NAME : _____ CLASS : _____

JURONG PIONEER JUNIOR COLLEGE
JC2 Preliminary Examination 2022

BIOLOGY
Higher 2

9744/01
23 September 2022

Paper 1 Multiple Choice

1 hour

Additional Materials: Multiple Choice Answer Sheet

READ THESE INSTRUCTIONS FIRST

Write in soft pencil.
Do not use staples, paper clips, glue or correction fluid.
Write your name, class and index number on the Answer Sheet in the spaces provided unless this has been done for you.

There are **thirty** questions on this paper. Answer **all** questions. For each question there are four possible answers **A**, **B**, **C** and **D**.
Choose the **one** you consider correct and record your choice in **soft pencil** on the separate Answer Sheet.

Read the instructions on the Answer Sheet very carefully.

Each correct answer will score one mark. A mark will not be deducted for a wrong answer.
Any rough working should be done in this booklet.
The use of an approved scientific calculator is expected, where appropriate.

This document consists of [redacted] printed pages.

For Trs copy

Qn	Ans	Qn	Ans	Qn	Ans
1	B	11	A	21	C
2	A	12	B	22	C
3	B	13	C	23	A
4	A	14	B	24	A
5	A	15	C	25	B
6	B	16	D	26	A
7	B	17	B	27	A
8	A	18	B	28	D
9	B	19	C	29	A
10	C	20	C	30	C

NAME : _____ CLASS : _____

JURONG PIONEER JUNIOR COLLEGE
JC2 Preliminary Examination 2022

BIOLOGY
Higher 2

9744/02
13 September 2022

Paper 2 Structured Questions

2 hours

Candidates answer on the Question Paper.
No Additional Materials are required.

READ THESE INSTRUCTIONS FIRST

Write your class and name in the spaces at the top of this page.
Write in dark blue or black pen.
You may use an HB pencil for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.

Answer **all** questions in the spaces provided on the Question Paper.

The use of an approved scientific calculator is expected, where appropriate.
You may lose marks if you do not show your working or if you do not use appropriate units.

At the end of the examination, fasten all your work securely together.
The number of marks is given in brackets [ ] at the end of each question or part question.

For Examiner's Use	
1	
2	
3	
4	
5	
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7	
8	
9	
10	
11	
Total	

This document consists of **32** printed pages.

Answer **all** questions.

1 Fig. 1.1 is an electron micrograph of a cell in the pancreas with structures labelled **X** and **Y**.

Fig. 1.1

(a) Identify structures **X** and **Y**. In each case, outline one visible feature that allows the structure to perform its functions.

structure **X** .....

visible feature related to its functions .....

structure **Y** .....

visible feature related to its functions .....

.....[4]

1. **Structure X: mitochondrion ;**
2. **Highly folded inner membrane / cristae for embedding electron carriers / ATP synthase for ATP synthesis ;**
3. **Structure Y: Golgi apparatus/body ;**
4. **Stack of flattened, membrane-bound sacs / cisternae for further modification / packaging of proteins ; OR**
5. **Swellings at end of sacs for vesicle formation /vesicles at ends of sacs ;**

MP 4 or 5 max 1

Protein production involves a complex sequence of events and number of cell structures. Cells in the pancreas secrete enzymes, such as amylase, into a duct.

(b) The first column in Table 1.1 shows some of the events that occur in the production of amylase in cells in the pancreas and its eventual release from the cell.

Table 1.1

event	sequence of events (numbers)	cell location (letters)
exocytosis		**F**
protein modification		
secretory vesicle formation		
transcription		
translation		

(i) In Table 1.1, write the sequence in which the events occur, using 1 as the first process in the sequence. [1]

1. **correct order of processes (5, 3, 4, 1, 2) ;**

(ii) From the list **A** to **F**, choose **one** cell location for each event and write the letter in Table 1.1. Each letter may be used once, more than once, or not at all. The first example, **F**, has been completed for you.

A Golgi apparatus

B lysosome

C nucleus

D rough endoplasmic reticulum

E smooth endoplasmic reticulum

F cell surface membrane [1]

1. **A and/or D, A, C, D ;**

event	sequence of events	cell location (letters)
exocytosis	**5**	F
protein modification	**3**	**A and/or D**
secretory vesicle formation	**4**	**A**
transcription	**1**	**C**
translation	**2**	**D**

(c) Explain how amylase that are secreted by cells in the pancreas are packaged into vesicles.

..... [4]

Answer can be given with reference to amylase/protein

1. **Transport vesicle (containing proteins) budded off from cisternae/membrane of rER and moves proteins to the cisternae at the cis face of GA ;**
2. **(Membrane of) transport vesicles will fuse with (the membrane of) the cisternae at the cis face of the Golgi apparatus/body ;**
3. **Proteins are further modified, sorted and packaged into secretory vesicles ;**
4. **Secretory vesicles containing the modified/mature proteins bud off from the cisternae (at the trans face) of GA ;**
5. **Vesicles are directed to the cell surface membrane via microtubules ;**
6. **Energy / ATP is required (for movement of vesicles / fusion with membrane) ;**
7. **Amylase/protein is released via exocytosis ;**

Mention "bud off" at least once in MP1 or MP4

[Total: 10]

2 Fig. 2.1 shows a section of the cell membrane of a red blood cell.

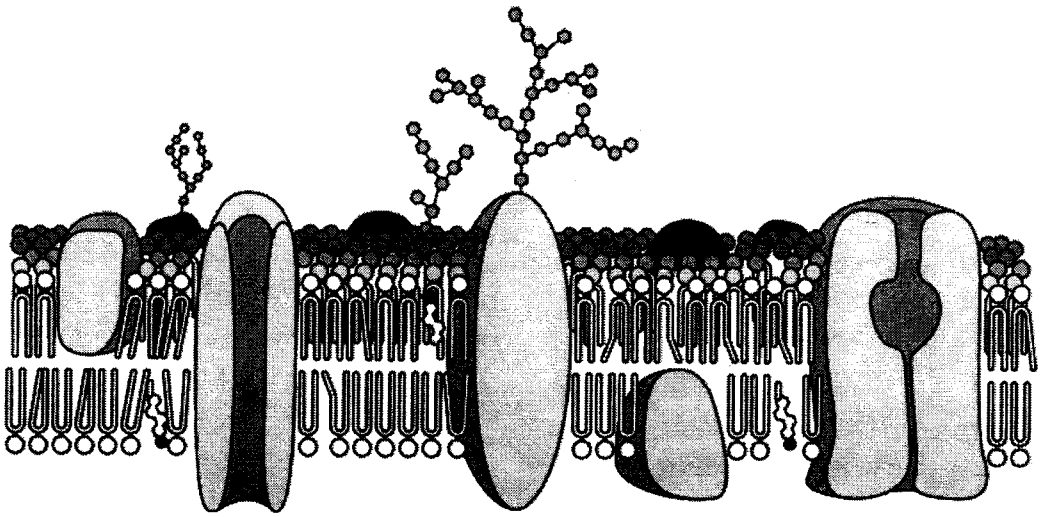

Fig. 2.1

(a) The arrangement of the various constituent biomolecules supports the fluid mosaic model of the cell membrane.

Explain why the cell membrane is referred to as fluid mosaic.

.....[3]

Fluid

1. **"Fluid" means that the phospholipids and proteins are free to move within the membrane ;**
2. **Phospholipids are held by (weak) hydrophobic interactions and move about rapidly by diffusion in their own layers ;**

Mosaic

3. **Proteins are embedded in the phospholipid bilayer in a random/scattered manner ;**

Cyanide is a poison that inhibits cytochrome c oxidase involved in aerobic respiration.

Fig. 2.2 shows how cyanide concentration affects the uptake of chloride ions by red blood cells. The rates of chloride ion uptake are given as percentages of those obtained in a control experiment with no cyanide.

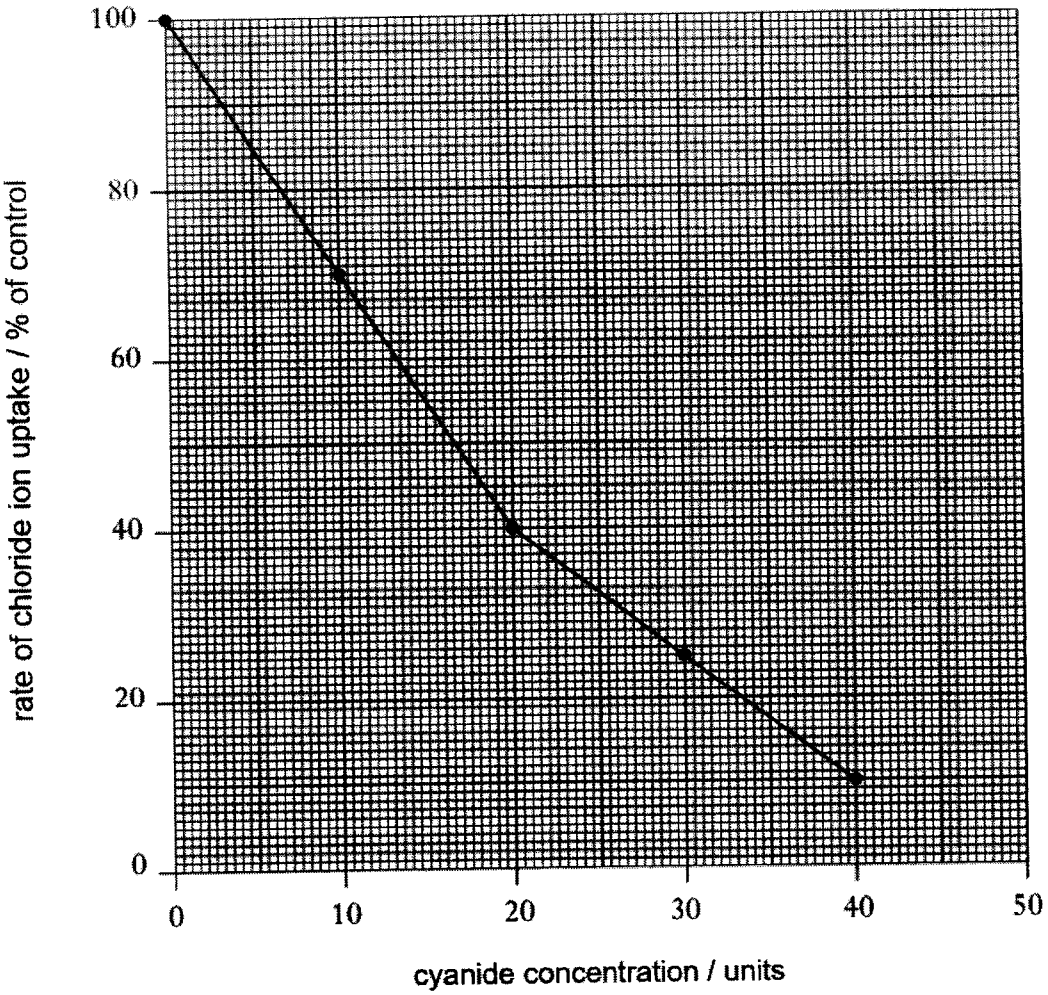

Fig. 2.2

(b) It is known that the uptake of chloride ions requires the presence of transmembrane proteins.

