	smooth, non-beaked	peach, beaked	smooth, beaked	peach, non-beaked
Number of F1 offspring	195	187	56	63

The conclusion that can be drawn from these results is that

A. **the genes for fruit skin type and fruit shape are linked.**

B. the genes for skin type and fruit shape are independent of each other.

C. the smooth, non-beaked and peach, non-beaked plants have the parental phenotypes.

D. the smooth, beaked and peach, beaked plants have the parental phenotypes.

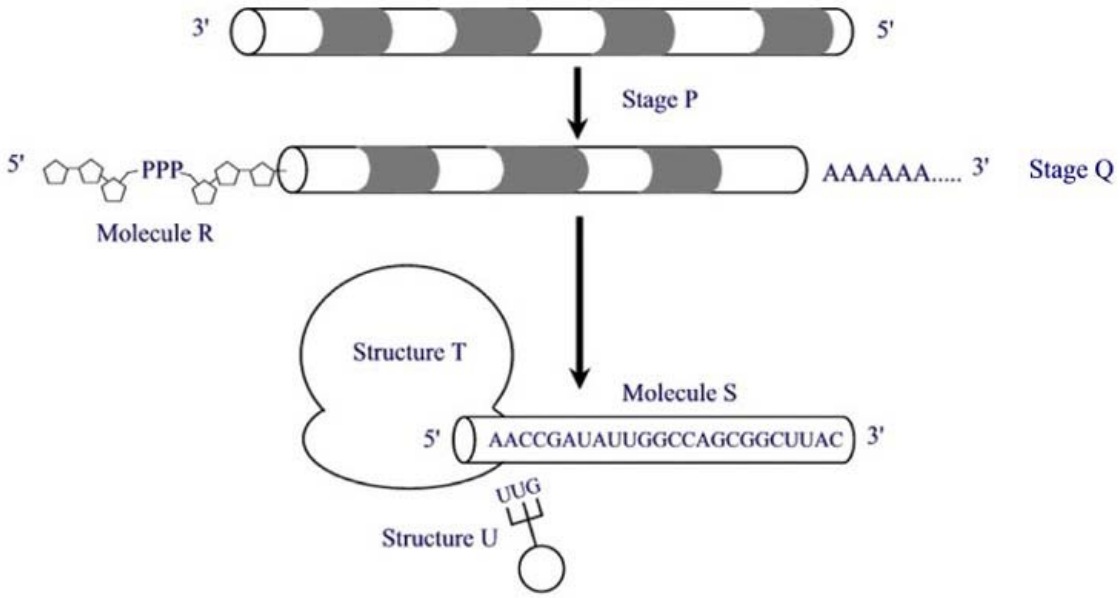
Answer is A

Explanatory notes

- A is correct – offspring are produced in the ratio expected when crossing over (recombination) has occurred, this is only possible if genes are linked.
- B is incorrect – offspring are not produced in the ratio expected (1:1:1:1) when independent assortment occurs, therefore the genes cannot be independent of each other and must be linked.
- C is incorrect – the smooth, non-beaked plants have the parental phenotypes but the peach, non-beaked plants have recombinant phenotypes.
- D is incorrect – the peach, beaked plants have parental phenotypes but the smooth, beaked plants have the recombinant phenotypes.

The following information relates to Questions 5, 6 and 7.

The following diagram shows the process of protein synthesis in a cell following the activation of DNA.



Question 5

The correct labels for the diagram are

	Stage P	Stage Q	Molecule R	Molecule S	Structure T	Structure U
A.	translation	splicing	methylated cap	mRNA	ribosome	amino acid
B.	transcription	translation	mRNA	methylated cap	mitochondrion	tRNA
C.	translation	transcription	mRNA	methylated cap	mitochondrion	amino acid
D.	**transcription**	**splicing**	**methylated cap**	**mRNA**	**ribosome**	**tRNA**

Answer is D

Explanatory notes

- A is incorrect – correct order is transcription, splicing, methylated cap, mRNA, ribosome and tRNA. Stage P shows production of mRNA from DNA (transcription). It cannot be translation as this occurs at a ribosome and involves the construction of a polypeptide chain using codons of the mRNA molecule. Stage Q is not splicing as this occurs before the addition of the methylated cap and poly-A tail. Molecule R is the methylated cap. Molecule S is mRNA. Structure T is a ribosome. Structure U is a loaded tRNA which transfers a specific amino acid from the cytoplasm to the ribosome.

- B is incorrect – correct order is transcription, splicing, methylated cap, mRNA, ribosome and tRNA. Stage P shows production of mRNA from DNA (transcription). Stage Q cannot be translation as this occurs at a ribosome and involves the construction of a polypeptide chain using codons of the mRNA molecule. Molecule R is the methylated cap not mRNA which has a methylated cap as part of its structure. Molecule S is therefore mRNA not the methylated cap. Structure T is a ribosome not a mitochondrion where aerobic respiration occurs (not polypeptide synthesis). Structure U is a loaded tRNA which transfers a specific amino acid from the cytoplasm to the ribosome.
- C is incorrect – correct order is transcription, splicing, methylated cap, mRNA, ribosome & tRNA. Stage P shows production of mRNA from DNA (transcription). It cannot be translation as this occurs at a ribosome and involves the construction of a polypeptide chain using codons of the mRNA molecule. Therefore Stage Q cannot be transcription. Molecule R is the methylated cap not mRNA which has a methylated cap as part of its structure. Structure T is a ribosome not a mitochondrion where aerobic respiration occurs (not polypeptide synthesis).
- D is correct – the Stages, Molecules and Structures are identified correctly and presented in correct order.

Question 6

At Stage P

A. DNA polymerase is active.

B. **RNA polymerase is active.**

C. removal of introns from DNA occurs.

D. removal of exons from pre-RNA occurs.

Answer is B

Explanatory notes

- A is incorrect – DNA polymerase is active when DNA is being replicated.
- B is correct – RNA polymerase is active during transcription when RNA is being synthesised from a DNA template.
- C is incorrect – introns are removed from pre-RNA, not from DNA.
- D is incorrect – introns are removed from pre-RNA, not exons.

Question 7

The DNA molecule involved in this process would have the nucleotide sequence

A. T T C C G T A T A A C G C G T C G C C G A A T G
B. T T G G C T A T A G A C T G T C G C C G A A T G
C. **T T G G C T A T A A C C G G T C G C C G A A T G**
D. T T G G C T T A T A C C G G A G C C C G A A T G

Answer is C

Explanatory notes

- Nucleotides in DNA and nucleotides in RNA pair in a complementary manner in the process of transcription. This is shown in the following table.

DNA	RNA
adenine (A) pairs with	uracil (U)
cytosine (C) pairs with	guanine (G)
guanine (G) pairs with	cytosine (C)
thymine (T) pairs with	adenine (A)

On the basis of this pairing:

- A is incorrect – base sequence in A would produce a strand of RNA with the sequence A A G G C A U A U U G C G C A G C G G C U U A C, which is not the sequence initially presented.
- B is incorrect – base sequence in B would produce a strand of RNA with the sequence A A C C G A U A U C U G A C A G C G G C U U A C, which is not the sequence initially presented.
- C is correct – base sequence in C would produce a strand of RNA with the sequence presented.
- D is incorrect – base sequence in D would produce a strand of RNA with the sequence A A C C G A A U A U G G C C U C G G G C U U A C, which is not the sequence initially presented.

Question 8

Ribonucleic acid (RNA) is composed of nucleotide subunits. Which of the following statements is correct for RNA nucleotides?

A. **Covalent bonds exist between ribose sugars and the bases.**

B. Adenine and uracil are the purine bases.

C. Adenine in RNA will pair with uracil in a strand of DNA.

D. The equivalent of a DNA triplet on an mRNA strand is an anticodon.

Answer is A

Explanatory notes

- A is correct – the bonds found between ribose sugars and bases ARE covalent bonds.
- B is incorrect – adenine and guanine are purine bases, uracil and cytosine are pyrimidine bases.
- C is incorrect – adenine in RNA pairs with thymine in DNA, there is no uracil in DNA.
- D is incorrect – the equivalent of a DNA triplet on an mRNA strand is a codon (anticodon in tRNA).

Question 9

The process of complementary base pairing between two RNA molecules takes place during the process of

A. DNA replication.

B. reverse transcription.

C. transcription.

D. **translation.**

Answer is D

Explanatory notes

- A is incorrect – during DNA replication there is only complementary base pairing between nucleotides of DNA molecules in DNA replication.
- B is incorrect – during reverse transcription there is only complementary base pairing between mRNA and DNA nucleotides.
- C is incorrect – during transcription there is only complementary base pairing between DNA and mRNA nucleotides.
- D is correct – during translation the nucleotide bases in an mRNA codon will pair in a complementary manner with the unpaired nucleotide bases on a tRNA anticodon.

Question 10

Apoptosis is a process that causes the natural death of cells and occurs in most tissues of the vertebrate body. An example of apoptosis would NOT include the

A. removal of cells with damaged DNA.

B. **phagocytosis of dead tissue.**

C. destruction of B and T cells following recovery from a disease.

D. loss of a tail in a tadpole as it metamorphoses into a frog.

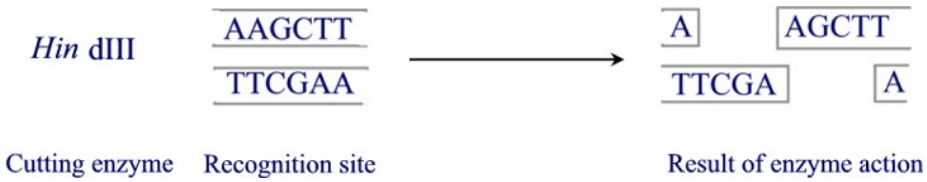
Answer is B

Explanatory notes

- A is incorrect – removal of cells with damaged DNA IS an example of programmed cell death.
- B is correct – phagocytosis of dead tissue is NOT an example of programmed cell death, as in this instance, the tissue is already dead and phagocytosis is a process to destroy and remove the dead tissue.
- C is incorrect – the destruction of B and T cells following recovery from a disease IS an example of programmed cell death.
- D is incorrect – loss of a tail in a tadpole as it metamorphoses into a frog IS an example of programmed cell death.

Question 11

The restriction enzyme *Hin* dIII has the recognition sequence AAGCTT and produces sticky ends.



