JC1 2023
H2 PROMOTIONAL EXAMINATION
ANSWERS

SECTION A: MCQ

1	**C**	6	**A**	11	**A**	16	**B**
2	**A**	7	**A**	12	**D**	17	**B**
3	**D**	8	**C**	13	**D**	18	**C**
4	**B**	9	**B**	14	**B**	19	**A**
5	**C**	10	**A**	15	**D**	20	**B**

SECTION B: STRUCTURED QUESTIONS

1 (a) Fig. 1.1 shows the behaviour of eight chromosomes in one stage of meiosis of a diploid plant cell.

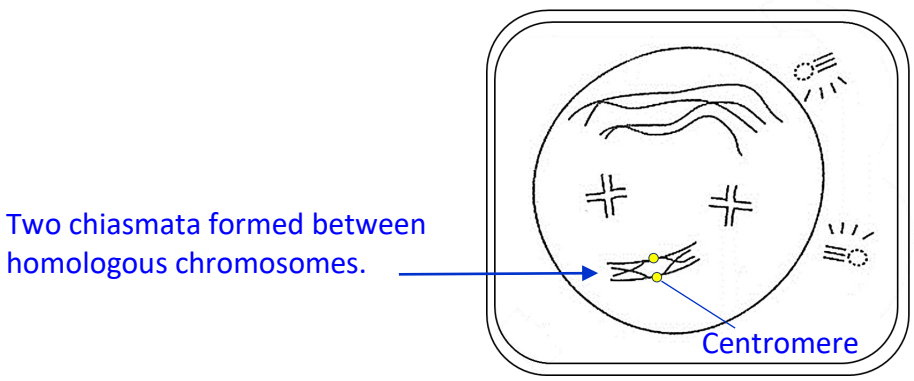
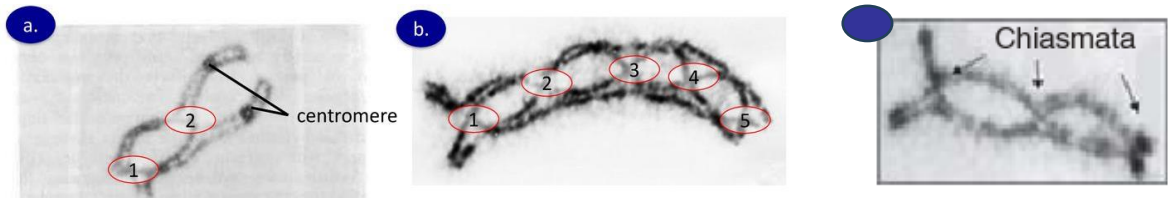


Fig. 1.1

Additional info. A pair of homologous chromosomes with multiple chiasmata.



(i) **Name** the stage of the nuclear division. [1]

Prophase I

(ii) Based on the observation of the chromosomes in Fig. 1.1, **explain why** it **cannot** be a stage in mitosis. [1]

During prophase of mitosis, homologous chromosomes do not pair up / no chiasmata formation / no crossing over. (Note the phrasing of the answer is with respect to mitosis.)

Accept opposite:
There is pairing of homologous chromosomes / chiasmata formation / crossing over between homologous chromosomes which only happen during prophase I of meiosis. (Note the phrasing of the answer to show that it cannot be a stage of mitosis.)

Feedback / comment

1. **Candidates are reminded to address the question fully instead of just describing the feature of prophase I. (See above answer)**

2. **[Phrasing error]: "There are pairs of homologous chromosomes."**
   [Conceptual error]: "There are no homologous chromosomes during mitosis".

   Both answers are rejected as there are homologous chromosomes in cells undergoing mitosis, but they do not pair up.

(iii) The diploid number of the flowering plant is 8. Complete Table 1.1 to show the number of chromosomes found in the cell at the end of each stage of the meiotic cell cycle.

