TEMASEK JUNIOR COLLEGE

2023 JC2 PRELIMINARY EXAMINATION

Higher 2

CANDIDATE NAME: **ANSWERS**

CENTRE NUMBER: S | | | | | INDEX NUMBER: | | | | |

BIOLOGY

9744/02

Paper 2 Structured Questions **(Part I)**

25 AUGUST 2023

2 hours

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

READ THESE INSTRUCTIONS FIRST

Write your Center number, index number 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.
DO **NOT** WRITE IN ANY BARCODES.
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 any working or if you do not use appropriate units.

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

For Examiner's Use	
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2	/ 11
3	/ 11
4	/ 10
5	/ 8

This document consists of **16** printed pages.

Answer **all** questions.

1 Fig. 1.1 shows an electron micrograph of a plant cell.

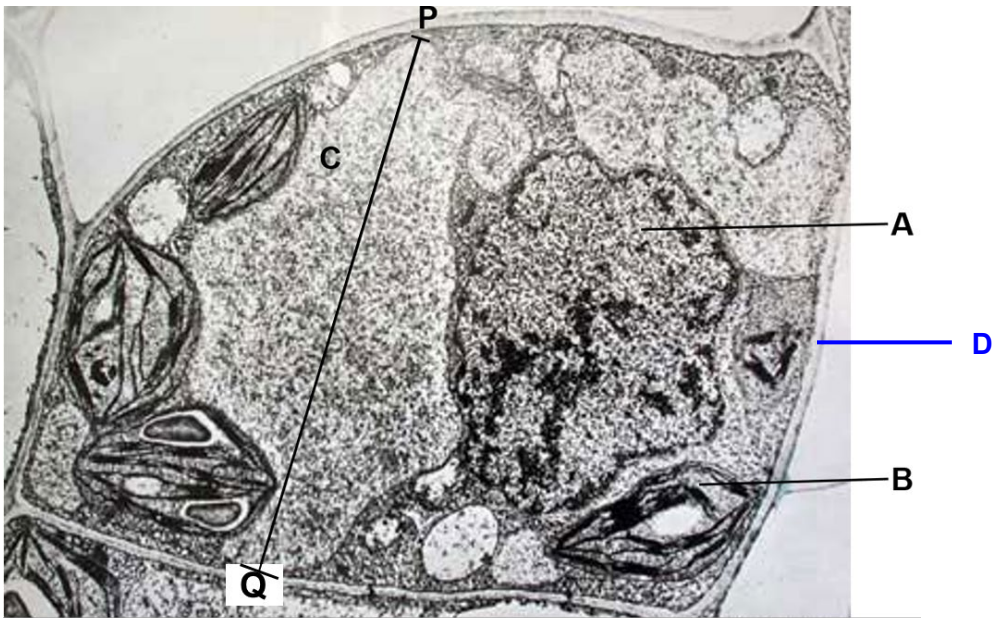

Fig. 1.1

(a) Identify the organelles labelled **A**, **B**, and **C** in Fig. 1.1.

A: **Nucleus**

B: **Chloroplast**

C: **Vacuole** [3]

(b) Use a line to label the cell wall, **D**. [1]

(c) The magnification of the photomicrograph is 560x.

Calculate the actual length of organelle **C** in µm, along the line **P**-**Q**. Show your working.

Length of PQ = 74 mm [1/2] (A: 73, 74, 75 mm)

Actual length of organelle C = $\frac{\text{length of image}}{\text{magnification}}$ **[1/2]**

$$= \frac{74 \times 1\,000\ \mu m}{560} = 132.1\ \mu m \text{ (A: 132.14 for 2 d.p.)}$$

actual length of organelle **C: 132.1 [1]** µm [2]

[1/2] – formula
[1/2] – state measurement of length PQ
[1] – correct final answer (number) on the line provided

(d) Compare the structural features of organelle **A** and organelle **B**. [2]

Similarities [any 1]:

1. **Both of them are bound by double membrane.**
2. **Both of them contain DNA (and RNA).**

Differences [any 1]:

3. **Nucleus has linear DNA while chloroplast has circular DNA.**
4. **Nucleus does not thylakoids while chloroplast has thylakoid membranes inside.**
5. **Nucleus does not contain ribosomes but chloroplast contain 70S ribosomes.**
6. **Presence of chlorophyll pigments/photosystems in chloroplasts vs absent in nucleus**
7. **Nucleus is larger / denser than chloroplast.**

AVP:
A outer membrane is continuous with RER, but not B
B has electron carriers / ATP synthase but not A
B has starch grains but not A

(e) A factor that can limit the rate of photosynthesis is the rate of regeneration of RuBP.

Sedoheptulose-1,7-bisphosphatase (SBPase) is an enzyme in the Calvin cycle that controls the rate of regeneration of RuBP. SBPase is coded for by the gene *SBPase*, which is present in most plants.

In an experiment, 2 wheat plants were studied.

- one was genetically modified to make more SBPase by introducing the *SBPase* gene from another grass species.
- one was not modified (wild type).

Fig. 1.2 shows the mean mass of plant for the wild type plants and genetically modified plants.

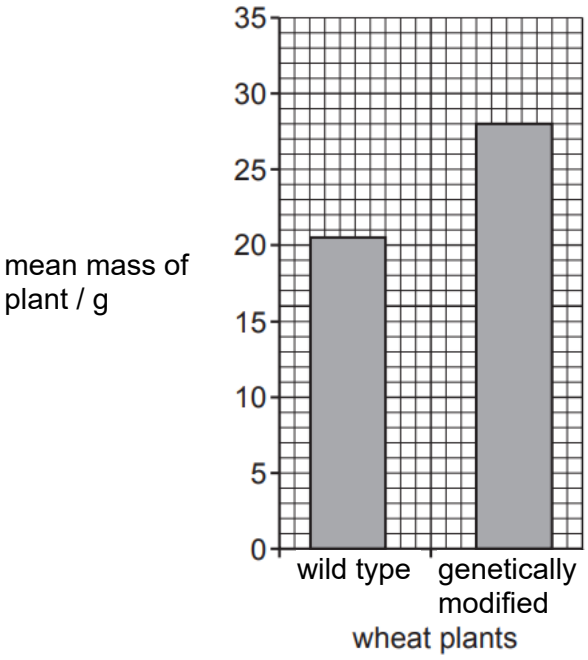

Fig. 1.2

Suggest and explain why genetically modified plants have a different mean mass than wild type plants. [4]

1. Must mention: genetically modified plants (GMP) has higher biomass of 28g than wild type with 20.5g [1]

   [1/2 each]
2. GMP plants have an extra copy of SBPase gene / new type of SBPase gene
3. (overall) increased, expression / transcription, of SBPase gene (so more SBPase)

4. increased rate of / more, regeneration of RuBP
5. (so) increased / more, carbon fixation / Calvin cycles / light independent reaction / TP / GP
6. more, glucose synthesized, for cellular respiration [1/2]

7. more starch is stored [1/2]
8. more amino acids [1/2] / proteins for growth [1/2]

[Total: 12]

2 Fig. 2.1 shows an electron micrograph of a mitochondrion. The labelled arrows **X** and **Y** both represent a structural feature of this organelle.

