OCR A-LEVEL BIOLOGY A · H420

BIOLOGY



EXAM QUESTION PACK

6.1.3 MANIPULATING GENOMES

SCORE	PERCENTAGE
/70	%

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Answer **all** the questions.

1(a). DNA fragments can be separated using electrophoresis.

Fig. 3.1 shows the result of electrophoresis of several DNA samples.

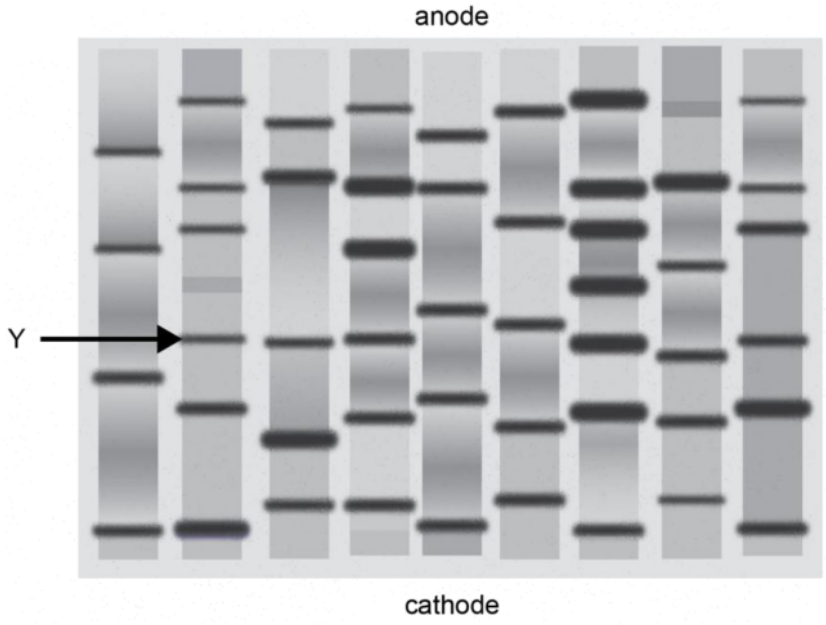


Fig. 3.1

(i) Describe how DNA can be visualised after electrophoresis has been completed.

---

[2]

(ii) Place a cross (X) **on Fig. 3.1** to indicate the position of a fragment of DNA with a mass greater than the DNA band labelled Y.

[1]

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(b).

(i) Mixtures of proteins can also be separated by electrophoresis.

- Proteins are heated before being placed in the electrophoresis gel.
- The gel contains a substance called SDS, which has a negative charge.
- SDS binds to proteins.

Suggest why proteins are heated before being placed in the electrophoresis gel.

---

[1]

(ii) Suggest why the binding of SDS to proteins is necessary for protein electrophoresis.

---

[2]

2. Which statement correctly describes a difference between somatic and germ line gene therapy?

A Germ line therapy involves the use of liposomes; somatic therapy involves use of viral vectors.
B Somatic therapy can target specific tissues in need of treatment, germ line therapy cannot.
C Somatic therapy is most successful when targeting single gene defects, but germ line therapy can target multiple defects.
D Long term success is theoretically more likely with somatic cell therapy than germ line therapy.

Your answer ☐

[1]

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3. An Iron Age farm was excavated by archaeologists. Some DNA was recovered from the tooth of an animal thought to be a type of domesticated milk cow.

A farmer keeps rare breed cows similar to those farmed on the Iron Age farm. DNA from the cows was obtained.

What technique would you plan to use, to compare digested and amplified fragments from the two DNA samples?

[1]

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4. Tissue traces from a crime scene often need to be identified. DNA from the tissue is 'amplified' by the polymerase chain reaction (PCR) to get samples large enough for further analysis.

Modern PCR technique uses DNA polymerase from the bacterium *Thermus aquaticus.* Why is this enzyme chosen?

---

[2]

5(a). The European corn borer moth, *Ostrinia nubilalis,* is a pest of agriculture. Its larvae develop inside maize stems and eat the contents, weakening the stems so that the plants collapse.

The bacterium *Bacillus thuringiensis* ('Bt') produces a protein that poisons the larvae of moths and butterflies. This protein can be isolated from cultures of Bt and packaged in fluids to be sprayed on the surface of plants.

The gene coding for the toxic protein has also been isolated. It has been incorporated into a genetically modified strain of maize called Bt corn. This makes the plant tissues poisonous to the corn borer moth.

Consider the statement:

'Genetically modified plants and animals should be classed as new species'.

Outline **one** experiment or investigation that would provide evidence to support or contradict the statement.

[3]

(b). A farmer wants to increase the yield of maize.

A friend recommends planting genetically-modified Bt corn as it would be more effective against European corn borer larvae rather than spraying unmodified corn with Bt toxin.

Which method would you recommend to the farmer? Justify your answer.

[1]

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(c). * Some students investigated the different ways of protecting maize plants against the corn borer moth. In each of **three** separate but close-together square plots, in the same field, they planted several hundred maize seedlings.

Plot A: untreated (control).

Plot B: sprayed daily with Bt toxin.

Plot C: the seedlings planted were genetically modified Bt corn.