Table 1.1

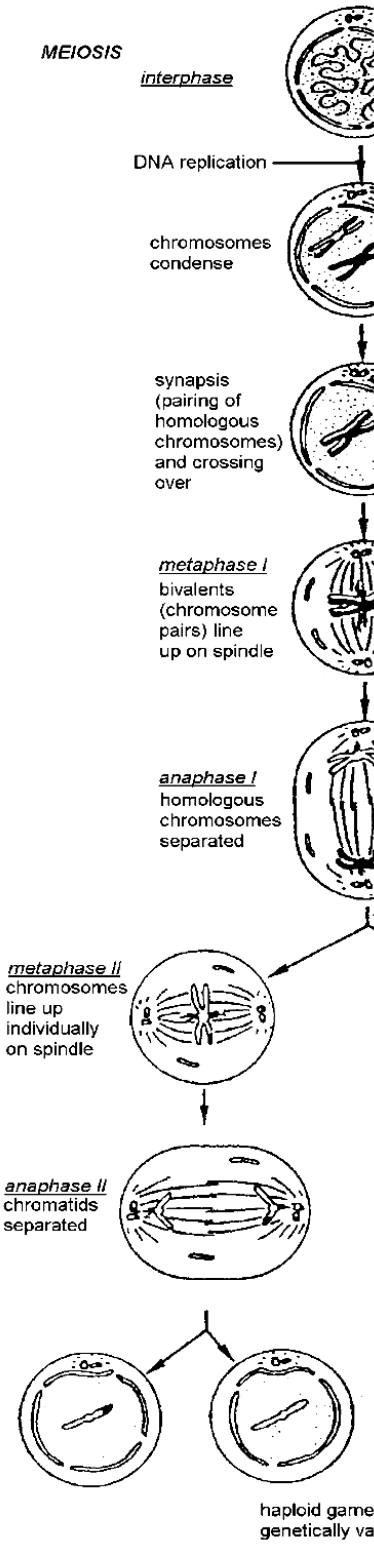
stage	no. of chromosomes per cell
G1	8
S phase **After DNA replication,** **2 DNA molecules (as 2 sister chromatids are joined together at centromere)** **→ each is 1 chromosome**	**8**
Anaphase I **Although homologous chromosome separates, cytokinesis has not taken place yet.**	**8**
Telophase I **Although homologous chromosome reach opp. poles of the cell, cytokinesis has not taken place yet.**	**8**
Cytokinesis I	4
Cytokinesis II **Chromatids separated and reach opp. poles of the cell + cell has divided into 2**	**4**

[2]

Feedback / comment

1. **Candidates generally found this question challenging and did not get full credit. However, some candidates sketched the chromosomes in empty spaces to help visualize the number and could get full credit.**

There are 2 chromosomes in Fig. 20, Cell cycle notes page 33.



Interphase (G1, S, G2)
No. of chromosomes per cell = 2

Prophase I
No. of chromosomes per cell = 2

Metaphase I
No. of chromosomes per cell = 2

Anaphase I
No. of chromosomes per cell = 2

Cytokinesis I
No. of chromosomes per cell = 1

Metaphase II
No. of chromosomes per cell = 1

Anaphase II
No. of chromosomes per cell = 2

Cytokinesis II
No. of chromosomes per cell = 1

For STQ 1a(iii)
No. of chromosomes per cell = 8 (given)

No. of chromosomes per cell = 8

No. of chromosomes per cell = 8

No. of chromosomes per cell = 8

No. of chromosomes per cell = 4 (given)

No. of chromosomes per cell = 4

No. of chromosomes per cell = 8

No. of chromosomes per cell = 4

(iv) With reference to Table 1.1, **explain** the change in the number of chromosomes per cell by the end of cytokinesis I. [1]

1. **During anaphase I, homologous chromosomes are separated to opposite poles.**

2. **Cytokinesis I resulted in two daughter cells. Each daughter cell has half the number of chromosomes from the original/parent cell / 4 chromosomes / 1 set of chromosomes.**

   Note: "Daughter cell" should be mentioned at least once.

Feedback / comment

1. **[Incorrect phrasing] "Homologous chromosomes are split into the daughter cells during cytokinesis I." (incorrect to say "split")**

   [Correct phrasing] Homologous chromosomes are separated equally into each of the 2 daughter cells during cytokinesis I.

Fig. 2.1 shows the change in the amount of DNA per nucleus during a meiotic cell cycle.