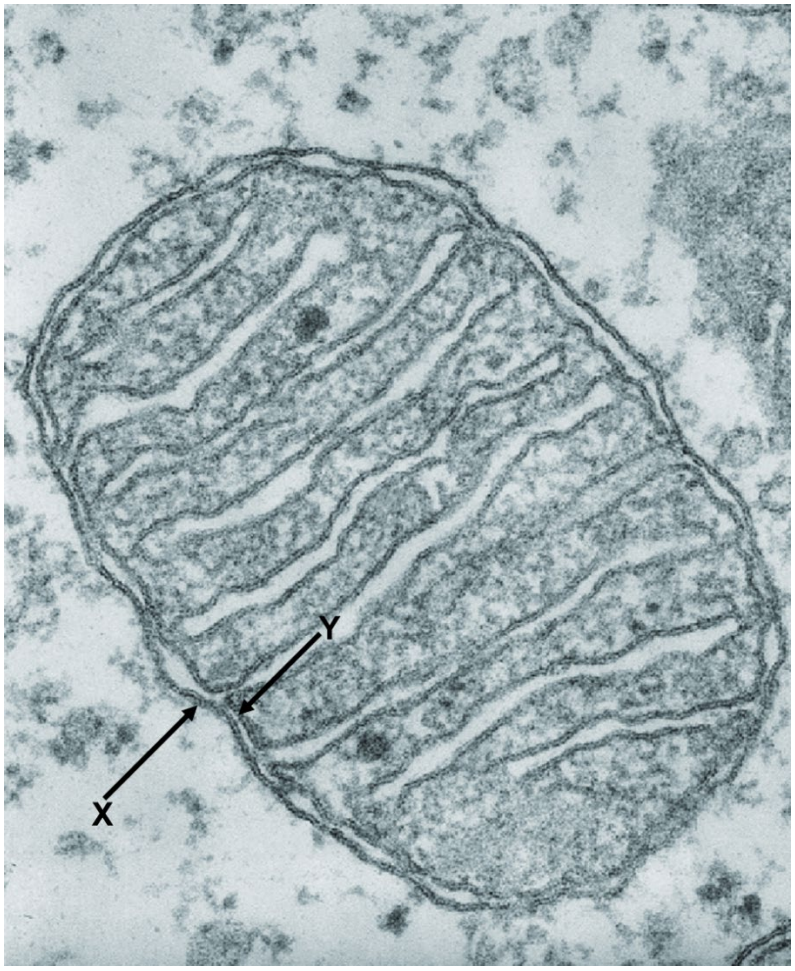

Fig. 2.1

The table below shows the protein composition of various areas in the mitochondrion in Fig. 2.1.

Table 2.1

labels	protein composition / %
X	6
Y	21
region between **X** and **Y**	6
inside mitochondria	67
total	100

(a) Using the information in Table 2.1 above,

(i) state the name of the structures labelled **X** and **Y**;

X outer mitochondrial membrane

Y inner mitochondrial membrane [2]

(ii) account for the abundance of protein inside the mitochondrion. [2]

1. **Protein composition inside W is high at 67% [1]**
2. **as there are abundant enzymes needed for Krebs cycle and link reaction [1]**

R: If candidate mentioned all processes e.g., glycolysis, link reaction, Krebs cycle, oxidative phosphorylation.

Newborns have a large amount of brown fat tissue, which contains abundant mitochondria. Brown fat cells express the protein, thermogenin, which is embedded in the inner mitochondrial membrane. Protons flow through the channel in thermogenin instead of ATP synthase. As a result, the proton gradient is less steep, and energy is released in the form of heat. This keeps the babies warm.

The mitochondrial matrix has a pH of about 7.8. The intermembrane space of mitochondria in different cells exhibits different pH values, as shown in Table 2.2.

Table 2.2

cells from which mitochondria are isolated	pH in intermembrane space
resting muscle	7.0
muscle during exercise	6.8
brown fat	7.4

(b) **(i)** Explain the difference in pH values in the intermembrane space and the matrix of the mitochondria in the resting muscle cells. [3]

1. **QF: The intermembrane space has a lower pH value of 7.0 compared to pH 7.8 in the matrix [1]**

2. **Reduced NAD and FAD release high energy electrons [1/2]**
3. **electrons are passed down the electron transport chain (electron carriers of decreasing energy levels), energy is released [1/2]**
4. **Energy is used to pump proton from the matrix into the intermembrane space, [1/2]**
5. **building a proton pool / maintain a proton gradient [1/2]**

(ii) Explain how low oxygen concentration will result in the newborns suffering from a drop in body temperatures. [2]

any 4 – ½ each

1. **Oxygen acts as the final electron and proton acceptor in the electron transport chain**
2. **When the concentration of oxygen is low, less reduced NAD and FAD molecules are able to release electrons into the ETC / less transfer of electrons down the electron carriers**
3. **Hence, less pumping of H+ from matrix to IMS**
4. **The proton concentration will reduced / reduction of proton gradient OWTTE**
5. **Less protons flow through thermogenin and ATP synthase, and less heat is produced**

(iii) The respiratory processes in the mitochondria require oxygen. Explain how oxygen is transported into the mitochondria. [2]

1. **Oxygen is a small [1/2]**
2. **and non-polar molecule [1/2]**
3. **Hence, it can diffuse across the hydrophobic core of the phospholipid bilayer of the mitochondrial membrane [1]**

[Total: 11]

3 Glycogen phosphorylase is an enzyme involved in glycogenolysis.

Fig 3.1 shows a model of the enzyme glycogen phosphorylase. Glycogen phosphorylase catalyses the hydrolysis of glycosidic bonds to break up glycogen into glucose subunits. The active site of glycogen phosphorylase is located in a slight depression on one side of the molecule. The three amino acids that form the active site are Serine, Histidine and Aspartic Acid. These three amino acids are some distance apart on the polypeptide chain but close together in the active site.

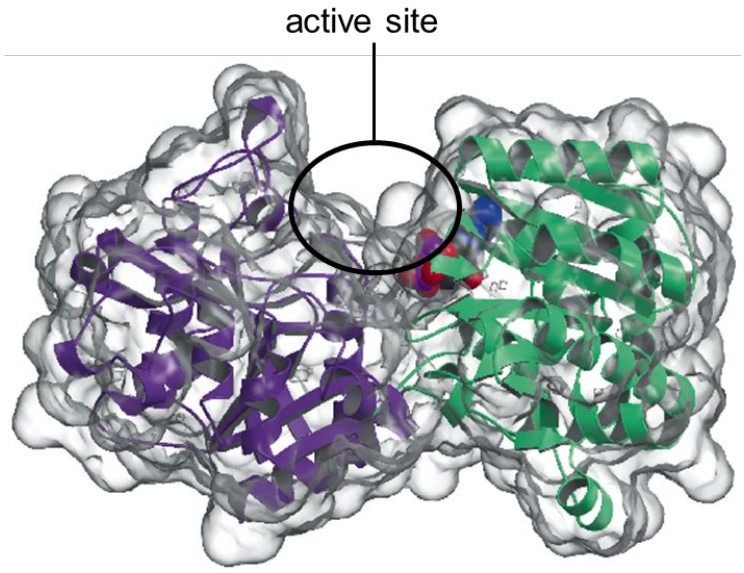

Fig. 3.1

(a) Explain how the substrate may be attached to the enzyme. [2]

1. **(Temporary) bonds are formed between substrate and R groups of contact residues of active site of the enzyme.**
   ½ mark if "contact residues" or "R groups" is missing.