On the first day of each week, one student would walk around the edge of a plot and count the number of maize plants that had collapsed in that plot. Each plot had a student responsible for counting. The results are shown in **Table 20.1.**

	Number of maize plants collapsed since the last weekly count		
Week number	**Plot A**	**Plot B**	**Plot C**
1	0	0	1
2	0	0	0
3	18	22	21
4	0	0	0
5	5	1	0
6	14	11	12
7	5	2	1
8	12	0	1
9	17	1	0
10	30	6	0
11	32	13	1
12	41	17	0
13	38	26	1
14	47	31	1
15	50	44	2
16	49	47	0

Table 20.1

The students' tutor raised a number of concerns about the investigation. In summary:

- **The methods were not a valid test of what was being investigated.**
- **The results may not be accurate.**

- **Some variables were not controlled.**

Explain why these concerns are justified and suggest improvements to the investigation.

[6]

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6(a). In order to sequence the whole genome of an organism it may be necessary to sequence billions of nucleotides. The human genome is approximately 3.2 billion nucleotides long.

Sequencing DNA requires a series of steps.

Place the following steps in the correct sequence. The first and last ones have been done for you.

A place sections in order by matching overlapping regions
B cut DNA into sections of varying length
C sequence short sections of DNA
D amplify the DNA (create many copies)
E extract samples of DNA from cells

E _____ _____ _____ **A**

[2]

The development of high-throughput sequencing techniques has enabled whole genomes to be sequenced more rapidly. Table 17.1 compares a number of DNA sequencing techniques.

Technique	**Rate of sequencing (Mb day^{-1})**	**Maximum length of nucleotide chain sequenced**	**Typical number of errors per 100 000 nucleotides**
Sanger (chain termination technique)	6	1000	5
Roche pyrosequencing	750	500	50
SOLiD	5000	50	500
Helicos	5000	32	1000

Table 17.1

(b). The protein coded for in a gene is 200 amino acids in length. How many errors could be expected in the exons of the sequenced gene when using the least accurate sequencing technique shown in Table 17.1.

Answer_____ **[2]**

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(c). Roche pyrosequencing relies on building a chain of nucleotides against a template. It involves the following steps:

- Nucleotides are washed over the template in a specific order.
- When the correct nucleotide is present it joins the new chain.
- The addition of a nucleotide to the chain releases energy.
- The energy is used to activate a protein called luciferin.
- Light released by luciferin is detected.
- If two identical nucleotides are added together then the intensity of the light emitted is doubled.

Fig. 17.1 shows a readout from a pyrosequencing machine.

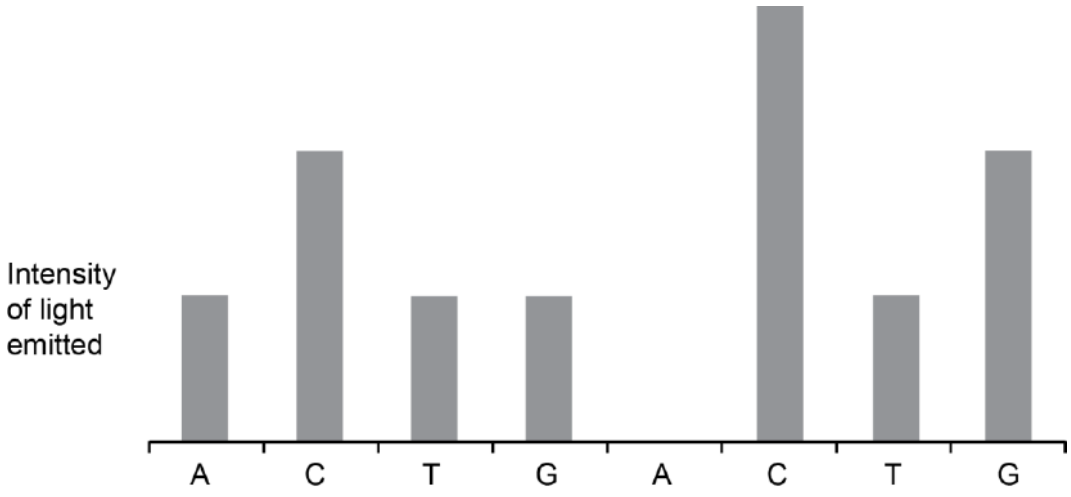


Fig. 17.1

Read off the sequence of bases in the length of DNA.

[1]

(d).

(i) A portion of a gene was sequenced from two members of the same family suspected of having a genetic disease.

The sequences are shown below:

A C G G T A T T G C T A C T T G A A T T A C G T
A C G G T A T T G A G C C T T G A A T T A C G T

What proportion of the sequence is different?

Answer = _____ **[2]**

(ii) To identify an allele that causes a genetic disease it must be sequenced accurately so that differences from the healthy allele are clear.

Using the information in **Table 17.1** decide which technique is best to use when sequencing a human gene that causes a genetic disease.

Explain your choice.

---**[2]**

(iii) Suggest how the interdisciplinary field of *bioinformatics* may be useful in determining whether a newly-sequenced allele causes a genetic disease.