Explain why chloride ions cannot freely pass through the phospholipid bilayer of membranes.

.....[2]

1. **Non-polar/hydrophobic fatty acids make up the hydrophobic core of the cell membrane/phospholipid bilayer of membranes, thus the membrane is impermeable to ions ;**
2. **Cl^- are charged and cannot move across the membrane because they are repelled by the hydrophobic core of the phospholipid bilayer of membranes ;**

(c) With reference to Fig. 2.2,

(i) describe how cyanide concentration affects the rate of chloride ion uptake

..... [2]

1. **As cyanide concentration increases from 0 units to 20 units, rate of chloride ion uptake <u>decreases sharply</u> from 100% of control to 40% of control ;**
2. **As cyanide concentration increases from 20 units to 40 units, rate of chloride ion uptake <u>decreases gradually</u> from 40% of control to 10% of control ;**

(i) identify how chloride ions are moved across the membrane of the red blood cells

..... [1]

1. **active transport ;**

(ii) account for your answer in **(c)(ii)**.

..... [2]

1. **When cyanide concentration increases, <u>rate of aerobic respiration decrease</u> leading to <u>decrease in (amount of) ATP synthesised</u> ;**
2. **Decrease in ATP synthesis is correlated to decrease in rate of chloride ion uptake, indicating that <u>ATP is required for the transport of Cl^-</u> (as active transport involves ATP expenditure) ;**

[Total: 10]

3 The DNA double helix can be successfully compacted into a nucleus with a diameter that is only a millionth of the length of DNA.

(a) Explain how DNA can be successfully compacted into a nucleus.

..... [4]

1. **Negatively charged DNA molecule winds around a positively charged histone octamer consisting of 2 molecules of H2A, H2B, H3 and H4 each to form a nucleosome ;**
2. **Individual nucleosomes are connected by strands of linker DNA and H1 histones to give (10nm) 'beads-on-a-string' / nucleohistone complex ;**
3. **With the aid of H1 histones, the 'beads-on-a-string' / nucleohistone complex coils (R: fold) to form a (30nm) chromatin fibre ;**
4. **The 30nm chromatin fibre folds (R: coil) to form looped domains that are attached to a base of scaffolding proteins / non-histones, forming the (300nm) chromatin fibre ;**
5. **that is further coiled and compacted to form the (highly-condensed) chromosome ;**

MP 1-5: max 4

Semi-conservative DNA replication occurs in the nucleus. This begins at the origins of replication, where the enzyme helicase causes the DNA molecule to unwind and unzip, causing the two parental strands to separate.

(b) Outline the role of **three other** enzymes in DNA replication.

..... [3]

1. **Primase catalyses the formation of a short RNA primer ;**

2. **DNA polymerase then binds to the RNA primer and adds free DNA nucleotides to the free 3' –OH end of the RNA primer / synthesises the new DNA strands in the 5' to 3' direction ;**
3. **DNA polymerase catalyses the formation of phosphodiester bonds between adjacent DNA nucleotides ;**
4. **DNA polymerase synthesises the leading strand continuously and the lagging strand discontinuously resulting in Okazaki fragments ;**

5. **Another DNA polymerase replaces RNA nucleotides of the RNA primers with DNA nucleotides ;**
6. **DNA ligase seals the gaps between DNA fragments by catalysing the formation of phosphodiester bonds between adjacent DNA nucleotides to form a continuous strand ;**

MP 2-4: max 1
Mention catalyse at least once for full credit

Besides DNA replication, transcription also occurs in the nucleus.

(c) Complete Table 3.1 using a tick (✓) to indicate which features apply to each of the processes. Use a cross (✗) for features that do **not** apply. The first row has been completed for you.

Table 3.1

feature	DNA replication	transcription
a single-stranded molecule is produced	✗	✓
hydrogen bonds are broken		
both strands of DNA act as templates		
covalent bonds are formed		

[3]

feature	DNA replication	transcription
a single-stranded molecule is produced	✗	✓
hydrogen bonds are broken	✓	✓
both strands of DNA act as templates	✓	✗
covalent bonds are formed	✓	✓

1 mark for each correct row ;

[Total: 10]

4 Fig. 4.1 shows some of the main structural features of an influenza virus. PA, PB1 and PB2 are RNA polymerases.

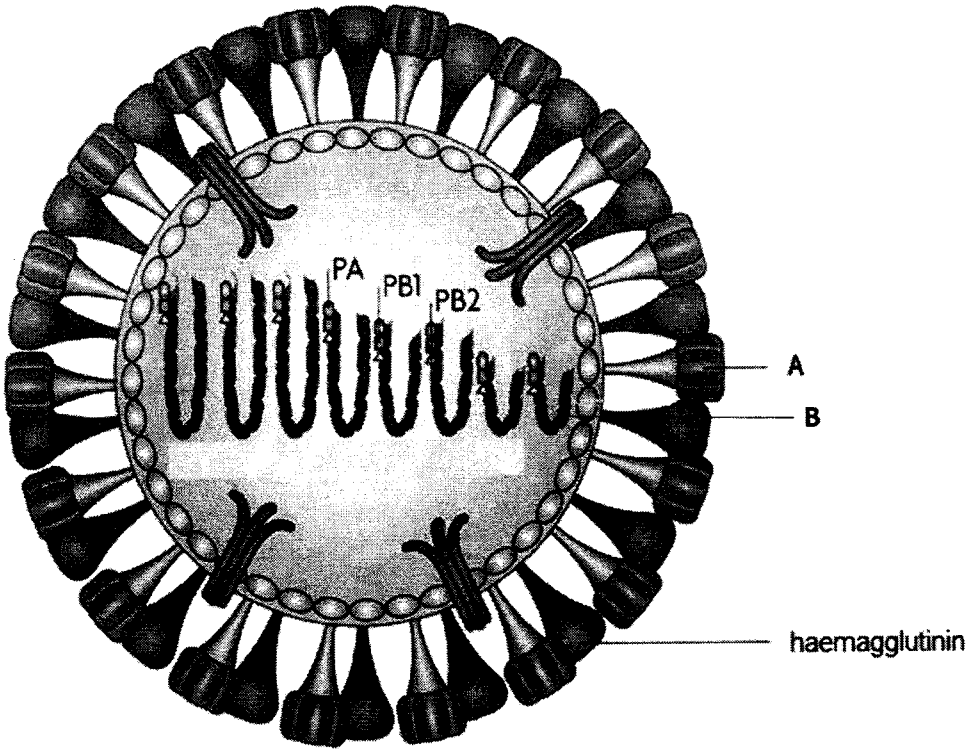

Fig. 4.1

(a) Identify the labelled structures and state their functions.

structure **A** .....

function .....

.....

structure **B** .....

function .....

.....

[4]

1. **A – neuraminidase ;**
2. **It (is an enzyme that) catalyses the cleavage of sialic acid residues from haemagglutinin ;**
   OR
3. **facilitating the exit and release of newly replicated influenza viruses from the (infected) host cell by budding ;**

4. **B – (single stranded) RNA (genome) ;** *I: double stranded*

5. **Viral RNA serves as the template for the synthesis of complementary RNA (cRNA), (using the viral RNA-dependent RNA polymerase) to express viral gene products (RNA and proteins) ;**

(b) Explain why the influenza virus requires its own RNA polymerases PA, PB1 and PB2.

.....[1]

1. **These RNA-dependent RNA polymerases are not present in the host cell A: host cell's RNA polymerases are DNA-dependent RNA polymerases ;**

(c) Discuss how viruses challenge the cell theory.

..... [2]

1. **Cells are basic units in living things, whether unicellular or multicellular but viruses are acellular (no cytoplasm or organelle) ;**
2. **Cells contain hereditary information in DNA which is passed from cell to cell during cell division but viruses contain only one type of nucleic acids/either DNA or RNA ;**
3. **All cells arise from pre-existing cells by division but viruses must replicate using the host cell's metabolic machinery/enzymes and ribosomes ;**

(d) Oseltamivir is an antiviral inhibitor used for the treatment of infection with influenza viruses.

Fig. 4.2 shows the number of copies of influenza genome per cm^3 plasma in two groups of infected patients – one group treated with oseltamivir and another control group without oseltamivir.

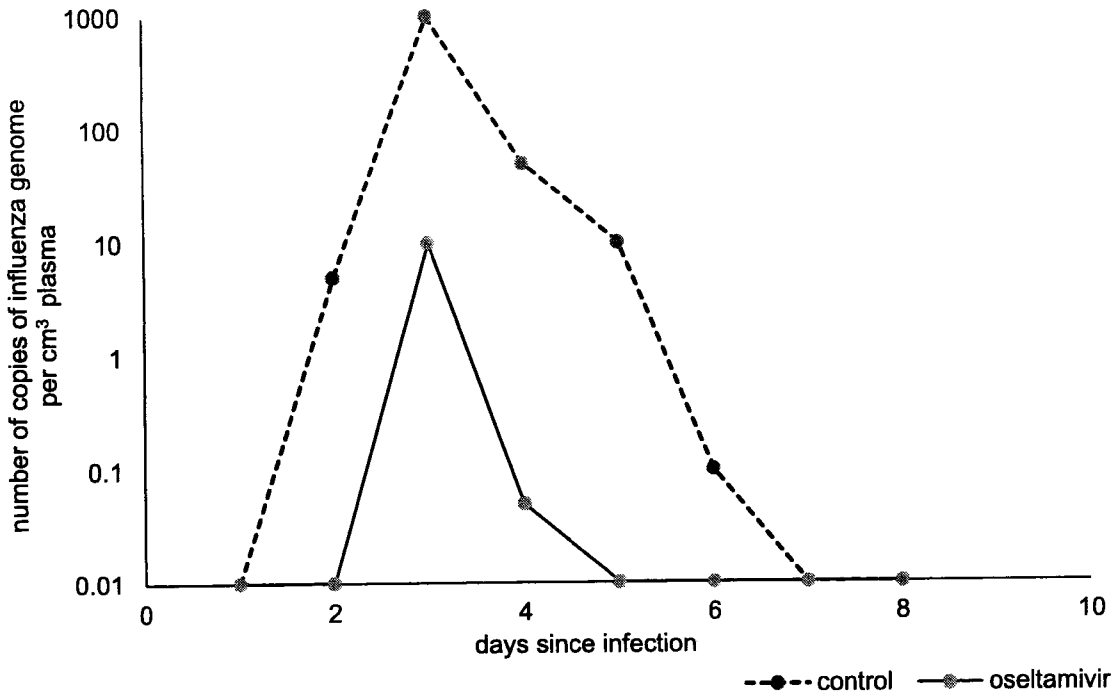

Fig. 4.2

Describe the effect of oseltamivir on the number of copies of influenza genome in patients, as shown in Fig. 4.2.

..... [3]

1. **<u>Maximum</u> number of copies of influenza genome per cm^3 plasma <u>reduced from 1000 to 10</u>, <u>3 days</u> since infection ;**
2. **Number of copies of influenza genome per cm^3 plasma lowered to <u>0.01</u> by <u>day 5</u> as compared to <u>day 7</u> of control/ not treated with oseltamivir ;**
3. **Influenza replicates for 3 days for those treated with oseltamivir vs. 6 days of those in control ;**

[Total: 10]

5 (a) Describe **two** ways in which the *lac* operon is **similar** to the *trp* operon.