2. **Hydrogen bonds / ionic bonds / hydrophobic interactions** *(any two)*
   ½ mark if only one named bond.

(b) Explain what determines the precise position of the three amino acids in the active site of the enzyme. [3]

1. **The sequence of nucleotides in the gene coding for glycogen phosphorylase**
2. **determines the specific sequence of amino acid in the polypeptide chain.**
3. **The polypeptide chain will proceed to fold into repeated alpha helix / beta pleated sheets.**
4. **Hydrogen bonds formed between -N-H and -C=O of peptide linkages.**
5. **Further fold into a compact, precise, globular, 3D molecule which allows the three amin acids to be found within the active site.**
6. **Hydrogen bonds / hydrophobic interactions / ionic bonds / disulfide bonds between R groups of amino acid residues.**

(c) On Fig. 3.2, draw the predicted changes in enzyme activity as pH changes.

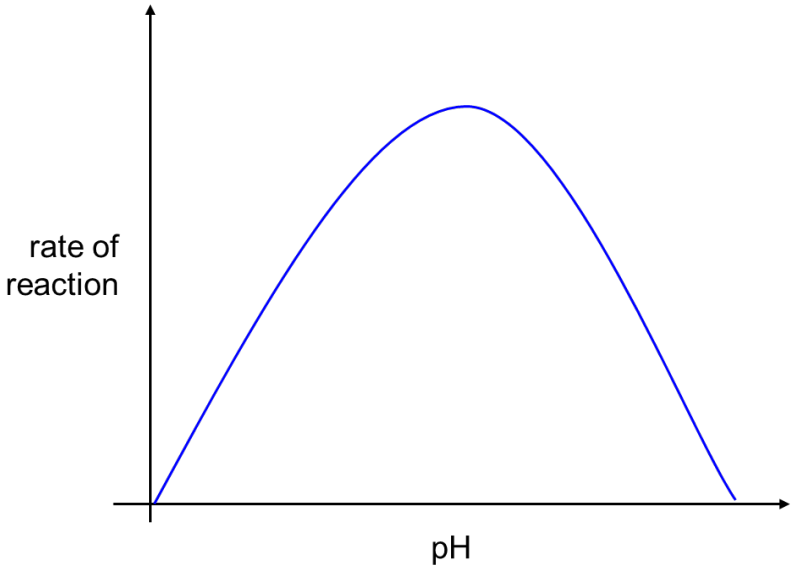

Fig. 3.2

[1]

Fig. 3.3 shows a cell signalling pathway that regulates the activity of glycogen phosphorylase.

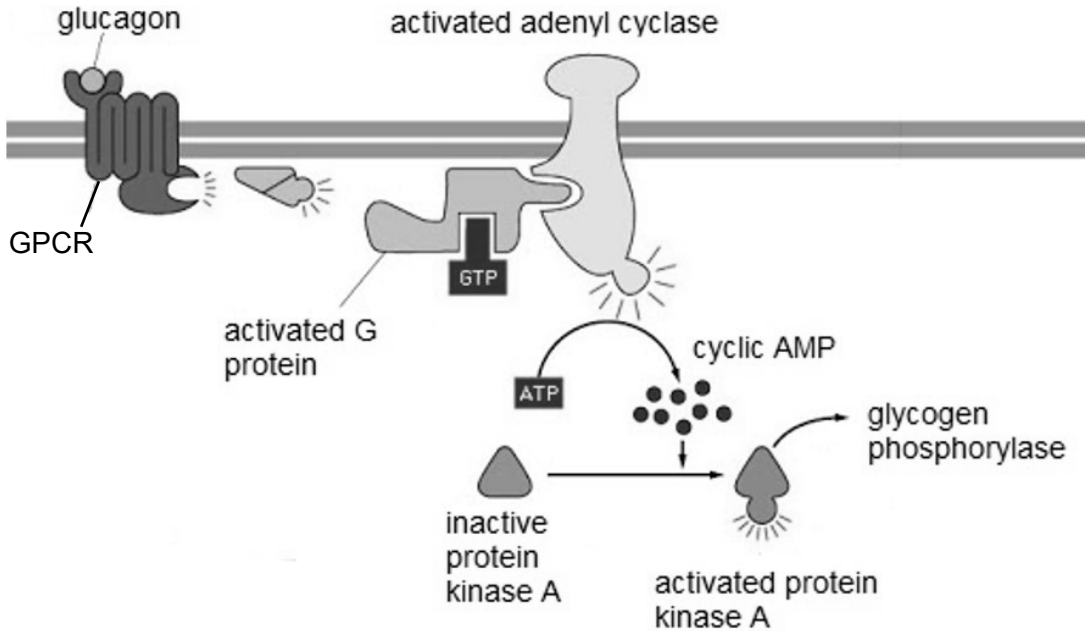

Fig. 3.3

(d) With reference to Fig. 3.3 and your own knowledge,

(i) describe how G protein is activated upon binding of glucagon to GPCR; [2]

1. **Binding of signal molecule results in the conformational change in the GPCR**
2. **and activates the GPCR**
3. **cytoplasmic side of the activated GPCR now binds to an inactive G protein.**
4. **causing a GTP molecule to displace the GDP molecule and activates the G protein.**

(ii) explain how the signal is amplified in the pathway. [1]

Activation of one adenylyl cyclase results in the production of many cyclic AMP molecules

(e) An inhibitor of protein kinase A is introduced into the cells of an individual. Predict and explain what would happen to the individual after prolonged hours of fasting. [2]

[Predict]

1. **Individual will feel faint due to lesser / no glucose for respiration / low blood glucose concentration.**
2. **Increased glucagon secretion by alpha cells of islets of Langerhans of pancreas.**

[Explain]

3. **(Inhibited) PKA cannot activate glycogen phosphorylase.**
4. **Glycogen cannot be hydrolysed to form glucose subunits.**

[Total: 11]

4 Using fluorescent dye, centromere can be visualised as a single dot. The centromere of a chromosome with pair of chromatids will appear as one dot.

The total number of dots corresponds to the total number of centromeres within the cell.

Table 4.1 shows the number of dots observed per cell, at various stages of meiosis.

Table 4.1

stage of meiosis	prophase I	prophase II	anaphase II	telophase II
number of dots observed per cell	16	8	16	16

(a) With reference to Table 4.1,

(i) complete Table 4.1 by stating the number of dots (i.e. centromeres) observed in prophase II and anaphase II respectively; [2]

(ii) explain your answer in **(a)(i).** [3]

1. **At the start / Prophase I, the cell has total of 16 chromosomes, giving rise to 16 dots.**
2. **Each chromosome consists of 2 sister chromatids joined together at the centromere.**
3. **End of meiosis I, homologous chromosomes have separated.**
4. **Prophase II: Only 1 set of homologous chromosomes / 8 chromosomes in each cell.**
5. **Anaphase II: Centromeres divide (C.D.) as chromatids separate and move to opposite poles of the cell.**
6. **Each chromatid has 1 centromere**

In a separate experiment, scientists studied the movement of chromosomes during meiosis in the animal cell.

The changes in distance between a corresponding region of a pair of homologous chromosomes (**X**) were measured over the course of the first meiotic division.

The results are shown in Fig 4.1 below.

