Civics Group	Index Number	Name (use BLOCK LETTERS)	**H2**

ST. ANDREW'S JUNIOR COLLEGE
2024 JC2 PRELIMINARY EXAMINATIONS

H2 BIOLOGY **9744/2**

Paper 2

Friday **23rd August 2024** **2 hours**

Materials: Question Paper Set A and Set B

READ THESE INSTRUCTIONS FIRST

Write your name, civics group and index number on all the work you hand in.
Write in dark blue or black pen on both sides of the paper.
You may use a soft pencil for any diagram, graph or rough working.
Do not use staples, paper clips, highlighters, glue or correction fluid.

Answer **all** questions.
Write your answers in the spaces provided on the question paper.

The number of marks is given in brackets [ ] at the end of each question or part question.

For Examiners' Use	
1	/10
2	/10
3	/12
4	/10
5	/9
6	/10
7	/10
8	/10
9	/5
10	/4
Total	**/100**

This document consists of **27** printed pages and **0** blank page.

[Turn over

QUESTION 1

(a) Table 1.1 lists cell structures that can be found in eukaryotic cells or prokaryotic cells. Some of these cell structures can be found in both types of cell.

Complete the table using a tick (✓) to show that the cell structure can be present in a particular type of cell and a cross (✗) to show that the cell structure cannot be present.

Put a tick or a cross in every box.

The top row has been completed for you.

Table 1.1

cell structure	eukaryotic cells	prokaryotic cells
nucleus	✓	✗
Golgi body		
circular DNA		
70S ribosome		

[2]

cell structure	eukaryotic cells	prokaryotic cells
nucleus	✓	×
Golgi body	✓	×
circular DNA	✓	✓
70S ribosome	✓	✓

1 mark for each correct column

(b) All cells have a cell surface membrane. Fig. 1.1 shows a transmission electron micrograph of part of two adjacent animal cells, cell 1 and cell 2.

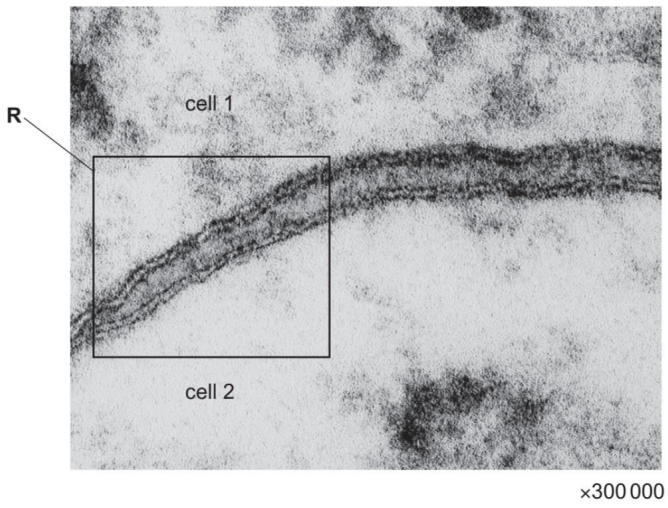


Fig. 1.1

In the space provided, draw a diagram of the region in the box labelled **R** in Fig. 1.1. Your diagram should show the four dark lines.

Label the diagram to identify what is shown by the dark lines and each of the three spaces between them.

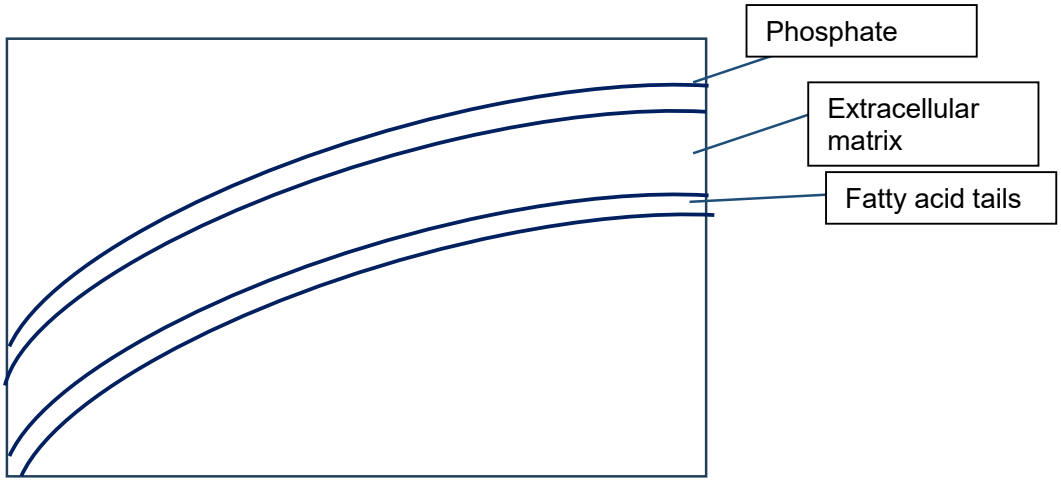
space for diagram:

diagram showing:

1 dark line(s) labelled as phosphate heads ;**Accept** phospholipid heads

2 clear area(s) between pairs of dark lines labelled as, fatty acid tails / hydrocarbon chains / hydrophobic core / AW ; Reject if pointing to intercellular space

3 clear area between the two cell surface membranes labelled as, interstitial fluid / tissue fluid / extracellular matrix / intercellular space ;**Accept** intercellular, area / region



[3]

Fig. 1.2 is a transmission electron micrograph of part of a hepatocyte showing some cell structures.

The peroxisome shown in Fig. 1.2 is a spherical organelle bound by a single membrane. It carries out a variety of enzyme-catalysed metabolic reactions, including detoxification. Some of these reactions require oxygen.

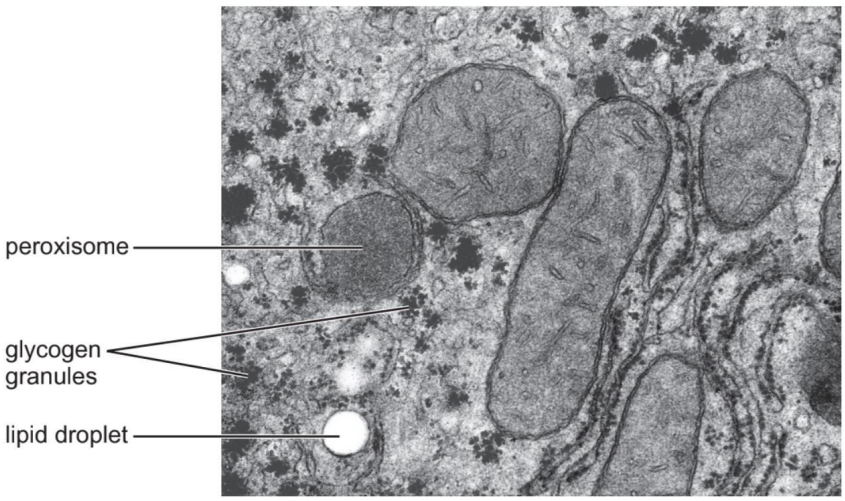


Fig. 1.2

(c) The mitochondria in Fig. 1.2 are larger than the peroxisome.
(i) State **one other** difference, **visible** in Fig. 1.2, between a peroxisome and a mitochondrion.

..... [1]

1 mitochondrion, bound by / has, double membrane / two membranes while peroxisome has (only) one membrane

2 peroxisome no cristae while mitochondrion has cristae ; **Reject cisternae**

3 peroxisome circular shape and mitochondria circular **and** rod shaped / AW ; I if only peroxisome shape stated **Reject oval shape**

Some of the enzymes used within mitochondria can be synthesised by the organelle.

Peroxisomes cannot synthesise any of the enzymes that they contain.

(ii) Suggest why a mitochondrion can synthesise enzymes, but a peroxisome cannot synthesise enzymes.

.....[2]

any two from:

1 mitochondrion has, DNA / genes coding for enzymes while peroxisome does not contain any genes coding for enzymes ;

2 A genetic, material / information, qualified with, transcription / ref. to mRNA / coding for enzymes

3 Mitochondrion contain 70S ribosomes for translation /to synthesise enzymes; **Reject 80S ribosomes**

4 Has the RNA polymerase/ enzymes for transcription ;

(**iii**) One of the enzymes present in peroxisomes is catalase. This enzyme catalyses the breakdown of hydrogen peroxide to harmless products.

