Insight Publications

INSIGHT

Trial Exam Paper

2008

BIOLOGY

Written examination 2

Solutions book

This book presents:

- correct solutions
- explanatory notes
- mark allocations

SECTION A – Multiple-choice questions

AREA OF STUDY 1 – Heredity

Question 1

There are alleles that can cause lethal conditions. In horses there are several known lethal alleles which occur when a horse is homozygous dominant for a gene. In Quarter Horses, coat patterning is due to the arrangement of white hairs mixed in the body colour hairs.

chestnut roan – ***Rr*** chestnut non-roan – ***rr***

In a cross between two chestnut roan Quarter Horses, the probability of producing a viable chestnut non-roan foal is closest to

A. 25%

B. 50%

C. **33%**

D. 66%

Answer is C

Explanatory notes

- A is incorrect – the lethal genotype ***RR*** means that there are only 3 possible viable outcomes.
- B is incorrect – the lethal genotype ***RR*** means that there are only 3 possible viable outcomes.
- D is incorrect – there is a 66% chance of producing a chestnut roan foal.

Question 2

Dominant lethal alleles are also known to persist in populations. In humans, Huntington's disease (HD) is a condition caused by a dominant lethal allele. Individuals with HD experience nerve degeneration and begin to show symptoms around the age of 40 years. HD is caused by a dominant lethal allele but it has persisted in the population because

A. mutations always occur in populations and they are passed on through gametes.

B. **it takes effect later in life when the individual who carries the allele(s) may have already passed it on to their offspring.**

C. when the individual is heterozygous for HD, the lethal allele can be passed on undetected.

D. some embryos are better adapted to survive lethal alleles.

Answer is B

Explanatory notes

- A is incorrect because mutations do occur in a population; however, mutation does not account for the frequency at which HD is currently maintained.
- C is incorrect because the allele for HD could never be passed on undetected as it is a dominant allele.
- D is incorrect because if a lethal allele is expressed during embryonic development, the embryo/foetus will die – there are no adaptations that allow a foetus to survive a lethal allele.

Question 3

One strategy which could be used to reduce the prevalence of HD in the population is

A. administration of medications to alleviate symptoms.

B. adherence to a specific diet which delays onset of the condition.

C. physical therapy to maintain physical fitness.

D. **presymptomatic testing to determine if an individual has inherited the lethal allele.**

Answer is D

Explanatory notes

- A is incorrect because administration of medication does not impact on the frequency of the lethal allele.
- B is incorrect because onset of the condition is not influenced by diet.
- C is incorrect because physical therapy improves physical fitness but does not change the frequency of the lethal allele.

Question 4

When a eukaryote cell prepares to divide it duplicates each of its chromosomes. The diagram shows a chromosome after duplication.

How many molecules of DNA are present in this duplicated chromosome?

A. 1

B. **2**

C. 4

D. hundreds

Answer is B

Explanatory notes

- B is correct because there are actually two molecules of DNA (each chromatid = 1 molecule of DNA).
- A, C and D are incorrect.

Question 5

Non-disjunction occurs when homologous chromosomes or sister chromatids fail to move apart properly producing offspring with too many (or too few) chromosomes. In one such example, a couple produces a daughter whose karyotype shows the full complement of autosomes and three X chromosomes (22XXX). The daughter's karyotype could **not** result from non-disjunction at

A. **anaphase I in the father.**

B. anaphase II in the father.

C. anaphase I in the mother.

D. anaphase II in the mother.

Answer is A

Explanatory notes

- A is correct because non-disjunction at anaphase I in the father produces sperm which contains either 22XY or 22--. All the mother's eggs would contain 22X. It is impossible to produce a daughter with the karyotype 22XXX, since the maximum number of X chromosomes in the daughter cell would be two.
- B is incorrect because it is possible to produce a female (daughter) karyotype 22XXX if non-disjunction occurs in anaphase II in the father, when an XX from disjunction in sperm fuses with a normal egg containing one X chromosome.
- C is incorrect because it is possible to produce a female (daughter) karyotype 22XXX if non-disjunction occurs in anaphase I in the mother, when an XX from disjunction in egg fuses with a normal sperm containing one X chromosome.
- D is incorrect because it is possible to produce a female (daughter) karyotype 22XXX if non-disjunction occurs in anaphase II in the mother, when an XX from disjunction in egg fuses with a normal sperm containing one X chromosome.

Question 6

During metaphase II of meiosis

A. homologous pairs of chromosomes are drawn apart to opposite sides of the dividing cell.

B. homologous pairs of chromosomes are assembled together on the spindle of the dividing cell.

C. sister chromatids separate and are drawn apart to opposite sides of the dividing cell.

D. **sister chromatids are still connected and assemble together on the spindle of the dividing cell.**

Answer is D

Explanatory notes

- A is incorrect because homologous pairs of chromosomes are drawn apart during anaphase I.
- B is incorrect because homologous pairs of chromosomes are assembled together during metaphase I.
- C is incorrect because sister chromatids separate and are drawn apart during anaphase II.

Question 7

At birth, Siamese kittens are completely white. Within weeks of birth the kittens begin to develop pigmentation which begins along the edge of their ears and gradually spreads until it reaches the face, ears, feet and tail. The pattern of pigmentation is most likely due to the

A. heat sensitive gene which produces pigment in cooler temperatures.

B. spread of the pigment tyrosinase to the extremities.

C. **interaction between the cat genotype and the temperature of the environment.**

D. interaction between the cat genotype and diet.

Answer is C

Explanatory notes

- A is incorrect because the gene is not heat sensitive, the enzyme produced by the gene is heat sensitive.
- B is incorrect because tyrosinase is not a pigment, it is an enzyme.
- D is incorrect because the interaction between genotype and diet has no outcome on pattern of pigmentation.

Use the following information to answer Questions 8 to 10.

In the fruit fly *Drosophila melanogaster*, two genes and their alleles are

Gene for wing type	*C*	straight	Gene for body colour	*E*	grey
	c	curly		*e*	ebony

Question 8

A straight winged grey fly (*C- E-*) is found, however, its pedigree and genotype are unknown. The correct test cross to establish its correct genotype would be

A. C- E- x Cc Ee

B. C- E- x Cc ee

C. C- E- x CC ee

D. **C- E- x cc ee**

Answer is D

Explanatory notes

- A is incorrect – a test cross should involve a parent who is homozygous recessive, this parent is heterozygous for both genes.
- B is incorrect – whilst this parent is homozygous recessive for the body colour gene, it is heterozygous for wing type and therefore not appropriate for a test cross.
- C is incorrect – whilst this parent is homozygous for both wing type and body colour, it is not recessive for both traits, therefore it is not appropriate for a test cross.

Question 9

The genotype of the fruit fly was established as ***Cc Ee*** and the gene loci were found to be on separate chromosomes. The following cross was then carried out

Cc Ee x *Cc Ee*

An F1 population of 160 fruit flies was produced and their phenotypes with respect to wing type and body colour was recorded. It is reasonable to expect that amongst the offspring there could be

A. **10 curly winged, ebony fruit flies**.

B. no more than 10 straight winged, grey fruit flies.

C. 10 straight winged, ebony fruit flies.

D. no more than 10 curly winged, grey fruit flies.

Answer is A

Explanatory notes

- B is incorrect because there would be around 90 straight winged, grey fruit flies produced in this cross.
- C is incorrect because there would be around 30 straight winged, ebony fruit flies produced in this cross.
- D is incorrect because there would be around 30 curly winged, grey fruit flies produced in this cross.