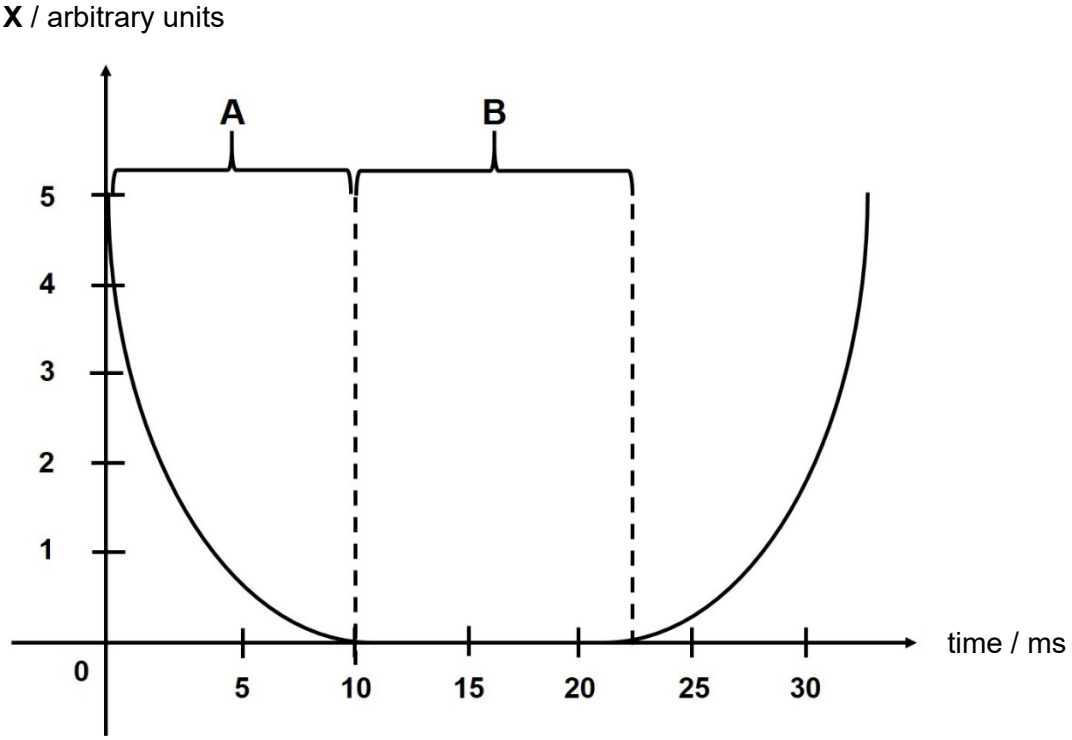

Fig. 4.1

(b) With reference to Fig. 4.1,

(i) identify the stage of meiosis at part **A**; [1]

Prophase 1

(ii) account for the changes at part **B**. [2]

1. **QF: X remains constant at 0 a.u.;**
2. **Homologous chromosomes pair up / synapsis of homologous chromosome**
3. **Arranged in 2 rows at the metaphase plate / equator**
4. **during metaphase I**

(c) State the role of the following processes in sexually reproducing organisms:

(i) meiosis [1]

meiosis produces haploid gametes

(ii) mitosis [1]

Any one:

1. **Maintain genetic stability of daughter cells**
   OR
   Leads to genetically identical daughter cells

2. **Growth and development of a multicellular organism**
   OR
   Development of zygote to embryo

3. **Replacement of cells of worn-out tissues**

4. **Immune response (cloning of activated B / T cells)**

[Total: 10]

5 Multicellular organisms are made up of different types of cells that form tissues and organs with specialised functions. All of these cells were originally stem cells.

(a) (i) Describe how totipotent stem cells differ from pluripotent stem cells. [2]

1. **Totipotent stem cells – have the ability to differentiate into any cell type to form whole organisms, as well as the placenta**

   while

2. **Pluripotent stem cells – have the ability to differentiate into almost any cell type except the placenta**

(ii) Stem cells differentiate to become specific cell types through a process called specialisation. Specialisation occurs through differential gene expression.

All totipotent stem cells contain the same genes. However, not all of these genes are ultimately expressed in specialized cells.

Suggest one way how this can take place. [1]

1. **DNA methylation**
2. **Long-term inactivation of genes**

   OR

3. **Genes are switched off**
4. **Packed into heterochromatin**

The differentiation of a eukaryotic stem cell into a specialised cell is controlled by many genes.

Fig. 5.1 summarises the interactions of some of these genes. The arrows represent the genes being switched on.

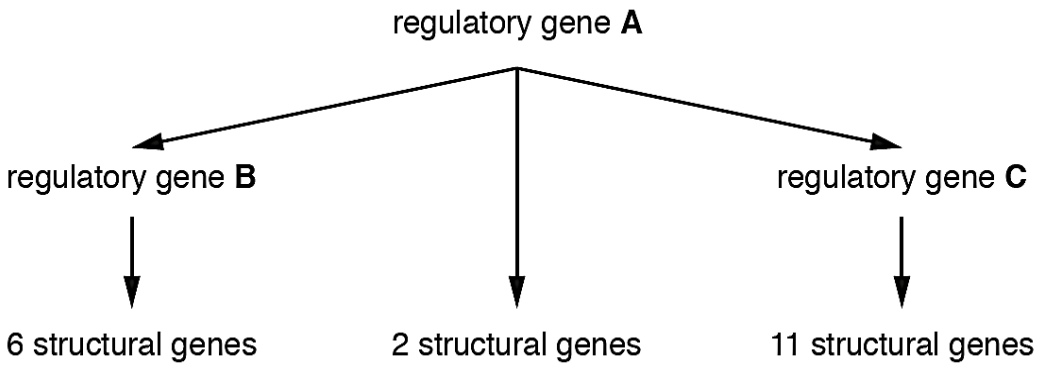

Fig. 5.1

(b) With reference to Fig. 5.1, explain how regulatory genes **A**, **B** and **C** are able to switch on other genes. [3]

1. Genes A, B & C code for activators [1/2]
2. which bind to enhancer. [1/2]
3. easier for RNA polymerase and general transcription factors to bind to promoter; [1/2]
4. transcription occurs at a faster rate; [1/2]

5. QF any 1 from Fig 5.1: [1]
   - gene A codes for TF/activator (a) which switches on 4 genes (b) / genes B and C and 2 other genes
     OR
   - gene B codes for TF/activator (a) which switches on 6 genes (b)
     OR
   - gene C codes for TF/activator (a) which switches on 11 genes (b)

In the differentiation of lymphoid stem cells, somatic hypermutation also occurs.

(c) Explain how somatic hypermutation differs from mRNA splicing. [2]

Any two:

1. Somatic hypermutation happens in activated B cells only whereas mRNA splicing happens in all cells that synthesise proteins.

2. Hypermutation involves mutation of gene segments/variable region coding sequences whereas mRNA splicing involves the removal of introns.

3. Hypermutation happens before transcription whereas mRNA splicing happens after transcription.

4. Hypermutation involves many point mutations whereas mRNA splicing does not involve mutations.

5. mRNA splicing involves snRNPs while hypermutation do not.

6. Hypermutation occurs at the DNA level while mRNA splicing occurs at the pre-mRNA level.

[Total: 8]

[End of Paper 2 Part 1]

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Answer **all** questions.