Suggest why it is useful to the cell for this reaction to take place within peroxisomes.

.....[2]

any two from:

1 peroxisome membrane bound, so rest of cell protected from hydrogen peroxide ; **Accept** hydrogen peroxide can have toxic effects on (rest of) cell / AW

2 peroxisome acts as a compartment / specific area / contained, for, more efficient breakdown of hydrogen peroxide / control of reactions ; **Accept** isolates (peroxisomes) enzymes from rest of cell

3 high concentration of enzyme in one location ; **Accept** more enzyme-substrate complexes can form

4 provides optimum conditions, for other peroxisome reactions

[Total: 10]

Question 2

Fig. 2.1 outlines the first three stages of respiration in aerobic conditions.

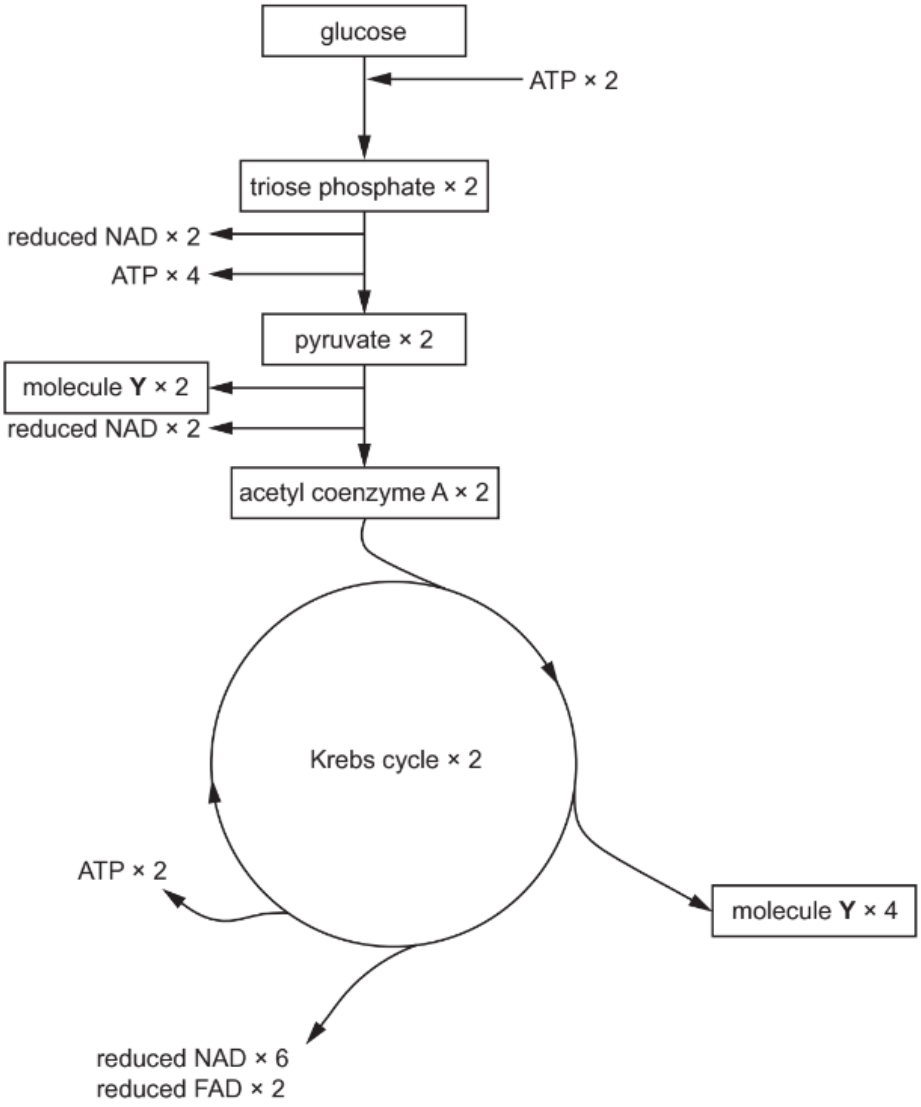


Fig. 2.1

(a) Name molecule Y in Fig. 2.1.

.....[1]

carbon dioxide Reject: CO_2

(b) At one time it was thought that the oxidative phosphorylation of:

• one molecule of reduced NAD results in the synthesis of 2.5 ATP molecules

• one molecule of reduced FAD results in the synthesis of 1.5 ATP molecules.

Using Fig. 2.1, a theoretical value for the net number of ATP molecules that are synthesised for each molecule of glucose can be calculated.

Modern research has shown that the actual net number of ATP molecules synthesised for each glucose molecule respired is much lower than this theoretical value.

(i) Using Fig. 2.1, calculate the theoretical value for the net number of ATP molecules that are synthesised for each molecule of glucose respired in all phosphorylation reactions.

Show your working.

(glycolysis & link rxn) + (Krebs)

(ATP + reduced NAD) + (ATP + reduced NAD + reduced FAD)

= (4 – 2) + (4× 2.5) + 2 + (6× 2.5) + (2× 1.5)

= 2 + 10 + 2 + 15 + 3 ;

= 32 ;

answer = ... [2]

More detailed explanation:
Glycolysis: net 2 ATP produced by substrate level phosphorylation (SLP); 2 NADH produced which results in 2 x 2.5 = 5 ATP molecules in oxidative phosphorylation
Link reaction: 2 NADH produced which results in 2 x 2.5 = 5 ATP molecules in oxidative phosphorylation
Krebs cycle: 2 ATP produced by SLP; 6 NADH produced which results in 6 x 2.5 = 15 ATP molecules in oxidative phosphorylation; 2 FADH2 produced which results in 2 x 1.5 = 3 ATP molecules in oxidative phosphorylation
Total ATP = 32 ATP

(ii) Suggest two reasons why the actual net number of ATP molecules synthesised is less than the theoretical number…….....…..[2]

1 ATP / energy, used to transport, pyruvate / reduced NAD / products of glycolysis, into (named part of) mitochondria ;

2 some protons leak from intermembrane space resulting in less steep proton gradient/less proton motive force ;

3 some energy lost as heat to the surrounding;

4 glucose may not be completely broken down / some intermediates are used in different metabolic processes ;

5 reduced NAD may be used for other (metabolic) reactions ;

(c) Outline the roles of NAD and FAD in aerobic respiration.

..... [2]

1 **coenzymes for dehydrogenases** / dehydrogenation reactions in ref. to glycolysis / link reaction / Krebs cycle

2 carry / transfer / transport / bring hydrogen ions & electrons/ H to ETC / inner mitochondrial membrane / crista ; Reject : bring electrons to ETC

(d) Rotenone is used as an insecticide. Rotenone kills insects by inhibiting the transfer of electrons in the electron transport chain of the mitochondrion.

Explain how rotenone affects ATP synthesis in the mitochondrion.

..... [3]

1 less or no energy release from electron transfer / ETC ;

2 fewer / no protons are pumped to intermembrane space so a less steep proton gradient/ no proton gradient form;

3 less / no chemiosmosis as fewer protons diffuse through ATP synthase hence less ATP synthesised ;

AVP No NAD and FAD regenerated, only glycolysis can occur so there is less ATP synthesize (max 1)

[Total: 10]

Question 3

The polymerase chain reaction (PCR) is used to produce large amounts of haemoglobin gene DNA from a very small original DNA sample. The main stages of a PCR are shown in Fig. 3.1.

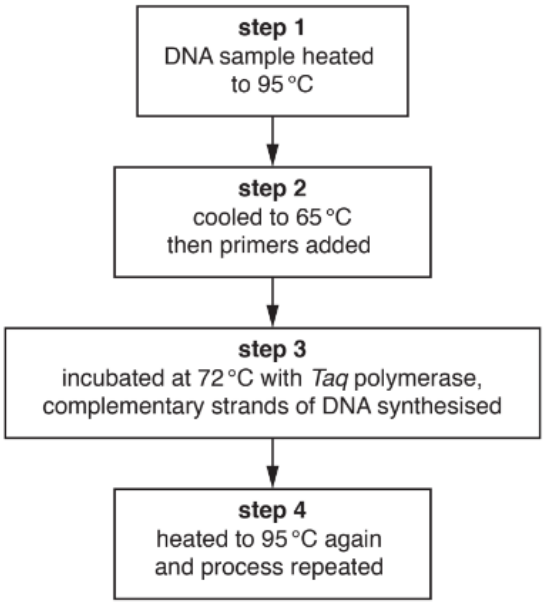


Fig. 3.1

(a) (i) Explain why the DNA sample is heated to 95°C in **step 1**.