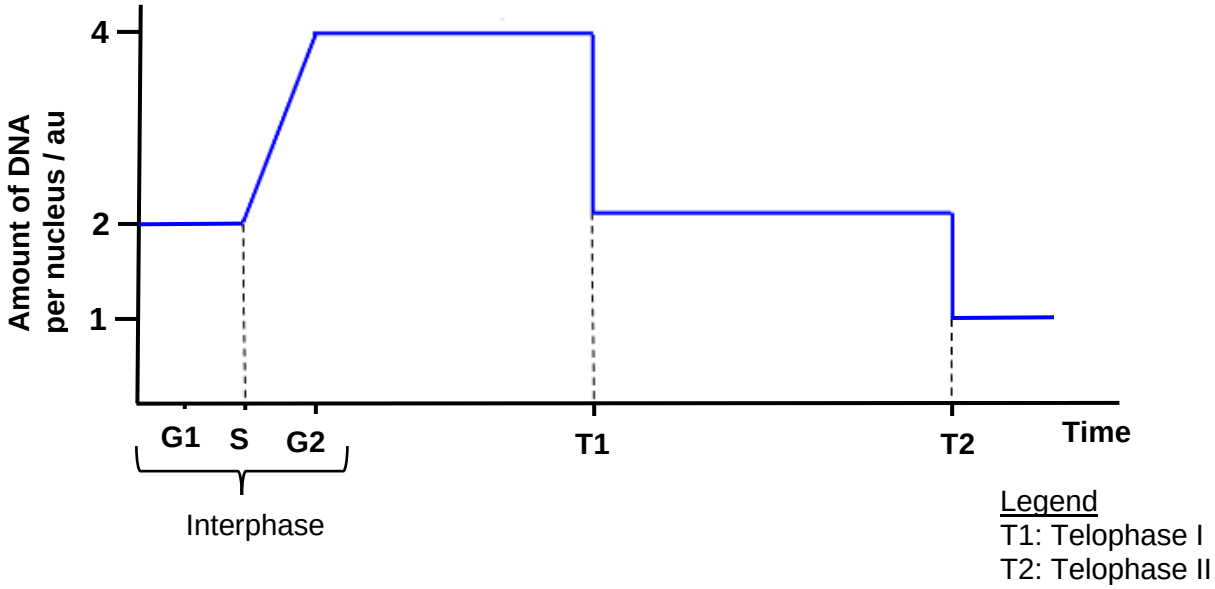


Fig. 1.2

(b) With reference to Fig. 1.2, **account for** the changes in amount of DNA per nucleus from the start of the cell cycle to the end of meiosis I. [2] **(Answer does not need to include meiosis II.)**

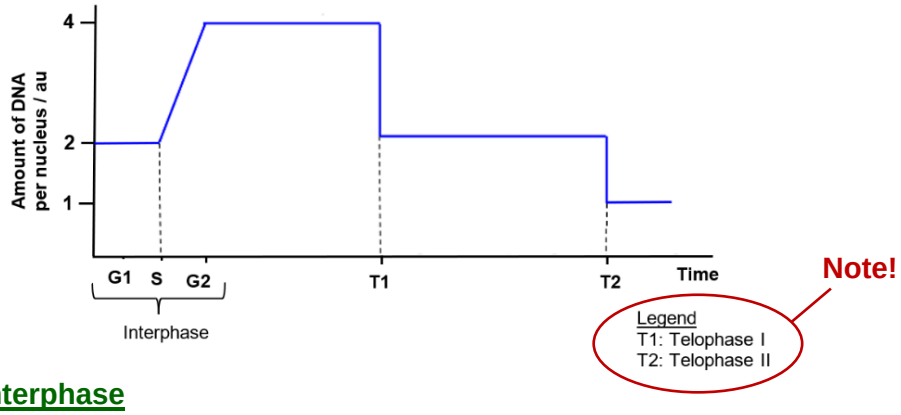
1. **[QF] The amount of DNA per nucleus in the parent cell doubles/increase from 2 to 4 au from S to G2.**
2. **as the cell undergone DNA replication during S phase of interphase.**
3. **By the end of telophase I, there are two daughter nuclei. (R: daughter cells)**
4. **[QF] The amount of DNA per nucleus is back to its original amount 2au.**