6 Fig 6.1 represents the main sequence of events in oxidative phosphorylation.

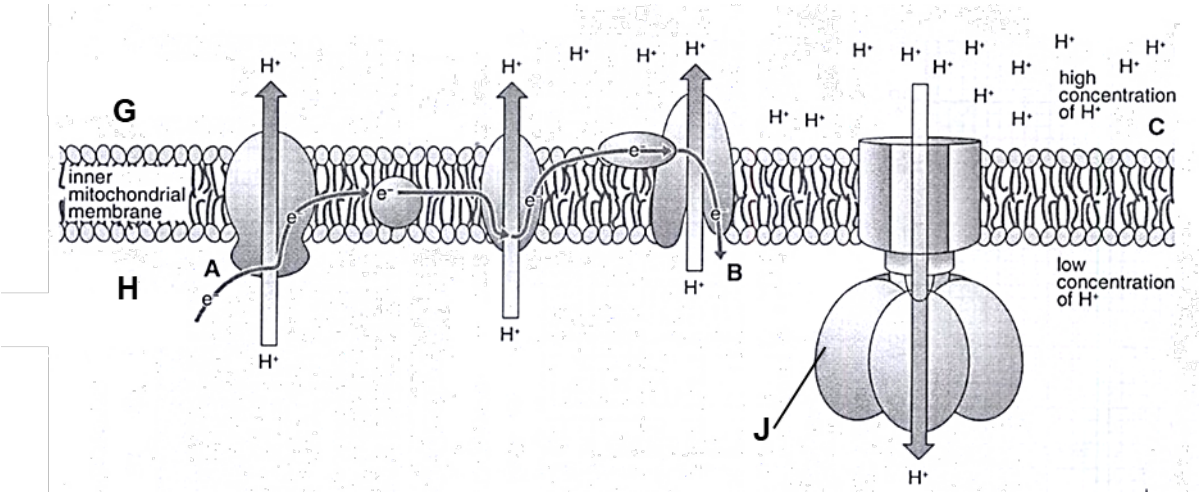

Fig. 6.1

(a) With reference to Fig. 6.1, identify the following:

Region **G**: **intermembrane space**

Region **H**: **mitochondrial matrix**

Protein **J**: **ATP synthase / stalked particle** [3]

(b) Briefly describe how ATP is synthesized during oxidative phosphorylation. [2]

1. **NADH and $FADH_2$ donate electrons to electron carriers of the electron transport chain.**
2. **Energy released from flow of electrons in electron transport chain is used to pump H^+ from matrix to intermembrane space (ecf: Accept from H to G) to**
3. **create a steep proton gradient.**
4. **Diffusion of H^+ from intermembrane space to matrix through hydrophilic channel of ATP synthase down concentration gradient releases energy**
5. **Which is coupled to ATP synthesis, catalysed by ATP synthase in a process called chemiosmosis.**

In the mitochondria, replication of mtDNA is gives rise to many copies of mtDNA per mitochondrion. Fig. 6.2 shows a schematic diagram of the initiation of mtDNA replication.

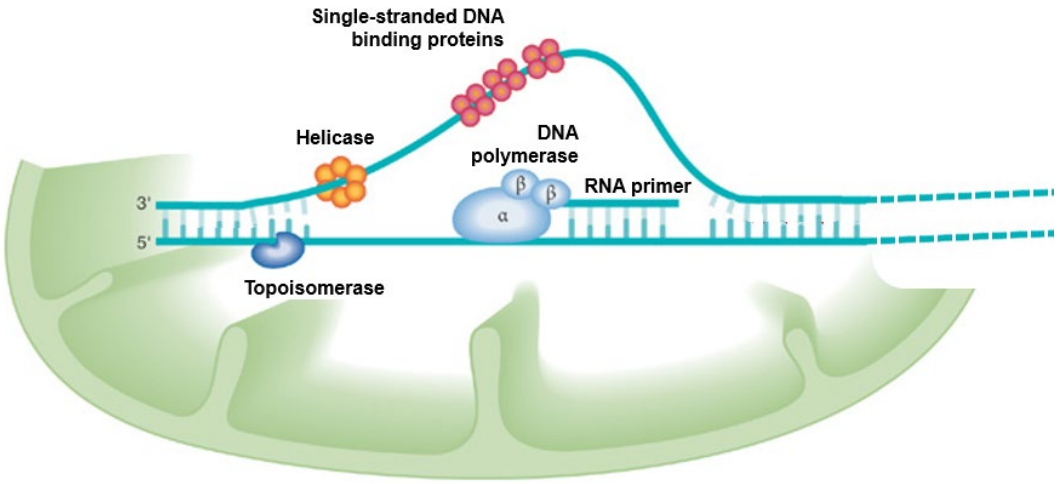

Fig. 6.2

(c) Compare the process in Fig. 6.2 and the polymerase chain reaction. [2]

Similarities (any 1)

1. **Both involve the synthesis of DNA / addition of free deoxyribonucleotides using DNA templates**
2. **Both involve DNA polymerases;**
3. **Both processes synthesise DNA using the semi-conservative mechanism / both DNA strands serve as templates for DNA replication / both involve complementary base pairing;**
4. **Both require primers for the elongation of new DNA strands;**
5. **New strands are synthesised in the 5' to 3' direction / template is read from 3' to 5' direction**

Differences (any 1)

6. **Helicase is required to separate the strands in mtDNA replication but PCR uses heating to 95°C**
7. **RNA primers used in mtDNA replication while DNA primers are used in PCR**
8. **Single-stranded DNA Binding Proteins (SSBPs) used in mtDNA replication but in PCR temperature is kept at a 55°C to allow annealing of primers but not reannealing of the template strands**
9. **DNA polymerase elongates DNA at body temperature / cellular conditions while thermostable Taq polymerase in PCR elongates DNA at 72°C**
10. **PCR only amplify a segment flanked by the primers but the whole mitochondrial DNA molecule can be replicated**
11. **Synthesis of new strands in PCR is continuous while in DNA replication the synthesis of leading strand is continuous and synthesis of lagging strand is discontinuous**

Mutations in the mtDNA often occur in the form of multiple or large-scale deletions involving several genes. As the number of mutated mtDNA copies increases in the cell, an individual will start to show symptoms such as lactate accumulation. The presence of normal and mutated mtDNA in the cells can be analysed using the following procedure.

1. Cells are homogenised. The cell mixture is first centrifuged at low speed and the pellet (solid residue) is removed.
2. The supernatant (liquid component) is then centrifuged again at a higher speed so that the mitochondria can be found in the pellet.
3. mtDNA is extracted from the mitochondria.
4. Restriction enzymes are added which cut the mtDNA at specific nucleotide sequences.
5. Gel electrophoresis is carried out.

Scientists carried out the above procedure using normal and mutated mtDNA from two different individuals – a patient suffering from lactate accumulation and a healthy individual. The results are shown in Fig. 6.4.

The DNA ladder was loaded in lane M. DNA sample from the patient was loaded in lane 1, while DNA sample from the healthy individual was loaded in lane 2.