.....[2]

two from

1 **to separate the two strands /denature DNA into single-stranded DNA**

2 by **breaking hydrogen bonds** between bases ;

3 so that bases are exposed to produce template strands for complementary copying ;

(ii) Explain why primers are added in **step 2**.

.....[2]

1 primer binds/ anneals to the **specific section of DNA/target gene for amplification** by complementary base pairing ; / Flank the target gene by binding of primers to specific DNA sequence

2 Provides 3'OH group for DNA polymerase to recognize and bind/attach nucleotides

AVP Primers reduce re-annealing of separated strands ;

(iii) Explain why the enzyme Taq polymerase is used in **step 3**.

.....[2]

1 synthesizes complementary DNA strands by catalyzing the formation of phosphodiester bond;

2 Taq polymerase, is heat stable/ able works at high temperature ;

3 Therefore **no need to add Taq polymerase again for each cycle /needs replacing only after a number of cycles** hence process is, more efficient / faster (than normal DNA polymerase) ;

(c) Gel electrophoresis can be carried out to test individuals for the different versions of haemoglobin: Adult haemoglobin(HbA) , Sickle cell haemoglobin (HbS) and Fetal haemoglobin (HbF).

• A buffer with alkaline pH is used to make all haemoglobin molecules negatively charged.

• HbS molecules have an additional positive charge compared to HbA.

• Fetal hemoglobin (Hb F) accounts for about two thirds of the infant's haemoglobin while HbA acounts for the rest of the haemoglobin.

(i) Describe and explain how gel electrophoresis is used to diagnose sickle cell anaemia.

..... [4]

1 current / potential difference / electric field applied across gel ;

2 protein / Hb moves towards/ attracted to the anode / positive electrode ;

3 HbS is more positive so it will moves more slowly/ move shorter distance / nearer to the negative end ;

4 compare the band positions to known haemoglobins reference bands if single band seen at HbS position person has sickle cell anaemia ;

(ii) Four individuals had their haemoglobin analysed by gel electrophoresis. One of the individuals was heterozygous for the HbA and HbS alleles and had a condition known as sickle cell trait (SCT).

Some of the results are shown in Fig. 3.2. In Fig. 3.2, lane 1 and lane 5 are complete.

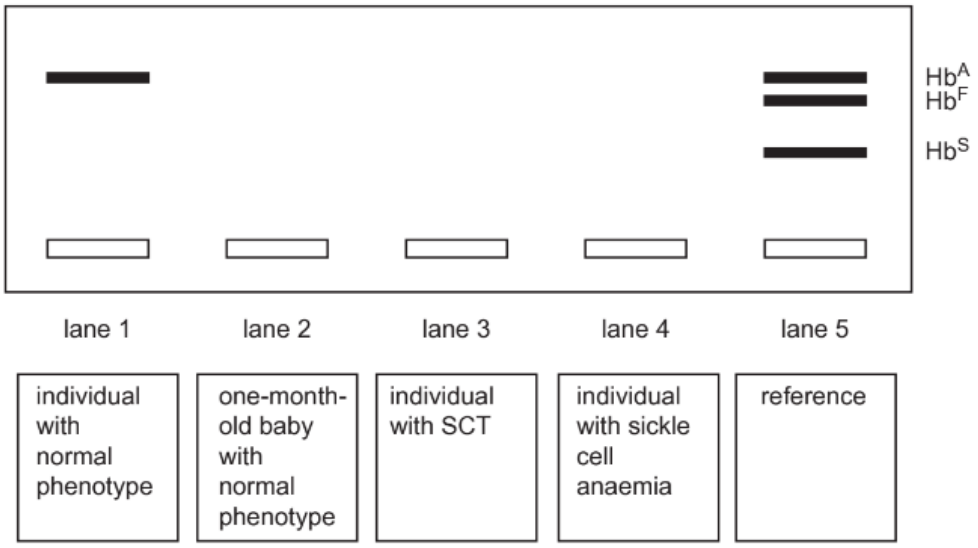
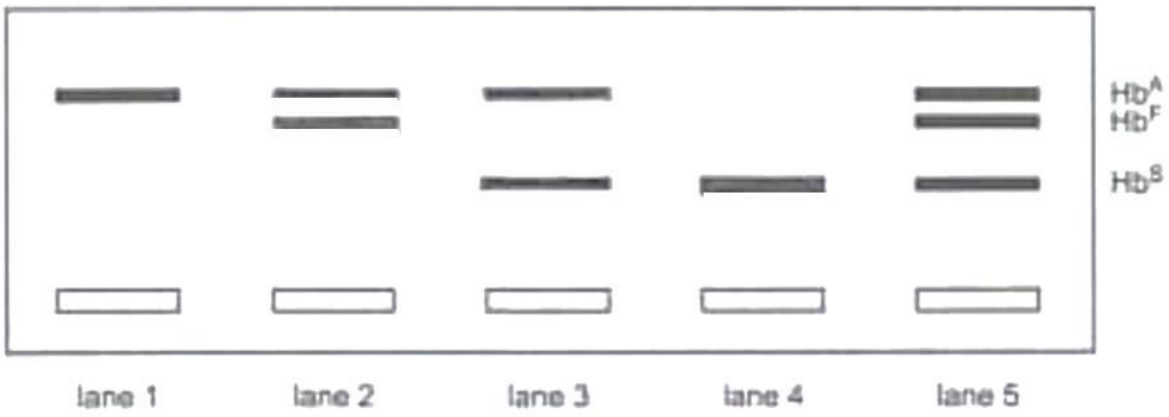


Fig. 3.2

Predict the results for the individuals analysed, by adding bands to lanes 2, 3 and 4 on Fig. 3.2. [2]



lanes 2, 3 and 4 correct position &thickness = 2 marks ;;

two correct = 1 mark

one or none correct = 0 marks

[Total: 12]

QUESTION 4

The enzyme glucose 6-phosphate dehydrogenase (G6PD) is active in all types of cells, is involved in the normal processing of carbohydrates.

Scientists investigated the activity of two isoforms of G6PD, J and K, at different concentrations of substrate. K is a form of the enzyme that results from a mutation that changes one amino acid in the polypeptide. The results are shown in Fig. 4.1.