Hin dIII cuts

A. covalent bonds only.

B. hydrogen bonds only.

C. **covalent and hydrogen bonds.**

D. ionic and hydrogen bonds.

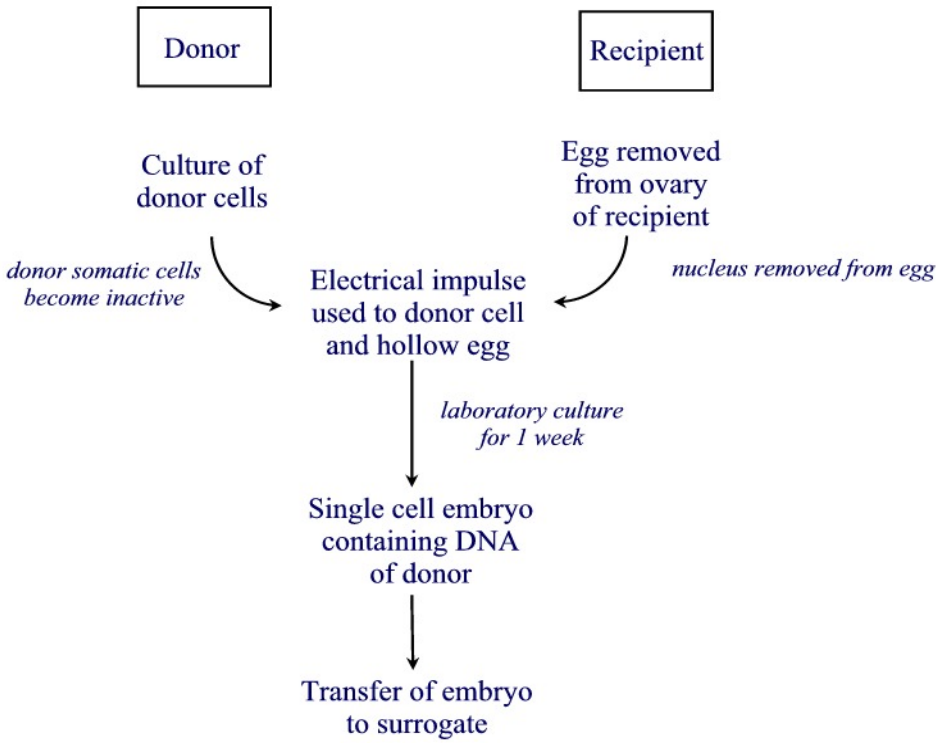
Answer is C

Explanatory notes

- A is incorrect – the production of sticky ends involves cutting the covalent bonds between the sugar and phosphate molecules AND the hydrogen bonds between nitrogen bases in DNA, not just covalent bonds.
- B is incorrect – the production of sticky ends involves cutting the covalent bonds between the sugar and phosphate molecules AND the hydrogen bonds between nitrogen bases in DNA, not just hydrogen bonds.
- C is correct – the production of sticky ends involves cutting the covalent bonds between the sugar and phosphate molecules and the hydrogen bonds between nitrogen bases in DNA.
- D is incorrect – the production of sticky ends involves cutting the covalent bonds (NOT ionic bonds) between the sugar and phosphate molecules AND the hydrogen bonds between nitrogen bases in DNA.

Question 12

The following diagram shows the steps involved in the technique of animal cloning by nuclear transfer.



Nuclear transfer involves the

A. removal of egg cells from a donor female which are fertilised *in vitro* by sperm from a male of the same species.

B. **removal of mature donor somatic cells and a recipient egg from a mature animal of the same species.**

C. artificial separation of the cells of an early stage embryo.

D. artificial insemination of female animals using semen from selected male animals.

Answer is B

Explanatory notes

- A is incorrect – removal of egg cells from a donor female which are fertilised *in vitro* by sperm from a male of the same species occurs in *in vitro* fertilisation (IVF), not nuclear transfer.
- B is correct – removal of mature donor somatic cells and a recipient egg from a mature animal of the same species is part of the process of nuclear transfer.
- C is incorrect – the artificial separation of the cells of an early stage embryo occurs in embryo splitting, not nuclear transfer.
- D is incorrect – the artificial insemination of female animals using semen from selected male animals occurs in artificial insemination, not nuclear transfer.

Question 13

Stem cells are undifferentiated cells that have the potential to differentiate into a wide range of different and specialised cells. Which of the following is NOT a term used to describe a stem cell?

A. **idempotent**
B. totipotent
C. pluripotent
D. multipotent

Answer is A

Explanatory notes

- A is correct – idempotent describes a mathematical quantity that remains unchanged when multiplied by itself; it is not associated with stem cells.
- B is incorrect – a totipotent stem cell gives rise to all cell types.
- C is incorrect – a pluripotent stem cell gives rise to most cell types.
- D is incorrect – a multipotent stem cell gives rise to particular cell types.

Question 14

The following table shows some mutagens and their observed effects. Which mutagen is most likely to cause a frameshift mutation?

	Mutagen	**Observed effect**
A.	nitrous acid	adenine in DNA is deaminated and behaves like guanine
B.	mustard gas	guanine in DNA is replaced by other bases
C.	**acridine orange**	**addition and/or removal of bases in DNA**
D.	colchicines	prevents spindle formation in mitosis, thus doubling the chromosome number

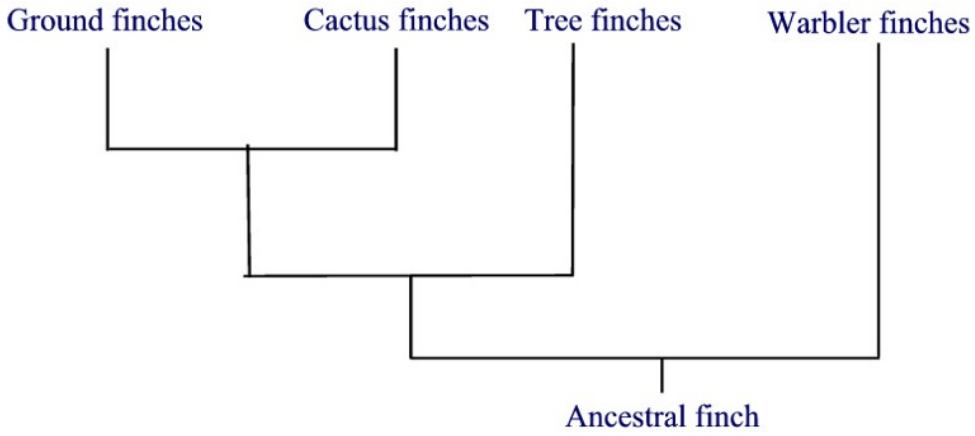
Answer is C

Explanatory notes

- A is incorrect – when adenine behaves like guanine, there is no addition or deletion, thus no frameshift.
- B is incorrect – when guanine is replaced by other bases, there is no addition or deletion, thus no frameshift.
- C is correct – acridine orange causes the addition and/or removal of DNA bases – a frameshift mutation.
- D is incorrect – colchicine stops the formation of spindles in mitosis therefore double-stranded chromosomes cannot be separated from each other. This does not lead to frameshift mutations, merely a doubling of chromosome number.

The following information relates to Questions 15 and 16.

The Galapagos Islands are home to 13 species of finches which are grouped into four genera. Small finches, the original colonisers of the islands, flew from South America across the Pacific Ocean to the Galapagos Islands. The diagram shows the evolution of these finches, also known as Darwin's Finches.



Question 15

The pattern of evolution observed in Darwin's Finches is known as

A. **divergent evolution.**
B. convergent evolution.
C. parallel evolution.
D. co-evolution.

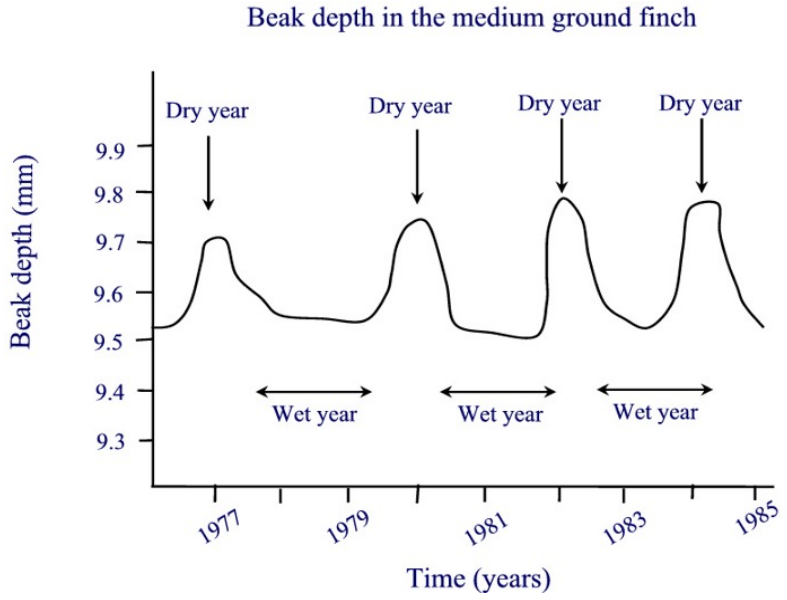
Answer is A

Explanatory notes

- A is correct – divergent evolution occurs when an ancestral species changes over time to produce several new species occupying different niches.
- B is incorrect – convergent evolution occurs when organisms with no recent common ancestry become similar in appearance due to their similar ways of life.
- C is incorrect – parallel evolution occurs when organisms with a recent common ancestry develop structural similarities due to similar environmental demands.
- D is incorrect – co-evolution occurs when two different species with a close ecological interaction develop changes which reinforce their interaction.

Question 16

The medium ground finch, *Geospiza fortis*, uses its beak to crush seeds. The finches actively choose small seeds over large seeds, probably because they are easier to crush. During wet years, small seeds are in abundance and the finches consume relatively few large seeds. In dry years, seeds of all sizes are more scarce and the finches tend to eat proportionally more large seeds. Over a 10-year period, the change in diet is correlated with a change in the average depth (from top to bottom) of the birds' beaks. The graph reflects this pattern of change.



What is the most likely explanation for this for this observation?

A. Beak size is a polygenic trait which shows continuous variation in *Geospiza fortis*.

B. Beak size is an acquired trait and increases in size when *Geospiza fortis* exercises its beak on large seeds.

C. The environment determines whether beaks are specialised for larger or smaller seeds, depending on the annual rainfall.

D. **Birds with stronger beaks have a feeding advantage and greater reproductive success during dry years.**

Answer is D

Explanatory notes

- A is incorrect – whether beak size is a polygenic trait which shows continuous variation in *Geospiza fortis* or a monogenic trait does not adequately explain the observation described.
- B is incorrect – beak size is NOT an acquired trait, it is inherited and variation is due to the genes present in the population.
- C is incorrect – the environment does NOT determine beak size in *Geospiza fortis*.
- D is correct – birds with stronger beaks survived the dry years to pass on their 'stronger beak' genes to their offspring.