---**[2]**

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(e). DNA profiling uses techniques to separate lengths of DNA to produce a profile that is unique to each individual.

Explain why only selected sections of non-coding DNA are used when profiling a human.

---

[3]

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7(a). Gene sequencing is an important technique in molecular biology.

Fig. 3.1 shows part of a computerised graph obtained from an automated gene sequencing machine.

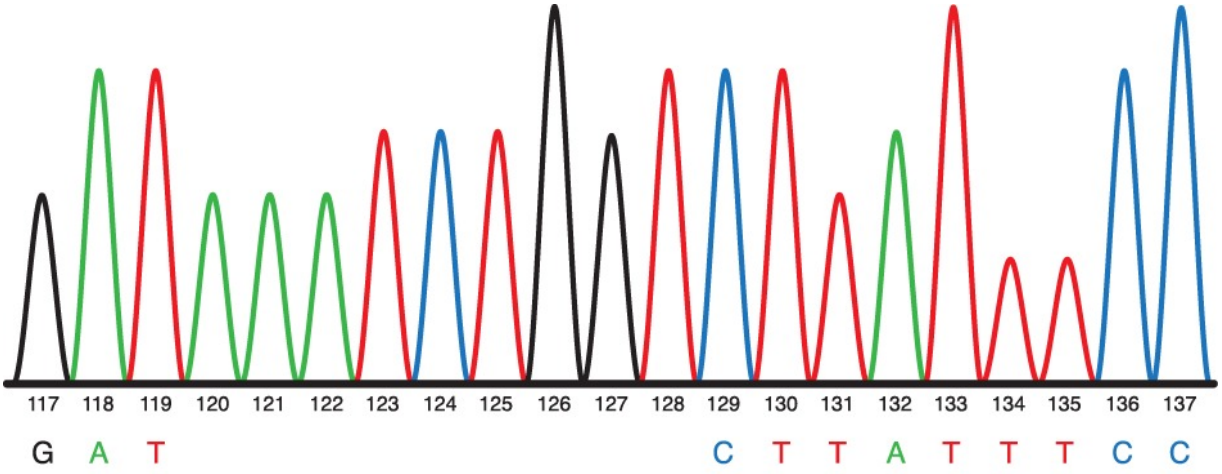


Fig. 3.1

- The section of the DNA molecule represented in Fig. 3.1 is from base position 117 (on the left of the graph) to base position 137 (on the right of the graph).
- The bases in the DNA sequence are labelled with four different coloured fluorescent dyes.
- The identities of some of the bases (117 to 119 inclusive and 129 to 137 inclusive) are indicated below the graph.

Use Fig. 3.1 to identify the order of bases from positions 120 to 128.

120	121	122	123	124	125	126	127	128
.....	.....	.....	.....	.....	.....	.....	.....	.....

[1]

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(b). To produce the type of graph shown in Fig. 3.1, the automated gene sequencing machine needs to be loaded with the following:

- the DNA to be sequenced
- short primer sequences specific to the DNA to be sequenced
- many normal DNA nucleotides
- some chain-terminating DNA nucleotides labelled with coloured dyes
- the enzyme *Taq* polymerase.

A regular cycle of temperature changes allows many DNA fragments of different lengths to be built up by the polymerase chain reaction (PCR).

Fig. 3.2 shows the end parts of the sequences of seven of these different length fragments, labelled 1 to 7. The end parts of the sequences for fragments 1 to 4 are complete but those for fragments 5 to 7 are not.
These seven fragments correspond to the **last seven peaks** on the right hand side of the graph in Fig. 3.1.

The letters in boxes represent labelled chain-terminating DNA nucleotides.
The letters not in boxes represent normal DNA nucleotides.

(i) Use the information in Fig. 3.1 to fill in the missing nucleotide bases on fragments 5 to 7 on Fig. 3.2.

You should distinguish between the normal and labelled nucleotides in the sequence for each fragment.

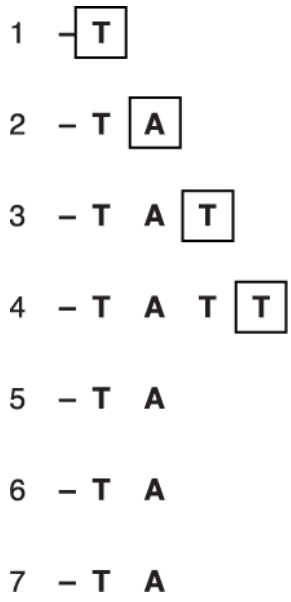


Fig. 3.2

[2]

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(ii) Explain how the automated sequencing machine orders the DNA fragments from the PCR reaction into the size order shown in Fig. 3.2.

---**[3]**

(c). Asthma in children may be treated with drugs. One of the most commonly used drugs is salmeterol.

Salmeterol acts by binding to protein receptors in the lining of the bronchioles. However, in approximately 14% of children with asthma, salmeterol is not very effective. This is thought to be the result of a genetic mutation in these children.

Suggest why this mutation reduces the effectiveness of salmeterol.

---**[3]**

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(d). In a recent medical trial, 62 children with this genetic mutation were studied.