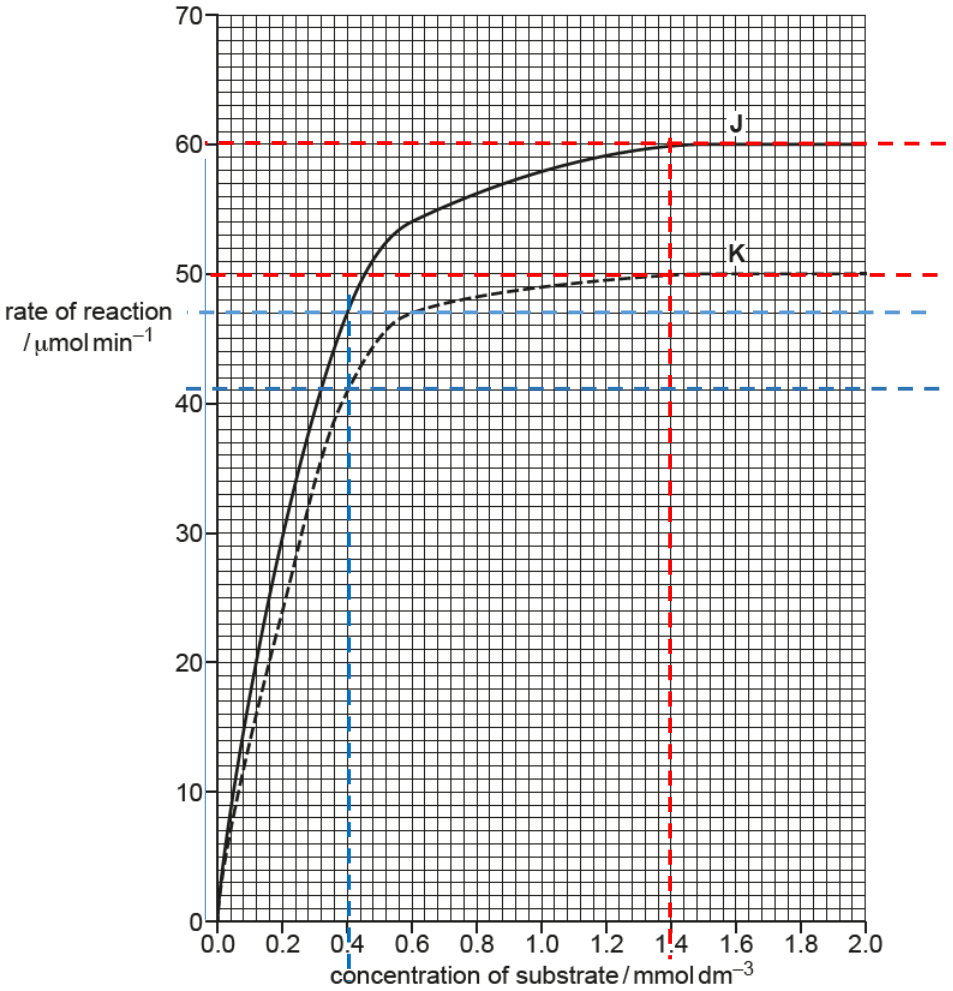


Fig. 4.1

(a) With reference to Fig. 4.1, account for the relationship when the concentration of substrate increases from 0.0 to 0.4 mmoldm^{-3} and rate of reaction for **J**. . [4]

1 [Relationship] As concentration of substrate increases from 0.0 to 0.4 mmol dm^{-3}, the rate of reaction increases linearly from 0 to 47 μmolmin^{-1};

2 [Explanation]Substrate concentration is limiting factor at low substrate concentration;
Active sites of enzyme molecules are not fully occupied by substrate;

3 Increasing substrate concentration, increase in frequency of effective collisions between enzyme and substrate molecules;

4 Increase in concentration of enzyme-substrate complexes formed per unit time;
Increase in concentration of products formed per unit time;

(b) Describe and suggest an explanation for the effect of the mutation on the activity of G6PD.[4]

1. [Describe] As concentration of substrate increases from 0.0 to 1.4 mmol dm^{-3}, the rate of reaction is higher from 0 to 60 $\mu molmin^{-1}$ for J and lower from 0 to 50 $\mu molmin^{-1}$ for K
   OR Rate of reaction is lower at all substrate concentrations for instance at 0.4 mmol dm^{-3} is 47 $\mu molmin^{-1}$ for J and 41 $\mu molmin^{-1}$ for K**;**

2. [Describe] As concentration of substrate increases from 1.4 to 2.0 mmol dm^{-3}, the rate of reaction is higher and remains constant at 60 $\mu molmin^{-1}$ for J and 50 $\mu molmin^{-1}$ for K

   OR Greater difference as substrate concentration increases from 1.4 to 2.0 mmol at 60 $\mu molmin^{-1}$ for J and 50 $\mu molmin^{-1}$ for K**;**

Award 1 mark if provided for general trend starting from 0.1

3. [Explanation] Missense Mutation brought about by **base substitution** as the **altered codon/nucleotides/triplet code encode for a different amino acid which has different chemical properties/R-group** as the original amino acid resulting in **protein with reduced functional activity.**
4. [Explanation]The replaced / changed amino acid is important in, **3D-shape/conformation, of active site/changed interaction between substrate and, active site** as it could be a part of **structural residues/contact (binding) residues/catalytic residues;**

[Include other variations to award mark for marker to see the difference]

Fig. 4.2 shows the dimeric arrangement of human G6PD enzyme consisting of the two subunits symmetrically located across a complex interface of β-sheets and each subunit binds to a Nicotinamide Adenine Dinucleotide Phosphate ($NADP^+$) molecule that confers structural stability.

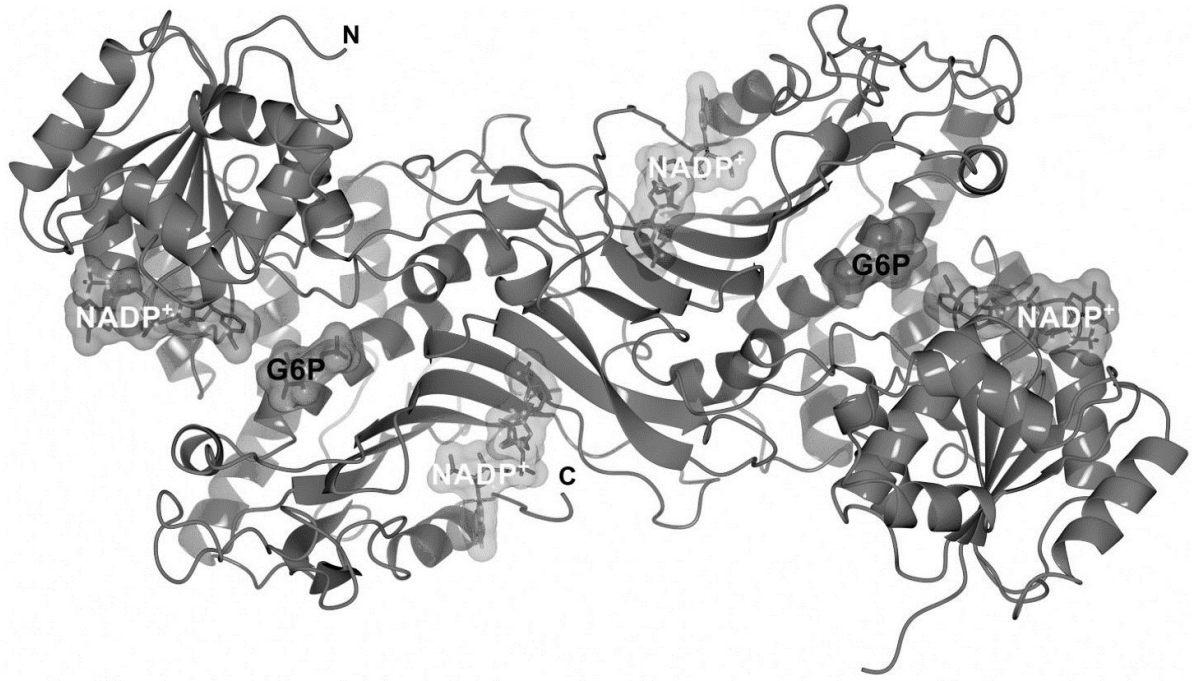


Fig. 4.2

(c) State the level of protein structure of G6PD and describe how the globular structure is held together. [2]

1. Quaternary Structure
2. Held together by hydrogen bonds, ionic bonds, disulfide bonds and hydrophobic interactions between R groups of amino acids from **different polypeptide chains** within the same protein

[Total: 10]

QUESTION 5

Fig. 5.1 shows the ends of a telomere elongated by a telomerase. Proteins associated with the telomerase and the RNA strand are shown.

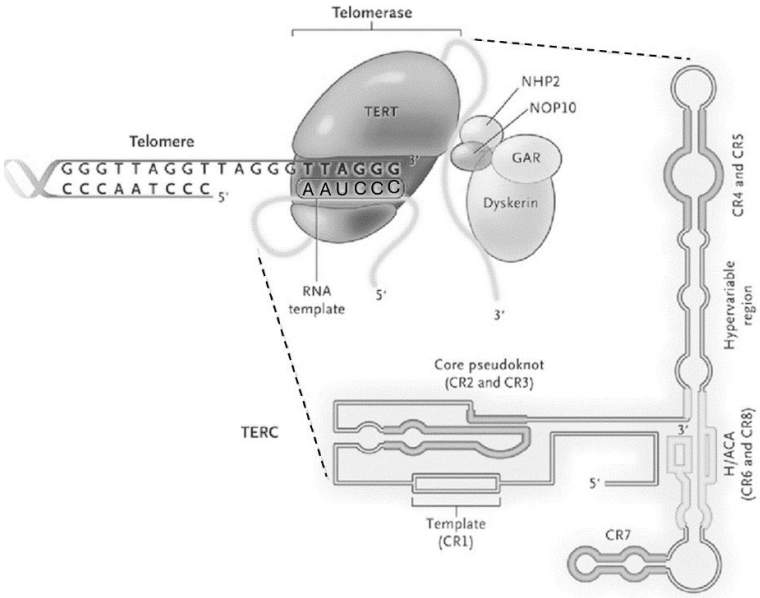


Fig. 5.1

(a) Explain why telomerase is known as a reverse transcriptase.