Question 17

An allele coding for plumage colour in a population of the red-headed crimson rosella *Platycercus elegans elegans* is most likely to be eliminated from the population if

A. genetic drift acts against the phenotype.

B. **it codes for the dominant phenotype which is selected against.**

C. it codes for the recessive phenotype which is selected against.

D. gene flow causes it to pass into other populations.

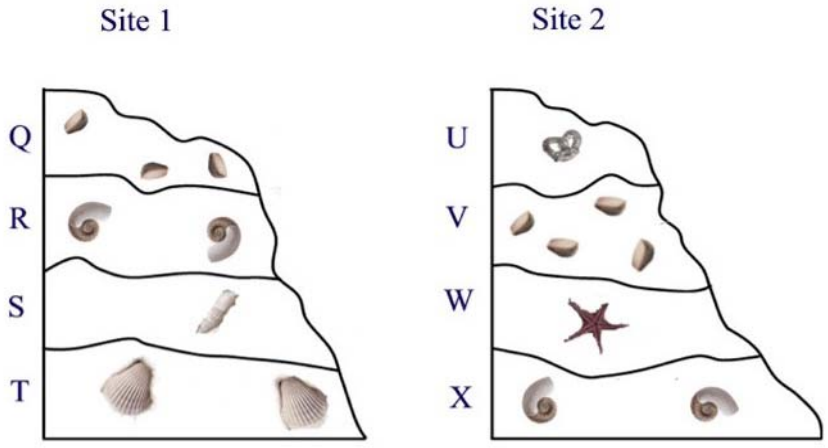
Answer is B

Explanatory notes

- A is incorrect – in small populations genetic drift can alter the frequencies of alleles but it would be less likely to lead to the elimination of an allele than that suggested in B.
- B is correct – if an allele codes for the dominant phenotype, it is always expressed. If it is selected against, it will be eliminated from the population.
- C is incorrect – if an allele codes for the recessive phenotype, it is only expressed in the homozygote. If it is selected against, it will not necessarily be eliminated from the population because it can remain 'hidden' in the heterozygote.
- D is incorrect – in small populations gene flow can alter the frequencies of alleles but it would be less likely to lead to the elimination of an allele than that suggested in B.

Question 18

The diagram shows a section through two samples of fossil-bearing strata discovered at two different locations.



From the data provided it could reasonably be concluded that

A. Stratum T contains fossils that are younger than those found in Stratum S.

B. Stratum U contains the oldest fossils.

C. Stratum R contains fossils of the same age as those found in Stratum X.

D. Stratum X contains the youngest fossils.

Answer is C

Explanatory notes

- A is incorrect – oldest layer is at the bottom of the sample, T is the oldest at Site 1, not S.
- B is incorrect – oldest layer is at the bottom of the sample, T is the oldest, not U.
- C is correct – fossils at R and X are the same indicating that these strata were laid down at the same time.
- D is incorrect – oldest layer is at the bottom of the sample, X is the oldest at Site 2, not the youngest.

Question 19

The technique of electron spin resonance (ESR) has been used to date corals, mollusc shells and human remains by analysing tooth enamel. ESR

A. is a relative dating technique.

B. **is an absolute dating technique.**

C. is used to date material of one million years and older.

D. measures the decay of potassium-40 to argon-40.

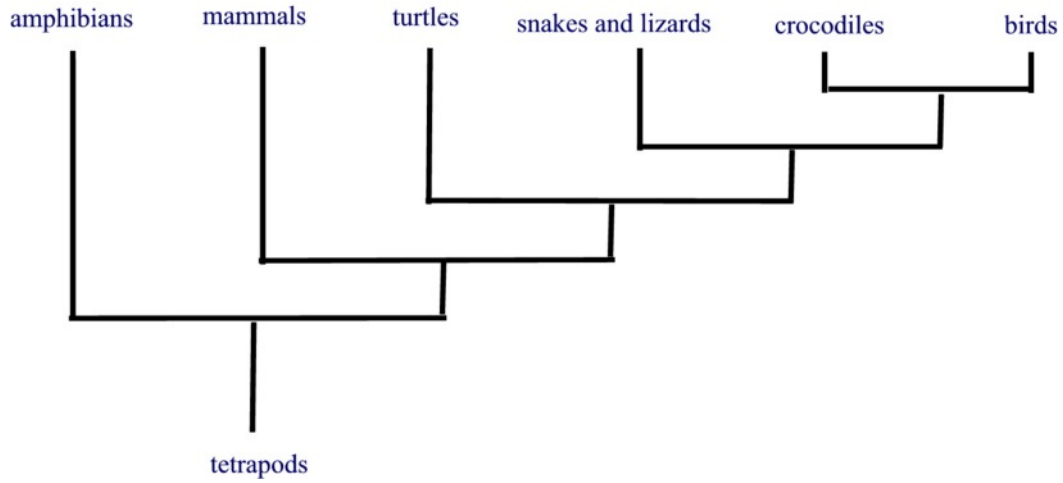
Answer is B

Explanatory notes

- A is incorrect – ESR assigns a numerical date to the sample being examined, it is not a relative dating technique.
- B is correct – ESR assigns a numerical date to the sample being examined therefore it is an absolute dating technique.
- C is incorrect – ESR is used to date material between 1000 – 1 000 000 years old.
- D is incorrect – ESR measures the microwave energy absorbed by samples previously heated or exposed to sunlight in the distant past. It does not measure the decay of potassium-40 to argon-40.

The following information relates to Questions 20 and 21.

The phylogenetic tree below depicts the evolutionary relationship between tetrapods based on comparative anatomy.



Question 20

Using the phylogenetic tree it can be concluded that the most closely related species to the crocodile is

A. turtles.

B. amphibians.

C. **birds.**

D. snakes and lizards.

Answer is C

Explanatory notes

- A is incorrect – in this phylogenetic tree, turtles are three times removed from sharing the greatest number of homologous structures with crocodiles, therefore they are not the most closely related.
- B is incorrect – in this phylogenetic tree, amphibians are the furthest removed from sharing homologous structures with crocodiles, therefore they are the most distantly related on this cladogram.
- C is correct – in this phylogenetic tree, birds share the greatest number of homologous structures with crocodiles, therefore they are the most closely related.
- D is incorrect – in this phylogenetic tree, snakes and lizards are two times removed from sharing the greatest number of homologous structures with crocodiles, therefore they are not the most closely related.

Question 21

It can also be concluded that

A. amphibians and birds have no common ancestors.

B. **snakes and lizards are more closely related to birds than they are to amphibians.**

C. snakes and lizards are the most closely related group to the crocodiles.

D. the most recent common ancestor of mammals and birds existed approximately 80 million years ago.

Answer is B

Explanatory notes

- A is incorrect – whilst the common ancestor to amphibians and birds is the most distant on this phylogenetic tree, there is still a shared common ancestry.
- B is correct – the most recent common ancestry occurs between snakes and lizards and birds; the common ancestry between snakes and lizards and amphibians is more distant in time.
- C is incorrect – birds are the most closely related group to the crocodiles, not snakes and lizards.
- D is incorrect – the phylogenetic tree does not present information about the time in which these animals existed, it only shows the evolutionary relationship based on shared anatomical characteristics.

Question 22

The term 'hominid' was once used to refer very broadly to humans and their extinct erect-walking ancestors. Currently, scientific journals and scientific institutions use the term 'hominin'. Which one of the following primates would NOT be considered a hominin?

A. ***Pongo pygmaeus*** **(orang-utan)**

B. *Australopithecus afarensis* (Lucy)

C. *Homo floresiensis* (The Hobbit)

D. *Kenyanthropus platyops* (Flatface)

Answer is A

Explanatory notes

- A is correct – *Pongo pygmaeus* (orang-utan) is a pongoid not a hominin.
- B is incorrect – *Australopithecus afarensis* (Lucy) is considered a hominin.
- C is incorrect – *Homo floresiensis* (The Hobbit) is considered a hominin.
- D is incorrect – *Kenyanthropus platyops* (Flatface) is considered a hominin.

The following information relates to Questions 23 and 24.

In East Africa, in the latter part of the Miocene, the climate became cooler and drier causing significant habitat changes for the arboreal dwelling hominids. Extensive areas of savannah became established and continued to expand as the forests continued to shrink. Fossils of early bipedal hominins have been found in a range of habitats including open woodland, closed woodland, forest and savannah.

Question 23

The most logical explanation for this observation is

A. hominins unable to adjust to the increasing areas of savannah retreated into the forests, existing in smaller populations.

B. hominins that retreated into the forests eventually became extinct.

C. bipedalism is a cultural response to habitat changes in the cooler and drier climate of East Africa.

D. **anatomical adaptations resulted when early hominins adopted new behaviour patterns, enabling them to survive the changing habitat.**

Answer is D

Explanatory notes

- A is incorrect – hominids that could not adjust to the increasing savannah did retreat into the forests and did exist for a time in small populations, BUT they were not hominins.
- B is incorrect – whilst the hominids that did retreat into the diminishing forests may have become extinct, hominins had not evolved at this time, therefore this is not correct.
- C is incorrect – bipedalism is not a cultural response, it is behavioural.
- D is correct – anatomical adaptations resulted when early hominins adopted new behaviour patterns, enabling them to survive the changing habitat.