Question 10

The relationship between the alleles for wing type and body colour in *D. melanogaster* show

A. incomplete dominance.

B. partial dominance.

C. **complete dominance.**

D. co-dominance.

Answer is C

Explanatory notes

- A is incorrect because incomplete dominance produces an effect which is intermediate between two different phenotypes, e.g. white x red snapdragons → pink snapdragons.
- B is incorrect because partial dominance is another name for incomplete dominance.
- D is incorrect because co-dominance produces an effect which is independently and equally expressed between two different phenotypes, e.g. red coat x white coat in horses → roan horses (coat with a mix of red hairs and white hairs).

Question 11

The ***p53* gene** is usually expressed to produce **p53 protein** when there is damage to the DNA in a cell. When p53 protein is produced it functions as a transcription factor, acting as a regulatory protein that binds to DNA and stimulates transcription of specific genes. If DNA damage is irreparable, p53 activates 'suicide' genes whose protein products cause

A. endocytosis.

B. symbiosis.

C. mycosis.

D. **apoptosis**.

Answer is D

Explanatory notes

- A is incorrect because endocytosis is the cellular uptake of material across the plasma membrane and is not associated with cell death.
- B is incorrect because symbiosis is an ecological relationship between two different organisms of different species and is not associated with cell death.
- C is incorrect because mycosis is a process in which fungi pass the resistance barriers of organisms establishing infections and is not associated with cell death.

Question 12

A single strand of a molecule of RNA has the base sequence

A A C C G A U A U U G G C C A G C G G C U U A C

The DNA molecule which produced this strand of RNA is

A. **T T G G C T A T A A C C G 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 C C G T A T A A C G C 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 A

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:

- 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 described.

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

Question 13

In prokaryotes and eukaryotes

A. transcription and translation occur in the nucleus.

B. the mRNA lasts for approximately the same duration of time**.**

C. there is post-transcriptional modification of mRNA.

D. **the ribosomes translate information in mRNA to produce polypeptides.**

Answer is D

Explanatory notes

- A is incorrect – prokaryotes have no nucleus therefore transcription and translation cannot occur there.
- B is incorrect – mRNA produced in prokaryotes lasts a few minutes, in eukaryotes it lasts hours or days.
- C is incorrect – post-transcriptional modification of mRNA does not occur in prokaryotes and does in eukaryotes.

Question 14

Many agricultural crop plants (e.g. oats, wheat, potatoes) grown for human consumption are polyploids. A polyploid is an organism

A. with genes from more than one species.

B. with three copies of one chromosome.

C. **which possesses more than two complete sets of chromosomes.**

D. which possesses one complete set of chromosomes.

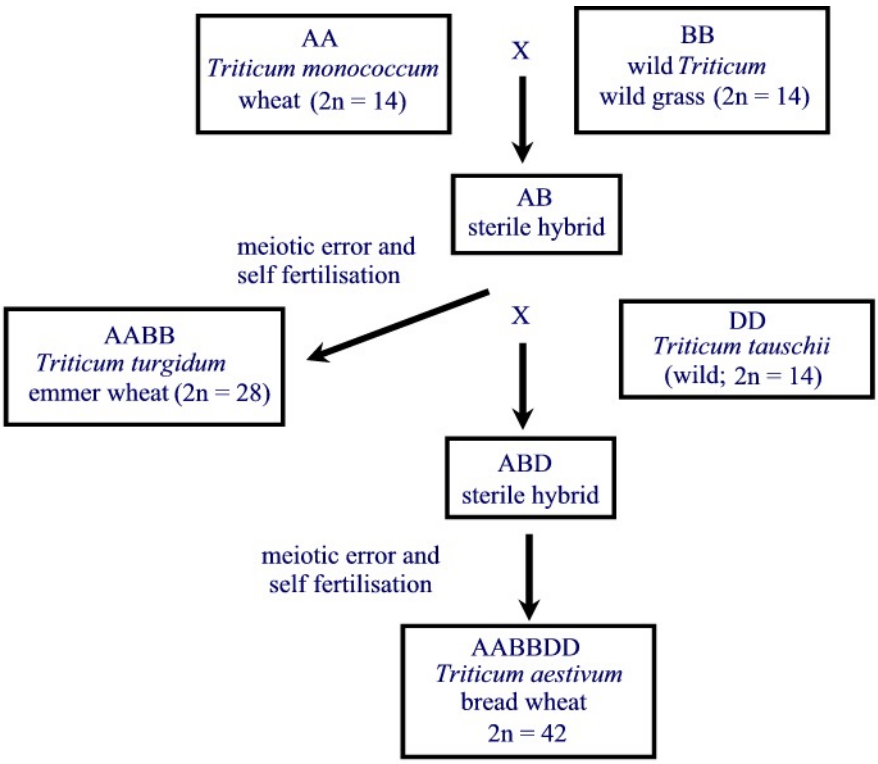
Answer is C

Explanatory notes

- A is incorrect because an organism with genes from more than one species is a hybrid.
- B is incorrect because an organism with three copies of one chromosome has a trisomy.
- D is incorrect because an organism with one complete set of chromosomes is diploid.

Question 15

Bread wheat is the evolutionary result of two hybridisation-meiotic error events. The first gave rise to emmer wheat, which has been cultivated in the Middle East for more than 11,000 years. The second event, which occurred about 8,000 years ago, produced bread wheat.



Emmer wheat and bread wheat are both examples of allopolyploids, which are a polyploid species produced when two or more different species interbreed and combine their chromosomes. From the diagram it is possible to deduce that the number of ancestors that bread wheat derives its chromosomes from is

A. 4
B. **3**
C. 2
D. 1

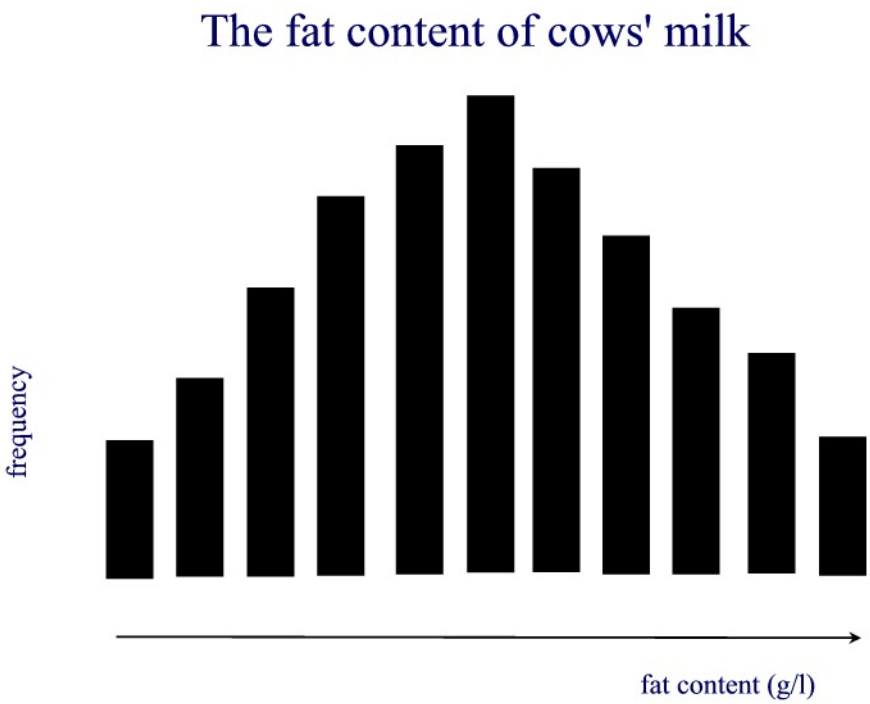
Answer is B

Explanatory notes

- A is incorrect because there are only three ancestors – *T. monococcum*, wild *Triticum* and *T. tauschi*, not 4.
- C is incorrect because there are three ancestors – *T. monococcum*, wild *Triticum* and *T. tauschii*, not 2.
- D is incorrect because there are three ancestors – *T. monococcum*, wild *Triticum* and *T. tauschii*, not 1.