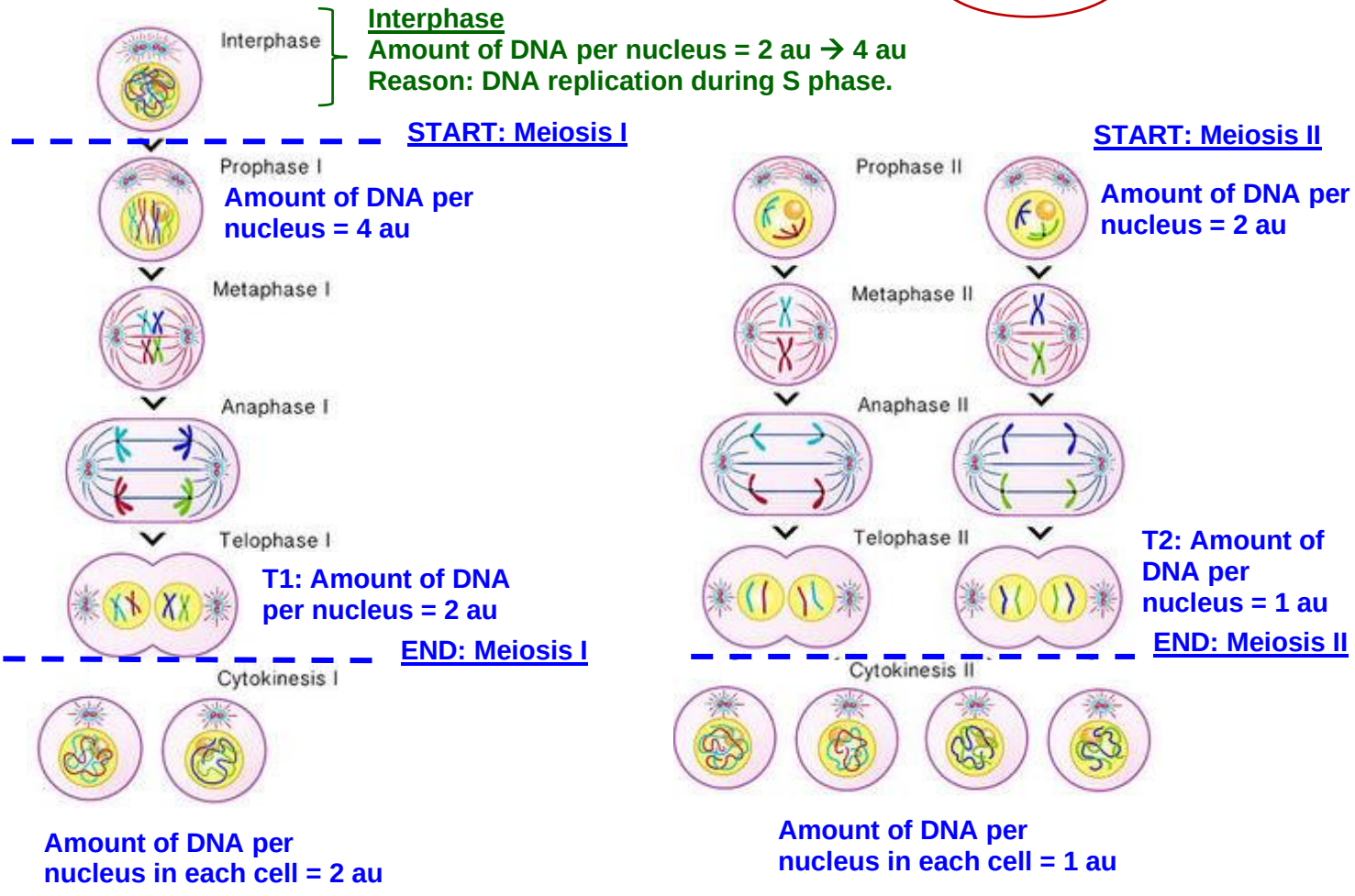
Feedback / comment

1. **Many candidates were not able to appreciate the difference between end of meiosis I and cytokinesis and so did not differentiate daughter nuclei and daughter cells in their answers.**

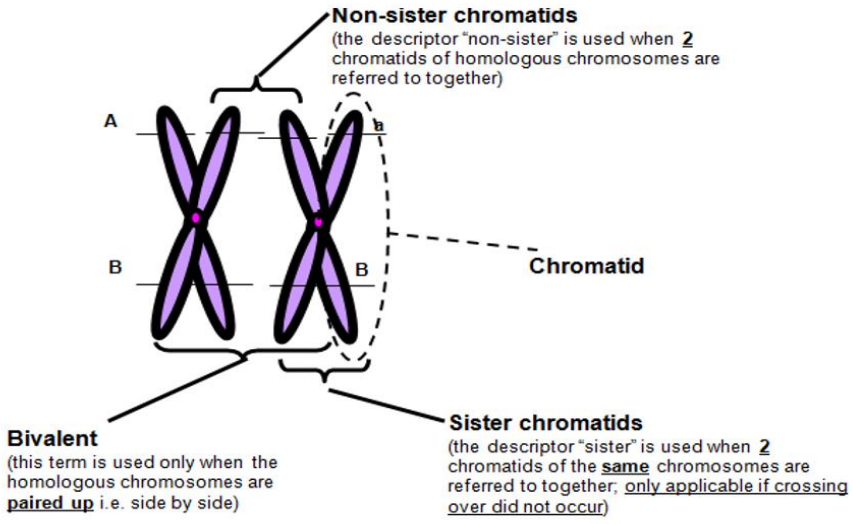
   Refer to the definition of meiosis (Cell cycle notes, page 3).

   At the end of meiosis I, two daughter nuclei are formed from one parental nucleus. At the end of cytokinesis, two daughter cells are formed, each daughter cell containing one daughter nucleus.





(c) **Describe** **one** difference between a pair of homologous chromosomes and sister chromatids of a chromosome. [1]

Feature	A pair of homologous chromosomes	Sister chromatids
1) Genetic similarity	**Not genetically identical to each other [1/2]**	**Genetically identical to each other before crossing over [1/2]**
2) Physical connection / attachment	**Not connected to each other**	**Connected to each other at the centromere**
3) Anaphase I	**Separate**	**Do not separate**
4) Alleles at corresponding gene loci.	**Same number and type of genes but may have different alleles for the same genes.** **Max ½ mark if "may" is missing from answer.**	**Same number and type of genes and have same alleles for the same genes.**
	Explanation: It is possible for the homologous chromosomes to have the same alleles for the same genes. In Fig 17 of Cell cycle notes (page 20), the pair of homologous chromosomes have different alleles for gene A/a but the same alleles for gene B/b.  	
5) Crossing over	**Crossing over occurs during prophase I.** **Max ½ mark if "prophase I" is missing.**	**No crossing over.**