..... [2]

1. **Both operons contain a <u>cluster of structural genes</u> that <u>make up a single transcription unit</u> ;**
   OR
2. **Both operons contain a <u>cluster of structural genes</u> that are <u>transcribed as a single / polycistronic mRNA</u> ;**
3. **(Expression of) Structural genes is under the control of the <u>same promoter and operator</u> ;**
4. **The structural genes code for enzymes / functionally related proteins involved in the same / a single metabolic pathway ;**
5. **When active repressor binds to the operator, it inhibits the transcription of the structural genes / operon is switched off ;**

MP1 and MP2: max 1

(b) Describe **four** ways in which the *lac* operon is **different** from the *trp* operon.

..... [4]

contrasting feature	*lac* operon	*trp* operon
1. type of operon ;	inducible	repressible
2. default state of operon expression ;	off (in the absence of inducer)	on (in the absence of co-repressor)
3. effector molecule ;	<u>allolactose</u> acts as an <u>inducer</u>	<u>tryptophan</u> acts as a <u>co-repressor</u>
4. effect of effector molecule on operon ;	(in the presence of inducer, allolactose) operon / transcription of structural genes is turned <u>ON</u>	(in the presence of co-repressor, tryptophan) operon / transcription of structural genes is turned <u>OFF</u>
5. default conformation of repressor ;	repressor synthesised in the active conformation	repressor synthesised in the inactive conformation
6. metabolic pathway involved ;	(protein products of operon involved in) catabolic pathway / breakdown of lactose	(protein products of operon involved in) anabolic pathway / synthesis of tryptophan

(c) Suggest the advantages to bacteria of arranging some genes in operons.

..... [2]

1. **Operons allow for the <u>simultaneous regulation of related genes with related functions</u> / which are involved in the same metabolic activity ;**
2. **Genes coding for proteins/enzymes of a single biochemical pathway / of related functions / same metabolic activity (such as the catabolism of carbohydrates) are <u>grouped together</u> into an operon for <u>easier control</u> ;**
3. **Operons enable the simultaneous regulation of related genes to <u>adapt and respond to environmental changes</u> ;**
4. **The genes on the operons are <u>only expressed when required</u>, allowing the bacteria to produce the proteins/enzymes that are required for <u>increasing efficiency / preventing wastage of energy and resources</u>.**
5. **Bacteria are able to <u>utilise a variety of carbohydrates</u> as respiratory substrates (for their energy requirement) ;**
6. **This <u>confers selective advantage</u> to the bacteria ;**

MP6 will only be awarded provided there is some prior elaboration and logical link provided (i.e. only if reference to any of the other MPs was made)

[Total: 8]

6 The polymerase chain reaction (PCR) is commonly used in medical and biological research to produce large quantities of DNA from a very small original sample.

(a) The main steps of one PCR method are shown in Fig. 6.1.

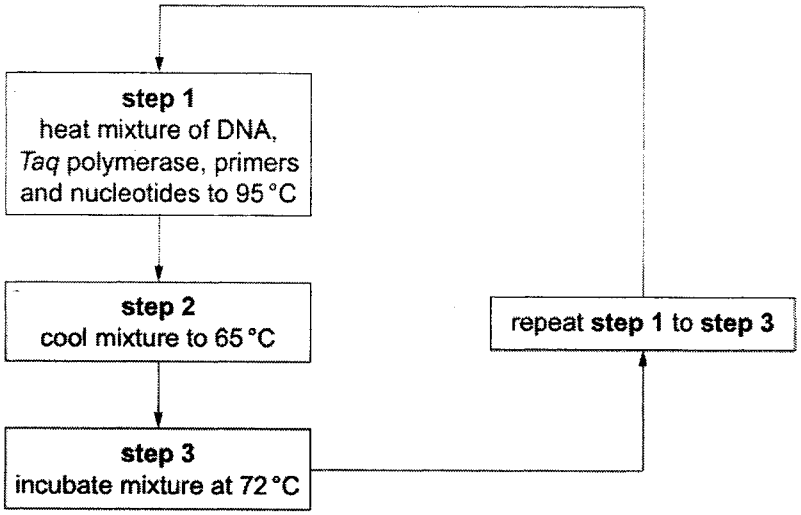

Fig. 6.1

(i) Explain why it is necessary to heat the mixture to 95 °C (**step 1**).

.....[2]

1. **To denature DNA / to separate the two DNA strands / double stranded DNA ;**
2. **By breaking hydrogen bonds between complementary base pairs (of the double-stranded DNA) ;**
3. **So that the bases are exposed to produce single-stranded DNA / template strands (for complementary base pairing with dNTPs) ;**

MP 1-3: max 2

(ii) Explain why the enzyme *Taq* polymerase, rather than any other type of DNA polymerase, is used in PCR.

.....[2]

1. ***Taq* polymerase is heat stable / works at high temperature ;**
2. **So it does not need to be replaced during each cycle of PCR ;**
   OR
3. **Other DNA polymerases are not heat stable ;**
4. **So they would have to be replaced during each cycle of PCR ;**

Another molecular technique used in medical and biological research is Southern blotting followed by nucleic acid hybridisation.

To visualise the results, autoradiography is carried out at the end. The images formed on the photographic X-ray film would correspond to the bands that contain the DNA sequence of interest.

(b) Outline the process of Southern blotting and nucleic acid hybridisation.

..... [4]

1. **Gel from gel electrophoresis is placed on top of a sponge soaked in alkaline solution, a nitrocellulose membrane, followed by a stack of paper towels, are placed on top of the gel ;**
2. **Alkaline solution is drawn upwards through the gel, denaturing the (double stranded) DNA fragments, transferring single-stranded fragments of DNA to the nitrocellulose membrane (where they adhere firmly in the same positions as they were in the gel) ;**
3. **Nitrocellulose membrane is placed in a sealed plastic bag containing radioactive single-stranded DNA probes (complementary to the DNA sequence of interest) ;**
4. **Which hybridise with DNA fragments (containing sequence of interest) on the nitrocellulose paper via complementary base pairing ;**
5. **Nitrocellulose membrane is removed from the bag and washed thoroughly to remove any unhybridised probes ;**
   Autoradiography is then carried out to visualise the results.

MP 1-5: max 4

Sickle cell anaemia is a genetic disease caused by a recessive mutant allele of the β-globin gene.

Scientists investigated the inheritance of the disease in one family. DNA was collected from each family member. PCR, restriction enzyme digestion using the enzyme *DdeI*, gel electrophoresis, Southern blotting and nucleic acid hybridisation were carried out.

Fig. 6.2 shows the autoradiography results from the final stage of this investigation.

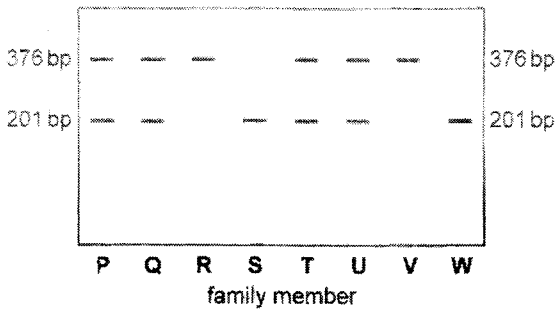

Fig. 6.2

Fig. 6.3 shows where the restriction enzyme *DdeI* cuts within the two different β-globin alleles and the sizes of the fragments produced.

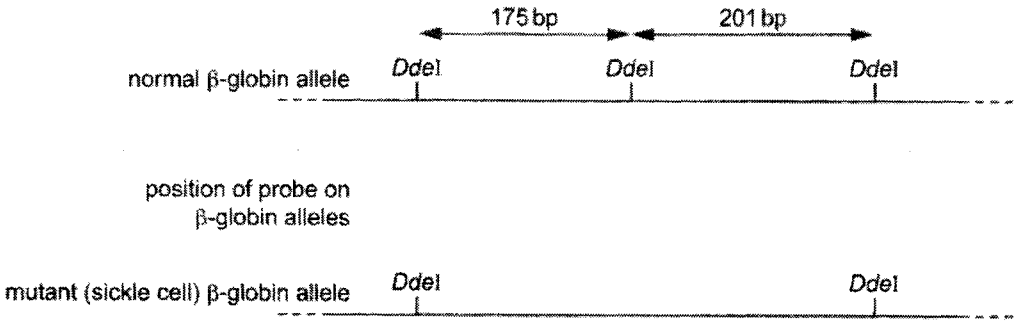

Fig. 6.3

(c) Using the information from Fig. 6.2,

(i) indicate in Fig. 6.3 the position of the probe that was used [1]

1. Indicates a region corresponding to the 201 bp fragment AND that does not overlap with any region in the 175 bp fragment of the normal β-globin allele ;

(ii) state which family members suffer from sickle cell anaemia.

.....[1]

1. Individual R and individual V ;

[Total: 10]

7 Fig. 7.1 shows an animal cell in a stage of the mitotic cell cycle.

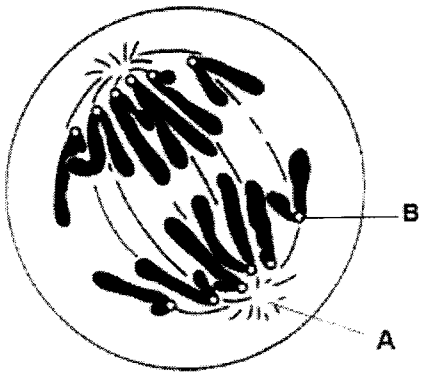

Fig. 7.1

(a) A pair of rod-like structures can be found in region **A**.

State **one other** feature of these structures and outline their role during mitosis in animal cells.

feature .....

role .....
[2]

Feature
1. **(The centriole pair is) positioned at right angles / perpendicular to each other ;**
2. **(transverse section shows) 9 triplets of microtubules arranged in a ring ;**

Role
3. **The <u>two pairs of centrioles move to the opposite poles</u> of the cell (during prophase) and <u>determine the polarity of the cell</u> ;**
4. **Centrioles act as the microtubule-organising centre (MTOC) – the centrioles <u>produce spindle fibres</u> (radiating from the centrioles) at the poles towards the equator of the cell ;**
5. **Centrioles <u>organise the synthesis of spindle fibres</u> which lead to the <u>separation of (sister) chromatids</u> during mitosis ;**

MP1/MP2 + any from MP3-5 for full credit

(b) Identify structure **B** and outline its structure and function.

B .....

structure .....

function .....

[3]

B

1. **Centromere ;**

Structure

2. **A constricted region on a chromosome ;**
3. **Consists of non-coding DNA made up of a series of tandem repeats / is (often) heavily methylated ;**
4. **Site at which (a number of centromere-associated) proteins bind, forming (a specialised structure called) the kinetochore ;**

Function

5. **Centromeres hold sister chromatids together (until anaphase of mitosis) ;**
6. **Centromeres divide to allow separation of sister chromatids (during anaphase of mitosis) ;**
7. **DNA at the centromere is essential for proper alignment and separation of sister chromatids to opposite poles of the cell during nuclear division ;**
8. **Centromeres ensure proper segregation of chromosomes by being the site on the chromosome where the kinetochore assembles and microtubules/spindle fibres from the centrioles attach during nuclear division ;**

MP1 + any from MP2-4 + any from MP5-8 for full credit

(c) With reference to Fig. 7.1, state **two** observable differences between the behaviour of chromosomes in mitosis and meiosis.