Question 24

Adaptations for bipedalism would NOT include

A. **position of the foramen magnum toward the back of the skull.**

B. outward slanting femur.

C. s-shaped curve in the vertebral column.

D. bowl-shaped pelvis.

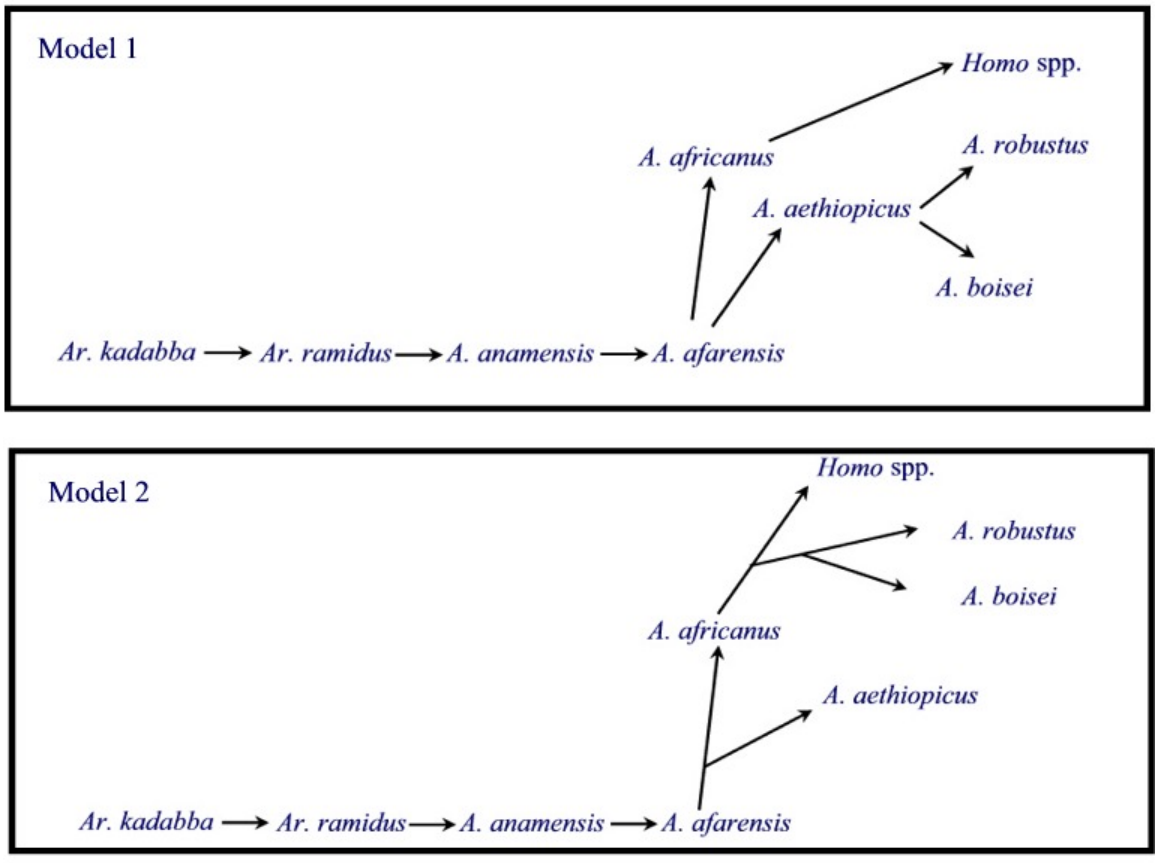
Answer is A

Explanatory notes

- A is correct – if bipedal, the foramen magnum is positioned forward in the skull, not toward the back, thus positioning of the foramen magnum toward the back of the skull is NOT an adaptation for bipedalism.
- B is incorrect – an outward slanting femur IS an adaptation for bipedalism, as it allows the knees to better support the body during upright walking.
- C is incorrect – an s-shaped curve in the vertebral column IS an adaptation for bipedalism, as it shortens the overall length of the torso giving it rigidity and balance for standing.
- D is incorrect – a bowl-shaped pelvis IS an adaptation for bipedalism, as it better supports the abdominal organs during standing.

Question 25

There is rarely complete agreement over schemes that describe evolutionary relationships. The diagram shows two models put forward to explain the possible ordering of species in the genus *Australopithecus*. Note that in the diagram of Model 1 and Model 2, *A.* is the abbreviation for the genus *Australopithecus* and *Ar*. is the abbreviation for the genus *Ardipithecus*.



Whilst the models are not identical, they do agree that

A. ***A. afarensis* gives rise to *A. africanus* and *A. aethiopicus*.**
B. *A. robustus* and *A. boisei* are direct descendants of *A. aethiopicus*.
C. *Homo* spp is the only descendant of *A. africanus*.
D. *Ar. ramidus* is a descendant of Australopithecines.

Answer is A

Explanatory notes

- A is correct – *A. afarensis* does give rise to *A. africanus* and *A. aethiopicus*.
- B is incorrect – *A. robustus* and *A. boisei* are not direct descendants of *A. aethiopicus* in Model 2.
- C is incorrect – *Homo* spp is not the only descendant of *A. africanus* in Model 2.
- D is incorrect – *Ar. ramidus* is an ancestor of Australopithecines.

END OF SECTION A

SECTION B – Short-answer questions

Question 1

In humans and other mammals, sex is determined by the sex chromosomes X and Y. The SRY gene is located on the Y chromosome and is responsible for triggering the development of the testis.

1a. What is the name given to the chromosomes that are **not** involved in sex determination?

1 mark

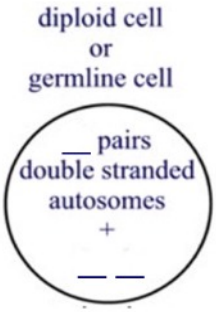
Answer

Autosomes

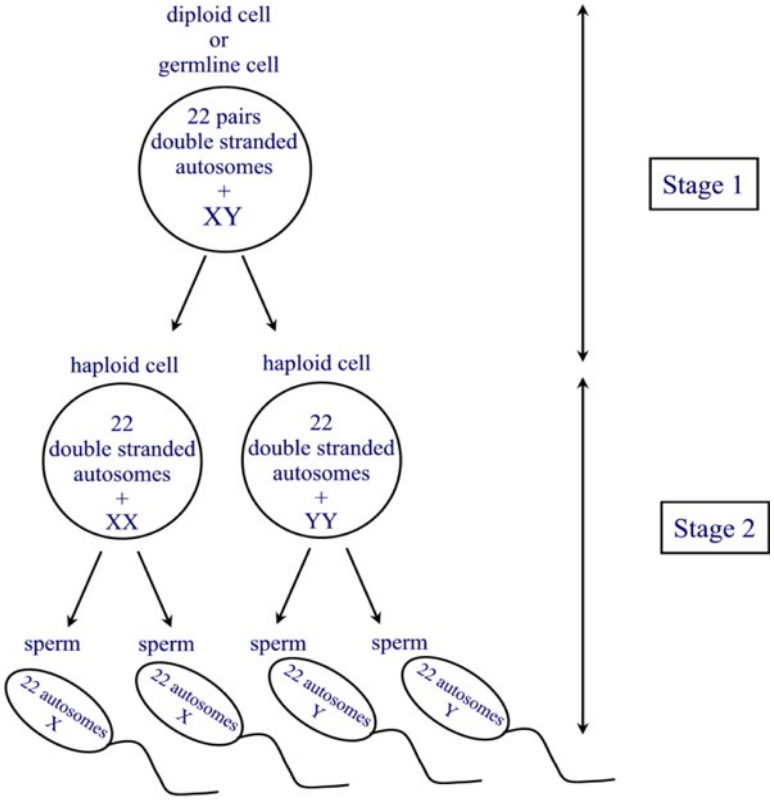
Explanatory notes

In a karyotype, chromosomes can be grouped as autosomes (non-sex chromosomes) and sex chromosomes (involved in sex determination and other characteristics found on the sex chromosomes).

1b. Using the diagram provided as a starting point, show the principle stages involved in gamete formation in a human male. Begin by filling in the blank spaces (dashes) in the diploid cell provided. Indicate how many chromosomes are found in each gamete. You do not need to show ALL stages of gamete formation, nor do you need to draw all the chromosomes involved in the process.



Answer



2 marks

Explanatory notes

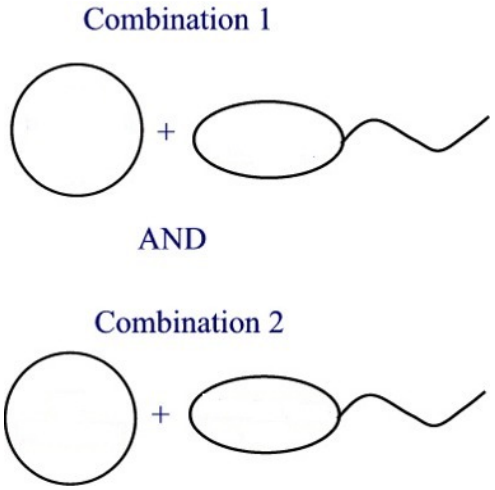
In the human male gametes are formed through the process of meiosis. Germline cells (which are diploid) contain the 22 homologous pairs of autosomes and a single non-homologous pair of sex chromosomes (in a male an X and a Y). The process of gamete formation occurs over two stages, meiosis I and meiosis II. In meiosis I, the pairs of double-stranded homologous chromosomes align themselves on the spindle of the dividing cell and then separate to opposite poles. A separate cell membrane then forms around each set of chromosomes. A second stage takes place (meiosis II) wherein the double-stranded chromosomes in each new cell align themselves along the spindle, the chromosomes separate and move to opposite poles, forming 2 new cells (4 cells in total) – each with half the original number of chromosomes (haploid).

Mark allocation

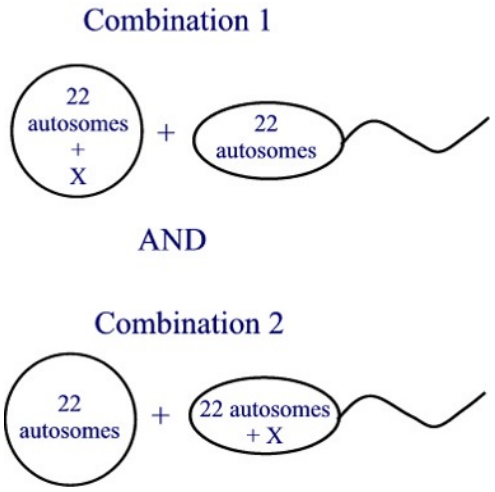
- 1 mark – correct completion of blank spaces in diploid cell (22 autosomes; XY), 2 stages of cell division (meiosis)
- 1 mark – 4 gametes produced with 23 chromosomes in each

Turner's syndrome is a genetic condition affecting 1 in 2500 females. Affected individuals show that they can be missing one X chromosome. Characteristics of the condition include short stature, absence of sexual maturation and webbing of skin between neck and shoulders.

1c i. Two possible combinations of gametes will produce zygotes with Turner's syndrome. Complete the following diagram to show the chromosomes present for each of these combinations.



Answer



2 marks

Mark allocation

- 1 mark – female gamete with X chromosome; male gamete with 0 chromosome
- 1 mark – female gamete with 0 chromosome; male gamete with X chromosome

1c ii. What error could have occurred during meiosis to produce these abnormal gametes?

1 mark

Answer

Non-disjunction of XX/XY chromosomes OR non-disjunction of XX chromatids OR failure of XX/XY chromosomes to separate during (the first division of) meiosis OR failure of X chromatids to separate during (the second division of) meiosis.

Explanatory notes

Turner's syndrome can occur as a result of chromosomal non-disjunction. If non-disjunction occurs, the gametes produced will show either 22 autosomes and 0 X chromosome or 22 autosomes and 2 X chromosomes. The incidence of chromosomal non-disjunction is known to increase with maternal age and this is the most likely cause for Turner's syndrome, however it is not certain that non-disjunction is the only cause of this condition.

The cotton plant *Gossypium sp.* has an ancestral haploid number of 13 (n = 13). Presently however, its chromosome number is 52 (4n = 52).

1d. What is the name used to describe the state of the chromosome number of *Gossypium sp.*?