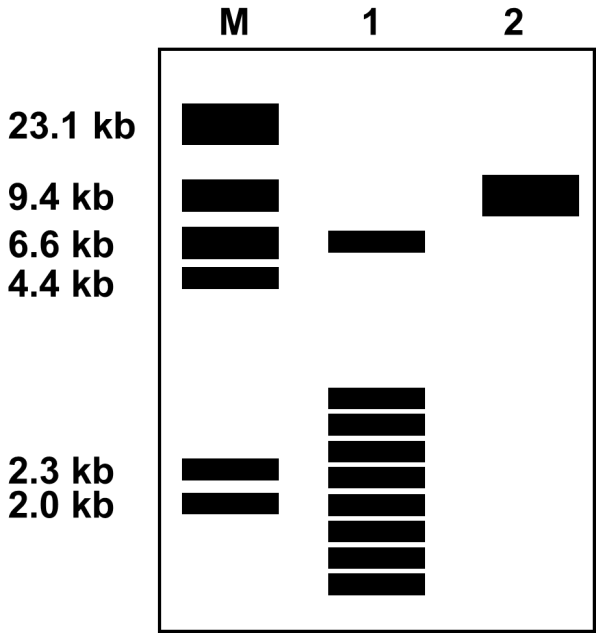

Fig. 6.4

(d) (i) Describe how the bands in a gel electrophoresis can be visualised. [2]

Ethidium bromide and UV light:

1. **EtBr is added to the agarose gel before it is poured into the gel casting tray.**
2. **After the DNA fragments are separated by gel electrophoresis, the agarose gel is placed under UV light to visualise the DNA bands.**

OR

Methylene blue:

1. **After the DNA fragments are separated by gel electrophoresis, the entire agarose gel is soaked in methylene blue overnight.**
2. **Methylene blue is able to bind to DNA, and each DNA band will be visible as a blue band.**

(ii) Explain why it was necessary to remove the pellet in step 1. [2]

1. **The largest and densest organelle is the nucleus and step 1 removes the nucleus**
2. **Nucleus contains genomic DNA which can contaminate the isolation of the mitochondrial DNA**

(iii) Using the information provided, explain why different band patterns are observed for lanes 1 and 2. [3]

any 3

1. **QF: In lane 1, there are smear / multiple bands corresponding to fragments of sizes below 9.4 kb, while in lane 2, there is a thick band corresponding to fragment of size 9.4 kb**
2. **Due to the accumulation of mutations, there are different nucleotide sequences**
3. **leading to different number of / more restriction sites found at different locations within the mtDNA (idea of different, either number or location is fine)**
4. **As many genes are deleted, many different / smaller fragments can be found further away from the well**

7 A study was carried out to examine the effectiveness of bacteriophages in treating *E. coli* bacterial infections.

(a) Name an example for

(i) a virulent phage;

T4 phage [1]

(ii) a temperate phage.

lambda phage [1]

(b) Suggest why the use of bacteriophages is a better alternative to antibiotic therapy. [1]

any 1

1. **Bacteriophages do not infect eukaryotic cells as they are host-specific. Hence, lesser side-effects to humans.**
2. **Bacteriophages will mutate alongside with the bacteria for long-term effectiveness (co-evolution)**
3. ***E.coli* may evolve resistance to the antibiotics over time.**

(c) Some Asian strains of the bacterium causing cholera, *Vibrio cholera*, have a gene named *SXT* on the F plasmid. The *SXT* gene confers resistance to commonly used antibiotics. *SXT* gene is also present in other bacterial species.

When some Asian strains of *Vibrio cholera* containing *SXT* gene is placed in a medium with other strains of *Vibrio cholera* which do not contain *SXT*, all the bacterial cells were found to contain *SXT* after some time.

(i) Name the process that enables *SXT* gene to be passed from Asian strains of *Vibrio cholera* containing *SXT* to strains of *Vibrio cholera* which do not contain *SXT*. [1]

Conjugation

(ii) Suggest **two** advantages of the process described in **(c)(i)** as compared to other mechanisms in generating genetic variation in bacterial cells.

[2]

any 2

1. **No need for the presence of a virus (transduction) / to make the cell competent (transformation);**
2. **Host cell is not lysed, unlike transduction;**
3. **Does not rely on chance e.g. chance that the host DNA fragments instead of phage genome are packaged (generalised transduction) / chance that the phage DNA is improperly excised (specialised transduction);**
4. **Higher chance of transferring genetic material as the donor and recipient bacterial cells make physical contact with each other;**
5. **Larger pieces of DNA can be transferred;**
6. **All defined genes of F plasmid are transmitted during conjugation vs random DNA fragments (via generalised transduction / transformation) OR only genes beside prophage (via specialised transduction);**

(d) Transfer of DNA from one species of bacterium to another is thought to be increased due to the so-called 'SOS response' of bacteria to DNA damage.

Measurements were made of the frequency of transfer of *SXT* gene from two species of donor bacteria grown in the presence or absence of two antibiotics.

- mitomycin, which is known to damage DNA;
- ciproflaxin, which is commonly prescribed for use against bacterial infections.

The results of the investigation are shown in Fig. 7.1.

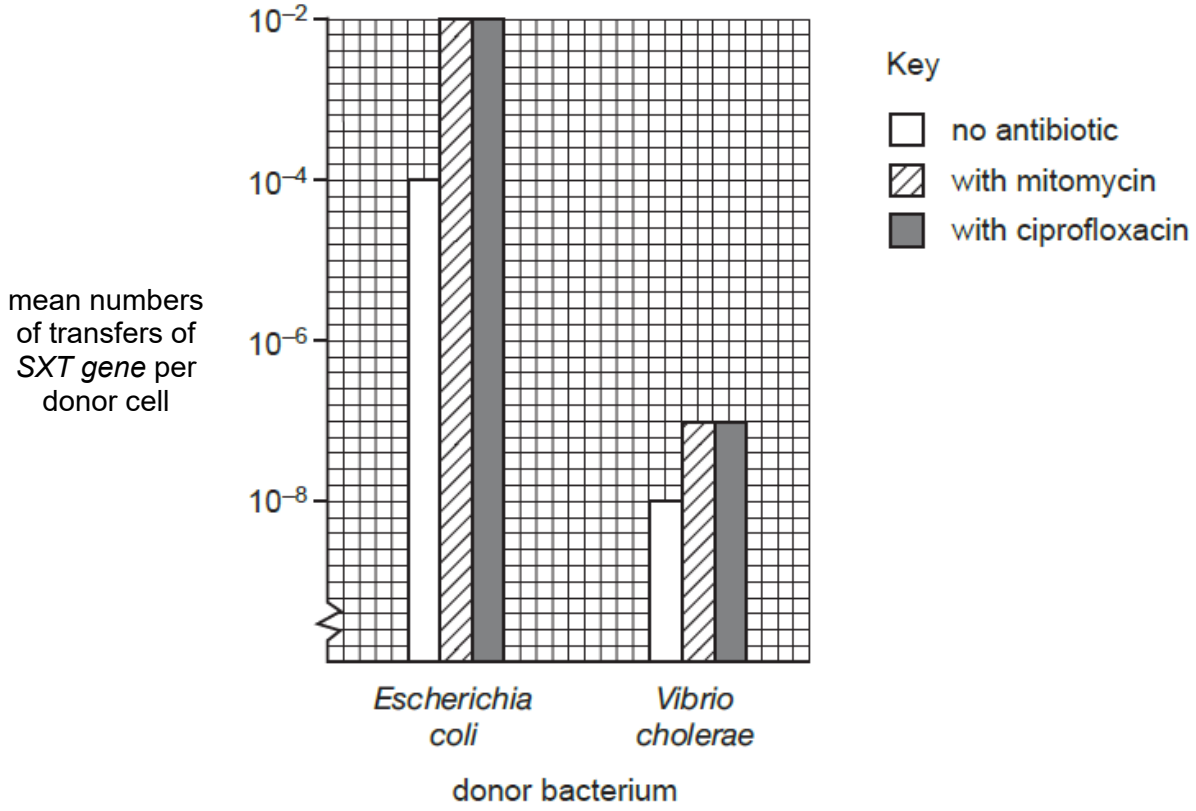

Fig. 7.1

(i) With reference to Fig. 7.1, compare the effect of the antibiotics on transfer of SXT from the two species of donor bacteria. [3]

any 3

1. **antibiotic increases transfer in both donors;**
2. **both antibiotics have same effect on both donors;**
3. **greater effect on *E. coli* than on *V. cholera*;**
4. **10x greater / 10^2 versus 10^1 / x100 versus x10;**