..... [2]

	mitosis	meiosis	
1.	(during anaphase) sister chromatids separate	(during anaphase I) homologous chromosomes separate	;
2.	(during anaphase) division of the centromere occurs	(during anaphase I) no division of centromere	;

(d) The stages and checkpoints of the mitotic cell cycle are closely regulated. Explain the need to regulate the mitotic cell cycle tightly.

..... [3]

1. **The mitotic cell cycle is controlled by checkpoints such as the G_1 checkpoint / G_2 checkpoint / M checkpoint (at least 1 e.g.) which determine whether or not the cell cycle can proceed ;**
2. ***(mark for idea)* Requirements of each checkpoint must be met before cells move on to next stage, e.g. accurate completion of DNA replication / bring about DNA repair mechanisms if required / cell cycle arrested when there is DNA damage etc. ;**
   (A: tight control is needed for normal cell division and cell development with some elaboration)
3. **Tight control of the mitotic cell cycle can thus prevent dysregulation of checkpoints of mitosis / cell division ;**
4. **preventing excessive cell cycle progression / rapid cell cycle / uncontrolled cell division which can lead to tumour formation and possibly cancer ;**

[Total: 10]

8 The fruit fly, *Drosophila melanogaster*, feeds on sugars found in damaged fruits.

A fruit fly with normal features is described as wild type. It has red eyes and its wings are longer than its abdomen. There are mutant variations such as purple eyes or short (vestigial) wings.

Fig. 8.1 shows a wild type fruit fly and a mutant fruit fly with purple eyes and vestigial wings.

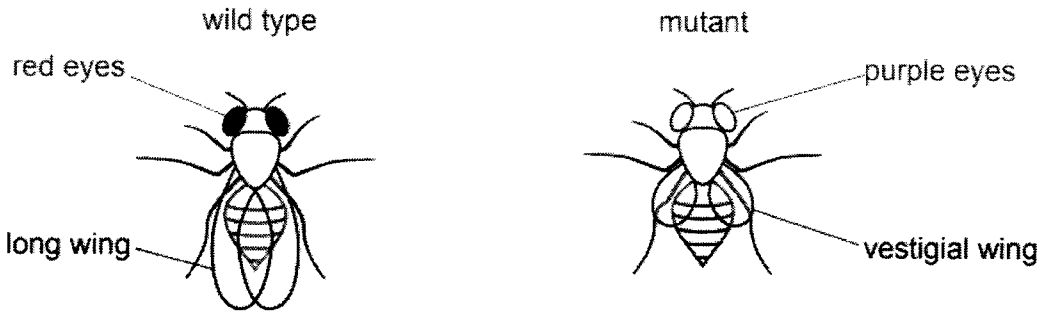

Fig. 8.1

- The genes coding for eye colour and wing length are located on the same chromosome.
- Allele **R** for red eyes is dominant to allele **r** for purple eyes.
- Allele **N** for long wings is dominant to allele **n** for vestigial wings.

(a) A wild type fruit fly, heterozygous for both genes, was crossed with a fruit fly that was homozygous recessive for both genes.

Table 8.1 is a summary of the cross.

Complete Table 8.1.

Table 8.1

	wild type parent		**double homozygous recessive parent**	
parental phenotype	**red eyes, long wings x purple eyes, vestigial wings**			
parental genotype	$\frac{RN}{rn}$ **x** $\frac{rn}{rn}$			
offspring				
offspring genotype	$\frac{RN}{rn}$	$\frac{rn}{rn}$	$\frac{Rn}{rn}$	$\frac{rN}{rn}$
offspring phenotype	**red eyes, long wings**	**purple eyes, vestigial wings**	**red eyes, vestigial wings**	**purple eyes, long wings**
number of offspring	1339	1195	151	154

1. **Correct parental phenotypes ;**
2. **Correct parental genotypes ;**
3. **Correct offspring genotypes (for all 4) ;**
   penalise under MP2 & MP3 if linkage notation not used
4. **Correct offspring phenotypes (for all 4) ;**

	wild type parent		double homozygous recessive parent	
parental phenotype	.....		.....	
	.....	X	.....	
parental genotype	.....	X	.....	
offspring				
offspring genotype	.....	.....	.....	.....
offspring phenotype	....	....	....	....
number of offspring	1339	1195	151	154

[4]

(b) A statistical test showed that the results of the cross were significantly different from those expected.

State the name of the statistical test used and explain why it would be useful to carry out the test on these results. No calculations are required to answer this question.

statistical test .....

explanation .....

[2]

1. **Chi-squared / χ^2 (test) ;**
2. **To estimate the probability that differences between observed and expected results were due to chance ;**

(c) Describe and explain the difference between the results of the cross in Table 8.1 and those expected.

..... [4]

Describe

1. **Expected ratio from the cross is 1:1:1:1 but observed ratio was 9:8:1:1 ;**
2. **The observed offspring of the cross are majority of parental combinations/phenotypes (A: red eyes, long wing and purple eyes, vestigial wing) / minority of recombinant combination/phenotypes ;**

Explain

3. **The 2 genes for eye colour and wing length are linked / the alleles of the 2 genes for eye colour and wing length are inherited together as one linkage group ;**
   reference to both traits required for MP3
4. **Resulting in a higher proportion of gametes/higher chances of getting gametes carrying the parental types ;**
5. **Crossing over between the 2 linked genes on non-sister chromatids of homologous chromosomes may occur ;**
6. **As crossing over is a chance event, this results in a lower proportion of gametes / lower chances of getting recombinant gametes ;**
7. **AVP – no independent assortment of homologous chromosomes occurs ;**

At least 1 from MP1-MP2 required for full credit

[Total: 10]

9 The red poppy, *Papaver rhoeas*, and several species of daisy often co-exist as weeds of wheat fields.

Fig. 9.1 shows changes in the percentage frequency of red poppies and daisies in an area of wheat fields over a six year period from 1998 to 2003. From 1985, the herbicide metsulfuron-methyl was used to control weeds in this area of wheat fields. This practice continued throughout the six year period.

1998 showed the first occurrence of a red poppy known as biotype X. This red poppy had a specific mutation not present in normal red poppies.

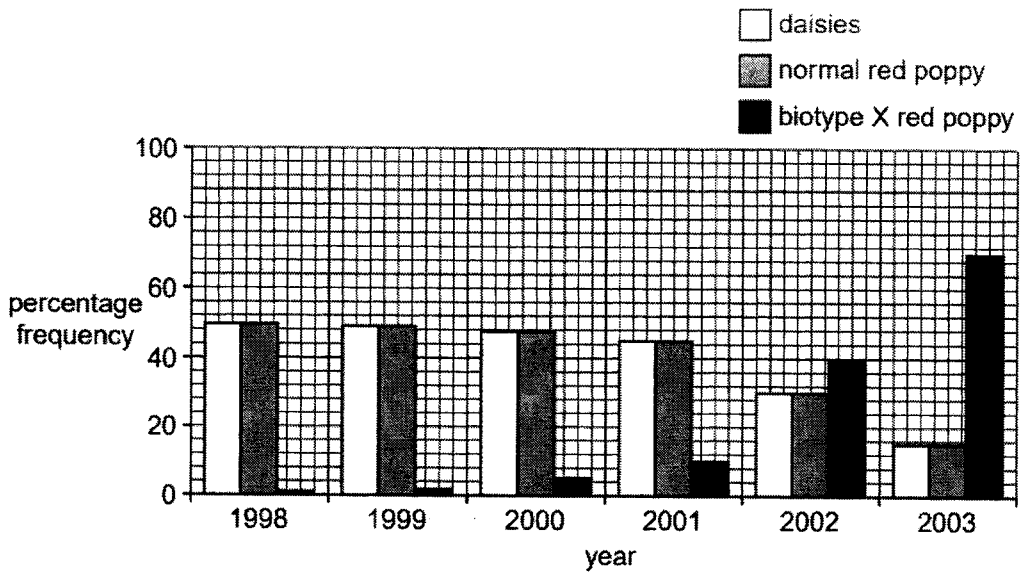

Fig. 9.1

(a) Describe how the percentage frequencies of red poppies and daisies changed over the six year period.

..... [3]

1. **From 1998 to 2003, percentage frequencies of daisies and normal red poppies decreased from 50% to 15% (A: 14-16%) ;**
2. **From 1998 to 2003, percentage frequencies of biotype X red poppy increased from 1% (A: 2%) to 70% ;**
3. **After 2001, there was a steep increase (30% increase by 2002 or 60% increase by 2003) in percentage frequencies of biotype X red poppy ;**
4. **From 1998 to 2003, total percentage frequencies of red poppies increased, from 51% (A: 52%) to 85% (A: 84-86%) ;**
5. **Percentage frequencies of daisies and normal red poppies were always equal throughout the six years ;**

(b) Suggest a reason for the distinct difference in percentage frequencies of normal red poppies and biotype X red poppy in the year 2003.

..... [1]

1. **Normal red poppies killed by / susceptible to metsulfuron-methyl but biotype X red poppy resistant to metsulfuron-methyl ;**
   OR
2. **The specific mutation present in biotype X red poppy enabled it to survive well even in the presence of metsulfuron-methyl ;**

Although biotype X red poppy and normal red poppies continue to grow within the same geographical location, after numerous generations, biotype X red poppy may eventually become a different species from the normal red poppies.

(c) Suggest why biotype X red poppy may eventually become a different species from the normal red poppies.

..... [2]

1. **<u>Physiological / reproductive isolation</u> (e.g. due to polyploidy, different flowering times) leading to <u>sympatric speciation</u> ;**
2. **<u>Prevents interbreeding</u> between biotype X and normal red poppies, leading to <u>disruption in gene flow</u> ;**

Daisies belong to the *Compositae* family, which is the largest family of flowering plants comprising more than 25 000 species. Many important evolutionary questions about the diversity in this family remain unanswered due to the lack of evidence to support major nodes of the phylogeny.

(d) Explain the advantages of using molecular methods to determine phylogenetic relationships within the *Compositae* family.

..... [3]

1. **<u>Unambiguous</u> and <u>objective</u>. A, T, G, C are easily recognised and one cannot be confused with another / not dependent on subjective judgements or observations involving qualitative differences in morphology ;**
2. **<u>Quantifiable</u> and can be converted to numerical form and open to statistical analysis ;**
3. **Homologous regions of DNA from different species provides <u>many points of comparison</u> as each nucleotide position is a point of comparison ;**
4. **Molecular evidence avoids pitfalls of convergent evolution when morphological evidence could be due to convergence ;**
5. **Molecular / nucleotide data can be used to trace evolutionary relationships of species that are so different that there is little morphological homology ;**
6. **Molecular / nucleotide can be used to assess phylogenetic relationships that cannot be measured by comparative anatomy / other non-molecular methods e.g. fossils ;**

Fossil evidence indicates that flowering plants first appeared about 125 million years ago and they have since been rapidly diversifying. The comparison of chloroplast genomes could provide insight into the evolution of flowering plants.

(e) Explain how evidence based on homologies identified in chloroplast genomes support Darwin's theory of evolution.