Feedback / comment

1. **Generally, well done although many candidates were unable to gain full credit for point 4 and point 5.**

(d) **State** the challenges of using embryonic stem (ES) cells for research or medical treatment and **explain** how induced pluripotent stem cells (iPSCs) may overcome each of these challenges. [3]

1. **Obtaining ES cells destroy human embryos which may be regarded as living human beings. Obtaining iPSCs do not involve killing human embryos so there is no ethical issue.**
   Note:
   Accept **both kill** OR **destruction of embryos**
   Refer to the destruction of embryos during the process of extracting ES cells + idea that embryos might be considered as living human beings.

   R: Destruction of ES cells.

2. **ES cells may cause immune rejection in the patients as they are foreign cells. iPSCs are derived from the patient and so the patient will not have any immune rejection.**
   Note:
   Need to mention the idea of "immune" rejection, and not merely donor rejection.
   OR
   Accept tissue rejection because the tissue is not compatible.

3. **Obtaining ES cells may take a long time as a suitable donor need to available. Obtaining cells from patients to create iPSCs are faster / do not need to wait.**
   Note: Need to mention the idea that iPSCs are derived from the patient at least once in point 2 or 3.

Feedback / comment

1. **Several candidates erroneously mentioned the destruction of embryonic stem (ES) cells instead of embryos. If ES cells are destroyed, they cannot be used for research or medical treatment.**

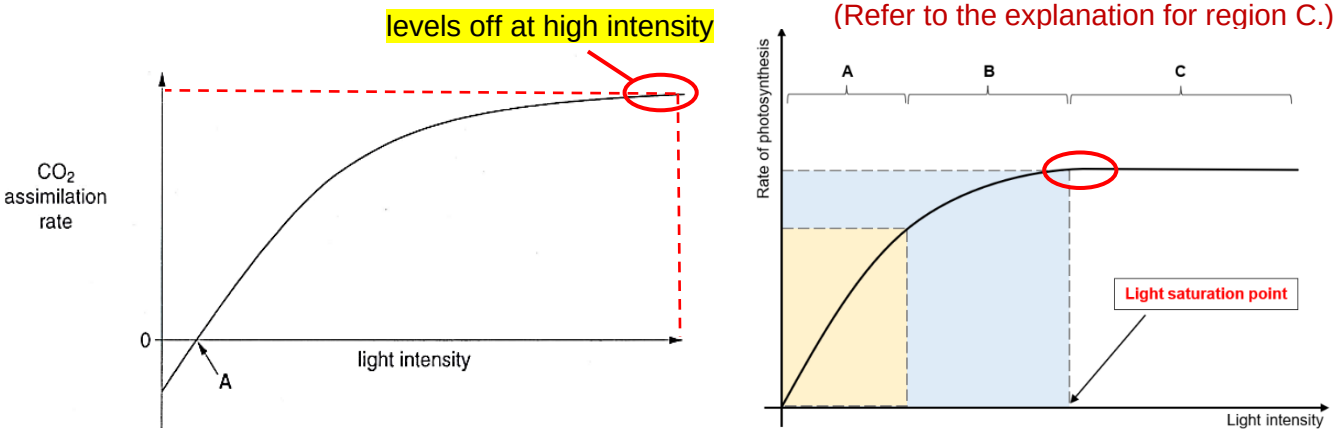
2. **Another error is the idea that ES cells might turn cancerous but not iPSCs. Note that there is always a risk that stem cells, including iPSCs, might turn cancerous.**

3. **Note that iPSCs are derived from specialized adult cells and not stem cells (refer to Stem cell notes, page 17).**

[Total: 11]

2 (a) Fig. 2.1 shows the relationship between CO_2 assimilation rate and increasing light intensity in a plant, when carbon dioxide concentration is not a limiting factor.

Refer to Photosynthesis notes page 22.
(Refer to the explanation for region C.)



(i) Explain why the CO_2 assimilation rate levels off at high intensity. [2]

1. **Light saturation point is reached OR all the photosystems / photosynthetic pigments are saturated with light energy.**
2. **Light reaction is occurring at maximum rate OR ATP and NADPH produced are at maximum.**
3. **Hence, dark reaction is occurring at its maximum rate.**
4. **Light intensity is no longer limiting factor, but other factor (e.g., temperature) may now be limiting.**

Feedback / comment

1. This proved to be a challenging question for most candidates.

   Some candidates have the misconception that light intensity is the limiting factor at high light intensity. Refer to the definition of limiting factor (Photosynthesis notes page 21).