(ii) Suggest the likely effect on the frequency of the *SXT* gene when an infected patient did not complete the full course of ciprofloxacin. [1]

frequency of resistant alleles increase (and results in increase in number of resistant bacteria)

[Total: 10]

8 It was hypothesized that persons with higher weight have a higher chance of contracting breast cancer. To investigate the hypothesis, a mini study was done by recording the weight of the persons with or without breast cancer.

Table 8.1 shows the results of the study.

Table 8.1

weight of person with breast cancer / kg	weight of person without breast cancer / kg
80	60
73	55
86	65
109	53
87	60
70	55
65	45
80	59
66	56
77	70

(a) State the null and alternative hypothesis for this study. [2]

null hypothesis

There is no significant difference between the means of weight of person with breast cancer and without breast cancer.

alternative hypothesis:

The mean weight of persons with breast cancer is higher than the mean weight of persons without breast cancer.

Table 8.2 shows the critical values for the *t*-distribution.

Table 8.2

degrees of freedom	probability, p, for one-tailed test				
	0.10	0.05	0.025	0.01	0.005
	probability, p, for two-tailed test				
	0.20	0.10	0.05	0.025	0.01
1	1.00	6.31	12.71	63.66	636.62
2	0.82	2.92	4.30	9.92	31.60
3	0.76	2.35	3.18	5.84	12.92
4	0.74	2.13	2.78	4.60	8.61
5	0.73	2.02	2.57	4.03	6.87
6	0.72	1.94	2.45	3.71	5.96
7	0.71	1.89	2.36	3.50	5.41
8	0.70	1.86	2.31	3.36	5.04
9	0.70	1.83	2.26	3.25	4.78
10	0.70	1.81	2.23	3.17	4.53
11	0.70	1.80	2.20	3.11	4.44
12	0.70	1.78	2.18	3.05	4.32
13	0.69	1.77	2.16	3.01	4.22
14	0.69	1.76	2.14	2.98	4.14
15	0.69	1.75	2.13	2.95	4.07
16	0.69	1.75	2.12	2.92	4.01
17	0.69	1.74	2.11	2.90	3.97
18	0.69	1.73	2.10	2.88	3.92
19	0.69	1.73	2.09	2.86	3.88
20	0.69	1.72	2.09	2.85	3.85

The formulae to calculate standard deviation and the *t* value are:

standard deviation $s = \sqrt{\frac{\Sigma(x-\bar{x})^2}{n-1}}$

t-test $t = \frac{|\bar{x}_1 - \bar{x}_2|}{\sqrt{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)}}$

Key to symbols

s* = standard deviation	$\sum$ = 'sum of'	$\bar{x}$ = mean
n = sample size (number of observations)	x = observation	
v = degrees of freedom	O = observed 'value'	

(b) Carry out the *t*-test in the space provided.

Mean weight of person with breast cancer = 79.3
Mean weight of person without breast cancer = 57.8

Standard deviation of weight of person with breast cancer = 12.9
Standard deviation of weight of person without breast cancer = 6.8

$$t = \frac{79.3 - 57.8}{\sqrt{(\frac{12.9^2}{10} + \frac{6.8^2}{10})}} = 4.66$$

[1] – calculate means
[1] – calculate standard deviation
(A: presented as table)
[1] – correct substitution of values into formula (ecf)

[3]

(c) State the conclusion for the *t*-test. [2]

1. **For 18 degrees of freedom,**
2. **The calculated t-value of 4.66 is more than 1.734 (for a one-tailed t-test)**
3. **Therefore, the p-value is less than 0.05. The difference in means of the 2 samples is statistically significant, and not due to chance.**
4. **Reject null hypothesis. Hence, the mean weight of person with breast cancer is higher than the mean weight of person without breast cancer.**

(d) Comment on the validity of this study. [1]

1. **Not valid.**
2. **Sample size is too few / deviation within each group too high.**

[Total: 8]

9 The *Oncorhynchus* genus of fish contains five species of Pacific Salmon residing in the Pacific Ocean.

Fig. 9.1 shows two different ways of classifying the same five species of Pacific Salmon where

- classification **X** is based on morphological characteristics,
- classification **Y** is based on genetic characteristics.

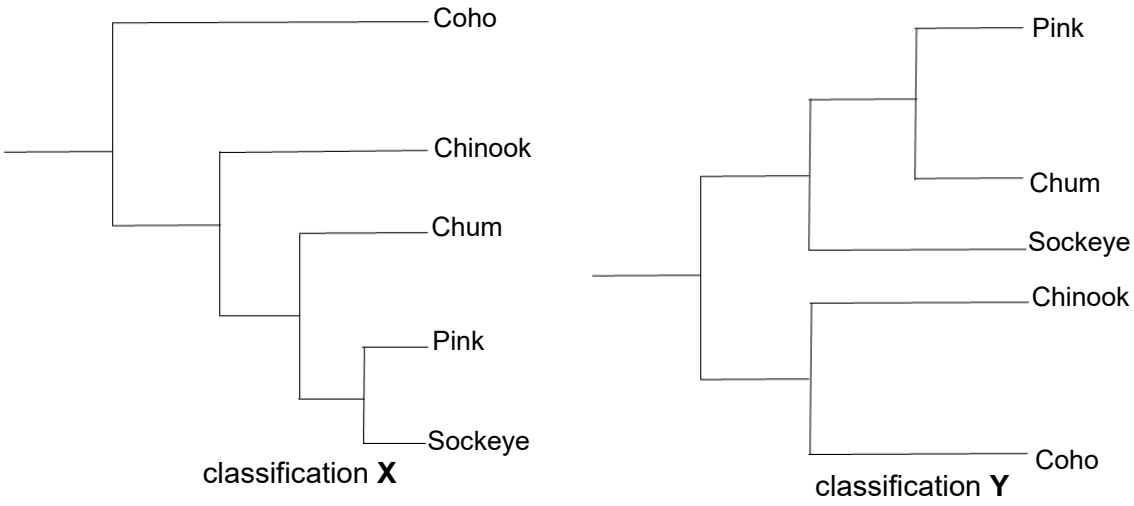

Fig. 9.1

(a) (i) Describe **two** differences in the evolutionary relationships amongst these five species of Pacific Salmon based on the two classifications shown in Fig. 9.1. [2]