……[1]

1 Telomerase uses a **RNA template** to **add complementary DNA nucleotides** to 3' end of the parental strand;

(b) Using your knowledge and Fig. 5.1, suggest how the telomerase maintains telomere length.

……[4]

1 [DNA binding phase] Telomerase uses the RNA template 3' AAUCCC 5' to **complementary base pairing** to the 3' end of the DNA parental strand

2 [Elongation phase] addition of new **deoxyribonucleotides to extend the telomeric end** with ref. telomeric (DNA) sequence 5' TTAGGG 3' being produced

3 Telomerase catalyses the formation of phosphodiester bonds between deoxyribonucleotides in the elongation of telomeric DNA

4 **RNA primers** are added to **complementary base pair with the newly synthesized telomeric sequence** to synthesize complementary DNA strand (by DNA polymerase)

(c) **(i)** State two structural similarities between the RNA strand found in telomerase and tRNA.

……[2]

[Any 2]

1 Both RNA nucleotides are joined by **phosphodiester bonds**

2 Both RNA and tRNA are **single stranded molecules**.

3 Both have double-stranded regions that can form loops

4 Both are made up of **ribonucleotides such as adenine, Guanine, uracil and cytosine** **Reject if only uracil mentioned**

(ii) Describe how tRNA is adapted to its role in translation.

……[2]

[Any 2]

	Structure	Function
1	3' CCA end	Attachment of a specific amino acid.
2	Specific sequence on anticodon complementary to mRNA codon	For correct sequencing of amino acids on the polypeptide chain from the mRNA.
3	Folded into specific shape complementary to active site of amino-acyl tRNA synthetase OR folded into specific shape complementary to P/A site in ribosome	to fit into active site for amino-acid activation OR Carries specific amino acid to ribosome to form polypeptide chain

[Total : 9]

QUESTION 6

In a sample of rat bladder tumours, more than a thousand different mutations in the *p53* tumour suppressor gene were found. A mutation frequency map of the mutated *p53* tumour suppressor gene is shown in Fig. 6.1. The mutation frequency map comprises the following:

- the incidence of tumour-derived mutation at each amino acid residue is indicated by the height of the bars,
- the amino acid sequence is indicated in a single-letter nomenclature,
- the underlined residues are those most highly conserved in the protein in normal rats, and
- the rectangles and arrows represent α-helices and β-pleated sheets respectively.

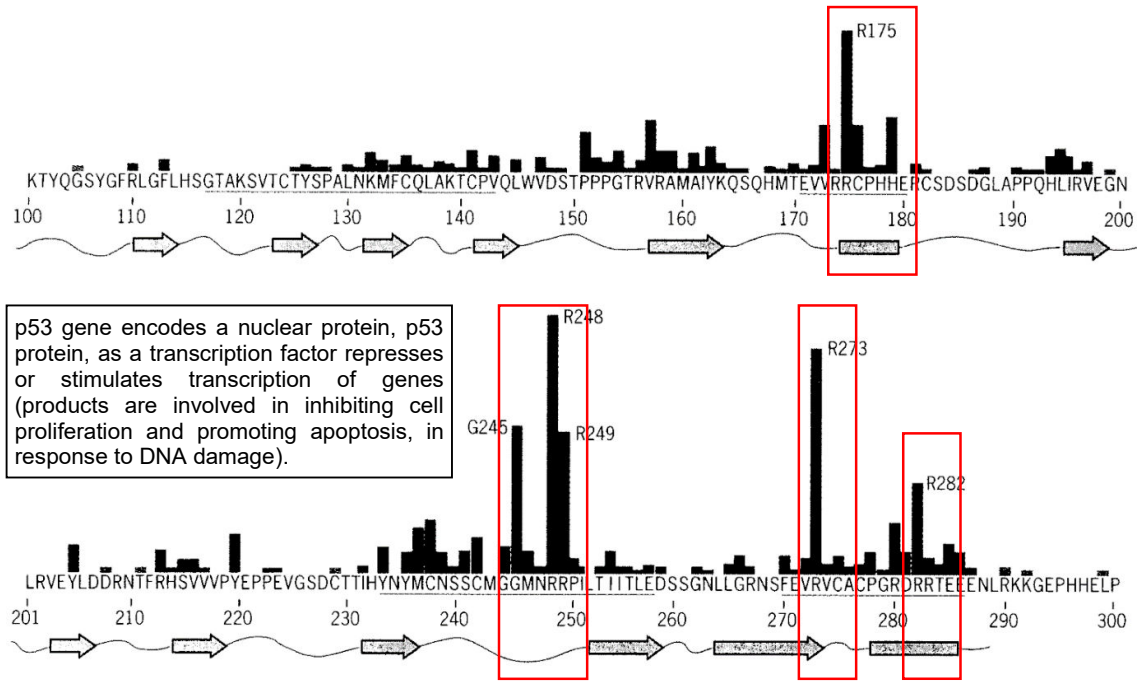


Fig. 6.1

(a) With reference to Fig. 6.1, deduce the relationship (state trend) between the locations of the mutations (identify the exact location) and their frequency of occurrence (refer to the height of bar – peaks) in the *p53* tumour suppressor gene.

……[2]

1 High incidence of mutations occurs at the conserved regions of the p53 tumour suppressor gene.

OR

which may be found in both α-helices and β-pleated sheets of the p53 tumour suppressor protein.

AND

2 at residues R175; at amino acid sequence EVVRRCPHHE/ at residues G245, R248, R249; at amino acid sequence GGMNRRPIL/ at residues R273 and R282; at amino acid sequence EVRVCACPGRDRR;

(b) explain how (elaborate and link) these mutations in the *p53* gene (loss-of-function) can contribute to the formation of rat bladder tumours.

…… [3]

1 Mutations are loss-of-function mutations therefore non-functional p53 transcription factor is produced.

2 unable to trigger expression of genes to results in **arrest at cell cycle checkpoints/ trigger apoptosis/ repair DNA;**

3 Resulting in uncontrolled cell division;

In the same sample of rat tumours, it was found that the concentration of epidermal growth factor was higher than other normal cells. Epidermal growth factor promotes cell growth and cell survival. Fig. 6.2 shows the cell signaling pathways of epidermal growth factor.

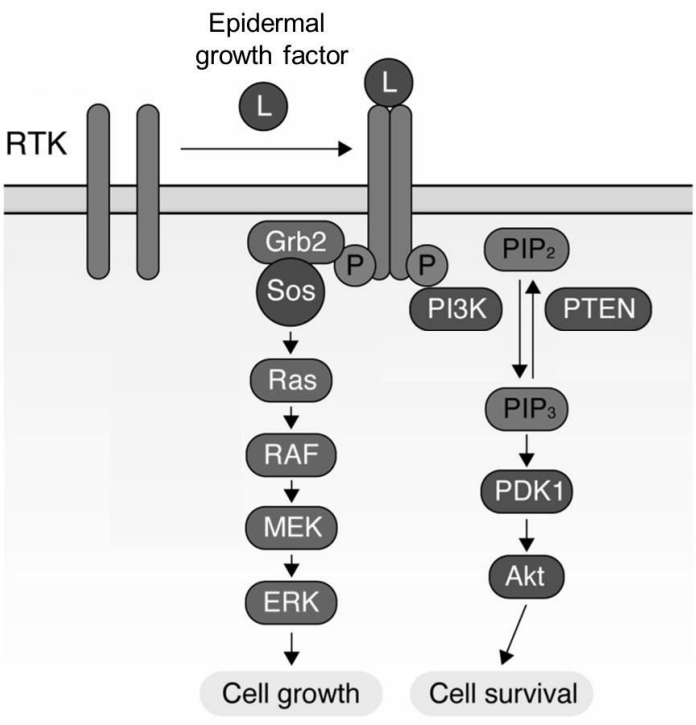


Fig. 6.2

(c) With reference to Fig. 6.2, describe how (present a step-by-step account) a higher concentration of epidermal growth factor (merge **increase** with account) contributes towards to formation of tumour.