2. Most candidates could not relate how light intensity would affect the rate of light reaction which would in turn affect the rate of the dark reaction (as shown by the CO_2 assimilation rate).

   Detailed explanation –

   - At high light intensity, light intensity is no longer the limiting factor.
   - The rate of light reaction is at its maximum.
   - Hence, the rate of production of ATP and NADPH is at its maximum.
   - Since the products of light reaction are used for the dark reaction, it also means that the dark reaction is at its maximum rate.
   - CO_2 assimilation rate, as a measure of the rate of dark reaction, is at its maximum rate (hence, the graph "levels off").

   R: idea that high light intensity damaged chloroplast/chlorophyll because this will cause the CO_2 assimilation rate to decline as the rate of light reaction will decrease.

(ii) Explain why the CO_2 assimilation rate is negative at the lowest light intensity. [2]

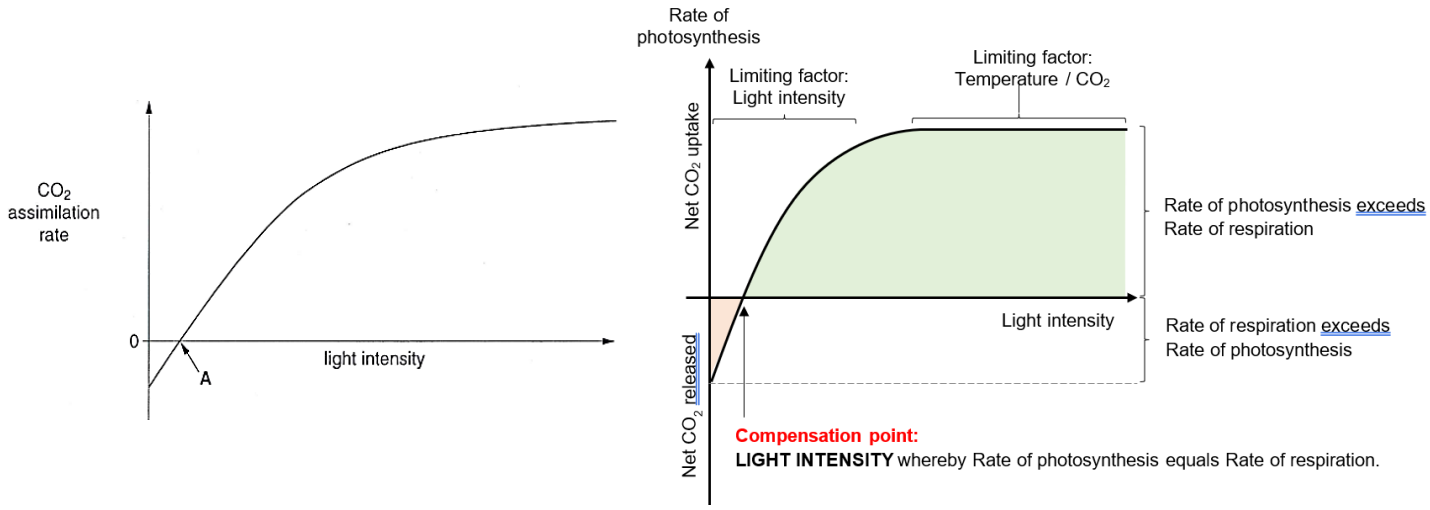
1. **Rate of respiration > rate of photosynthesis. [1]**
2. **More CO_2 released than taken in by the plant. [1]**

OR

3. **At lowest light intensity, the rate of photosynthesis is low (or absent).**
4. **Little (or no) CO_2 is assimilated / uptake.**

5. **However, respiration is still on-going.**
(Note: Must convey idea that respiration is occurring all the time.)
6. **CO_2 is produced.** (Must be clear that it is due to cellular respiration)

Refer to Photosynthesis notes page 23.



Feedback / comment

1. Generally, candidates fared better for this question although a few candidates have the misconception that at low light intensity, plants undergo the dark reaction.

   Note that while dark reaction is independent of light, it needs the products (ATP and NADPH) of the light reaction. Hence, dark reaction will NOT take place if there is the absence of light.
   (Hence, dark reaction needs light indirectly.)

2. Candidates must be careful in their phrasing which may be misleading. The statements (in the left column) seem to suggest that respiration does not take place when photosynthesis is taking place.

Misleading statements	Correct statement
"At low light intensity, photosynthesis does not take place. Instead, respiration takes place." "Respiration occurs instead of photosynthesis."	"At low light intensity, photosynthesis does not take place. Instead, **only** respiration takes place." "At low light intensity, photosynthesis does not take place. **Meanwhile**, respiration takes place."
"At low light intensity, photosynthesis cannot occur. Hence, respiration will occur."	"At low light intensity, photosynthesis cannot occur. However, respiration is **still occurring / ongoing**."