- Their asthma was not controlled well by salmeterol.
- 31 children continued using salmeterol and the remaining 31 were given an alternative drug, montelukast.
- Montelukast is not routinely prescribed because salmeterol is far more effective for most children with asthma.

(i) After one year, the children taking montelukast had better control of their asthma and were able to reduce their use of montelukast.

Suggest why these children responded better to montelukast than to salmeterol.

---**[2]**

(ii) Comment on the reliability of the results of this medical trial.

---**[1]**

(iii) It is proposed that a simple saliva test could identify those children who have the mutation.

What would be the source of the genetic material used in this test?

---**[1]**

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8. Samples of DNA were taken from frogs **A**, **B**, **C** and **D**.

Electrophoresis was used to separate the different lengths of DNA after cutting.

Fig. 1.2 shows the results.

These results are known as genetic profiles. Only the genetic profile of frog **C** is identified. The remaining profiles are labelled **1** to **3**.

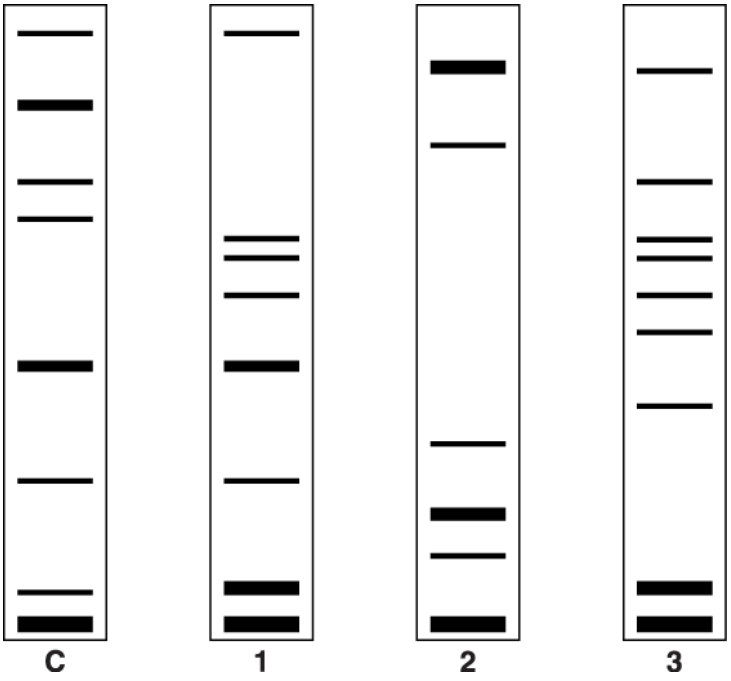


Fig. 1.2

(i) Identify which of the frogs in Fig. 1.1 gave genetic profiles corresponding to **1**, **2** and **3** in Fig. 1.2.

Write the letters **A**, **B** and **D**, as appropriate, in the table below.

Genetic profile number	Letter of frog
1	
2	
3	

[3]

(ii) Mitochondrial DNA from the frogs was sequenced.

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State, giving a reason, which of the frogs **A**, **B** and **C** would have a mitochondrial DNA sequence identical to **D**.

---**[1]**

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9. In a colony of bees, about 5% of the workers are more adventurous than other workers. These bees are known as scout bees. They actively seek out new food sources and, if necessary, new nest sites.

Researchers investigated how gene expression differed in the brains of the scout bees compared to the normal worker bees.

- The researchers extracted mRNA from the brain cells of **normal worker** bees.
- This mRNA was used to produce lengths of single-stranded DNA, which were then attached to a fluorescent dye.
- These lengths of single-stranded DNA were used as gene probes fixed onto a device known as a 'microarray DNA chip'.
- mRNA extracted from the brain cells of **scout** bees would only bind to the gene probes that matched it, causing these probes to fluoresce.
- The locations of the brightest fluorescent spots on the DNA chip revealed which genes were most active.

(i) Name the enzyme that can be used to convert mRNA to single-stranded DNA.

---

[1]

(ii) Explain how the locations of the fluorescent spots on the DNA chip reveal which genes are most active.

---

[3]

(iii) The researchers found many differences in gene activity in the scout bees compared to the normal worker bees. One of these differences in activity was in a gene used to make the neurotransmitter, dopamine.

In a follow-up experiment, scout bees became less adventurous if dopamine signalling was prevented.

Use your knowledge of the DRD4 dopamine receptor in humans to comment on the findings of this research into scout bee behaviour.

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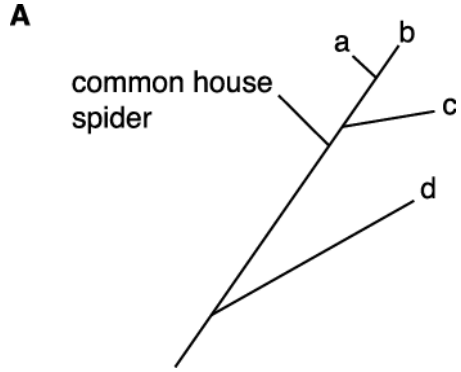
[3]

10. Scientists sequenced the DNA of the common house spider and four other species a, b, c and d that look similar. Analysis revealed the following differences from the DNA of the common house spider.