……[5]

1 Higher concentration of epidermal growth factor leads to more RTK activated via autophosphorylation of tyrosine residues;
2 **More relay proteins Grb2 and SOS** are activated;
3 **More activation** of Ras, Raf, MEK and ERK (at least 2)
4 Leading to more cell growth

OR

1 Higher concentration of epidermal growth factor leads to more activation of RTK;
2 **More relay proteins PI3K are activated/More conversion of PIP2 to PIP3**;
3 **More PDK1 and Akt** activated
4 Leading to better/increased cell survival/ cells do not undergo apoptosis and leads to formation of tumour;

AND

5 Causes more rounds of cellular division and leads to formation of tumour;

[Total: 10]

QUESTION 7

(a) Describe the stages(must state and expand on specific stages) in meiosis that allows variation(context – link to the identified stages) to occur. [4]

1. Chiasmata are formed during Prophase I, which are points where **non-sister chromatids cross over each other and may break and re-join** where **crossing over** may occur at the chiasmata, i.e. the breakage and rejoining of non-sister chromatids of homologous chromosomes to **exchange equivalent parts** of the chromatid.
2. **Exchange of alleles** occurs between homologous chromosomes (human average 2 - 3 cross over per chromosome) results in chromosomes with **new combinations of alleles** (➔ genetic variation)
3. Independent assortment of **homologous chromosomes** at metaphase I followed by segregation of **homologous chromosomes** at anaphase I; **OR**
4. Independent assortment of **chromatids** at metaphase II followed by segregation of **chromatids** at anaphase II ;
5. Results in gametes with different combination of paternal and maternal chromosomes (➔ genetic variation)

Inheritance of wing shape and eye colour in the fruit fly, *Drosophila melanogaster*, is controlled by two genes.

Gene **N**/**n** controls wing shape. Allele **N** for wrinkled wings is dominant to allele **n** for normal wings
Gene **E**/**e** controls eye colour. Allele **E** for rosy eyes is dominant to allele **e** for red eyes

A biologist predicted that, if the genes are on **different** chromosomes, the ratio of the phenotypes of the F2 generation would be 9:3:3:1. (dihybrid cross- genes on two chromosomes)

The biologist carried out a breeding experiment.

- Homozygous dominant fruit flies with wrinkled wings and rosy eyes (NNEE) were crossed with homozygous recessive fruit flies with normal wings and red eyes (nnee).
- All the F1 fruit flies had wrinkled wings and rosy eyes (NnEe – dominant alleles – wrinkled wing and rosy eyes).

Observed and Predicted Frequency do not tally. There is partial linkage between the genes for wing shape and

The F1 fruit flies were crossed with each other.

Table 7.1 shows the results for the F2 generation and the biologist also calculated the predicted frequency using the 9:3:3:1 ratio.

Table 7.1

F2 phenotypes	Observed Frequency	*Predicted frequency*
wrinkled wings rosy eyes	**60** Non-recombinant phenotype	***45(9/16)***
wrinkled wings red eyes	**6** **Recombinant phenotypes**	***15(3/16)***
normal wings rosy eyes	**4**	***15(3/16)***
normal wings red eyes	**10** Non-recombinant phenotype	***5(1/16)***
Total	**80**	***80***

(b) Using the symbols provided, draw a genetic diagram to explain the cross between the F1 generation and the results of the F2 generation. [4]

Genetic Cross:

F_1 phenotypes: wrinkled wings, rosy eyed x wrinkled wings, rosy eyed

F_1 genotypes: $\frac{N\ E}{n\ e}$ x $\frac{N\ E}{n\ e}$

F_1 gametes: (N E) (n e) x (N E) (n e)

Non-recombinant gametes (majority)

Non-recombinant gametes (majority)

(N e) (n E)

Recombinant gametes (minority)

Recombinant gametes (minority)

Please remember to state which are Non-recombinant gametes and which are recombinant gametes

F_2 genotypes: (N E) (N e) (n E) (n e)

	(N E)	(N e)	(n E)	(n e)
(N E)	$\frac{N\ E}{N\ E}$ (Wrinkled, rosy)	$\frac{N\ e}{N\ E}$ (Wrinkled, rosy)	$\frac{n\ E}{N\ E}$ (Wrinkled, rosy)	$\frac{n\ e}{N\ E}$ (Wrinkled, rosy)
(N e)	$\frac{N\ E}{N\ e}$ (Wrinkled, rosy)	$\frac{N\ e}{N\ e}$ (Wrinkled, red)	$\frac{n\ E}{N\ e}$ (Wrinkled, rosy)	$\frac{n\ e}{N\ e}$ (wrinkled, red)
(n E)	$\frac{N\ E}{n\ E}$ (Wrinkled, rosy)	$\frac{N\ e}{n\ E}$ (Wrinkled, rosy)	$\frac{n\ E}{n\ E}$ (Normal, rosy)	$\frac{n\ e}{n\ E}$ (normal, rosy)
(n e)	$\frac{N\ E}{n\ e}$ (Wrinkled, rosy)	$\frac{N\ e}{n\ e}$ (Wrinkled, red)	$\frac{n\ E}{n\ e}$ (Normal, rosy)	$\frac{n\ e}{n\ e}$ (Normal, red)

There is no need for phenotypic ratio as it cannot be determined.

F_2 phenotypes:	Wrinkled wings, Rosy eyes	Normal wings, Red eyes	Wrinkled wings, Red eyes	Normal wings Rosy eyes
	Non-recombinant phenotypes		Recombinant phenotypes	
Observed numbers	45	15	15	5

*Indicate recombinant / non-recombinant phenotypes; Use a **bracket** to combine 2 phenotypes*

Note!

(c) Explain (provide reasons) for the difference in the observed and predicted frequency of the F2 generation (why the numbers will be different). [2]

1 *(Explain)* There is no independent assortment of genes ; as the **genes for wing shape and eye colour** are located on the same chromosome/partial linkage of genes for wing shape and eye colour;

2 Recombinants are present due to **occasional** crossing over that breaks the linkage between the 2 genes on the same chromosome ;

[Total: 10]

QUESTION 8

In 1946, Lederberg and Tatum performed an experiment to determine if genetic transfer occurs between bacteria cells. They used two strains of bacteria lacking in essential genes. Strain A does not encode for biotin (bio^-) and methionine (met^-) while strain B does not encode for phenylalanine (phe^-) and threonine (thr^-). Bacteria lacking in essential genes cannot grow on minimal media.

These two strains were also mixed in the same test tube and then plated on minimal media.

Fig. 8.1 shows the experiment and the results obtained.

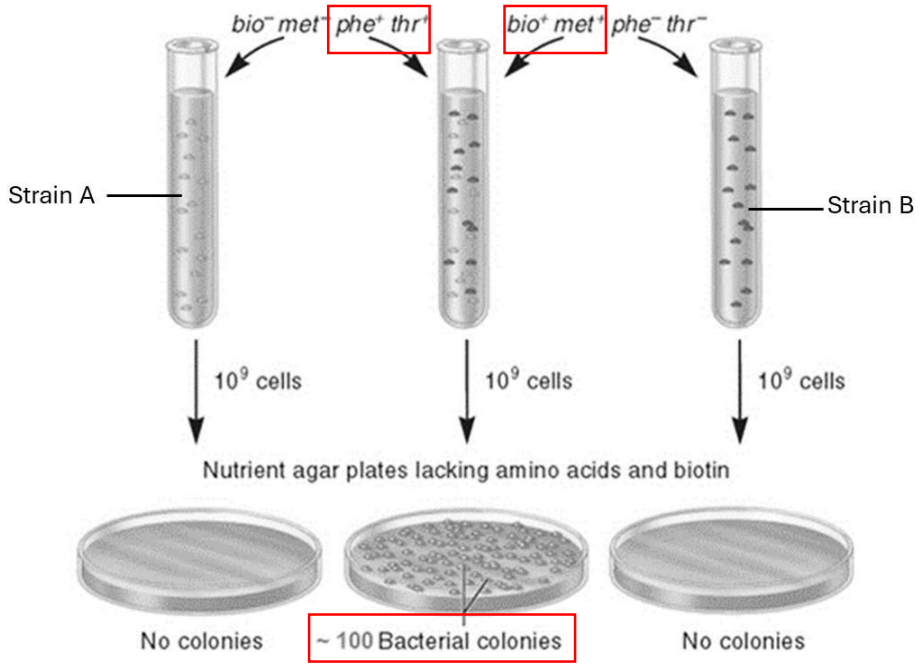


Fig. 8.1

(a) **(i)** With reference to the results and the information provided, infer (account for the results by linking to the preamble) the conclusion of this experiment.