1 mark

Answer

polyploidy

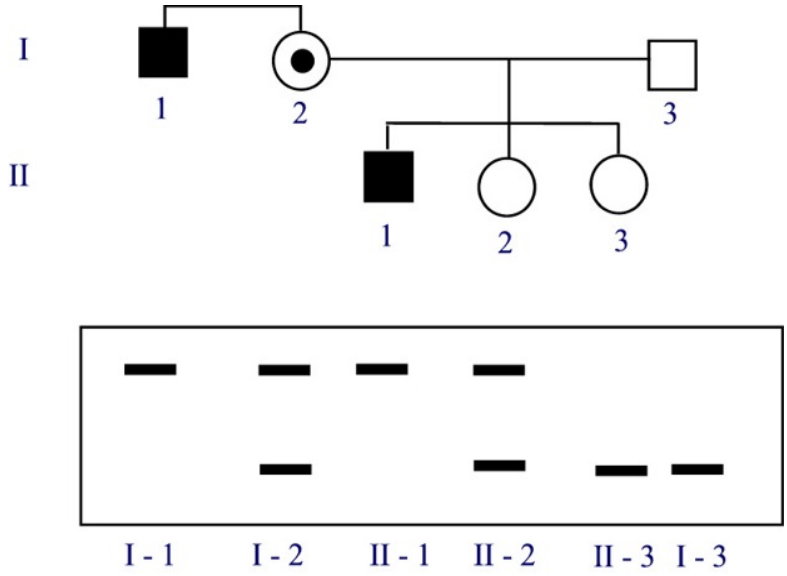
Explanatory notes

- Polyploidy is a state in an organism where instead of having the normal diploid chromosome complement, they have more than two sets. Polyploidy can occur in animals but is more common in plants.

Total 1 + 2 + 2 + 1 + 1 = 7 marks

Question 2

Haemophilia is an X-linked condition in which the body's ability to clot or coagulate blood is severely impaired. There are three types of haemophilia, A, B and C, each of which is due to the absence of clotting Factor VIII, IX and XI respectively. The diagram shows the RFLP patterns taken from a family in which some members have haemophilia.



2a. Explain what is meant by the abbreviation RFLP.

1 mark

Answer

The abbreviation stands for Restriction Fragment Length Polymorphism. RFLPs are the differences in the lengths of DNA sequence on homologous chromosomes obtained by digesting their chromosomes with restriction enzymes.

Explanatory notes

- Restriction fragment length polymorphisms are differences in DNA sequence on homologous chromosomes that can be detected in members of a family by digesting their chromosomes with restriction enzymes. The presence or absence of a restriction enzyme cutting site in a sequence of DNA or gene will indicate a short or a long fragment/sequence of DNA which can then be compared with other family members.

2b. Using the pedigree above, complete the table to show what is indicated by the following symbols.

Symbol	Explanation
	–
	–

2 marks

Answer

Symbol	Explanation
	– affected individual (male or female)
	– carrier (female)

Explanatory notes

- Symbols used in pedigrees are standard. A square is used to represent a male, a circle a female. If the shape is unfilled, the individual does not show the condition; if the circle is filled, the individual has the condition. If the shape has a filled circle within it, the individual is a known carrier of the condition.

Mark allocation

- 1 mark – affected individual
- 1 mark – carrier

2c. Of the individuals II-1, II-2 and II-3, explain which is a carrier of haemophilia.

2 marks

Answer

Individual II-2 is a carrier of haemophilia. Female carriers will be heterozygous for haemophilia; they will show two RFLP fragments/sequences, one for each allele.

Explanatory notes

- Only females can be carriers (due to their hemizygous nature, males will express the condition if they carry the allele for the recessive trait) and female carriers will be heterozygous for haemophilia. Thus they will show two RFLP fragments/sequences, one for each allele.

Mark allocation

- 1 mark – individual II-2
- 1 mark – individual II-2 shows 2 RFLP fragments, is therefore heterozygous and a carrier

Total 1 + 2 + 2 = 5 marks

Question 3

Huntington disease (HD) is an autosomal dominant disorder in which individuals experience nerve degeneration and gradual deterioration of physical, cognitive and emotional abilities. It is a condition that affects adults and usually appears between the ages of 30 and 50. However, it can affect people under the age of 20 (Juvenile HD) and in the later stages of life.

3a. Suggest why the allele for HD has remained in the human population despite it being a fatal condition with no known cure.

1 mark

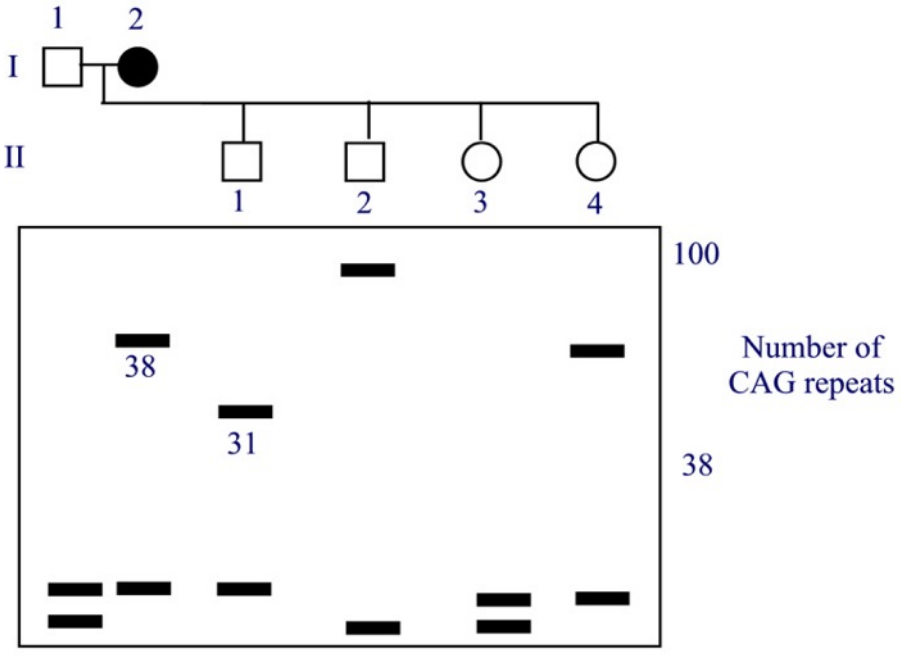
Answer

Allele has remained in the population because individuals who have the dominant trait reproduce (and pass on the allele) before they are aware that they have the condition.

Explanatory notes

- Lethal alleles can escape detection and elimination if they are late acting. By the time symptoms of the condition become apparent the lethal allele will have been transmitted to the offspring.

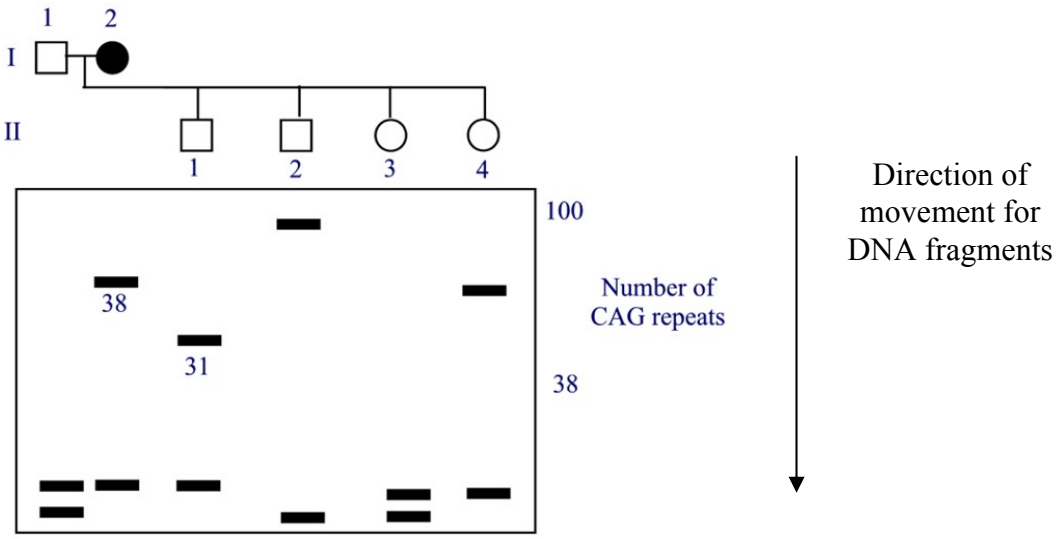
The diagram below shows the result of electrophoresis for a family whose mother has HD. PCR fragments have been amplified using probes for the altered HD site. The region of the chromosome under observation has a variable number of repeating CAG sequences. Individuals who do not have the condition can have up to 30 copies of each sequence, but individuals with HD have 37 to more than 100 copies. The number that appears below the band from the PCR fragment indicates the age at which the symptoms first began.



3b. Draw an arrow on the diagram to indicate the direction of movement of DNA fragments.

1 mark

Answer



Note: An arrow pointing down the page (on either side of the diagram) shows the direction of band movement.

Explanatory notes

- Gel electrophoresis uses an electric current to sort fragments of DNA according to their size. An electric field is set up and the negatively charged DNA fragments are drawn toward the positive terminal at the far end of the gel. The shortest fragments move most quickly (and also the furthest). On the diagram, the number of CAG repeats provides an indication of the positive end of the gel. Fragments with fewer than 38 CAG repeats will move toward the positive end of the gel faster.

3c. Using the electrophoresis results, complete the following table, showing the possible phenotypes and genotypes of Individual II-2 and Individual II-3.

For each phenotype select from:

- will develop Huntington disease
- will not develop Huntington disease
- not possible to determine from information provided

Use the following symbols to represent the alleles involved: H, h.

	Phenotype	**Genotype**
Individual II-2		
Individual II-3		

2 marks

Answer

	Phenotype	Genotype
Individual II-2	will develop Huntington disease	HH
Individual II-3	will not develop Huntington disease	Hh

Explanatory notes

- Individual II-2 shows two bands in the gel. The faster moving (smaller) band has fewer than 30 copies of each CAG sequence and so must be the allele for the recessive trait; however, the slower moving (larger) band has close to 90 copies of each CAG sequence and is therefore the allele for the dominant trait. Thus Individual II-2 is heterozygous for the condition and will develop HD. Individual II-3 shows two bands in the gel. Both the faster moving (smaller) and slower moving (larger) band have less than 30 copies of each CAG sequence and must be alleles for the recessive trait. Thus Individual II-3 is homozygous for the condition and will not develop HD.

The restriction enzyme *Eco* P151 was used to prepare the fragments for the gel electrophoresis. The recognition site for *Eco* P151 is CAGCAG.