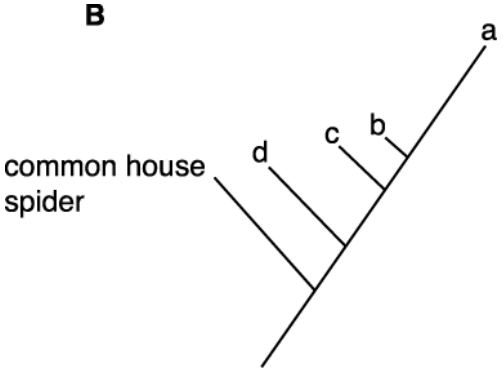
Species	Number of differences from DNA of common house spider
a	23
b	72
c	6
d	18

Which phylogenetic tree matches these data?

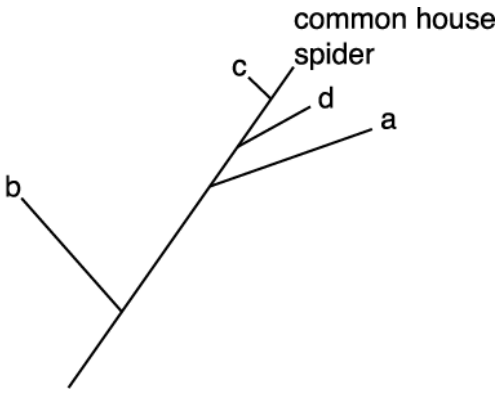
A



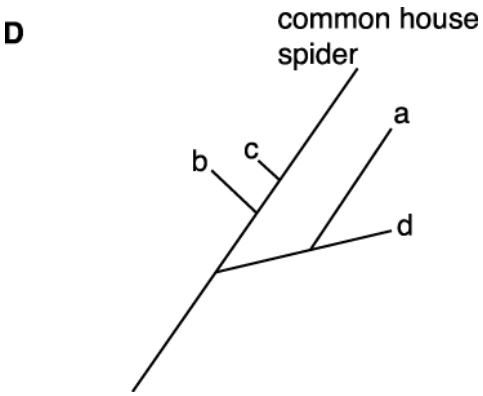
B



C



D



Your answer

[1]

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11. What is the main advantage of the polymerase chain reaction (PCR) when it is used as part of the process to sequence the genome of an endangered species?

A it is cheaper than rearing animals
B it never makes mistakes
C it reproduces DNA rapidly
D only a small sample of DNA is required

Your answer

[1]

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12. Fig. 22 shows four nucleotides.

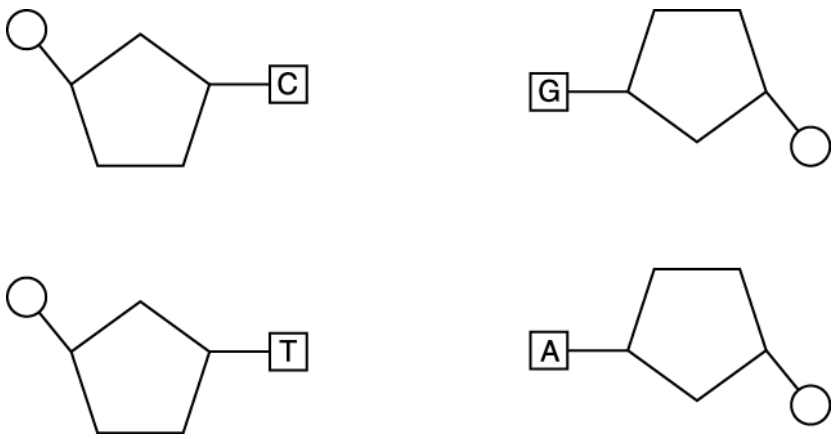


Fig. 22

(i) **On Fig. 22**, use the letter **R** to label a bond that would be made by the action of a ligase enzyme.

[1]

(ii) **On Fig. 22**, use the letter **P** to label a bond that would be broken during the hottest step of the PCR reaction.

[1]

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13(a). *Scientists have genetically engineered many different species of plant.

Aubergine plants, *Solanum melongena*, can suffer damage from moth larvae.

Scientists have produced a variety of aubergine that is resistant to moth larvae. To create the resistance, scientists transferred a gene from the *Bacillus thuringiensis* bacterium.

Describe the process the scientists could have used to produce the pest-resistant aubergines.

[6]

(b). Potatoes often suffer bruising, which reduces their value as a food crop.

A variety of crop potato that does not bruise has been developed using a technique called gene silencing.

Scientists carry out gene silencing by inserting small sequences of RNA into potato cells. These RNA sequences are complementary to mRNA from genes responsible for bruising.

Use this information to suggest why the technique is called 'gene silencing'.