Question 16

The graph shows the fat content of milk produced by dairy cows on several farms owned by one farmer.



A student was asked to explain the pattern shown by the data. What reasonable conclusion could be drawn?

A. Fat content is a monogenic trait which shows continuous variation in this population of dairy cows.

B. **Fat content is a polygenic trait which shows continuous variation in this population of dairy cows.**

C. Fat content is a monogenic trait which shows discontinuous variation in this population of dairy cows.

D. Fat content is a polygenic trait which shows discontinuous variation in this population of dairy cows.

Answer is B

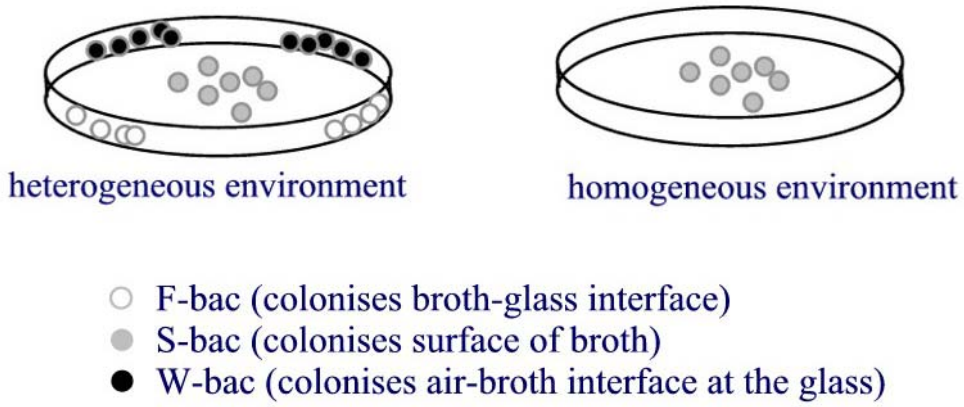
Explanatory notes

- A is incorrect – the continuous variation in fat content indicates polygenes in action, not monogenes.
- C is incorrect – the variation presented on the graph is continuous NOT discontinuous and indicates polygenes in action, not monogenes.
- D is incorrect – the variation presented on the graph is continuous NOT discontinuous.

Use the following information to answer Questions 17 to 19.

Bacteria have short generation times and can show evolutionary change within relatively short time frames.

Evolution in *Pseudomonas fluorescens* (*P. fluorescens*) was studied experimentally. Colonies of *P. fluorescens* were cultured in a heterogeneous broth medium in a glass petri dish. After a short period of time the ancestral population (S-bac) was observed to have adapted to the different environments to produce two new morphs (F-bac and W-bac) with clear niche specificity. After the initial experiment, using identical incubation conditions, researchers cultured the S-bac in a homogeneous broth (created by shaking the broth before pouring into the petri dish). The results are shown in the diagram.



Question 17

The results of these experiments demonstrate that

A. there is no genetic variation in S-bac.

B. **bacteria have the ability to evolve to occupy available niches.**

C. conditions in the broth medium were not optimal for the bacteria in the second experiment.

D. there is no competition between strains of *Pseudomonas fluorescens*.

Answer is B

Explanatory notes

- A is incorrect because genetic variation must exist to produce the three morphs in the heterogeneous medium.
- C is incorrect because growth of S-bac has occurred therefore conditions for growth must have been optimal.
- D is incorrect because the growth of S-bac is due to its ability to outcompete the F-bac and W-bac, therefore competition is evident.

Question 18

The ability of *Pseudomonas fluorescens* to resist antibiotics is an example of evolutionary change which has occurred in a relatively short time frame. Such change can have widespread effects. Antibiotic resistance does **not** occur

A. **primarily to natural mutations that occur in the bacterial genome.**

B. due to overuse of antibiotics to treat bacterial infections in humans.

C. as a result of the presence of antibiotics in animal feed.

D. due to the use of antibiotics by immunosuppressed patients.

Answer is A

Explanatory notes

- A is correct because antibiotic resistance (AR) in bacteria **is not** primarily due to naturally occurring mutations in the bacterial genome, but instead due to extrachromosomal plasmids carrying resistance genes.
- B is incorrect because overuse of antibiotics to treat bacterial infections in humans **does** lead to AR.
- C is incorrect because the presence of antibiotics in animal feed **does** lead to AR.
- D is incorrect because the use of antibiotics by immunosuppressed patients **does** lead to AR.

Question 19

Antibiotic resistance and the ability of *Pseudomonas fluorescens* to exploit a heterogenous growth medium are both examples of

A. adaptive convergence.

B. heterozygote advantage.

C. **adaptive radiation.**

D. allopatric speciation.

Answer is C

Explanatory notes

- A is incorrect because adaptive convergence would produce a uniformity in the phenotypes of *Pseudomonas fluorescens*, not a difference.
- B is incorrect because there is not enough information to confirm this as an example of heterozygote advantage.
- D is incorrect because there is no geographic isolation which physically separates the bacterial population and produces a new species.

Question 20

In the 1890s the population of northern elephant seals in North America was reduced to around 20 individuals by intense hunting. The seals were declared a protected species and since then the population has increased to over 30 000 animals. Researchers have analysed 24 gene loci in a significant proportion of the population and no genetic variation was found. The fixing of a single allele at each of the 24 loci is most likely due to

A. **a bottleneck effect.**

B. the absence of mutation over time.

C. natural selection.

D. gene flow.

Answer is A

Explanatory notes

- B is incorrect because it is highly unlikely that the population will be mutation free over 100 years.
- C is incorrect because the hunting that caused the fixing of the allele was not a natural selection event.
- D is incorrect because gene flow is usually due to the migration of fertile individuals or gametes between populations.

Question 21

Reproductive isolation occurs when two or more species are prevented from producing viable fertile offspring. Reproductive isolating mechanisms (RIMs) can be categorised as prezygotic or postzygotic depending on whether they form before or after fertilisation. An example of a prezygotic RIM is

A. **the production of incompatible gametes in species of freshwater fish.**

B. the failure of hybrid offspring of frogs from the genus *Rana* to complete development.

C. the production of a sterile hybrid mule when a horse and a donkey breed.

D. hybridisation of fertile cotton that produces offspring which die as seeds or grow into weak, defective plants.

Answer is A

Explanatory notes

- A is correct because this is an example of a prezygotic RIM – the gametes are not able to meet.
- B, C and D are incorrect because in all examples offspring have been produced after zygote formation, therefore they are postzygotic RIMs.

Question 22

In October 2004, the fossil of a new hominin species was found in a cave on Flores Island in Indonesia. The 18 000-year-old adult female fossil included a skull, teeth and jaw and was named *Homo floresiensis.* Scientists hypothesised that *Homo floresiensis* hunted, killed and butchered animals. Evidence that would support this hypothesis could include

A. the small brain capacity.

B. small teeth in a parabolic-shaped jaw.

C. **bones from animals showing evidence of cutting.**

D. animal hides with puncture marks, held together with fibres.

Answer is C

Explanatory notes

- A is incorrect because brain capacity is not necessarily an indicator of ability to hunt and kill.
- B is incorrect because the size and shape of teeth and jaw is used to distinguish between apes and hominins.
- D is incorrect because animal hides with puncture marks, held together with fibres are indicative of ability to sew and not necessarily hunt, kill and butcher.