3d i. On the **continuous** sequence of a single strand of DNA below, circle all the recognition sites that would be cut by the enzyme *Eco* P151.

TCACCCGATCAGCAGCGAGGCAATCCTTAGCCGATCAGCAGCCCCGGGGTAT

TCCGACTCAGCAGAGGTCACACCCCAGCAGAATGGGTACCAG

Answer

TCACCCGATCAGCAGCGAGGCAATCCTTAGCCGATCAGCAGCCCCGGGGTAT

TCCGACTCAGCAGAGGTCACACCCCAGCAGAATGGGTACCAG

3d ii. How many fragments of DNA will be created by digesting the fragment with *Eco* P151?

1 mark

Answer

Five fragments

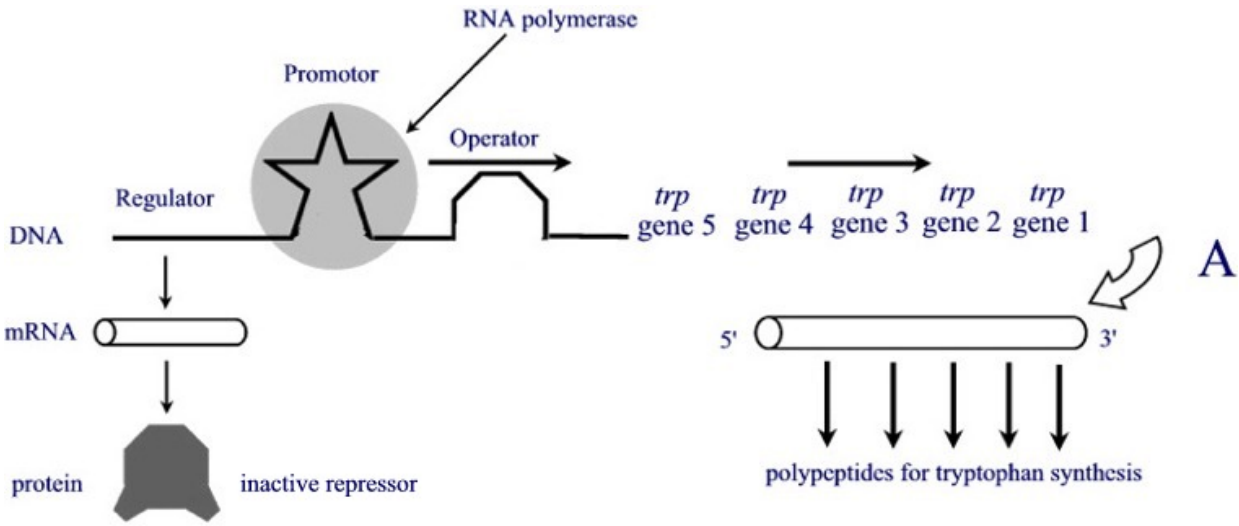
Explanatory notes

There are four recognition sites in the DNA sequence shown. If four cuts are made in one continuous sequence of DNA, there will be five pieces produced from the cuts.

Total 1 + 1 + 2 + 1 + 1 = 6 marks

Question 4

Escherichia coli (*E. coli*) is a bacterium which lives in the environment of the human colon which is constantly changing due to the dietary habits of the host. *E. coli* relies on an amino acid, tryptophan (*trp*), to survive and is capable of synthesising it from a precursor molecule. The diagram illustrates the *trp* operon in the absence of tryptophan.



4a. What is an operon?

1 mark

Answer

The entire sequence of DNA required for the production of mRNA (and ultimately enzyme production/gene expression)

4b. Identify and describe the function of **two** components of an operon.

Component 1:

Component 2:

2 marks

Answer

Possible components and functions include:

operator – a DNA sequence that provides a binding site for the regulatory protein and controls the access of RNA polymerase to the gene

promoter – a DNA sequence along which RNA polymerase binds therefore enabling a gene to be transcribed

genes – a DNA sequence that codes for the production of mRNA

Explanatory notes

An operon is a unit of genetic function consisting of co-ordinately regulated clusters of genes with related functions. An operon is comprised of an operator, a promoter and the genes they control.

Mark allocation

- 1 mark – correct identification of component 1 AND its function
- 1 mark – correct identification of component 2 AND its function

4c. What process is occurring at **A**?

1 mark

Answer

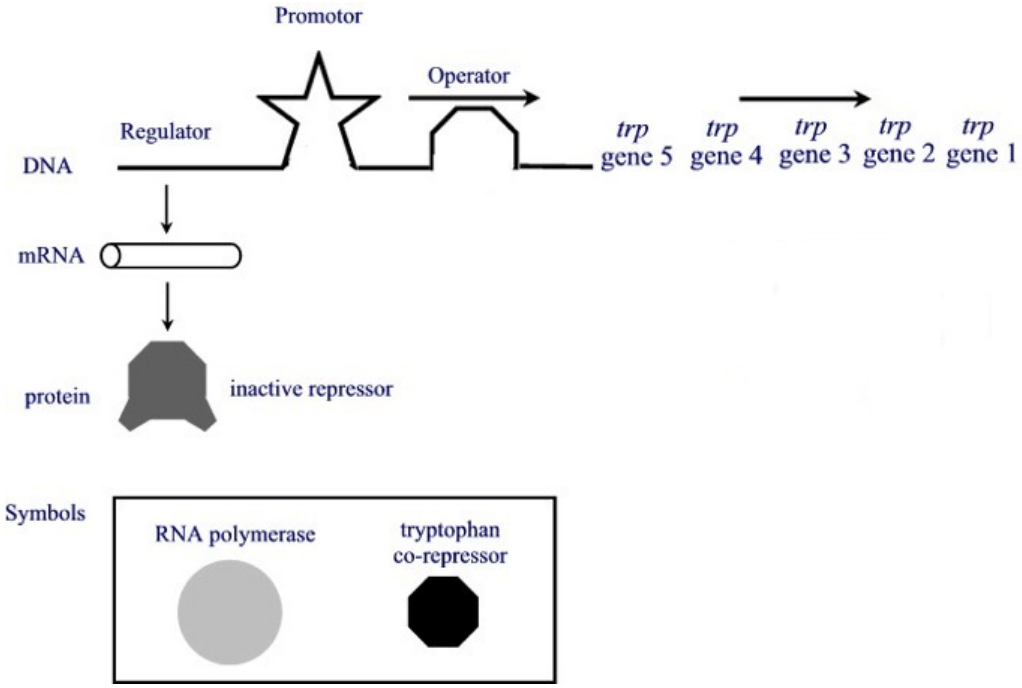
The production of mRNA

Explanatory notes

- In this model, tryptophan is absent which means the repressor is inactive and the operon is switched on. As a result, RNA polymerase binds to the promoter and gains access to the genes via the operator. When this happens, mRNA is synthesised.

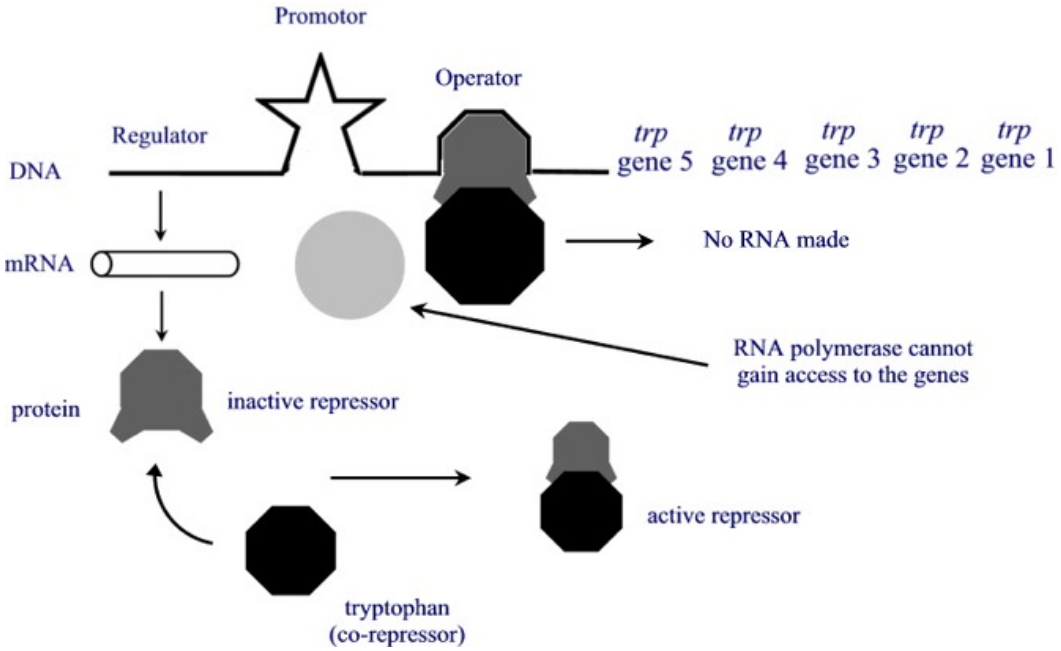
Tryptophan is also available through the dietary intake of the host. When tryptophan is readily available to the cell *E. coli* will stop its own synthesis, using the amino acid already supplied.

4d. Using the symbols provided below, add to the diagram to illustrate what would occur in the *trp* operon when tryptophan is readily available.



2 marks

Answer



Explanatory notes

When tryptophan is present and accumulating in a cell, it inhibits its own production by activating the repressor protein. The tryptophan binds to the repressor protein and causes its conformation to change. The repressor is now able to bind to the operator and switch off the operon. RNA polymerase is not able to gain access to the genes and mRNA is not synthesised.

Mark allocation

- 1 mark – tryptophan acting as a co-repressor
- 1 mark – indicating no mRNA produced
  (0 marks awarded for representation of regulator gene – *trp* operon as it is provided at beginning of the question)

Total 1 + 2 + 1 + 2 = 6 marks

Question 5

Australian researchers at the Centre of Excellence for Kangaroo Genomics (KanGo) have produced the first detailed map of the kangaroo genome, revealing large sections in common with the human genome. The tammar wallaby, *Macropus eugenii* (*M. eugenii*), is a marsupial with around 20 000 genes located on its 16 chromosomes. The human genome has 20 000 – 25 000 genes. Humans are placental mammals and have 46 chromosomes in their karyotype.

5a. How many chromosomes are found in the germline cells of *M. eugenii*?

1 mark

Answer

16

Explanatory notes

A germline cell is diploid (2n) and gives rise to haploid cells (n) or gametes, which have half the diploid number of chromosomes.

The tammar wallaby has a similar number of genes to humans (20 000), yet they are significantly different organisms.

5b. Explain the basis for this anomaly in terms of chromosome number and phenotype.