---

[2]

END OF QUESTION PAPER

Question			Answer/Indicative content	Marks	Guidance
1	a	i	radioactive, labels / tags (1) fluorescent, labels / tags (1) UV, light / radiation (1) (named) visible stain (1)	2	
		ii	X placed on any fragment below Y (1)	1	X can be placed in any of the 9 lanes, but must be touching a DNA band that is lower in the image (nearer the cathode) than Y
	b	i	denature / unfold, protein **AND** *idea of* exposes charges or hydrophobic region (1)	1	
		ii	*idea that* different proteins have different overall charges (1) *idea that* (binding of) SDS makes all proteins negatively charged (1) *idea that* proteins will be separated by, mass / length (1) *idea that* proteins move in the same direction (1)	2	
			Total	**6**	
2			B	1	
			Total	**1**	
3			electrophoresis	1	
			Total	**1**	
4			thermostable **OR** does not, denature / AW, at 95 °C (during DNA strand separation) (1) so PCR can be cycled repeatedly without stopping (to reload with enzyme) (1)	2	**ALLOW** temperature values 93 – 97 °C in correct context. **DO NOT ALLOW** "killed“ for denatured. **IGNORE** refs to optimum working temperature, which would apply equally to less thermostable polymerases.
			Total	**2**	

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Question			Answer/Indicative content	Marks	Guidance
5	a		*Fertility* breed GM stock with non-modified stock (1) see if offspring fertile (1) if so they should be classed as the same species (1) **ora** *Morphology* Compare several individuals from GM and non-GM groups (1) in respect of several physical structures (1) if similar they should be classed as one species (1) **ora** *Ecology* observe how both function in the wild (1) occupy the same or different niche(s) (1) if same niche they should be classed as one species (1) **ora** *Genetics* compare DNA (1) by electrophoresis (1) same pattern should be classed as one species (1) **ora**	3	Marks awarded should be from **one** outlined investigation **and** the conclusion from its results. If more than one investigation suggested, mark the first investigation and **IGNORE** the others.
	b		recommend GM Bt corn, because spray may not reach all larvae / larvae are inside plant (stem) / shielded from spray (1)	1	
	c		* **Level 3 (5–6 marks)** A complete explanation detailing objections and improvements for validity, accuracy and control. The evaluation of the data / procedures is critical, providing refinements that address all the significant issues concerned. *There is a well-developed line of reasoning which is clear and logically structured. The information presented is relevant and substantiated.* **Level 2 (3–4 marks)** A partial explanation detailing objections and improvements for some of the teachers concerns **OR** objections and improvements for all of the teachers concerns.	6	**IGNORE** professions of agreement with the tutor. **Indicative scientific points may include:** **Results not valid** **Objections:** • cause of collapse not recorded / plants may have collapsed for different reasons • number of collapsed less meaningful than percent **Improvements:** • determine which plants collapsed due to corn borer • dissect stems to seek larvae • use percent collapsed out of, original / still standing, numbers.

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Question			Answer/Indicative content	Marks	Guidance
			A range of aspects of the data / procedures are evaluated resulting in sound but not comprehensive refinements. *There is a line of reasoning presented with some structure. The information presented is in the most-part relevant and supported by some evidence.* **Level 1 (1–2 marks)** A simple explanation, linking some objections or improvements to some of the teachers concerns. Evaluation and / or refinement, links to data / procedure in some respects but links are not clearly shown. *The information is basic and communicated in an unstructured way. The information is supported by limited evidence and the relationship to the evidence may not be clear.* **0 marks** No response or no response worthy of credit.		**Results may not be accurate** **Objections:** • collapsed plants may have been counted twice from plot-edge • some collapsed plants may not have been noticed from plot-edge • students may have counted differently from each other **Improvements:** • remove / mark, collapsed when counted • use narrow strips as plots so that collapsed not missed • have all plots counted by the same student • have more than one student counting • average the counts. **Variables not controlled** **Objections:** • no account of natural variation in plant susceptibility • genetic variations between Bt and regular corn **Improvements:** • use, cloned / genetically identical, plants in each plot. • perform genetic modification to Bt on same clones as used for other plots. **ALLOW** references to repeating the procedure.
			Total	**10**	

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Question			Answer/Indicative content	Marks	Guidance
6	a		B, D, C (1)(1)	2	One mark for D after B and one for C after D
	b		6 (1)(1)	2	Correct response = 2 marks If response incorrect **ALLOW** one mark for 600 nucleotides / bases **ALLOW** one mark for idea of one error every 100 nucleotides
	c		A C C T G C C C T G G	2	
	d	i	1/8 or 0.125 (1)(1)	2	Correct response = 2 marks If response incorrect **ALLOW** one mark for working e.g. 3/24 **ALLOW** 12.5%
		ii	Sanger / chain termination technique (1) Only 5 errors per 100 000 nucleotides compared to, 50 in Roche pyrosequencing / 500 in SOLiD / 1000 in Helicos (1)	2	
		iii	base sequence of normal allele and (known) alternatives held (in database) (1) computational analysis allows rapid comparison of sequences with newly sequenced allele (1) amino acid sequence / protein structures, also held (in database) (1) *idea of* computer modelling of new protein structure from base sequence (1)	2	
	e		in most people, the genome is very similar / most genes the same (1) using coding sequences would not provide unique profiles (1) (parts of) non-coding DNA contains variable numbers of, short tandem repeats / repeating sequences (1)	3	
			Total	**14**	

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Question			Answer/Indicative content	Marks	Guidance
7	a		AAA TCT GGT;	1	**Examiner's Comments** The vast majority of candidates were able to identify the bases correctly from the automated sequencing graph, with base 6 labelled as A being the most common error.
	b	i	the correct bases inserted in **all** 3 rows before box; correctly identifying the last base in each sequence as the labelled base; 5 **T** **T** [**T**] 6 **T** **T** **T** [**C**] 7 **T** **T** **T** **C** [**C**]	2	**Examiner's Comments** This was also well answered by the majority of candidates, though some candidates failed to attempt the question. The most common error was a failure to inset the correct sequence of bases in all three rows, before putting in the labelled base.