Question 23

The regional continuity (multiregional) and out-of-Africa (monogenesis) hypotheses for the origin of modern humans confer that

A. *Australopithecines* migrated out of Africa.

B. the ancestors of modern humans in Europe are Neanderthals.

C. the origin of modern *Homo sapiens* is from Africa only.

D. ***Homo erectus*** **had an African origin.**

Answer is D

Explanatory notes

- A is incorrect because neither hypotheses believe *Australopithecines* migrated out of Africa.
- B is incorrect because there is overlap in time between modern humans and Neanderthals, therefore Neanderthals cannot be ancestral to modern humans in Europe.
- C is incorrect because the regional continuity hypothesis suggests that the origin of modern *Homo sapiens* occurred in parallel in different parts of the world.

Question 24

Transgenic organisms (TGOs) possess foreign genes or DNA as part of their genome following experimentation. An example of a TGO is

A. a cat with the 'cat allergen' gene silenced.

B. ***E. coli* with plasmids carrying the gene for human insulin.**

C. a cow produced by cloning.

D. a hybrid produced by breeding wheat and rye plants together.

Answer is B

Explanatory notes

- A is incorrect because cats with the 'cat allergen' gene silenced do not possess foreign genes or DNA.
- C is incorrect because cows produced by cloning do not possess foreign genes or DNA.
- D is incorrect because hybrids do not possess genetically engineered foreign genes or DNA.

Question 25

Which of the following is **not** an example of a reproductive technology that would be used in selective breeding programs for commercial herds and flocks?

A. artificial insemination (AI)

B. **artificial pollination (AP)**

C. oestrus synchronisation (OS)

D. multiple ovulation and embryo transfer (MOET)

Answer is B

Explanatory notes

- B is correct because artificial pollination is NOT a reproductive technology used for commercial herds and flocks (animals) – it is used for plants.
- A is incorrect because artificial insemination IS a reproductive technology that would be used in selective breeding programs for commercial herds and flocks.
- C is incorrect because oestrus synchronisation IS a reproductive technology that would be used in selective breeding programs for commercial herds and flocks.
- D is incorrect because multiple ovulation and embryo transfer (MOET) IS a reproductive technology that would be used in selective breeding programs for commercial herds and flocks.

END OF SECTION A

SECTION B – Short-answer questions

Question 1

In the honey bee *Apis mellifera* colony, the adult queen bee is the reproductive female. Honey bees are classified in the order Hymenoptera and demonstrate haplodiploidy, where males develop from unfertilised eggs and so are haploid drones, and females are diploid individuals.

If a queen bee mates only once with a drone, her daughters will be highly related to one another and are known as supersisters.

a. Why would the daughters be so closely related?

Solution

Degree of relatedness is so high because the drone's sperm are all identical

1 mark

Explanatory notes

- Drones are haploid, they develop from unfertilised eggs, therefore all their chromosomes have come from their mother and all sperm cells will be identical.

Female bees have 16 chromosomes in their germ cells.

b. How many chromosomes would be present in the somatic cells of drones?

Solution

16

1 mark

Explanatory notes

- The diploid number for female bees is 32. Male bees develop from unfertilised eggs, which means they are haploid. If drones are haploid they will only have 16 chromosomes in their somatic cells.

It was previously thought that sex determination in a colony was controlled by the queen and that on return from a mating flight she could 'choose' whether to lay fertilised or unfertilised eggs which would develop into females or males, respectively. It is now known that sex determination in bees is controlled by alleles at a single locus. If a bee has two different alleles it will be female, if it has a single allele it will be a normal fertile male, if it has two identical alleles it will be an infertile male.

c. **i.** What is a locus?

Solution

The position of a gene on a chromosome.

1 mark

Explanatory notes

- A locus is the position occupied by a gene on a chromosome and is likened to the address (locus) or a house (gene) on a street (chromosome).

ii. What is the term used to describe the genotype of a normal fertile male honey bee?

Solution

Hemizygous

1 mark

Explanatory notes

- Hemizygous is the term used to describe the genotype of an organism which has only one allele of a chromosome or gene instead of the normal two.

iii. Is a colony of honey bees monomorphic or polymorphic for sex determination?

Solution

Polymorphic

1 mark

Explanatory notes

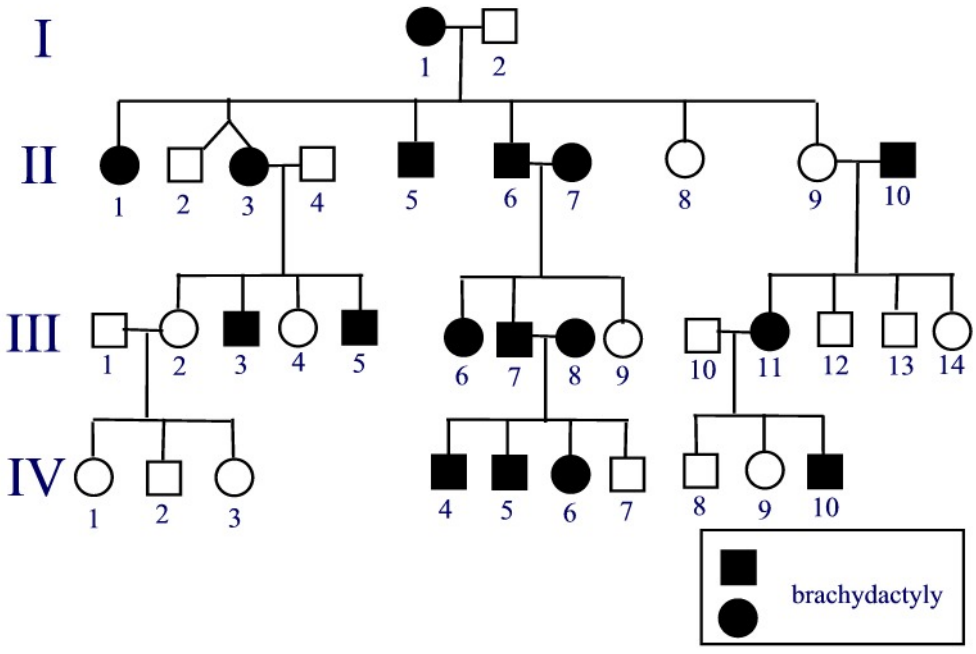
Where members of a population show two or more variations of a trait caused by a single gene locus, the population is regarded as being polymorphic. The honey bee population in a colony would show the phenotypes fertile female, fertile male and infertile male. There are three phenotypes and therefore three variations of the trait, thus the population is polymorphic.

Mark allocation

Total 5 marks

Question 2

Brachydactyly (BD) is a condition in humans in which underdevelopment of the bones in the hands and feet leads to shortening of the fingers and toes. The pedigree represents a family, some members of which have brachydactyly.



It has been suggested that brachydactyly is an autosomal dominant trait.

a. What evidence from the pedigree supports this suggestion?

Solution

The condition affects both males and females AND two parents in generation II (II6 and II7) who have the trait, produce a child (III9) who does not.

1 mark

Explanatory notes

- As a rule, for autosomal dominant traits both females and males are affected evenly, all affected individuals will have at least one affected parent (phenotype appears in every generation), both parents can pass the trait to both male and female offspring and parents who have the trait can produce offspring who do not have the trait (due to a recessive allele in heterozygous individuals).