(iii) Describe the significance of point **A** to the growth of the plant. [2]

1. **A is the compensation point**
2. **whereby rate of photosynthesis = rate of respiration (rate of CO_2 assimilation in photosynthesis equals to that of CO_2 production in respiration)**
3. **There is no (net) growth (R: constant growth)**
4. **As all products of photosynthesis are used up in respiration to obtain ATP for the plant.**

Feedback / comment

1. Candidates were generally able to explain point A but few could addressed its significance to the growth of the plant.

(b) The conditions in which young plants are grown affects their ability to photosynthesise at high and low temperatures when they are mature.

Young maize and wheat plants were grown to maturity at high and low temperatures. When they were mature, their rate of photosynthesis was measured at different temperatures.

The results are shown in Fig. 2.2.

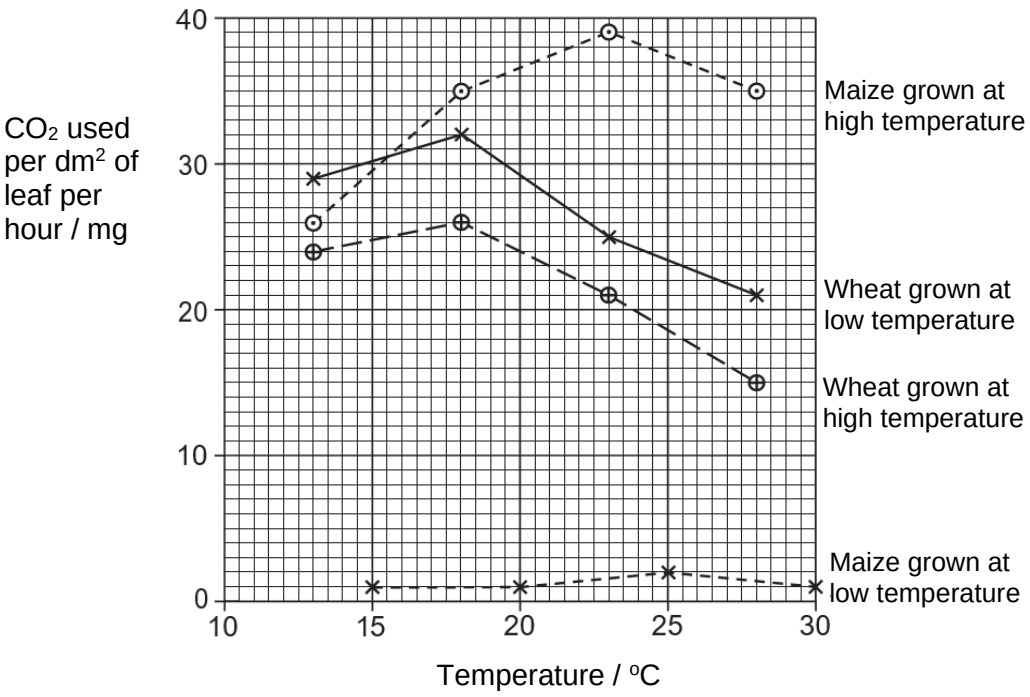


Fig. 2.2

(i) With reference to Fig. 2.2, compare **one** effect of temperature on the rate of photosynthesis of maize plants and wheat plants that were grown at high temperature. [2]
Any 1

Differences:
1a) Maize has higher rate of photosynthesis compared to wheat at all temperatures.
1b) [QF]
At 13°C, maize uses 26 mg CO_2 per dm^2 of leaf per hour compared to 24 mg for wheat.
At 28°C, maize uses 35 mg CO_2 per dm^2 of leaf per hour compared to 15 mg for wheat.

2a) At higher temperatures, maize has a (much) higher rate of photosynthesis than that for wheat compared to lower temperatures.
2b) [QF]
At 28°C, CO_2 used per dm^2 of leaf per hour is 35mg for maize compared to 15mg for wheat (difference of 20mg) whereas it is only 26mg compared to 24mg at 13°C. (difference of 2mg)

3a) Maize has a higher optimum temperature compared to that of wheat.
3b) [QF]
The optimum temperature for maize is 23^0C compared to 18^0C for wheat.

4a) Maize has a higher maximum rate of photosynthesis than that for wheat.
4b) [QF]
Max. rate for maize is 39 mg per dm^2 of leaf per hour compared to 26 mg per dm^2 of leaf per hour for wheat.

5a) Maize shows an initial steeper increase in rate of photosynthesis as temperature increases.
5b) [QF]
From 13^0C to 18^0C, CO_2 used for maize increased from 26 to 35 mg CO_2 used per dm^2 of leaf per hour (difference of 9 mg) compared to up to 24 to 26 mg CO_2 used per dm^2 of leaf per hour (difference of 2 mg) for wheat.