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Question			Answer/Indicative content	Marks	Guidance
		ii	electrophoresis; (negatively-charged DNA) moves towards, positive electrode / anode; smallest/smaller (fragments) move, fastest / faster; **ora** resolution on gel sufficient to register 1, nucleotide / base;	3 max	 **ACCEPT** positive, end /terminal **IGNORE** ref to distance **ACCEPT** lightest / shortest **ACCEPT** description 'machine detects fragments to one base in length' **IGNORE** pair **Examiner's Comments** This question proved to be a good discriminator, with few candidates gaining full marks. Most candidates realised the question was asking them to explain the process of electrophoresis, though some explained the PCR process instead, or the process gene sequencing in general. Many explained that the DNA was negatively charged so moved towards the positive anode, but many then failed to get the third marking point as they stated that the smallest fragment moved further and failed to say that they moved fastest, possibly because this had been the correct marking point in a previous question. In this case the question was related to the use of electrophoresis in sequencing,rather than as a method of just separating fragments. A number of candidates lost a marking point for saying 'the fragments moved towards the positive cathode'.

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Question			Answer/Indicative content	Marks	Guidance
	c		(mutation) change in (DNA) nucleotide/ base, sequence; (mutation causes) change in, amino acid sequence / primary structure (of protein); change in, tertiary structure/ 3D shape / binding site, of <u>receptor</u>; salmeterol unable to bind; *idea that* no response triggered in cell / no second messenger system activated;	3 max	**IGNORE** triplet / codon / gene / frameshift **DO NOT CREDIT** active site **ACCEPT** salmetorol not complementary shape to <u>receptor</u> **ACCEPT** salmeterol cannot bind as easily e.g. adenyl cyclase not activated **IGNORE** 'has no effect' **Examiner's Comments** This question discriminated well, with many candidates gaining 3 marks, for correctly linking a change in nucleotide sequence to a change in primary and tertiary structure of the receptor, so that salmeterol was unable to bind. A common error was to talk about proteins in general, rather than receptors, or to not mention that a mutation leads to a change in base sequence. Weaker candidates related their answers to enzymes, and discussed changes to the shape of active sites which gained no credit.

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Question			Answer/Indicative content	Marks	Guidance
	d	i	(mutation resulted in) <u>receptor</u> having complementary shape to montelukast; montelukast able to bind; (whereas) salmeterol cannot; montelukast may have a different <u>receptor</u>;	2 max	**DO NOT CREDIT** active site **IGNORE** fit **ACCEPT** attach **ACCEPT** cannot bind as easily **ACCEPT** montelukast receptors not damaged **Examiner's Comments** Many candidates scored both marks on this question by applying their knowledge about receptors to this new situation, and suggesting that montelukast could bind to the mutated receptor due to it being complementary in shape, whilst salmeterol could not. Other acceptable suggestions included that montelukast had different receptors which were unaffected by the mutation or that the drug worked in a different way which did not involve the mutated receptors. A minority of candidates talked about building up a resistance to salmeterol or having no resistance to montelukast, which did not gain credit.
		ii	not reliable because, sample size **too** small / **only** 62 children in study; **or** could be reliable because 31 is quite a large sample;	1	**<u>Note</u>** *31 is a suitable number for a phase 1 trial* **Examiner's Comments** A surprisingly large number of candidates failed to get this mark, which asked about the reliability of this trial. Some candidates talked about the lack of a control group, length of study or age range of the group, rather than the fact that the sample size was too small to be reliable. Generalised statements such as 'if you increase the sample size then reliability will be increased' were not credited.

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Question			Answer/Indicative content	Marks	Guidance
		iii	(epithelial) cells lining cheek;	1	**ACCEPT** (named) white blood cells in saliva / salivary gland cells **Examiner's Comments** It was surprising to many examiners that most candidates struggled to answer this question. Many candidates believed that genetic material can be found in proteins and enzymes, or just in saliva in general. Few candidates realised that cells from the cheek, white blood cells and salivary gland cells can be found in saliva, and that this can be used as a source of DNA.
			Total	**13**	