Mark allocation

- 1 mark – Evidence for the condition being autosomal AND dominant must be made.

b. Assign allele symbols to represent brachydactyly and normal hand and foot development.

Solution

B – brachydactyly, b – normal hand development

1 mark

Explanatory notes

- Trait is autosomal therefore there is no need to consider X and Y chromosomes. Allele symbols need to follow the convention of capital letter for dominant trait and lowercase letter for recessive trait. Actual choice of letter used is not important, however B/b seems a logical choice.

c. Use the symbols assigned in **2b** to complete the table. Show the genotypes and state the phenotypes of individuals I2 and II5.

Solution

	genotype	phenotype
Individual I2	**bb**	**normal hands and feet**
Individual II5	**Bb**	**brachydactyly**

2 marks

Explanatory notes

- Genotypes MUST use same allelic symbols as in 2b. Correct genotype and phenotype must be given for each individual.

Mark allocation

- 1 mark – bb; normal hands and feet
- 1 mark – Bb; brachydactyly

d. If the couple III10 and III11 were to have another child, what is the likelihood that it will have brachydactyly? Show your working using a Punnett square.

Solution

	B (0.5)	b (0.5)
b (0.5)	Bb (0.25)	bb (0.25)
b (0.5)	Bb (0.25)	bb (0.25)

Pr (Bb) = 0.25 + 0.25 = 0.5 (brachydactyly)

Pr (bb) = 0.25 + 0.25 = 0.5 (normal hands and feet)

Probability of a fourth child with brachydactyly is 50% or 0.5 or ½.

2 marks

Explanatory notes

- At every conception there is a 0.5 chance of producing a child with brachydactyly.

Mark allocation

- 1 mark – appropriate construction of Punnett square – with proportions and genotypes
- 1 mark – probability of a fourth child with brachydactyly is 50% or 0.5 or ½

Total 6 marks

Question 3

Escherichia coli (*E. coli*) is a bacterium which lives in the environment of the human colon. This is a constantly changing environment due to the dietary habits of the host. *E. coli* is capable of modifying its metabolism to survive in the fluctuating conditions. One strategy used by *E. coli* is to activate the production of new enzymes in response to the presence of a new substrate.

a. What mode of reproduction is shown by E. coli?

Solution

Binary fission.

1 mark

Explanatory notes

- *E. coli* is an asexually reproducing organism and uses the method of binary fission to reproduce.

b. What is the name of the process which enables *E. coli* to initiate the production of new enzymes?

Solution

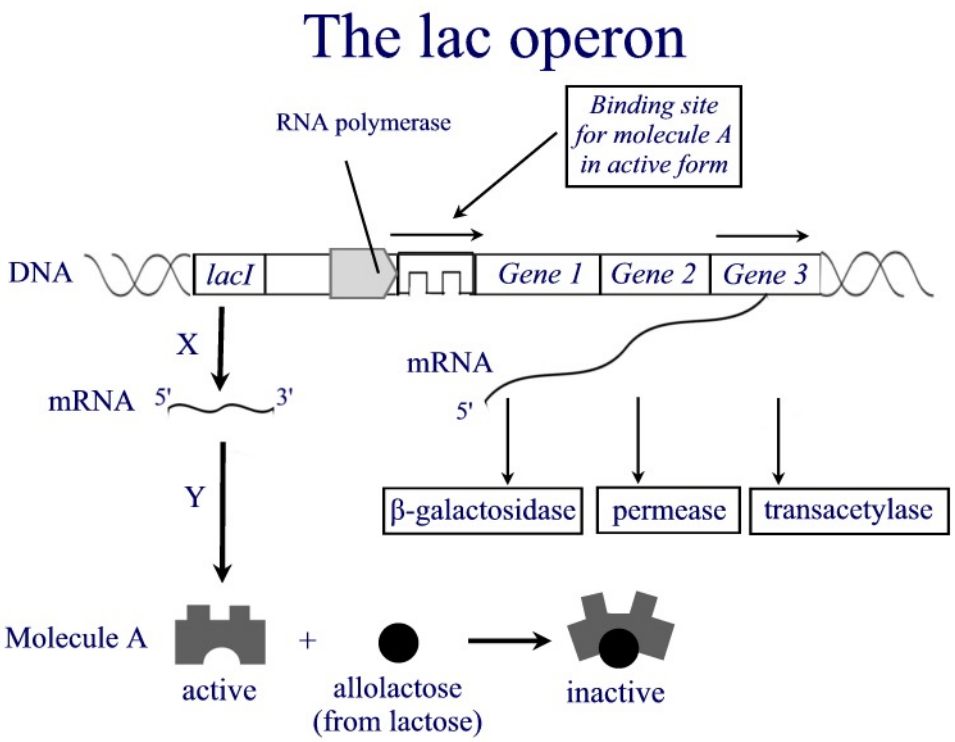
Gene regulation OR regulation/control of gene expression.

1 mark

Explanatory notes

- The rates of specific metabolic pathways can be adjusted by regulating gene expression (synthesising new enzymes) or by regulating the catalytic pathway of existing enzymes.

In *E. coli,* lactose can be absorbed, broken down for energy or used as a source of organic carbon for synthesising other compounds. Lactose metabolism relies on the enzyme β-galactosidase which is only present in very small amounts in bacteria that have been growing in the absence of lactose (in a host with a low dairy product diet). However, if lactose is added to the nutrient medium of *E. coli*, within 15–20 minutes the amount of β-galactosidase increases one thousand times. The diagram below shows the outcome of adding lactose to a nutrient medium.



c. **i.** Identify the processes occurring at X and Y respectively.

Solution

X: transcription

Y: translation OR protein production

1 mark

Explanatory notes

- Both answers need to be given in correct order for mark to be awarded.

ii. What is the function of Molecule A?

Solution

Molecule A is a regulatory protein OR a repressor protein.

1 mark

Explanatory notes

- The regulatory protein is active and in the absence of lactose is responsible for switching off the *lac* operon by binding to the operator. This prevents the formation of β-galactosidase which breaks down lactose.

iii. What is the function of the molecule allolactose?

Solution

Allolactose induces the gene to produce enzymes for lactose metabolism and its role is to inactivate the repressor protein (or it acts as a derepresser of the operon).

1 mark

Explanatory notes

- Allolactose is an isomer formed from lactose. When lactose is introduced to the nutrient medium, allolactose is formed and binds to the repressor protein that normally switches off the lac operon. The repressor protein is inactivated or derepressed which means that the lac operon can now produce mRNA for the enzymes of the lactose pathway.

E. coli only produces increased quantities of β-galactosidase when lactose is included in the nutrient medium.

d. Explain the selective advantage in this metabolic strategy.

Solution

If *E. coli* produces the enzymes it requires only when the nutrient is present/available, the cell avoids synthesising enzymes/proteins that will have nothing to metabolise. The synthesis of protein/enzyme is an anabolic process and if the protein is not required, the cell can instead allocate its available energy to other uses. There will be no unnecessary use of cellular energy.

2 marks

Explanatory notes

- It is essential to clarify the relationship between protein/enzyme synthesis and the energy required. If *E. coli* is metabolising proteins unnecessarily, it will cost the cell energy that could be used more effectively for other processes.

Total 7 marks

Question 4

The protein SATB1 is found in the nuclei of cells and acts as a genome organiser. SATB1 is produced by the SATB1 gene which regulates the immune response and antibody production in healthy individuals; however, if a person has cancer, it can act as a master regulator.

a. Explain what is meant by the term 'master regulator'.