Chromosome number:

Phenotype:

2 marks

Answer

i. Chromosome number: Whilst they may share a similar number of genes, these genes will not necessarily be the same length or be distributed in the same way to make up the same number of chromosomes.
ii. Phenotype: Each of the corresponding genes is likely to be composed of a different nucleotide sequence and also a different number of nucleotides. Differences in phenotype are determined by the sequences of the nucleotides in each species, interactions between genes and also when they are switched on and off during development.

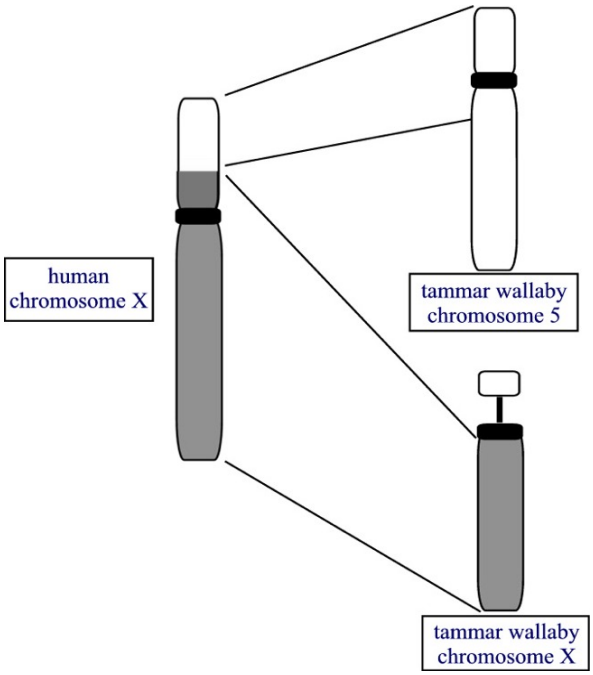
Explanatory notes

- Whilst the number of genes in the tammar wallaby and humans is quite similar the number of chromosomes and expression of phenotype is significantly different for several reasons. Each gene is composed of a sequence of nucleotides. The nucleotide sequence for the same genes in different species can be different in terms of the nucleotide bases of which it is comprised AND the number of nucleotides in the sequence. Furthermore, the nucleotide sequence and when it is activated during development, will determine the phenotypic expression of the gene.

Mark allocation

- 1 mark – nucleotide sequences of corresponding genes have different lengths, and will not necessarily be distributed in the same way to make up the same number of chromosomes
- 1 mark – phenotype determined by the sequence of the nucleotides in a gene in each species, interactions between genes and when they are switched on and off

The human X chromosome is made up of segments from the number 5 and X chromosomes of *M. eugenii*. The two segments joined around 150 million years ago. Further, it has been found that the q-arms of the X chromosome of humans and *M. eugenii* are homologous.



5c. What circumstances might have existed to produce a human X chromosome that is a composite of chromosomes 5 and X in the tammar wallaby?

1 mark

Answer

Humans and the tammar wallaby (kangaroos) shared a common ancestor before the chromosome segments joined 150 million years ago.

Explanatory notes

- The genetic material found in the genome of both organisms was present in the common ancestor to these present day species. Marsupials last shared a common ancestor with humans 130 million years ago.

Total 1 + 2 + 1 = 4 marks

Question 6

The bacterium *Bacillus thuningensis* (*B. thuningensis*) produces crystal proteins of insecticidal endotoxins, coded for by the *cry* 1 Ac gene located on the bacterial chromosome. When ingested the crystal proteins are activated by an alkaline gut pH. Once activated, they become embedded in gut cell membranes, causing swelling, lysis and death. The *cry* 1 Ac gene has been introduced into the cotton plant *Gossypium sp.*, creating cotton that is resistant to moths, butterflies, mosquitoes, flies and beetles. This cotton is also known as Bt cotton.

6a. Having identified the *cry* 1 Ac gene on the chromosome of *Bacillus thuningensis*, what steps would be required to produce Bt cotton?

2 marks

Answer

Steps involved should include:

1. Isolate the *cry* 1 Ac gene from the chromosome of *Bacillus thuningensis* using a restriction enzyme.
2. Prepare plasmid from *Bacillus thuningensis* by cutting with the same restriction enzyme used to isolate the *cry* 1 Ac gene.
3. Make recombinant plasmid.
4. Transform cotton plant cells by introducing recombinant plasmid to cotton plant cells.

Explanatory notes

- The process of making Bt cotton relies on two bacteria *Bacillus thuningensis* (from which the resistance gene is obtained) and *Agrobacterium tumefaciens* (used to introduce the recombinant plasmid to cotton plant cells). *A. tumefaciens* is capable of transferring its own DNA into the genome of the host plant cell and when it carries a transformed plasmid, the genes on the plasmid are introduced to the plant cell as well. The transformed plant cell is then cultured on a growth medium until it reaches an embryogenic state forming very tiny embryos, just like the embryos found in cotton seeds, each with a root end and a cotyledon end. The embryos can be grown on a different culture medium and then germinated like a seed to produce a small plant that can be potted in soil and will eventually become a normal flowering plant which can set seed and will pass the introduced genes on to their progeny through normal reproduction.

Mark allocation

- 1 mark – isolate gene AND prepare plasmid
- 1 mark – make recombinant plasmid AND transform cotton plant cells

6b. By distinguishing between genetically modified organisms (GMOs) and transgenic organisms (TGOs), indicate whether Bt cotton is a GMO or a TGO.

2 marks

Answer

GMOs have genotypes which have been artificially changed; however, the modifications do not involve the insertion of genes from a different species. TGOs have genes in their genomes that have been artificially introduced from another species. Bt cotton is a TGO.

Explanatory notes

- Bt cotton receives genes from the bacterium *Bacillus thuningensis.* As the Bt cotton genome is receiving genes from another species, it is classified as a transgenic organism (TGO) however it is not a genetically modified organism (GMO) because by definition, GMOs do not receive genes from other species.

Mark allocation

- 1 mark – distinguishing between GMO and TGO
- 1 mark – Bt cotton is a TGO

6c. Explain a benefit of growing Bt cotton.

1 mark

Answer

Reduction in the use of insecticides means less likelihood of environmental impacts from pesticides.

OR

Increased crop production and reduced spending on chemical pesticides results in better economic return.

Explanatory notes

- Growing Bt cotton results in the reduction of the use of insecticides and consequently, a decreased likelihood of environmental impacts on farmers, field workers and agriculturalists from pesticides.

OR

- The growth of Bt cotton increases the amount of cotton grown successfully which increases the amount of cotton available for trade. Increased crop production and reduced spending on chemical pesticides result in better economic return.

Whilst the development of Bt cotton has been widely successful it should not be considered the solution to the problem. The cotton bollworm moth, *Helicoverpa armigera* (*H. armigera*), is insecticide resistant to nearly every class of chemical insecticide used for its control. Recently, *H. armigera* has shown resistance to Bt cotton.

6d i. Explain what is meant when the bollworm moth is described as insecticide resistant.

1 mark

Answer

The cotton bollworm moth has developed a decreased susceptibility to insecticides and cannot be killed or controlled by this class of chemicals.

6d ii. Name the process by which the cotton bollworm moth would have become insecticide resistant.

1 mark

Answer

Natural selection

Explanatory notes

- Insecticide resistance occurs when an insect population targeted by an insecticide shows an adaptation to the insecticide which results in a decreased susceptibility to that chemical. The insect population develops a resistance to a chemical through natural selection. The most resistant organisms are the ones to survive and pass on their traits to their offspring. After the population has been exposed to an insecticide for many generations it no longer kills them as effectively.

Total 2 + 2 + 1 + 1 +1 = 7 marks

Question 7

In the 1930s, the cane toad *Bufo marinus* (*B. marinus*) was introduced to Australia in an effort to control the beetles that were damaging sugar cane crops. The cane toad releases a potent cardiac toxin from a large gland on its shoulder and there are many reports of cane toads causing the death of native predators. Native animals that are known to eat the cane toad include quolls, crocodiles, lizards and snakes. Amongst these native animals, there is variable vulnerability to the toxin, ranging from susceptibility to tolerance.

In Australia, the cane toad places a selective pressure on the predator population.

7a. What characteristic must be present in a population if a selecting agent is to have any effect?

1 mark

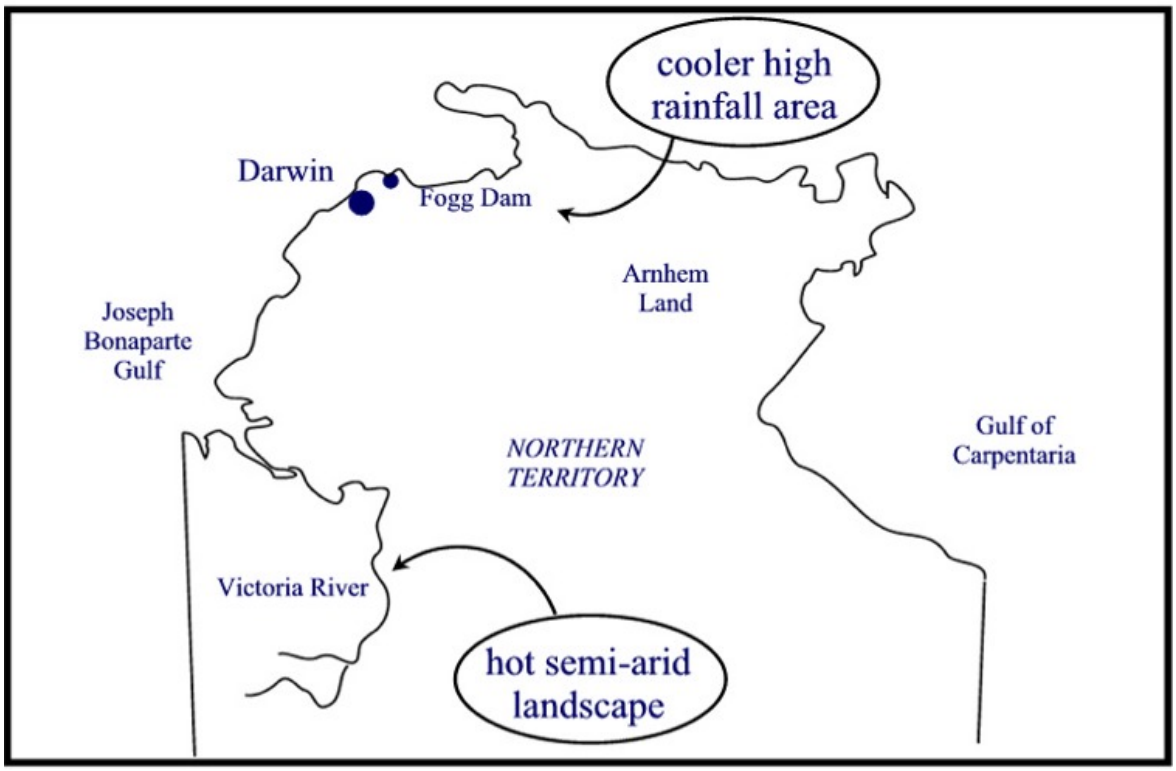
Answer

A selecting agent is an environmental factor that acts differentially on phenotypes in a population meaning some phenotypes have a better chance of survival and reproduction. This will occur if the population is polymorphic for the trait under selection.