Classification X	Classification Y
1. **Pink and Sockeye share a more recent common ancestor than Chum**	**Pink and Chum share a more recent common ancestor than Sockeye**
2. **Chinook shares a more recent common ancestor with Chum, Pink & Sockeye than with Coho**	**Chinook shares a more recent common ancestor with Coho than with the other 3 species**

(ii) State **one** reason why classification **Y** is a better representation of evolutionary relationships than classification **X**. [1]

1. **Molecular methods can be used for all organisms, living or dead.**
   - **All living organisms have nucleic acids and proteins so comparisons can be made.**
   - **Molecular methods can also be applied to dead or extinct organisms as long as DNA or protein can be obtained. E.g. DNA may be extracted from fossils.**

2. **Molecular methods are objective.**
   - **For example, DNA sequences in the form of A, T, C and G are unambiguous. Thus, differences in DNA sequences between organisms can be determined objectively.**
   - **This is unlike comparing certain morphological structures (e.g. shape) that are hard to distinguish resulting in subjective interpretation of the differences.**

3. **Molecular methods are quantitative.**

    - **Molecular data can be easily converted to numerical form for computation and analysis.**
    - **Thus, the degree of relatedness between species can be inferred by calculating number of nucleotide / amino acid differences between species.**
    - **Furthermore, molecular data can be uploaded into online electronic databases for easy retrieval in the future, or access by other scientists in other parts of the world.**
    - **This is not possible for morphological method which requires physical specimens.**

4. **Molecular methods are more accurate in establishing evolutionary relationships of organisms.**

    - **It avoids the pitfalls of convergent evolution where organisms appear morphologically similar due to adaptation to similar habitats but do not share a common ancestor (e.g. flying squirrel and sugar glider).**
    - **Conversely, it can be used to establish the evolutionary relationship between organisms that appear very differently but are actually closely related. This is because major phenotypic differences may be due to small genetic differences.**

The coho salmon spend equal time in freshwater streams, when they are young, and in the salt water, when they are adults.

Adults migrate back to the freshwater stream to spawn (release sperm or eggs).

Some males, known as jacks, begin the migration to the freshwater stream much earlier in their adult lives than the normal breeding adult males, known as hooknoses.

Fig. 9.2 depicts hooknoses and jacks. Jacks are much smaller than hooknoses and do not develop the hooked snout and large teeth.

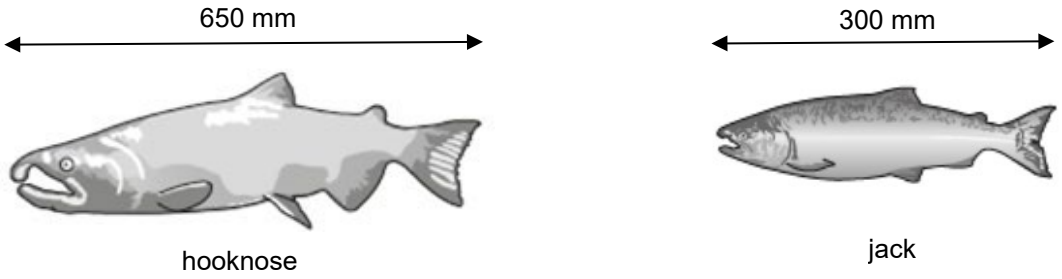

Fig. 9.2

Jacks and hooknoses employ different breeding strategies in order to spawn successfully.

- Jacks sneak around the smaller boulders on the stream bed and attempt to stealthily mate with a female.
- Hooknoses swim within the open water and fight aggressively amongst one another for the opportunity to mate with a female.

(b) Suggest **two** reasons why jacks are able to spawn as successfully as hooknoses. [2]

1. **jacks are smaller and hence can hide from predators**
2. **jacks spend less time in ocean and hence have higher chances of escaping predators**
3. **jacks lack large teeth and hence have different source of food**

Fig. 9.3 shows the variation in the body length of reproductively mature males in an original population of coho salmon, **before** evolution of the jack reproductive phenotype.

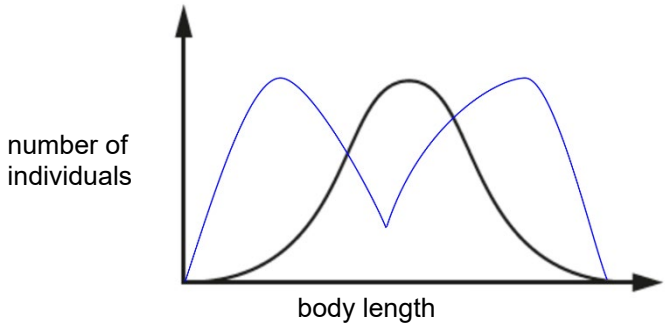

Fig. 9.3

Selection has since acted over time on this original population to change the distribution of body length in reproductively mature male salmon.

(c) (i) Sketch a curve on Fig. 9.3 to show the new distribution of body length in the present-day population of reproductively mature male salmon. [1]

Ans: Two peaks on both sides of normal peak

(ii) Explain the type of selection that has occurred. [2]

1. **disruptive selection [1]**
2. **selection pressure is exerted by breeding environment**
3. **jacks are smaller and are able to sneak better around boulders in stream bed, hooknoses are larger and are able to fight more aggressively**

[Total: 8]

10 A person who is confirmed as SARS-CoV-2-positive has also tested positive for the presence of antibodies to the virus.

(a) Outline the events that lead to the production of antibodies specific to SARS-CoV-2. [5]

max marking

1. **When SARS-CoV-2 infects a person, the primary immune response will be stimulated**
2. **SARS-CoV-2 /viral antigen is taken up by an antigen-presenting cell (APC),**
3. **via phagocytosis.**
4. **The antigen is processed by the APC and is bound to MHC class II receptors on the cell membrane of the APC.**
5. **The antigen is presented to naive CD4 T cells.**
6. **Naive CD4 T cells become activated,**
7. **proliferate and differentiates to form helper T cells**
8. **SARS-CoV-2 /viral antigen is also recognised by/ binds to B cells**
9. **Helper T cells fully activate B cells,**
10. **via release of cytokines.**
11. **B cells proliferate and differentiate to form plasma cells**
12. **that produce antibodies specific to SARS-CoV-2.**

As of June 2023, there are currently 8 common variants of the SARS-CoV-2 virus. These variants were observed to have slightly different glycoprotein spikes.

(b) Describe how these slightly different variants of the SARS-CoV-2 virus come about. [2]

1. **Antigenic drift [1]**
2. **Viruses have high mutation rates. [1/2]**
3. **Spontaneous random mutations result in conformational changes in the structure of viral glycoprotein spikes. [1/2]**

Various anti-SARS-CoV-2 antibodies, which can bind to different parts of the same virus, are found in the infected person.

(c) Suggest the significance of having various anti-SARS-CoV-2 antibodies produced in the infected person. [1]

any one

1. **To increase chances of binding to SARS-CoV-2**
2. **To increase chances of removal of SARS-CoV-2 by macrophages**
   Note: after the antigen-binding site of SARS-CoV-2 antibody binds to SARS-CoV-2, the Fc region can bind to receptor on macrophages, which will take up the virus and destroy the virus (using lysosomes)

3. **High mutation rates of SARS-CoV-2 could lead to changes in antigen on the virus→ but having various anti-SARS-CoV-2 antibodies means that the virus could still be recognised by the antibodies**

[Total: 8]

[End of Paper 2 Part 2]