Solution

A master regulator is a gene that controls the expression of many (hundreds or thousands) of other genes.

1 mark

Explanatory notes

- The SATB1 gene alters the behaviour of more than 1000 other genes within breast tumour cells.

SATB1 causes loops of DNA to clump together and as a result, the spatial arrangement of the DNA can change. Consequently, the position of proteins which surround some sections of the genome can be changed.

b. What is the likely effect of changing the position of the proteins which surround the genome?

Solution

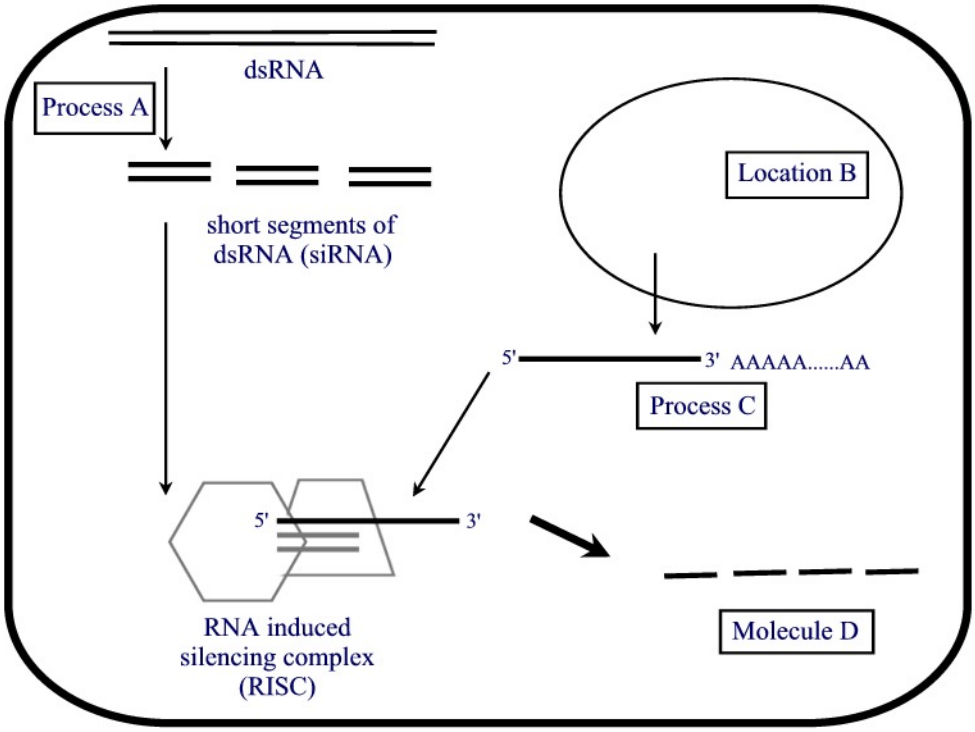
Changing the position of the proteins can result in the turning on of some genes and turning off of others.

1 mark

Explanatory notes

- Changing the position of the proteins can cause different interactions between proteins and DNA thus having the effect of turning some genes on and others off.

Research indicates that SATB1 acts a marker in tumour cells. Once it is expressed in breast cancer cells it is inevitable that they will proliferate and spread (metastasise). In a series of experiments on mice, the SATB1 gene in tumour cells was 'knocked out'. The technique removed the RNAs required for SATB1 gene multiplication. The process is summarised in the following diagram.



c. **i.** What is the name given to the technique?

Solution

RNA interference (RNAi)

1 mark

Explanatory notes

RNA interference is the process whereby adding double-stranded RNA (dsRNA) to cells causes one or more specific genes to be switched off/silenced.

ii. Complete the diagram with appropriate labels.

Solution

Label **Process A –** RNA dicing/cleavage

Label **Location B –** nucleus

Label **Process C –** transcription

Label **Molecule D –** degraded/cleaved mRNA

2 marks

Mark allocation

- 2 marks – 4 labels correct
- 1 mark – 2 or 3 labels correct
- 0 marks – 0 or 1 labels correct

iii. Explain the outcome of 'knocking out' the SATB1 gene in this experiment.

Solution

SATB1 gene is switched off/not expressed.

1 mark

Explanatory notes

- 'Knocking out' the SATB1 gene using RNAi involves introducing dsRNA to a cell. An enzyme known as a dicer cuts the dsRNA into small pieces called siRNA which combine with cellular proteins to form an RNA-induced silencing complex (RISC). The RISC targets a base sequence in the mRNA with a base sequence complementary to one strand of siRNA. When they come into contact, the RISC breaks down the target mRNA. This has the effect of switching off the SATB1 gene.

d. What could be an unintended negative consequence of this technique?

Solution

Interfering with the function of SATB1 in cancer cells could interfere adversely with the normal regulation of immune response and antibody production.

1 mark

Explanatory notes

- The SATB1 gene is found in the nuclei of cells and acts as a genome organiser. SATB1 is produced by the SATB1 gene which regulates the immune response and antibody production in healthy individuals; however, if a person has cancer it can act as a master regulator. If its function in cancer cells can be manipulated, there is no guarantee at this stage that there will be no side effects on its normal functions in a cell.

Total 7 marks

Question 5

Serious breeders of guinea pigs strive to produce strong pedigrees by mating their animals with strong genetic stock. When pups are sold to breeders, their family pedigrees are required. A breeder selling pups (GP26, GP27, GP28, GP29) claimed they were bred by a prize winning male (GP30) and female (GP25) was challenged as to whether the claim was true. To confirm or exclude GP30 as the breeding male of the pups, DNA profiles using STRs were prepared. The results are shown in the following table.

Parentage Evaluation Report – DNA Profiles														
LAB ID	STR1		STR2		STR3		STR4		STR5		STR6		STR7	
Claimed breeding female: GP25 (Carrie)	172	172	243	243	111	119	189	189	279	287	136	142	197	201
GP26 (Brownie)	172	188	238	243	111	111	180	189	279	315	120	142	194	197
GP27 (Tiny)	168	172	238	243	111	111	180	189	287	315	120	142	201	204
GP28 (Patch)	172	172	243	245	111	119	189	189	279	287	142	142	197	201
GP29 (Snowball)	172	172	233	243	111	119	189	189	279	287	142	142	201	201
Claimed breeding male: GP30 (Pete)	168	188	238	245	111	111	180	190	315	315	120	142	194	204

a. What is an STR?

Solution

STR is the abbreviation for short tandem repeat.

1 mark

Explanatory notes

An STR is the position on a chromosome where multiple copies of a short DNA sequence, which are joined end to end, are found.

b. What do the numbers entered in the columns labelled STR represent?

Solution

The number of repeats of each STR

1 mark

Explanatory notes

- As the variation in the number of tandem repeats increases, the relatedness decreases.

A scientist analysing the results of the DNA profile assumes that a female passes one of her two alleles at each STR locus to her offspring.

c. Explain clearly whether this assumption is correct.

Solution

Assumption is correct. Each parent contributes one chromosome from each homologous pair to each pup. Consequently, there will only be one allele from the female at each STR locus.

2 marks

Explanatory notes

- It is necessary to indicate whether the assumption is correct AND provide a clear justification for this decision. Students should remember to affirm their response by referring to the question.

Mark allocation

- 1 mark – assumption is correct
- 1 mark – 1 chromosome from each parental homologous pair to pup, therefore, one allele from female at each STR locus

d. Explain whether Pete is the breeding male of the pups.