..... [2]

1. **(Molecular) homology identified in the chloroplast genomes suggest <u>common ancestry / descent from a common ancestor</u> ;**

2. **Cumulative changes in chloroplast genome sequences show <u>descent with modification</u> ;**
   OR
3. **Comparisons of homologies in chloroplast genome between species show how a population may have been modified into descendent species (through natural selection and changes in allele frequency) ;**

Although plant fossils are usually rare compared to fossils of bones, teeth and shells, there are many great fossil sites in the world that have excellent preservation of plant materials.

(f) Suggest why plant fossils are usually rare.

..... [1]

1. **Plant material (e.g. leaves) are soft and decompose rapidly ;**

[Total: 12]

10 Measles is a common viral infection. A vaccine has been available for measles since the 1960s. There are vaccination programmes for many diseases including measles. Babies are born with a passive immunity to measles so the vaccine is not given in the first few months after birth.

(a) Explain how active immunity differs from passive immunity.

..... [3]

Feature	Active immunity	Passive immunity
Involvement of T or B cell ;	immune response involves clonal selection and expansion (A: activation) of B cells or T cells	does not involve B cells or T cells
Source of antibodies ;	antibodies are synthesised from plasma cells	antibodies are acquired from mother
Durability of immune response	long-lived effect of active immunity	short-lived effect of passive immunity
Lag time for immune response ;	immune response of active immunity is not immediate	immune response of active immunity is almost immediate
Memory cell production ;	memory cells are produced	memory cells are not produced
Removal of antibodies from circulation ;	antibodies are not removed	antibodies are removed

The World Health Organisation (WHO) publishes data on the vaccination programmes for infectious diseases. The WHO recommends vaccination rates of over 90% of children.

Each health authority in a country reports its success in vaccinating children in their district. The WHO uses these figures to estimate the percentage of districts in each country that vaccinate 90% of children against measles.

The WHO also collects statistics on death rates of children under the age of 5 from all causes, including infectious diseases.

Fig. 10.1 shows these statistics for 24 countries for the year 2007.

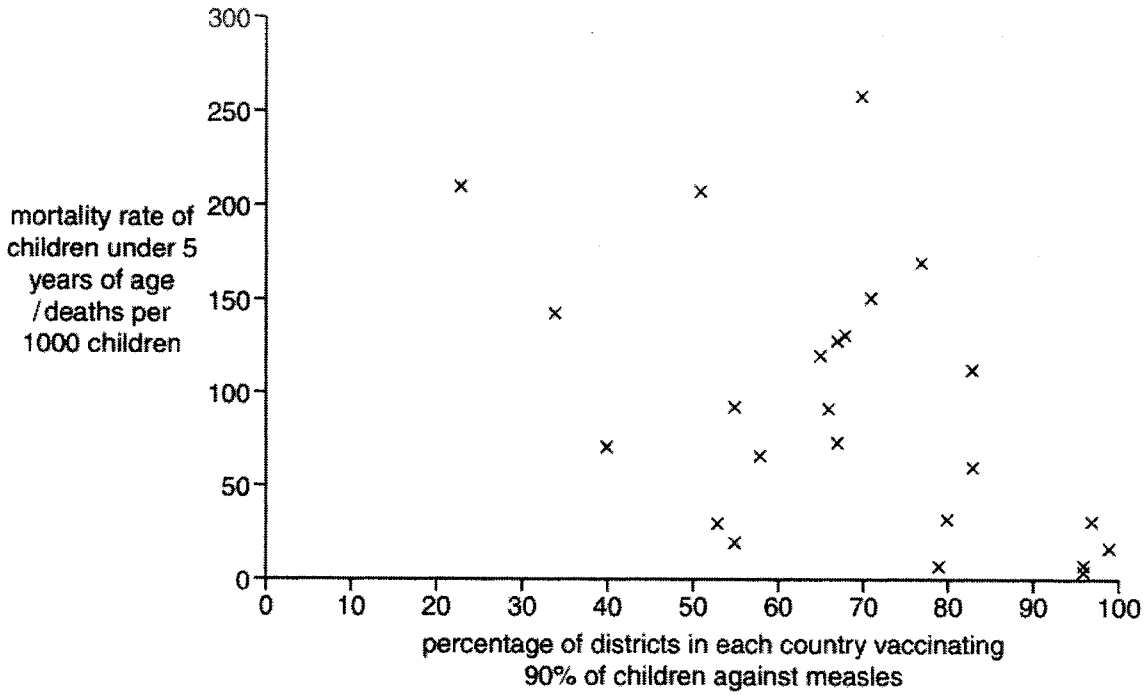

Fig. 10.1

(b) Use the information in Fig. 10.1 to explain why the WHO recommends immunisation of 90% of children.

..... [2]

1. **All countries with <u>>90%</u> (A: 96-99%) of districts reporting 90% of children vaccinated have <u>very low death rates</u> /5 deaths per 1000 children under 5 years of age ;**
   OR
2. **Countries with <u>less than 90%</u> of districts (A: appropriate data e.g. 20% district), has <u>high</u> death per 1000 children (A: appropriate data e.g. 210 deaths per 1000 children under 5 years of age) ;**
3. **Herd immunity is achieved for countries with >90% district vaccination ;**

MP 1 or 2 + MP 3 for max 2

[Total: 5]

11 The concept of climate change and global warming has been of concern to scientists for many years.

(a) One way to collect data about atmospheric concentrations of greenhouse gases in the past is to study samples of ice from ice sheets in Antarctica. Ice samples from deep in the ice sheets were formed hundreds of thousands of years ago, while those near the surface were formed recently.

As ice forms, small bubbles of air are trapped in the ice. These air bubbles can be analysed to determine the concentration of carbon dioxide present. It is also possible to use chemical techniques to determine when the air bubbles were trapped.

Scientists studying climate change measured carbon dioxide concentrations in air bubbles from ice samples of known age, collected from near the surface.

Fig. 11.1 shows the concentration of carbon dioxide measured in air bubbles that were trapped in ice from 1959 to 1990. Direct measurements of atmospheric carbon dioxide from 1948 to 1978 are also shown.

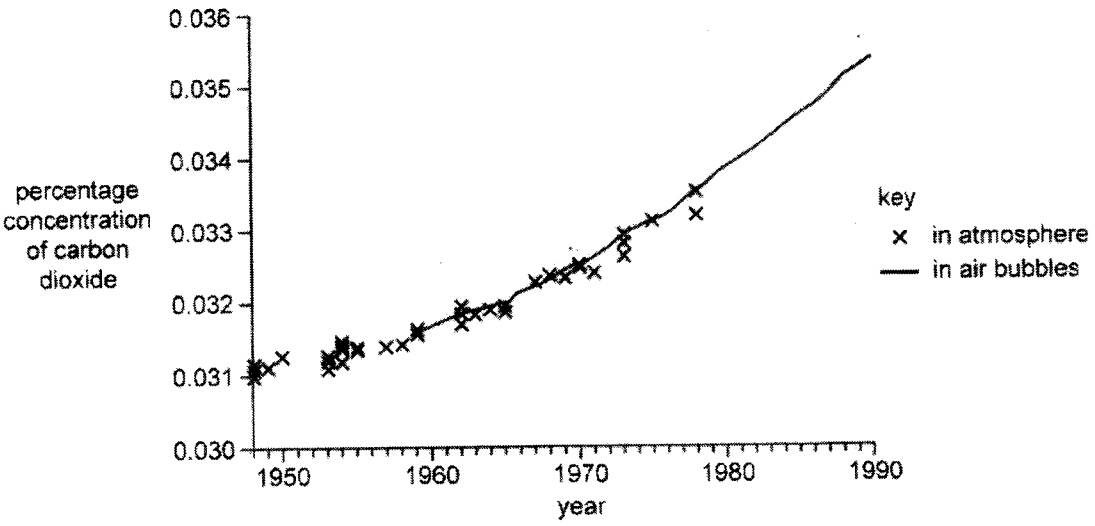

Fig. 11.1

With reference to the information provided, suggest and explain how climate change scientists can estimate atmospheric carbon dioxide concentrations 10 000 years ago.

..... [2]

Suggest

1. **Scientists can analyse the concentration of carbon dioxide in air bubbles trapped deeper in the ice sheets 10 000 years ago (as an estimate of the atmospheric carbon dioxide concentrations then) ;**

Explain

2. **The graph in Fig. 11.1 shows that the concentration of carbon dioxide measured in air bubbles trapped in ice is a good/accurate match with the direct measurements of atmospheric carbon dioxide at the time when the air bubbles were formed ;**
   Idea that air bubbles could be regarded as samples of the atmosphere from the time at which they formed

(b) Volcanic eruptions, which eject large volumes of gases such as water vapour and carbon dioxide to heights of 16 to 32 kilometres above the Earth's surface, have had an effect on the climate of the Earth.

Toba is a volcano in Sumatra that erupted approximately 12 000 years ago. Fig. 11.2 shows the location of Sumatra.

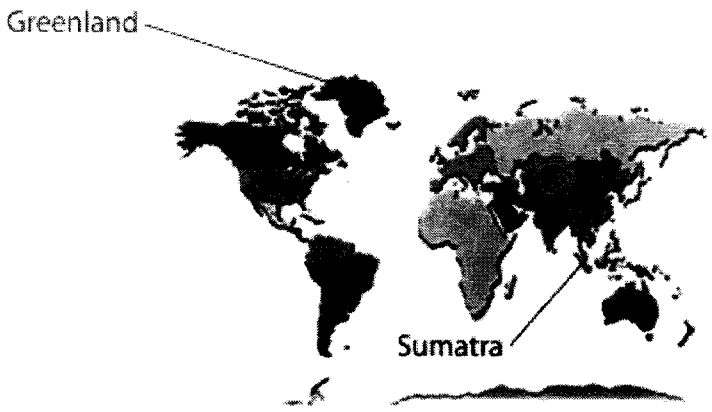

Fig. 11.2

Fig. 11.3 shows the changes to sea levels, compared to the present day, in the oceans around Greenland.

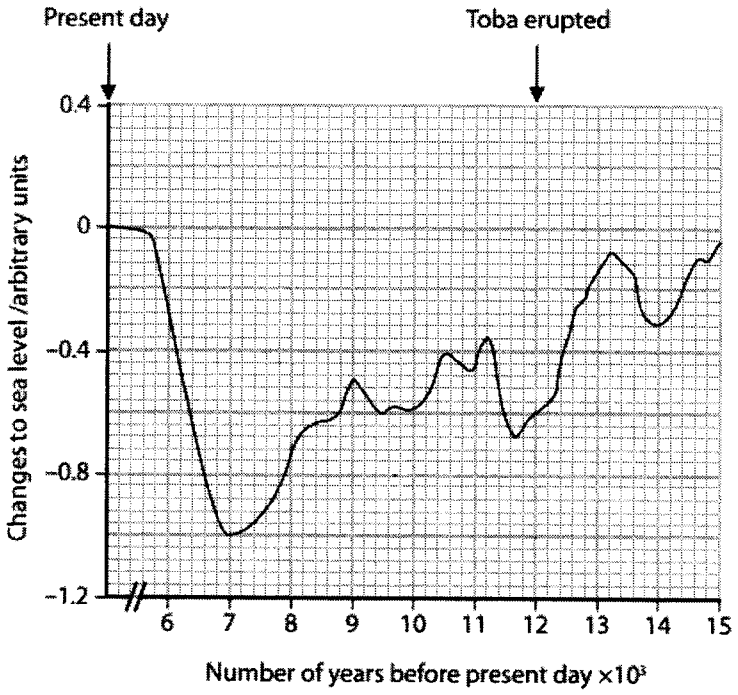

Fig. 11.3

It is claimed that the volcanic eruption of Toba caused a change in world climate.