.....[2]

1 (ref. to results) Bacteria from test tube mixed with strain A and strain B **contains all essential genes bio^+ $met^+$$phe^+$ thr^+** as the **bacteria colonies grew in minimal media**;

2 Therefore it can be concluded that **genetic transfer has occurred between the two strains of bacteria**;

Reject : conjugation and transformation

In 1950, Bernard Davis performed a similar experiment. He put two strains of bacteria, each lacking in essential genes, into a U-tube and separated them with a filter (Fig. 8.2). The filter has pores small enough to allow the passage of genetic material and viruses but too small to permit the passage of bacterial cells. The application of alternating pressure and suction promoted the movement of liquid through the filter.

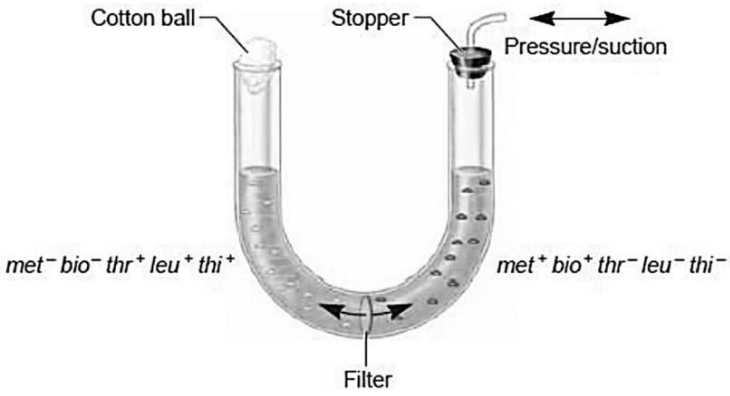


Fig. 8.2

Bacteria from either side of the tube were placed on minimal media. No bacteria colonies grew on the plates.

(ii) Based on both Lederberg and Tatum's and Davis's experiments, explain why no bacteria colonies grew from either side of the tube.

……[2]

1 Gene transfer can only occur by conjugation;
2 Conjugation cannot occur as bacteria cells **cannot come into contact** with each other;

In bacteria, the concentration of the amino acid methionine is regulated by the *met* operon. The *met* operon is a repressible operon that functions in the same way as the *trp* operon .

(iii) **(i)** Using your understanding of the *trp* operon, discuss how synthesis of methionine can be repressed.

……[3]

1 **At high methionine concentration**, methionine act as a **co-repressor** and binds to the repressor;
2 This changes the conformation of the repressor to make it active, it binds to the operator;
3 Blocks the binding of the RNA polymerase/ prevents the RNA polymerase from transcribing the structural genes.

(ii) In a population of bacteria infected by lambda phage (lysogenic/temperate phage), methionine was synthesised regardless of the concentration of methionine (always switched ON). Suggest how (provide a reasonable explanation based on mark allocation) this may occur.

……[3]

1 Phage DNA inserted into the gene coding for repressor protein;
2 **No repressor/non-functional repressor produced unable to** bind to operator
3 RNA polymerase can **bind to promoter at all times**

[Total: 10]

Question 9

Twenty million years ago, an ocean covered the area where the country of Panama is now located. There was a gap between the continents of North America and South America through which the waters of the Atlantic and Pacific Oceans flowed freely.

The porkfish, *Anisotremus sp*, lived in this area between North America and South America.

Fig. 9.1 shows a porkfish.

Fig. 9.1

Inhabiting shallow inshore waters over reefs and rocky bottoms, the porkfish is found at depths of 6-65 feet (2-20 m).

About 3 million years ago, volcanic activity and sedimentation formed a narrow strip of land, Panama, joining North America and South America.

Twenty million years ago, porkfish in the Atlantic and Pacific Oceans were able to breed successfully and produce fertile offspring.

Fig. 9.2 shows the area 20 million years ago and now.

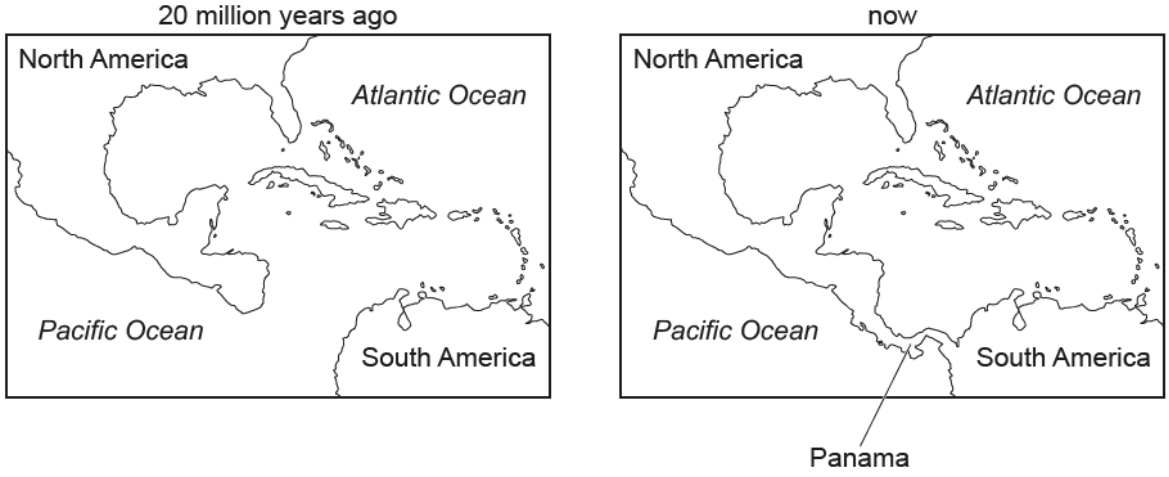


Fig. 9.2

(a) Using your knowledge on the species concept, explain why (link it to the preamble to elaborate) the Atlantic porkfish and Pacific porkfish were considered one species twenty million years ago.

……[2]

1 Atlantic and Pacific Oceans' porkfish were able to breed successfully and produce fertile offspring and there was **no geographical barrier/gene flow**

2 Aligned to biological species concept as closely related organisms which are capable of interbreeding in nature to produce viable, fertile offspring and are reproductively isolated from other species

(b) Explain why (link to the preamble and figure to elaborate) Atlantic porkfish and Pacific porkfish are now not able to breed successfully to produce fertile offspring.

……[3]

1 Allopatric speciation

2 It occurs as a result of geographic isolation occurred **due to volcanic activity and sedimentation formed a narrow strip of land, Panama/**disruption of gene flow in a population of Porkfish

3 each sub-population subjected to different selection pressures with different change in allele frequency within gene pool of each sub-population

AVP

4 Other evolutionary agents such as mutations and genetic drift occurs, leading to accumulation of genetic differences over time

Fig. 9.3 shows forelimb skeletal pattern of four vertebrates,

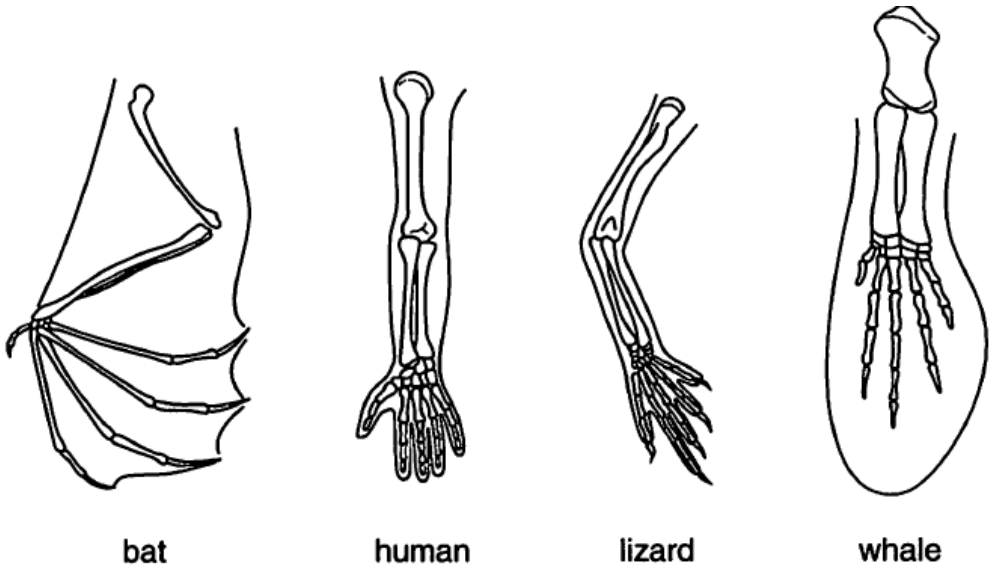


Fig. 9.3

(c) Explain how the relationship between the structures in Fig. 9.3 provide evidence to support the theory of evolution.