Solution

DNA profile indicates that Pete is NOT the boar. The pups Patch and Snowball cannot have Pete as a father. Using STR4 they both need to have 189 repeats from Carrie AND either 180 or 194 repeats from Pete. They do NOT, instead they both have 2 loci with 189 repeats.

OR
Pete can also been excluded with evidence from STR5. Both pups should have inherited an allele with 315 repeats from Pete. They did NOT.

OR

STR8 shows the inheritance of 242 repeats – neither Pete nor Carrie have 242 repeats.

2 marks

Explanatory notes

Mark allocation

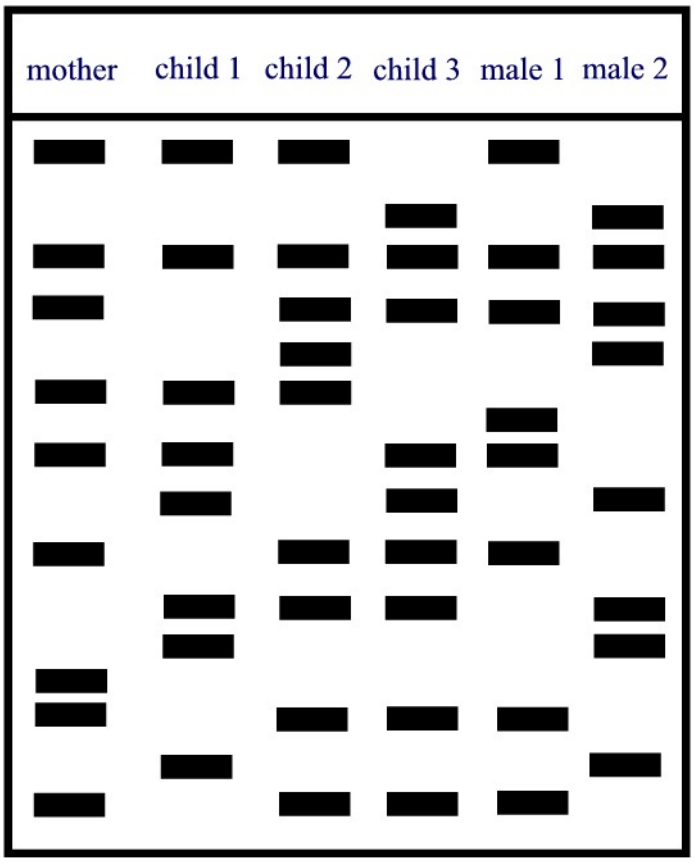
- 1 mark – Pete is not the boar that sired the pups in the litter.
- 1 mark – a correct and reasonable explanation which supports the question.

Total 6 marks

Question 6

On 17 July 1918, it was reported that all the Romanovs (Tsar Nicholas II, his wife Alexandra, their four daughters and one son), the Russian royal family and several of their attendants were killed and buried in an unmarked grave. In 1991, in a forest near Ekaterinberg in Russia, a shallow unmarked grave was found to contain the skeletal remains of nine people – three young females, three adult females and three adult males. Analysis of nuclear DNA suggested that there were five members of the same family and four unrelated individuals.

The results of a variable region analysis carried out on the remains are shown in the following diagram.



a. Explain which of the males is the father of the children.

Solution

Male 2 is the father of the three children. To be the father, the male must have provided all of the alleles that the mother has not. Male 1 does not satisfy this requirement and Male 2 does.

2 marks

Mark allocation

- 1 mark – Male 2 is the father of the three children.
- 1 mark – the male must provide all alleles that the mother has not, Male 1 does not satisfy this requirement and Male 2 does.

In order to confirm identities, it was necessary to analyse the D-loop of the mitochondrial DNA (mtDNA) from each of the skeletons. The mtDNA was extracted and then amplified.

b. **i.** Why is it necessary to use the D-loop of mtDNA specifically in this analysis?

Solution

The D-loop contains non-coding DNA that is inherited (without change) through the maternal line and is highly variable in unrelated individuals. If there is no variation present in the mtDNA of the mother and the children, identities can be resolved.

2 marks

Explanatory notes

- It is important to demonstrate an awareness that the D-loop contains non-coding maternal DNA AND that maternal descendents will have identical D-loop regions whereas unrelated persons will have highly variable D-loop regions.

Mark allocation

- 1 mark – the D-loop contains non-coding maternal DNA.
- 1 mark – maternal descendents have identical D-loop regions; unrelated persons have highly variable D-loop regions.

ii. What is the name of the technique is used to amplify the mtDNA extracted from the skeletons?

Solution

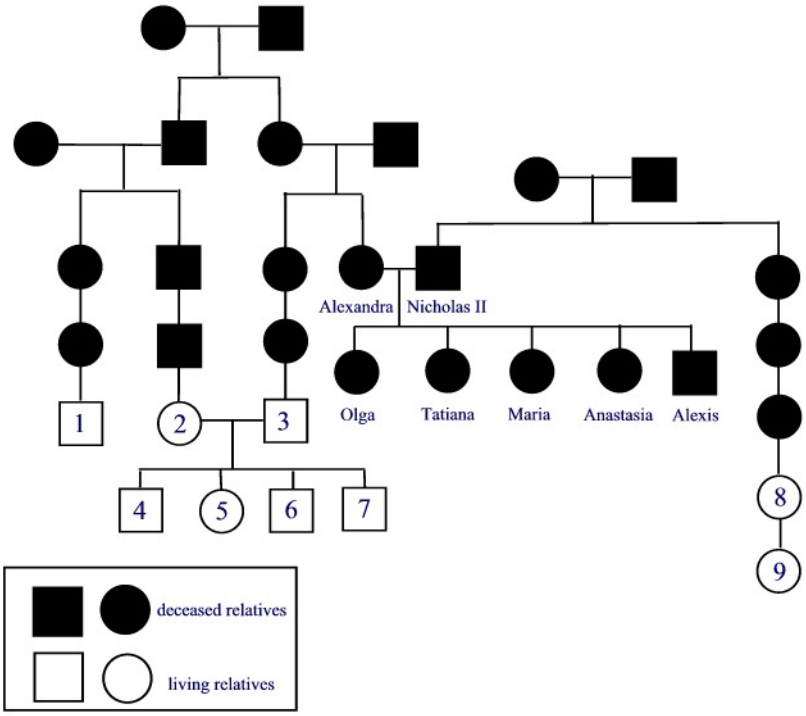
Polymerase chain reaction (PCR)

1 mark

Explanatory notes

- The question asks for the NAME of the technique – not the acronym of the name. It is essential to write polymerase chain reaction, not just PCR.

The relationship between the adult female and the three female children was confirmed, they were mother and daughters. However, whether they were the remains of Tsarina Alexandra and three of her daughters was yet to be determined. The pedigree shows part of the family tree of the Romanovs.



c. Explain which living relative would be the best person to confirm the remains of Tsarina Alexandra?

Solution

Individual 3 (male) would be the only person whose mtDNA could be used to confirm the Tsarina's identity. The living relative must be a descendant from the same maternal line and Individual 3 is the only person who meets this criterion.

2 marks

Explanatory notes

- Recognition that Alexandra's mother is also the great grandmother of Individual 3 therefore Alexandra and Individual 3 will share identical mtDNA.