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Question			Answer/Indicative content	Marks	Guidance
8		i	<table><tr><th>Genetic fingerprint number</th><th>Letter of frog</th></tr><tr><td>1</td><td>**D**</td></tr><tr><td>2</td><td>**A**</td></tr><tr><td>3</td><td>**B**</td></tr></table> ; ; ;	3	**Mark the first answer in each box.** If an additional answer is given that is incorrect or contradicts the correct answer, then = **0 marks** **If no letters in the table <u>at all</u>**, look at the diagram and award marks if the profiles are identified correctly. **Examiner's Comments** Genetic profile 2 was often correctly identified, but many candidates mixed up profiles 1 and 3. *Teaching tip – candidates may find it useful to draw horizontal lines between the genetic profiles to see how they relate to each other*.
		ii	cytoplasm / mitochondria, came from **A** **or** mitochondria / (mitochondrial) DNA, in cytoplasm of **A**;	1	**If frog not identified correctly = 0 marks** **Must refer specifically to frog A** **Must refer specifically to frog A** **Examiner's Comments** Many candidates remembered that mitochondria are found in the cytoplasm, and have their own DNA, but failed to apply the information from the start of the question to identify the correct frog which had the same sequence as D.
			Total	**4**	

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Question			Answer/Indicative content	Marks	Guidance
9		i	reverse transcriptase;	1	**Mark the first answer.** If the answer is correct and an additional answer is given that is incorrect or contradicts the correct answer then = **0 marks** **DO NOT CREDIT** DNA (reverse) transcriptase **Examiner's Comments** Surprisingly few candidates could correctly identify the enzyme. A variety of incorrect answers were given, including DNA / RNA polymerase, restriction endonuclease and ligase.
		ii	**1** mRNA binds to, (gene) probes / cDNA / ssDNA, by complementary base pairing; **2** *idea that* the ***more*** active the gene the ***more*** mRNA produced; **3** during transcription; **4** ***more*** fluorescence indicates ***more*** mRNA (bound);	3 max	**1 DO NOT CREDIT** in the context of the gene probe binding to DNA **3 IGNORE** translation **Examiner's Comments** This was a challenging question, which few candidates scored full marks on. Many missed the point of what an active gene means in terms of mRNA transcription, and so referred to the gene binding to the gene probe, rather than mRNA. Some candidates did not understand the use of a gene probe in this context, and referred to gel electrophoresis and automated gene sequencing, or just restated the question by saying the most active gene fluoresced the most.

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Question			Answer/Indicative content	Marks	Guidance
		iii	**1** dopamine linked to, ADHD / addiction / risk-taking / adventurous behaviour / hyperactivity / erratic behaviour (in humans); **2** *idea of* common mechanism in bees and humans (for adventurous behaviour); **3** *idea that* as they are different organisms the mechanisms may not be comparable (even though apparently similar); **4** AVP;	3 max	**1 IGNORE** ref to schizophrenia / Parkinson's **This mark is for the effect of the *chemical* dopamine, not the dopamine receptors alone.** **2** e.g. ***both*** have, DRD4 / dopamine receptors e.g. dopamine has the same effect in ***both*** **4** e.g. other genes also involved in, bee / human, behaviour **Note:** 'both have dopamine receptors which are linked to adventurous behaviour' = **1 mark** (mp 2 only) 'both have dopamine receptors and dopamine is linked to adventurous behaviour' = **2 marks** (mps 2 & 1) **Examiner's Comments** Many candidates did not link dopamine to its effect on humans, but rather stated it was the receptor or gene alone causing the effect. However, most did gain credit for identifying a common mechanism in both humans and bees.
			Total	**7**	
10			C ☐	1	
			Total	**1**	
11			D ☐	1	
			Total	**1**	
12		i	**R** used to label a phosphodiester bond ☐	1	
		ii	**p** used to label a hydrogen bond ☐	1	
			Total	**2**	

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Question			Answer/Indicative content	Marks	Guidance
13	a		***Please refer to the marking instructions on page 4 of this mark scheme for guidance on how to mark this question.*** ***In summary:*** *Read through the whole answer. (Be prepared to recognise and credit unexpected approaches where they show relevance.)* *Using a 'best–fit' approach based on the science content of the answer, first decide which of the level descriptors,* ***Level 1****,* ***Level 2*** *or* ***Level 3****, best describes the overall quality of the answer.* *Then, award the higher or lower mark within the level, according to the* ***Communication Statement****(shown in italics):* • *award the higher mark where the Communication Statement has been met.* • *award the lower mark where aspects of the Communication Statement have been missed* • ***The science content determines the level.*** • ***The Communication Statement determines the mark within a level.***		

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Question			Answer/Indicative content	Marks	Guidance
			Level 3 (5–6 marks) Describes the process in detail, with no significant errors. *There is a well-developed line of reasoning, which is clear and logically-structured and uses scientific terminology at an appropriate level. All the information presented is relevant and forms a continuous narrative.* **Level 2 (3–4 marks)** Describes some details of the process, with only minor errors. *There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.* **Level 1 (1–2 marks)** Describes aspects of the process, but with significant omissions or errors. *The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.* **0 marks** No response or no response worthy of credit.	6	**Indicative scientific points may include:** • method for gene extraction from the bacterium (e.g. conversion of mRNA to cDNA with reverse transcriptase, or removal of gene with restriction enzymes) • use of appropriate vector (e.g. *Ti* plasmid of *Agrobacteriumtumefaciens*) • electroporation • use of DNA ligase • reference to marker genes and their purpose • electrofusion
	b		base sequence in genes is unchanged □ *idea that* mRNA is inhibited, therefore translation does not occur □ gene is not expressed □	2 max	
			Total	**8**	

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