(i) Describe the evidence in Fig. 11.3 that supports this claim.

..... [1]

1. **The volcanic eruption of Toba was followed by an increase in sea level 300 years later/11 700 years ago, from -0.68 arbitrary units to __ (e.g. -0.36) arbitrary units (accept any relevant data point) ;**
   OR
2. **The volcanic eruption of Toba was followed by a decrease in sea level (over the next 300 years), from -0.6 arbitrary units to -0.68 arbitrary units ;**

(ii) Suggest why this claim may not be true.

..... [2]

1. **<u>Prior to the eruption of Toba</u>, fluctuations in sea level / changes in climate were already taking place (e.g. 14 000 years ago) ;**
2. **Changes in sea level / Climate change might be due to other factors, e.g. anthropogenic activities, rather than the eruption of Toba ;**
3. **The changes in sea level in Fig. 11.3 are <u>only for one area/around Greenland</u> but might not be applicable to the world ;**

[Total: 5]

NAME : _____ CLASS : _____

JURONG PIONEER JUNIOR COLLEGE
JC2 Preliminary Examination 2022

BIOLOGY
Higher 2

9744/03
21 September 2022

Paper 3 Structured and Free-response Questions

2 hours

Candidates answer on the Question Paper.
No Additional Materials are required.

READ THESE INSTRUCTIONS FIRST

Write your class and name in the spaces at the top of this page.
Write in dark blue or black pen.
You may use an HB pencil for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.

Section A
Answer **all** questions in the spaces provided on the Question Paper.

Section B
Answer any **one** question in the spaces provided on the Question Paper.

The use of an approved scientific calculator is expected, where appropriate.
You may lose marks if you do not show your working or if you do not use appropriate units.

At the end of the examination, fasten all your work securely together.
The number of marks is given in brackets [ ] at the end of each question or part question.

For Examiner's Use	
1	
2	
3	
Section B	
Total	

This document consists of **17** printed pages.

Section A

Answer **all** the questions in this section.

1 Colorectal cancer and hepatocellular carcinoma (HCC) are amongst the leading causes of cancer-related deaths worldwide. Colorectal cancer is the cancer of the colon or rectum. It is amongst the top three causes of cancer in both men and women globally, with more than a million people diagnosed with colorectal cancer each year.

Most colorectal cancers are due to old age and lifestyle factors, with only a small number of cases due to underlying genetic factors.

(a) State two environmental causes of cancer.

..... [2]

1. **Ionising radiation such as nuclear radiation/X-rays/gamma rays/UV radiation ;**
2. **Chemical carcinogens such as tobacco/tar in cigarette smoke / ethidium bromide / asbestos ;**

(b) Colorectal cancer often begins as an adenoma – a benign tumour that develops at the inner lining of the large intestine. Though benign, Fig. 1.1 shows how adenomas may transform to become malignant as a result of genetic alterations over time.

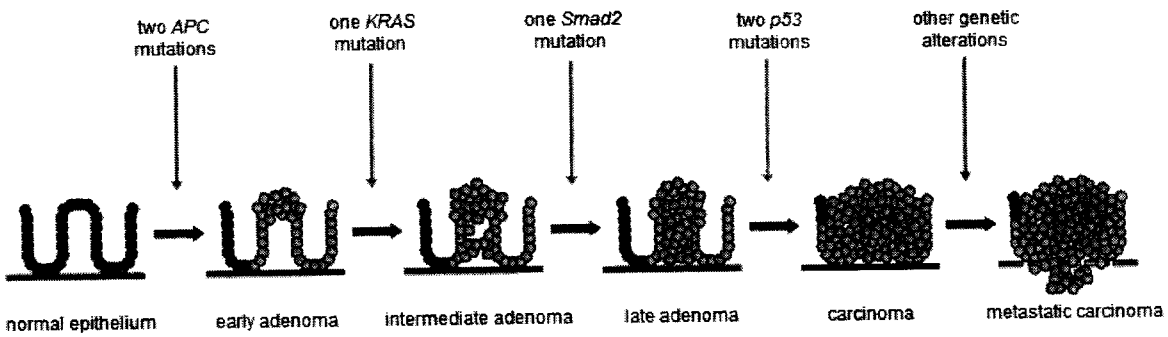

Fig. 1.1

Explain how Fig. 1.1 provides evidence for the development of cancer as a multi-step process.

..... [4]

1. **Fig. 1.1 shows that a single cell needs to accumulate more than one (somatic) mutation to become a cancerous cell ;**
2. **Mutations in the tumour suppressor genes *APC* / *p53* / proto-oncogenes *KRAS* / *Smad2*, as well as other genetic alterations in the same somatic cell ;**
3. **results in the rate of cell division to be greater than the rate of cell death, hence leading to uncontrolled cell division (and tumour formation) ;**
4. **When cells of a tumour *(accept: carcinoma)* invade surrounding tissue, and metastasise to other sites, the tumour is considered to be malignant and cancer has developed ;**

MP1/MP2: reference to single/same somatic cell at least once

(c) Different types of gene mutation have been found to affect tumour suppressor genes.

Explain why a base pair deletion in a tumour suppressor gene is more likely to produce a non-functional protein than a base pair substitution.

..... [3]

1. **Base pair deletion results in a <u>frameshift mutation</u> where the reading frame is altered and <u>nucleotides downstream from the deletion are improperly grouped into</u> (incorrect) <u>codons</u> ;**
2. **Resulting in extensive missense mutation / primary structure / many amino acids in the polypeptide chain will be changed, which will greatly alter the 3D conformation of the protein ;**

3. **Whereas for base pair substitution, it may result in a <u>silent mutation</u> where the <u>same amino acid is still coded</u> for due to the <u>degeneracy of the genetic code</u> ;**
   OR
4. **Base pair substitution may result in a <u>missense mutation</u> / a <u>different</u> amino acid is coded for, where the <u>amino acid has similar R-group properties</u> to the original amino acid coded for ;**
   OR
5. **Base pair substitution may result in a <u>missense mutation</u> / a <u>different</u> amino acid is coded for, but the amino acid is <u>not found in a critical region</u> of the protein ;**

Pt 1 + Pt 2 + Pt 3/4/5 for full credit

Unlike colorectal cancer, the incidence of HCC can be attributed to different genetic and epigenetic alterations. Epigenetics refers to heritable states of gene expression without alteration to the DNA sequence itself. Epigenetic changes such as DNA hypermethylation or hypomethylation, dysregulation of histone modification patterns, chromatin remodelling and aberrant expression of micro-RNAs (miRNAs) are associated with HCC.

miRNAs are non-coding single-stranded RNAs that are typically 19 to 25 nucleotides in length. They mostly function as negative gene regulators by binding to their complementary sequence located at the 3' untranslated region of their target mRNA, thereby forming miRNA-mRNA duplexes and silencing gene expression.

(d) State the level at which miRNAs regulate gene expression.

..... [1]

1. **Translational level ;**

(e) Fig. 1.2 shows how chronic liver damage and the replacement of normal liver tissue by fibrous scar tissue can lead to liver cirrhosis. Cirrhosis is generally irreversible once it occurs; more often than not, it leads to HCC.

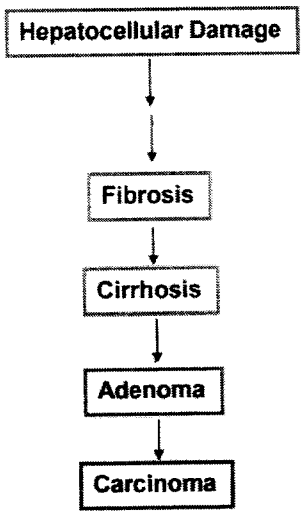

Fig. 1.2

A study investigated the association between differential levels of miRNA expression in liver cirrhosis. Non-cirrhotic and cirrhotic liver samples were used and the results are shown in Fig. 1.3.

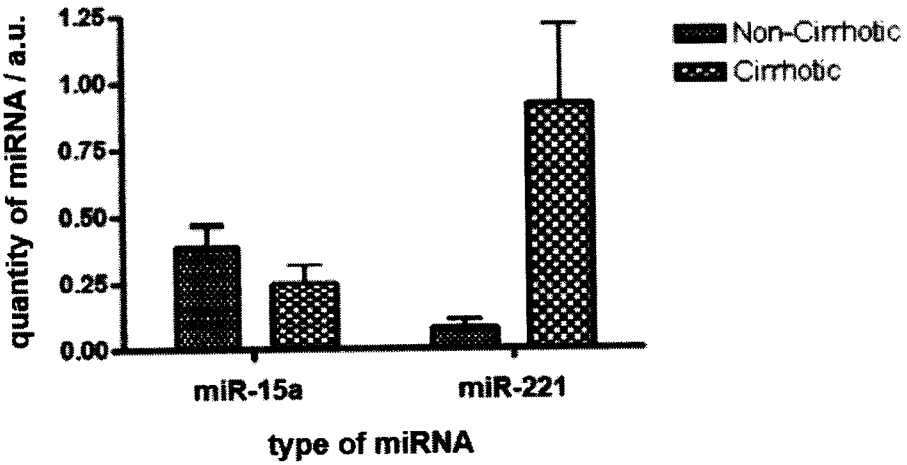

Fig. 1.3

(i) Compare the effect of the relative quantities of miRNA in leading to liver cirrhosis.

..... [3]

Describe (Quote data)
miR-15a

1. **The quantity of miR-15a decreased from (an average of) 0.40 a.u. in non-cirrhotic liver samples to (an average of) 0.25 a.u. in cirrhotic liver samples / decreased by 0.33% (OTWWE) ;**

miR-221

2. **The quantity of miR-221 increased from (an average of) 0.07 a.u. in non-cirrhotic liver samples to (an average of) 0.91 a.u. in cirrhotic liver samples / increased by 13 times (OTWWE) ;**

Similarity

3. **Changes in the relative quantities of each miRNA contributed to the progression towards liver cirrhosis ;**

Difference

4. **An increase in the quantity of miR-221 and a decrease in the quantity of miR-15a led to liver cirrhosis ;**

(ii) 'oncomiRs' are miRNAs that promote oncogenesis by negatively regulating important tumour suppressor genes. On the other hand, 'anti-oncomiRs' are miRNAs that exert tumour-suppressive effects by repressing oncogenes.

Deduce if miR-15a and miR-221 is an 'oncomiR' or 'anti-oncomiR' and justify your answer.

miR-15a .....

justification .....

.....

miR-221 .....

justification .....

.....

[4]

1. **miR-15a: anti-oncomiR ;**
2. ***(mark for idea)* Down-regulation of miR-15a led to a reduced repression of oncogenes / increased levels of oncogene expression, which was correlated with the progression towards liver cirrhosis ;**

3. **miR-221: oncomiR ;**
4. ***(mark for idea)* Up-regulation of miR-221 led to a greater extent of repression of tumour suppressor genes / reduced levels of TS gene expression, which was correlated with the progression towards liver cirrhosis ;**

(f) The molecular genetics of HCC have recently been extensively characterised. One of the most consistent epigenetic changes in HCC is that of DNA hypermethylation at the promoters of target genes.