……[3]

1 Organisms with anatomical homology have morphological structures (e.g. bones, organs, body plan) that they inherited from a common ancestor.

2 These **Pentadactyl (1-2-5) limb structure in forelimbs of bat, human, lizard and whale** are homologous structures that may have **different functions** but are **highly similar in structure with those of the common ancestor;**

3 It shows descent with modification as the ancestral structure was altered by natural selection in the different organisms to suit their specialised functions/environments, resulting in variations of the ancestral structure showing divergent evolution has occurred.

HoxA/D cluster genes are active during limb development, and over the last two decades, have been the focus of many studies aimed at gaining insights into the evolutionary origin of limb-specific morphologies.

(d) State two advantages of using molecular methods in classifying organisms.

……[2]

[Any two]

1 Molecular data such as nucleotide and amino acid sequences are quantifiable, in abundance and open to statistical analysis.

2 Molecular data can be easily described in an unambiguous manner. Protein and nucleic acid sequence data are precise and accurate. This facilitates the objective assessment of evolutionary relationships.

3 Molecular data is based strictly on heritable material.

4 All organisms can be compared with the use of some molecular data as all living organisms have nucleic acids and proteins, so molecular data can be collected from any organism.

5 DNA information provides abundance of data for analysis and it allows easy homology assessment.

[Total: 10]

Question 10

Fig. 10.1 is a simplified diagram representing a section through the human immunodeficiency virus (HIV) particle that causes HIV/AIDS. The diagram shows the virus particle about to attach to the cell surface membrane of a T-helper cell at a receptor protein called CD4. A second protein (coreceptor) called CCR5 is also necessary for the virus particle to enter and then infect the T-helper cell.

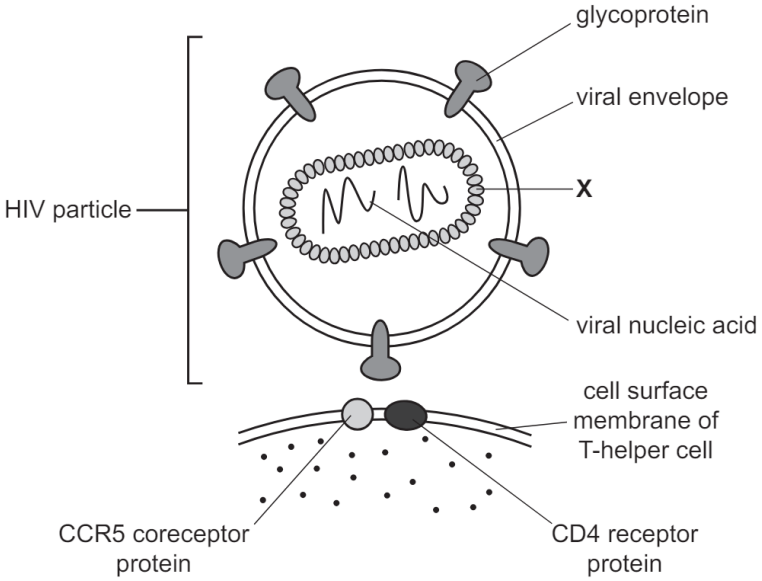


Fig. 10.1

(a) Identify structure X in Fig. 10.1.

……[1]

capsid ;
Accept : capsomere or protein coat
Reject : protein / glycoprotein / capsid

(b) Explain how the ability of the immune system to resist the damaging effects of a pathogen is affected by destruction of T-helper cells.

……[3]

[Any three]

1 fewer cytokines released ;
2 fewer plasma cells therefore fewer antibodies produced ;
3 fewer macrophages stimulated / less antigen presentation by macrophages ;
4 fewer CD8 T cells to kill infected cells;
5 fewer memory cells produced by the primary response;

(c) Studies have shown that some individuals did not become infected with HIV even though they were repeatedly exposed to the virus. Later discoveries indicated that these individuals had a mutation in the gene for the CCR5 coreceptor protein. Suggest how mutation of the gene for the CCR5 coreceptor protein provided protection against HIV infection.

……[1]

- virus cannot enter the T-helper cell / CCR5 unable to trigger fusion of viral particle

[Total: 5]

Question 11

Fig. 11 shows the number of bleaching events around the world.

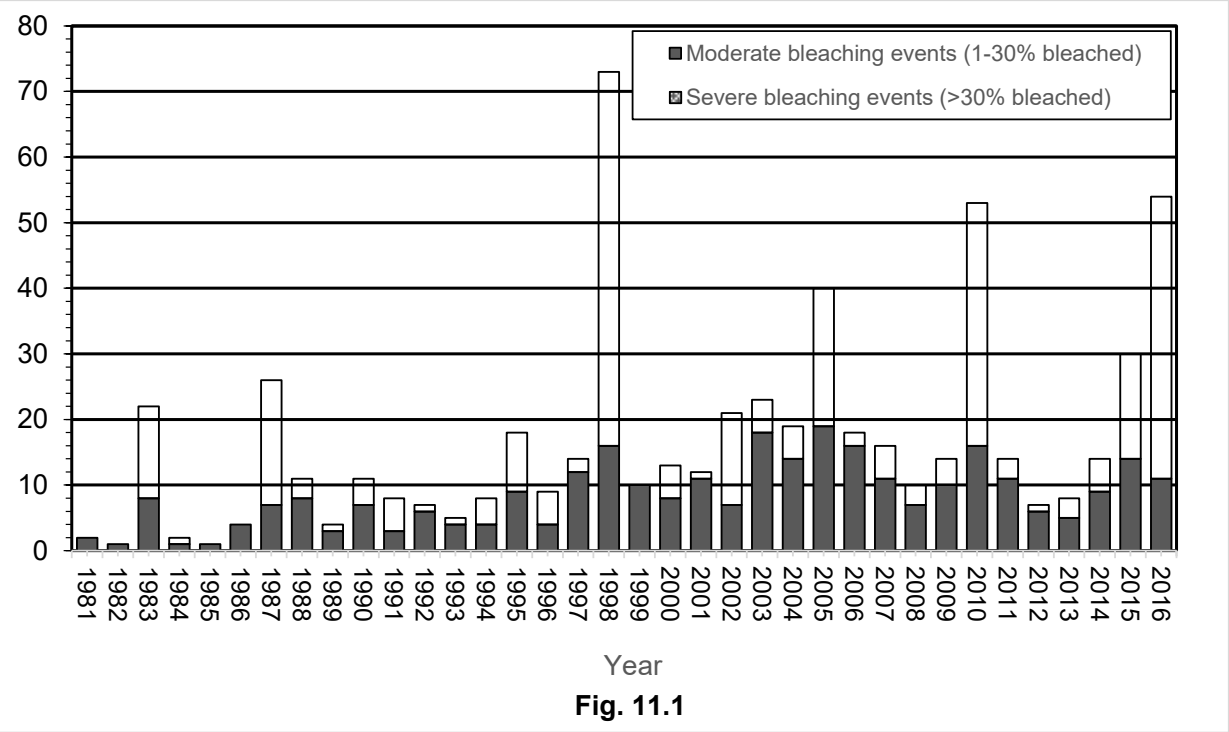


Fig. 11.1

(a) With reference to Fig. 11.1, state the differences in the number of bleaching events in 1981 and 2016.

……[2]

1 2 moderate events in 1981 which is lower compared to 11/12 events in 2016.
2 0/No severe events in 1981 which is lower compared to 42/43/44 events in 2016.

(b) Describe how climate change causes severe bleaching events. [2]

1 Heat stress/increase in temperature disrupts the photosynthesis process in the zooxanthellae and it produces an **excess of products that become toxic damages** the metabolism of the coral polyp, **which expels the zooxanthellae**, leaving the coral skeleton a stark, 'bleached' white.
2 Ocean acidification, **hard coral s cannot absorb the calcium carbonate** they need to maintain their skeletons/the stony skeletons that support **corals will dissolve**.

[Total: 4]