Mark allocation

- 1 mark – Individual 3 (male)
- 1 mark – living relative must be a descendant from the same maternal line (Individual 3)

Total 7 marks

Question 7

To establish whether giant pandas and lesser pandas are true bears or members of the racoon family, their evolutionary relationship was analysed using DNA-DNA hybridisation. In this process, single-stranded DNA from the species being compared was mixed and complementary base sequences allowed to anneal.

a. Why is single-stranded DNA used in the process of DNA-DNA hybridisation?

Solution

DNA-DNA hybridisation depends on the formation of bonds between the DNA from two different species. Single-stranded DNA has unpaired nucleotide bases, which will readily pair with the unpaired nucleotide bases found in another strand of DNA.

1 mark

Explanatory notes

- The process depends on the ability of the separate strands of DNA to anneal. When one strand of DNA is single stranded it has free nucleotides which can readily form H-bonds with the other single strand of DNA.

After the strands of DNA have annealed, the stability of the bonds is tested by heating the double-stranded molecule until the bonds separate again. The results of such a process are shown in the following table.

Species	Temperature at which DNA strands separate (°C)
1 and 2	77
1 and 3	81
2 and 3	74

b. i. Explain with reference to the results in the table, the significance of the different temperatures.

Solution

The DNA of species 1, 2 and 3 separate from each other at different temperatures on heating. The higher the temperature at which the DNA strands separate, the more closely matched the nucleotide bases will be. This indicates a closer evolutionary relationship.

2 marks

Explanatory notes

Results show a difference between species 1, 2 and 3 in the temperature at which they separate from each other on heating. The higher the temperature at which the DNA strands separate, the more stable the molecule, the stronger the bond and the closer the matching of nucleotide bases. This indicates a closer evolutionary relationship and a higher degree of relatedness.

Mark allocation

- 1 mark – difference between species 1, 2 and 3 in the temperature at which they separate.
- 1 mark – the higher the temperature at which the DNA strands separate, the more stable the molecule etc.

ii. Which two species seem more closely related?

Solution

Species 1 and 3

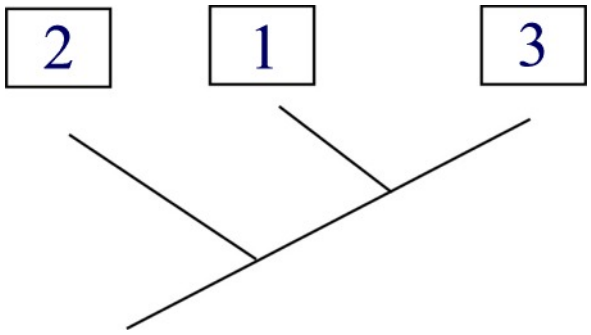
1 mark

Explanatory notes

Hybridised DNA of species 1 and 3 required the highest temperature (81^{o}C) to separate. It can be inferred that they have formed the most stable bonds due to the close match between complementary bases.

iii. Use the results of the DNA-DNA hybridisation to demonstrate the evolutionary relationship between the three species using a cladogram (phylogenetic tree).

Solution



1 mark

Explanatory notes

- Final diagram is determined by degree of similarity between complementary base sequences of DNA-DNA hybrids. The greater the similarity, the higher the temperature at which they separate. The DNA-DNA hybrid of species 1 and 3 separates at 81^{o}C which is the highest temperature – therefore they are most closely related. The DNA-DNA hybrid of species 2 and 3 separates at 74^{o}C and that of species 1 and 2 at 77^{o}C. Species 2 and 3 separate at the lowest temperature – therefore must be the furthest apart. Order based on this must be 2 1 3.

c. Of what does the technique of DNA-DNA hybridisation provide a measure?

Solution

It measures the similarity of the genetic material of two species, and gives an estimate of the genetic distance between them.

1 mark

In the past, scientists have studied single genes to gain knowledge about evolution. Researchers can now use comparative genomics to clarify evolutionary history.

d. Explain how comparative genomics enables the clarification of evolutionary history.

Solution

Comparative genomics allows researchers to identify conserved genes and make inferences about the evolutionary history of a species.

OR

Comparative genomics provides evidence of the occurrence of processes such as gene duplication and horizontal gene transfer.

1 mark

Explanatory notes

- By comparing the genomes of different species it is possible to gather information about how evolution has occurred and facilitates the progress of medicine and furthers research in ecology and biodiversity.

Total 7 marks

Question 8

The Riversleigh world heritage area in Northern Queensland is a renowned fossil location. In the late 1990s, a near-complete skeleton of *Nambaroo gillespieae*, a prehistoric kangaroo, was unearthed. The new species is one of the earliest known predecessors of the modern kangaroo.

The skeleton of *Nambaroo gillespieae* was dated at 25 million years old.

a. Describe the dating techniques which would have been used to date the skeleton of *Nambaroo gillespieae*.

Solution

Relative dating of rock strata to determine the age of the rock in which the skeleton of *Nambaroo gillespieae* was found **AND** radiometric potassium-argon (K-Ar) dating (absolute dating).

2 marks

Explanatory notes

- Actual fossils can very rarely be dated directly. As a rule, the rocks in which they are found are dated (relative dating techniques) and then the age of the rock is attributed to the fossil. The fossil can be more specifically dated using absolute dating techniques. The skeleton of *Nambaroo gillespieae* is dated at 25 million years old, which would have been determined by potassium-argon (K-Ar) dating (or ^{14}C radiocarbon dating). Potassium-argon dating is likely to be most accurate from 4.3 billion to 100 000 years before the present.

Nambaroo gillespieae was about the size of a small dog and had canine fangs, large muscular forearms, opposable big toes and flexible feet, and lived in dense forest.

b. Using evidence, describe two possible methods that *Nambaroo gillespieae* used to move around.

Solution

Method 1. Large muscular forearms – galloped or bounded along

Method 2. Opposable big toes and flexible feet – climbed in trees

2 marks

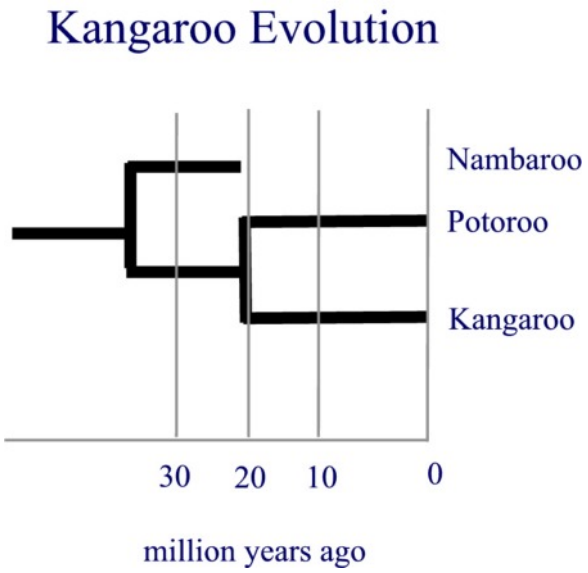
Explanatory notes

Physical characteristics (such as size and organisation of bones, shape and size of teeth) provide clues about how an animal lived in its environment (its ecology). By observing the bones of the forearm and the structure of the feet, it is possible to use structural evidence to infer how the Nambaroo moved around.

Mark allocation

- 1 mark – large muscular forearms **AND** galloped or bounded along
- 1 mark – opposable big toes and flexible feet **AND** climbed in trees

The Nambaroo is part of an extinct group of kangaroos known as the Balbaridae which have been replaced over time by the direct predecessors of contemporary kangaroos. The diagram below shows the evolutionary history of the kangaroo.



c. What kind of evolution has produced this history?

Solution

Divergent evolution

1 mark
Total 5 marks

END OF SOLUTIONS BOOK