(i) Describe how DNA hypermethylation at promoters can alter expression levels of the target genes.

..... [3]

1. **DNA (hyper)methylation physically blocks the binding of general transcription factors and RNA polymerase to the promoter (of the target genes) ;**
2. **hence preventing formation of the transcription initiation complex, preventing transcription ;**
3. **DNA (hyper)methylation also leads to recruitment of transcriptional repressors / histone deacetylases / other repressive chromatin remodelling complexes, thereby forming more compact chromatin / tighter nucleosomes / DNA more tightly coiled around nucleosomes, preventing transcription ;**

MP2/MP3: reference to preventing T/C must be made at least once for full credit

(ii) The *p16INK4a* gene is located on chromosome 9 and is one of the most frequently altered genes observed in HCC. The prevalence of hypermethylation of its promoter in various types of liver tissues are shown in Tables 1.1 and 1.2.

Table 1.1

sample	percentage of samples which showed *p16INK4a* promoter hypermethylation
HCC	54.5
non-tumourous	15.6

Table 1.2

sample	percentage of samples which showed *p16INK4a* promoter hypermethylation
cirrhotic	22.7
non-cirrhotic	9.2

Predict whether *p16INK4a* is an oncogene or tumour suppressor gene and suggest a possible role of its protein product in the cell cycle.

..... [2]

1. ***p16INK4A* is a tumour suppressor gene ;**

2. **Role of protein product – inhibit cell cycle progression / triggers cell cycle arrest (OWTTE) ;**
3. **AVP – triggers apoptosis etc. ;**

(g) Another common hallmark of HCC is that of telomerase reactivation.

A student made the following claim:

"*In eukaryotes, telomerase synthesises additional lengths of DNA that are added to the ends of chromosomes, thus solving the end-replication problem that results from each round of DNA replication.*"

(i) Account for the end-replication problem.

..... [4]

1. **DNA polymerase can only add DNA nucleotides to the free 3' –OH end of an existing strand ;**
2. **With the removal of the RNA primer from the 5' end of the newly synthesised strand ;**
3. **There is <u>no free 3'</u> (–OH) <u>end</u> for DNA polymerase to add (free) nucleotides to / the RNA primer is <u>not replaced</u> (with DNA nucleotides) ;**
4. **This results in a daughter strand that is shorter than the parental/template DNA strand / progressive shortening of telomeres (in eukaryotes) / a 3' overhang at the end of the chromosome ;**

(ii) Evaluate the validity of the student's claim that the addition of DNA to chromosomal ends solves the end-replication problem.

..... [2]

<u>Not valid</u>

1. **The end-replication problem can never be solved / shortening of chromosomal ends in (linear) eukaryotic chromosomes continues to occur with each round of DNA replication due to the removal of the RNA primer (OWTTE) ;**

<u>Valid</u> to a certain extent in that:

2. **With each round of DNA replication, the shortening of <u>telomeres</u> occurs without deleterious effects / genes within the chromosome will not be lost / loss of important genetic information is prevented (OWTTE) ;**

(iii) Telomerase is **not** present in prokaryotic cells. Suggest why prokaryotes do **not** have telomerase.

..... [2]

1. **Prokaryotes have circular DNA / do not have linear chromosomes / do not have telomeres (A: DNA has no ends) ;**
2. **Thus they do not encounter the end-replication problem ;**
   so there is no need for telomerase in prokaryotic cells.

[Total: 30]

2 Gene expression in eukaryotes is regulated at different levels and involves various regulatory proteins and enzymes. At translational level of regulation, regulatory proteins such as translation initiation factors and translational repressors are involved.

(a) Describe how gene expression may be regulated by translational repressors.

..... [2]

1. **Translational repressors recognise and bind to specific sequences, usually the 5' untranslated region (5' UTR) of mature mRNA ;**
2. **Blocking / preventing ribosomes from binding to mature mRNA so that initiation of translation cannot take place ;**

Another regulatory protein, ubiquitin, is a highly conserved protein comprising 76 amino acids, ubiquitously expressed in all tissues in eukaryotes.

(b) State the role of ubiquitin in regulating gene expression in eukaryotes.

..... [1]

1. **Marks proteins for degradation by proteasome ;**

Fig. 2.1 shows the structure of an ubiquitin molecule.

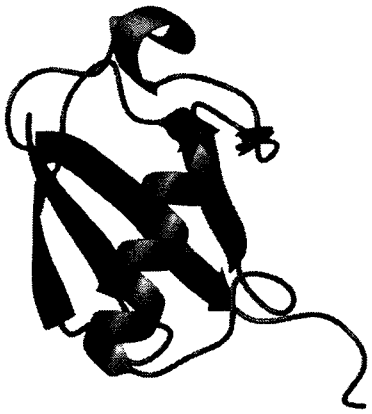

Fig 2.1

(c) Describe **two** similarities between the secondary structures found in ubiquitin.

..... [2]

Both α-helices and β-pleated sheets

1. **are maintained by (intramolecular) hydrogen bonds between the (O of) C=O group and (the H of the) -NH group in the polypeptide backbone ;**
2. **contain hydrogen bonds formed at regular intervals in the polypeptide chain ;**
   OR
3. **are geometrically regular repeating structures in the polypeptide chain ;**
4. **These hydrogen bonds are disrupted by heat / changes in pH ;**

α-helices and β-pleated sheets must be mentioned for full credit

Ubiquitin is synthesised at cytosolic ribosomes. mRNA, tRNA and rRNA are involved in the synthesis of ubiquitin.

(d) Describe the roles of tRNA in the synthesis of ubiquitin.

..... [2]

1. **To act as an intermediate molecule between the codon of mRNA and the amino acid sequence of the polypeptide chain ;**
2. **To carry the correct amino acid from the cytoplasm to the polypeptide chain being synthesised at the ribosome ;**

During protein synthesis, transcription precedes translation. Researchers measured the error rates during transcription and translation in yeast cells. The results are shown in Table 2.1.

Table 2.1

process	error rate
transcription	10^{-5} per base
translation	10^{-3} per codon

(e) Suggest why such a difference in error rates during transcription and translation is tolerated by the yeast cell.

..... [3]

1. **Error rate during transcription is <u>lower</u> than error rate during translation (or vice versa) ;**
2. **Each error in transcription leads to the subsequent translation of the mRNA molecule with an incorrect sequence into many copies of non-functional protein ;**
3. **Whereas each error during translation only results in one copy of non-functional protein ;**

[Total: 10]

3 Algae are aquatic photosynthetic protoctists. Some researchers genetically modified the unicellular alga, *Chlorella vulgaris*, to try to increase the rate of the light independent stage of photosynthesis.

C. vulgaris was modified to increase the expression of the gene coding for aldolase. Aldolase is an enzyme that causes an increase in the concentration of rubisco.

Two cultures of *C. vulgaris*, one that was not genetically modified (unmodified) and one genetically modified, were grown under controlled conditions for 14 days. Samples were taken from the cultures at regular intervals during the 14 days to obtain measurements of dry mass. The results are shown in Fig. 3.1.

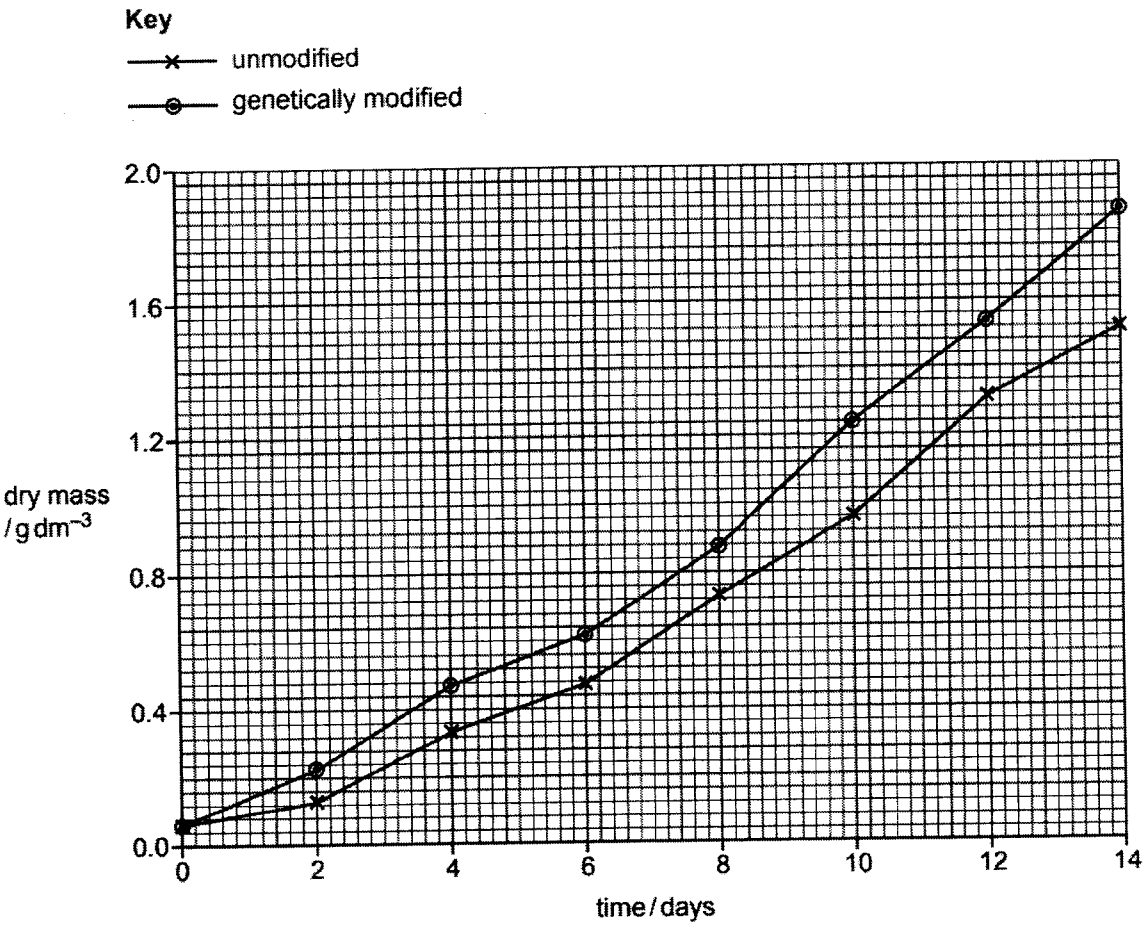

Fig. 3.1

(a) With reference to Fig. 3.1, describe the differences between the results for the two cultures.