Explanatory notes

- A selecting agent is an environmental factor that acts differentially on phenotypes in a population. Therefore, the agent is capable of removing some alleles from the predator population (alleles that make predators vulnerable to toads) but other traits are not affected. Consequently the genetic composition of the population is changed. Selecting agents can only have an effect if variation exists in the trait under pressure.

The freshwater crocodile *Crocodylus johnstoni* (*C. johnstoni*), inhabits the Victoria River and is also found at Fogg Dam in the Northern Territory. The map shows the location of Fogg Dam and Victoria River in the Northern Territory.



Researchers have documented massive mortality of *C. johnstoni* due to the effect of cane toad toxin. At Victoria River dead crocodiles spanned a wide size range. Population densities of crocodiles plummeted by as much as 77% following toad invasion, and population size structures have changed over several generations.

Crocodiles surveyed at Victoria River during Study	
Size range of live crocodiles	0.25–3.0 metres
Full size range of dead crocodiles	0.6–2.1 metres
Size range of most dead crocodiles	0.6–1.5 metres

7b i. From the table, what can be concluded about mortality rates in *C. johnstoni*?

1 mark

Answer

Crocodiles most likely to be killed by cane toad toxin occur within the size range 0.6–1.5 metres.

7b ii. Identify what evolutionary process is taking place in the population of *C. johnstoni*.

1 mark

Answer

Microevolution is taking place.

Explanatory notes

- The cane toad toxin is killing crocodiles within a particular size range (0.6–1.5 metres). This leads to a small scale change in the composition of the gene pool and is defined as microevolution.

The impact of cane toads on *C. johnstoni* increases with increasing aridity. The negative impact of toads on crocodiles appears to be greater in hot semi-arid landscapes (Victoria River) than in cooler, higher rainfall areas (Fogg Dam).

7c. Suggest why the environmental conditions at Victoria River and Fogg Dam have different outcomes for *C. johnstoni*.

1 mark

Answer

Victoria River is hotter and drier forcing cane toads and crocodiles into close proximity at the water's edge, resulting in crocodiles being poisoned by cane toad toxin if the crocodiles attack them.
AND
At Fogg Dam, crocodiles have access to a wider prey base (more water = more animals) and do not prey on cane toads as much.
OR
At Fogg Dam crocodiles are less likely to come in contact with cane toads (and their toxin) because there are more small, scattered water bodies and puddles available in these areas for toads to rehydrate.

Explanatory notes

- The environmental conditions (aridity) have an impact on the behaviour of both the crocodiles and the cane toads. Both animals seek hydration and will move toward water bodies whether they be billabongs, rivers or lakes. If they come in contact with each other, it is highly likely that the crocodiles will prey on the cane toads and be exposed to the deadly toxin. In semi-arid landscapes (Victoria River) there is less free water available in a given area and as a result crocodiles and cane toads are forced into close proximity. In cooler, higher rainfall areas (Fogg Dam) there is an increased likelihood that there are more bodies of water available. This is likely to increase the numbers of animals frequenting the area. There are two outcomes associated with this environmental condition. The first is that the crocodiles and cane toads are less likely to come into close contact with each other (there is a greater area from which they can seek hydration). The second is that due to the increased numbers of animals coming to the area, the crocodiles will have access to a wider prey base and will not prey on cane toads as much.

Different species of Australian snakes show variation in their response to cane toad toxin.

Generally, snakes with larger ratio of body length to head size are less affected by cane toad toxin. The longer a snake, the smaller its head is compared to its overall body length. Given that the size of a snake's head limits the size of its prey, a longer snake is less likely to eat a toad large enough to poison it.

An evolutionary biologist hypothesised that the body shape (length) of snakes has evolved in response to exposure to cane toad toxin. She studied four species of snake found in Queensland and in order to test her hypothesis, predicted that two of the species would be highly sensitive to cane toad toxin and that the other two would not.

High sensitivity	No sensitivity
Pseudechis porphyriacus (red-bellied black snake)	*Hemiaspis signata* (swamp snake)
Dendrelaphis punctulatus (green tree snake)	*Tropidonophis mairii* (keelback snake)

7d i. What are **three** essential factors that should be included by the biologist in the design of her research?

3 marks

Answer

Factors should include:

Use all four species of snake

Compare body-length to head-size ratios *before* and *after* cane toads were introduced into their area

Use a large sample size (between 100–150 snakes per treatment) with 50% from 'before cane toads' and 50% 'after cane toads'

Mark allocation

- 1 mark for each factor

7d ii. What result would support the hypothesis?

1 mark

Answer

After introduction of cane toad to Australia it would be expected that:

snakes with no sensitivity to cane toad toxin – show no change in body length to head size ratio

AND

snakes with high sensitivity to cane toad toxin – show a gradual increase in body length to head size ratio

Explanatory notes

- The hypothesis would be supported by results showing no change over time in body length to head size ratio for populations of snakes with no sensitivity to cane toad toxin AND a gradual increase in body length to head size ratio for populations of snakes with high sensitivity to cane toad toxin following the introduction of cane toads to Australia. Snakes with no sensitivity to the cane toad toxin would not be affected by the selection pressure and would not experience genetic drift. Snakes with high sensitivity to the toxin are affected by the selection pressure. Snakes with a larger head size to body length ratio will be able to swallow cane toads. The longer the snake the greater its ability to withstand the toxic venom from the cane toad, those that survive pass their genes for increased head size to body length ratio onto the next generation, leading to a gradual increase in head size to body length ratio over time.

Total 1 + 1 + 1 + 1 + 3 + 1 = 8 marks

Question 8

In 2005, archaeologists in Germany uncovered a multiple burial grave site in Eulau, Saxony-Anhalt. One of the graves contained the 4600-year-old skeletons of four *Homo sapiens* – a female, a male and two children. *Homo sapiens* (*H. sapiens*) are the only species to have reached this time period, also known as the Neolithic Age. Some paleoanthropologists believe there is strong evidence to show that *H. sapiens* evolved from the species *Homo erectus* (*H. erectus)*.

8a. Identify and compare **two** significant structural features in the skulls of *H. erectus* and the skeletons of the family found at Eulau.

Structure 1:

Structure 2:

2 marks

Answer

Any two of:

Structure	***Homo erectus***	***Homo sapiens***
Teeth	larger	smaller
lower jaw	U-shaped	parabolic
brain case	smaller	larger
forehead	low, flat	vertical
top of skull	ridged	no ridge
back of skull	pointed	rounded
nasal opening	large	small

Explanatory notes

- It is essential that students identify the structure and then compare between the two species, stating clearly in their response the appearance of the structure for both species.

Mark allocation

- 1 mark – identification of structure 1 and comparison between the two species
- 1 mark – identification of structure 2 and comparison between the two species

In their analysis of the remains at Eulau, researchers used several sources of data, including information from autosomal and Y chromosomes, to determine that the group was a family consisting of a mother, a father and two sons. The results of the analysis provide the earliest evidence, dating back to the Stone Age, of a nuclear family.

8b. What technique would have been used to establish the relationship between the individuals?

1 mark

Answer

mtDNA analysis.

Explanatory notes

- Mitochondrial DNA (mtDNA) is the DNA found in the mitochondria and contains 37 genes, all of which are essential for normal mitochondrial function. MtDNA is inherited only from the mother, because all mitochondria are descended from maternal egg cells. Mitochondrial DNA is passed from a mother to her offspring and only daughters can pass their mtDNA to their offspring. This mode of inheritance makes mtDNA useful for tracing individuals' maternal lineage. In what is known as a maternal lineage test, mtDNA can be extracted from samples such as hair shafts and bone fragments. The mitochondrial DNA (mtDNA) sequences of two or more individuals are compared and if they are biologically related they will share similar mtDNA sequences. The woman and both children share the same mtDNA haplogroup K1b (a haplogroup is a group defined by differences in mtDNA).

Researchers were also able to learn about the social organisation of the group using strontium isotope analysis. Strontium is found in food and is incorporated into growing teeth. By measuring the strontium isotopes in the teeth of the skeletons, researchers were able to draw conclusions about where the skeletons had spent their pre-adult years.

8c. How can the measurement of strontium isotopes be used to indicate the place where these people grew up?

2 marks

Answer

When the level of strontium in teeth is determined it can be matched to the geographical region with the same strontium levels, thus determining the location in which the person/people grew up.

Explanatory notes

- Modern geochemical fingerprinting by strontium and other isotope analyses can yield conclusive data on the origin, mobility and migration of the members of ancient communities. Strontium isotopes in tooth enamel correlates with dietary strontium derived from soils during childhood and shows variation between individuals from distinct geological regions. They can be used to infer the childhood geological location of an individual and hence identify subsequent movement, which may be related to subsistence behaviour or mass migrations.

Mark allocation

- 1 mark – strontium levels are determined and matched to corresponding geographical area
- 1 mark – if strontium levels are the same, it can be concluded that the person grew up there

The strontium analysis showed that the female had spent her childhood in a different region from the male and children. This is a demonstration of the practice of exogamy (marrying out) and patrilocality (females moving to the area of the males).

8d i. What would be the importance of the practices of exogamy and patrilocality to the people of this group?

1 mark

Answer

The practices of exogamy and patrilocality would enable the group to avoid inbreeding and to establish kinship networks with other communities.

The practice of burying the dead is one example of the cultural changes that have occurred in human societies over time.

8d ii. Explain the difference between biological and cultural change.

1 mark

Answer

Biological evolution is the genetic process of change in members of a species, over a long period of time, as a result of natural selection; whereas cultural change is associated with rapid changes in human societies over time where changes are socially transmitted (by knowledge), not genetically.

Explanatory notes

- Biological evolution is a relatively slow process which can only take place through inheritance, where adaptations are passed from generation to generation. There is no choice about which traits will be inherited and the process is generally unplanned and random. In contrast, cultural change is often based on technological development and occurs very rapidly in human populations, and changes can be transmitted within or between generations. Individuals can choose whether to accept or reject cultural traits and consequently the process is conscious and deliberate.

Total marks 2 + 1 + 2 + 1 + 1 = 7 marks

END OF SOLUTIONS BOOK