..... [3]

1. **genetically modified (GM) culture has <u>higher</u> (dry) mass throughout the experiment than unmodified culture + quote relevant data from day 2 to 14**
   - **e.g. At day 2, dry mass of GM culture is 0.24 g dm^{-3}, higher than the dry mass of unmodified culture of 0.12 g dm^{-3} ;**
2. **GM culture has a (slightly) <u>higher rate</u> of/steeper, increase in dry mass ;**
3. **the largest difference in (dry) mass between the 2 culture is after day 8 ;**
4. **processed data to show difference (see table for computed values) ;**
5. **AVP: rate of growth over 14 days**
   - **rate of growth for GM → 1.86 – 0.08 / 14 = 0.13 g dm^{-3} day^{-1}**
   - **rate of growth for unmodified → 1.52 – 0.08 / 14 = 0.10 g dm^{-3} day^{-1}**

time / days	dry mass / g dm^{-3}		
	genetically modified ± 0.02	unmodified ± 0.02	difference between the two ± 0.04
2	0.22	0.13	0.09
4	0.48	0.34	0.14
6	0.62	0.48	0.14
8	0.88	0.74	0.14
10	1.24	0.96	0.28
12	1.54	1.31	0.23
14	1.86	1.52	0.34

(b) Explain how the Calvin cycle was affected by the genetic modification of *C. vulgaris*.

..... [3]

1. **More rubisco leads to greater rate of/more carbon dioxide fixation ;**
2. **Greater rate of glycerate phosphate (GP) / PGA produced ;**
3. **Greater rate of triose phosphate produced (from GP/ PGA);**
4. **Greater rate of/more regeneration of RuBP;**
5. **Greater rate of/more Calvin cycle ;**

(c) Intermediate products of the Calvin cycle are needed to produce organic molecules for use by the cell. One such organic molecule is phospholipid, a major constituent of cell membranes.

Outline the functions of membranes within cells.

..... [3]

1. **Membranes of cell organelles enable separate compartments to be formed inside the cell, thereby allowing specialised metabolic pathways to take place ;**
2. **Selective barrier – the hydrophobic core of membranes acts as a selective barrier, restricting the movement of charged ions or polar molecules across the membrane ;**
3. **Transport – channel proteins or carrier proteins embedded in membranes regulate the movement of polar molecules/charged ions into and out of the cell/organelles ;**
4. **Signal transduction (cell signalling) – specific signals on the extracellular surface of the cell are detected and relayed to the inside of the cell, triggering a specific cellular response within the cell ;**
5. **Membranes are the site where enzymes may be embedded and ordered to carry out sequential steps of a metabolic pathway ;**
6. **Membranes allow for transport proteins/enzymes/receptors to be embedded, leading to an increase in surface area for metabolic reactions to occur efficiently ;**

(d) Planting large numbers of trees is one way to reduce global atmospheric CO_2 concentration. Large scale culture of genetically modified *C. vulgaris* could also reduce global atmospheric CO_2 concentration.

Suggest one advantage of using genetically modified *C. vulgaris* instead of trees to reduce global atmospheric CO_2 concentration.

..... [1]

1. **Faster growth rate / reproduction ;**
2. **Cheaper to set up ;**
3. **Can culture algae in lab / not using land to grow algae / not constrained by lack of space ;**

[Total: 10]

NAME : _____ CLASS : _____

Section B

Answer **one** question in this section.

Write your answers on the lined paper provided at the end of this Question Paper.

Your answers should be illustrated by large, clearly labelled diagrams, where appropriate.

Your answers must be in continuous prose, where appropriate.

Your answers must be set out in parts **(a)** and **(b)**, as indicated in the question.

4 (a) Describe how transformation, transduction and conjugation give rise to variation in prokaryotic genomes and explain why genetic variation is important in bacteria. [15]

Transformation

1. **A (competent) bacterium takes up foreign DNA ;**
2. **The foreign DNA is incorporated into bacterium's chromosome via homologous recombination ;**
3. **By crossing over where there is sufficient homology between the DNA fragments and bacterial chromosome ;**
4. **Segments of the bacterium's genome are replaced ;**

Transduction

5. **Bacterial DNA / genes are transferred from one bacterium to another via a bacteriophage ;**
6. **When a (virulent) bacteriophage undergoes lytic cycle, a small piece of the host bacterial cell's degraded DNA is (mistakenly) packaged within the capsid of a defective phage ;**
7. **Defective phage infects another bacterial cell and injects the piece of host bacterial DNA into the newly infected bacterial cell cytoplasm ;**
8. **When a (temperate) bacteriophage enters into lytic cycle from lysogenic cycle, a small region of the host bacterial DNA that was adjacent to the prophage is improperly excised and the phage-host hybrid DNA is packaged within the capsid (of a defective phage);**
9. **The defective phage infects another bacterial cell and injects the phage-host hybrid DNA into the newly infected bacterial cell cytoplasm ;**
10. **The host bacterial DNA/ phage-host hybrid DNA is incorporated into recipient bacterium's genome / DNA via homologous recombination ;**

Conjugation

11. **F^+ donor cell produces sex pilus to attach to F^- recipient cell ;**
12. **Sex pilus retracts upon contact, pulling the two cells closer and forming a temporary cytoplasmic mating bridge between F^+ donor cell and F^- recipient cell ;**
13. **A single strand of F plasmid breaks at a specific point (origin of transfer) and the F plasmid is transferred as a single strand ;**
14. **From F^+ donor cell into the F^- recipient cell via the cytoplasmic mating bridge ;**
15. **Each single stranded DNA in each respective cell (donor and recipient cells) now acts as a template for the synthesis of a complementary daughter strand ;**
16. **F^- recipient cell (without F plasmid) is now a F^+ cell ;**

Why genetic variation is important

17. **Genetic variation is important in bacteria so that bacteria may acquire new alleles / genes ;**
18. **That confer selective advantage under a particular selection pressure (e.g. antibiotic resistance is a selective advantage, in the presence of antibiotics) ;**
19. **Bacteria with selective advantage are selected for and reproduce (via binary fission) to pass on favourable alleles to subsequent generations ;**

- **Pt 1-16: max 13**
- **Pt 1-19: max 14**

QWC [1]

Clearly expressed and well structured, with all 4 parts of question addressed using correct terminology.

(b) Describe the structures and organisation of viral, prokaryotic and eukaryotic genomes. [10]

Viral genome

1. **A virus contains nucleic acid either DNA or RNA as its genome but never both ;**
2. **Viral genome might consists of a single nucleic acid molecule or several nucleic acid molecules (i.e. segmented) ;**
3. **The nucleic acid molecules may be circular or linear ;**
4. **The nucleic acid can be single-stranded (ss) or double-stranded (ds) ;**
5. **The genetic material may sometimes be associated directly with nucleoproteins, known as nucleocapsid ;**
6. **Genes ranges from 4 to 100 base pairs (depending on the type of virus) ;**

Prokaryotic genome

7. **Genome is usually found on 1 main chromosome (excluding plasmids) ;**
8. **Circular / Looped chromosome ;**
9. **The chromosomal DNA must be compacted by forming looped domain and supercoiling of the loop DNA ;**
10. **Naked / associated with nucleoid-associated proteins (H-NS proteins) ;**
11. **Small genome size / fewer genes present compared to eukaryotic genome ;**
12. **Presence of operons / cluster of genes controlled by single promoter ;**

Eukaryotic genome

13. **Genome is divided into many different chromosomes (no. of chromosomes is species-dependent) ;**
14. **Linear chromosomes ;**
15. **Large genome size / more genes present ;**
16. **(Very high degree of compaction) "beads-on-a-string" where DNA winds around histone proteins to form nucleosomes. Nucleosomes undergo further packing to form 30 nm chromatin fibre → 300 nm chromatin fibre.**
17. **May further condense during nuclear division ;**
18. **DNA associates with histones (forming nucleosomes) / scaffolding proteins ;**
19. **Presence of introns interspersed within a gene ;**
20. **Presence of centromeres / telomeres in a linear chromosome;**
21. **Besides promoters, eukaryotes typically contain enhancers and/or silencers as regulatory sequence in their DNA ;**
22. **Genes involved in the same pathway are usually separated on different chromosomes, with each gene under the control of 1 promoter ;**

- **MP 1-6: max 3**
- **MP 7-12: max 3**
- **MP 13-21: max 3**

QWC [1]

Clearly expressed and well structured to address structures of all 3 genomes and organisation of prokaryotic & eukaryotic genomes using correct terminology.

[Total: 25]

5 (a) Outline and contrast chemiosmosis in photosynthesis and respiration. [15]

During photosynthesis and respiration in aerobic conditions,

1. **Flow of electrons down the electron transport chain (ETC) releases energy to pump H^+ across the membrane (via active transport) ;**
2. **generating a <u>proton gradient</u> across the membrane ;**
3. **ref. membrane impermeable to H^+ ;**
4. **Chemiosmosis occurs when <u>H^+ diffuse down</u> their (electrochemical and) <u>proton gradient</u> ;**
5. **through the ATP synthase ;**
6. **Releasing (electrical potential) energy ;**
7. **which drives the <u>phosphorylation of ADP to ATP</u> ;**
8. **<u>catalysed by ATP synthase</u> ;**

Differences between chemiosmosis in photosynthesis and respiration:

Features		Photosynthesis		Respiration
occurs during	9.	photophosphorylation ;	10.	oxidative phosphorylation ;
location	11.	occurs at thylakoid membrane of chloroplast ;	12.	occurs at the inner mitochondrial membrane ;
source of energy for ATP synthesis	13.	energy for ATP synthesis comes from light ;	14.	energy for ATP synthesis comes from glucose oxidation ;
source of electrons	15.	from water	16.	from reduced NAD and reduced FAD
accumulation of protons in	17.	thylakoid lumen / space ;	18.	intermembrane space ;
flow of protons through ATP synthase	19.	from thylakoid lumen to stroma ;	20.	from intermembrane space mitochondrial matrix ;

- **Pt 1-20: max 14**

<u>QWC [1]</u>
Clearly expressed, using correct terminology to address chemiosmosis and marking clear features of contrast between chemiosmosis in photosynthesis and respiration.

(b) Describe how the molecular structure and properties of cellulose are related to its functions. [10]

Structure

1. **A cellulose molecule consists of a (long) straight chain ;**
2. **of (many) β-glucose residues ;**
3. **joined by β-1,4 glycosidic bonds ;**
4. **Successive β-glucose residues are rotated 180° with respect to the adjacent residue ;**
5. **which results in the –OH groups projecting outwards from each cellulose chain in all directions ;**
6. **Hydrogen bonds are formed between the –OH groups of (neighbouring) cellulose chains ;**
7. **lying in parallel ;**
8. **resulting in (extensive) cross-linking ;**
9. **that binds the chains rigidly together to form microfibrils and macrofibrils ;**

Properties

10. **which confer high tensile strength, stability and support ;**
11. **AVP – (the extensive hydrogen bonds) result in cellulose being insoluble (in water) ;**

Function

12. **Cellulose is the main structural component of plant cell walls ;**
13. **The high tensile strength of microfibrils prevents the plant cell from bursting/lysing when water enters by osmosis ;**
14. **As a plant cell inflates with water, pressure develops inside it and the cell becomes turgid (turgid cells help support plants which lack wood) ;**
15. **The arrangement of fibres around the cell helps to determine the shape of the plant cell as it grows ;**
16. **AVP – the arrangement of fibres at angles/criss-cross allows passage of water (A: named substances) / makes cell wall permeable ;**

- **Pt 1-11: max 9**
- **Pt 11 & 16: max 1**
- **Award for accurately drawn + annotated diagram if MP not scored for response in prose**

QWC [1]

Clearly expressed using the correct terminology and communicated without ambiguity to describe molecular structure, properties and function of cellulose ;

[Total: 25]