6a) Maize shows a decrease in rate of photosynthesis at a higher temperature than for wheat.
6b) [QF]
Rate starts to decrease from 23^0C for maize compared to 18^0C for wheat.

Similarity
7a) For both plants, their rate of photosynthesis increased initially before decreasing.

7b) [QF] Maize: CO_2 used per dm^2 of leaf per hour increased from 26 to 39 mg from 13 to 23°C before decreasing to 35mg by 28°C.

[QF] Wheat: CO_2 used per dm^2 of leaf per hour increased from 24 to 26 mg from 13 to 18°C before decreasing to 15mg by 28°C.

Feedback / comment
1. This question was challenging for some candidates.
   - Some candidates misinterpreted the question and compared the effect of high versus low temperatures for each plant.
   - Some candidates merely described the shape of the 2 graphs instead of using a common reference (e.g., temperature range, optimum temperature, maximum rate, etc.) for the comparison.
2. Note that if the number of comparisons is not stated in the question, candidates are expected to provide one similarity and one difference based on the 2 marks allocation.

(ii) It was observed that low temperatures reduced the formation of the thylakoid membranes inside the chloroplasts of maize leaves, but not in wheat leaves.

Using this information and the results in Fig. 2.2, suggest a possible reason for the different results for maize and wheat grown at low temperatures. [2]

(Note: Reference to both plants should be mentioned in the answer.)

1. **Reference to maize having (much) lower rate of photosynthesis than wheat.**
   [QF] CO_2 used per dm^2 of leaf per hour range between 1-2 mg from 15 to 30°C for maize compared to 21 to 32mg from 13 to 28°C for wheat.
   (Note: Present data as range of CO_2)

2. **Less thylakoid membranes in maize as compared to wheat.**
   Reject: Reduced formation of thylakoid membrane which is merely a repeat of the preamble. Instead, the outcome of the reduced thylakoid formation should be mentioned.
3. **Result: less chlorophyll to absorb light.**
   Or less electron carriers to pass the electrons through the electron transport chain.
4. **Reduces rate of light reaction / light dependent stage / photophosphorylation.**
5. **Less products (NADPH and ATP)**
6. **Reduced rate of dark reaction, so amount of CO_2 used per dm^2 of leaf per hour was drastically reduced.**

Feedback / comment

1. Most candidates were able to explain in terms of the function of the thylakoid membranes and linked it to dark reaction where CO_2 was used.

2. Some candidates did not read the preamble carefully and mentioned that no thylakoid membranes were formed, and so light reaction and dark reaction did not occur. It is not the case as the graph in Fig. 2.2 showed a low level of CO_2 used by maize grown at low temperature. This means that photosynthesis occurred, but the rate was low.

   Candidates are reminded to be precise in their analysis of the question and data provided in the future.

3. A few candidates made reference to the effects of high temperatures (involving enzymes) on the rate of photosynthesis which was irrelevant to the question.

4. Note that reduction in the formation of thylakoid membranes results in lesser thylakoid membranes in the plant cells, and NOT “thinner” thylakoid membranes. A membrane is a bilayer structure, and it cannot become even “thinner”.

(c) Describe **two** differences between Calvin cycle and Krebs cycle. [2]
(Note: "Describe" → some elaboration of the difference is needed)

Feature of comparison	Calvin Cycle	Krebs Cycle
1. Location R: If only organelle is mentioned.	• **Stroma of chloroplast**	• **Matrix of mitochondrion**
2. (Starting) intermediate regenerated	• **Ribulose-1,5-bisphosphate (RuBP)**	• **Oxaloacetate**
3. Compounds exiting cycle	• **glyceraldehyde-3-phosphate, $NADP^+$, ADP**	• **NADH, $FADH_2$, ATP**
4. Involvement of CO_2	• **Fixed by rubisco / reference to CO_2 fixation**	• **Released during oxidative decarboxylation.**
5. Role of electron / hydrogen carrier	• **NADPH provides reducing power for carbon reduction.**	• **NADH is a product formed during oxidation of acetyl-CoA.**
6. Role of ATP	• **Use ATP for** **1) phosphorylation of glycerate-3-phosphate to form glyceraldehyde-3-phosphate.** **2) regeneration of RuBP**	• **Synthesize ATP by substrate level phosphorylation**
7. Type of metabolic process / enzyme reaction	• **Anabolic (Carbon is fixed to synthesize organic compounds)**	• **Catabolic (Carbon is removed as CO_2 from organic compound)**

Feedback / comment

1. Candidates are reminded to answer the question using point to point comparison (PTPC). Refer to the 1st column (feature of comparison) for valid comparisons.

2. Furthermore, avoid combining different points together.

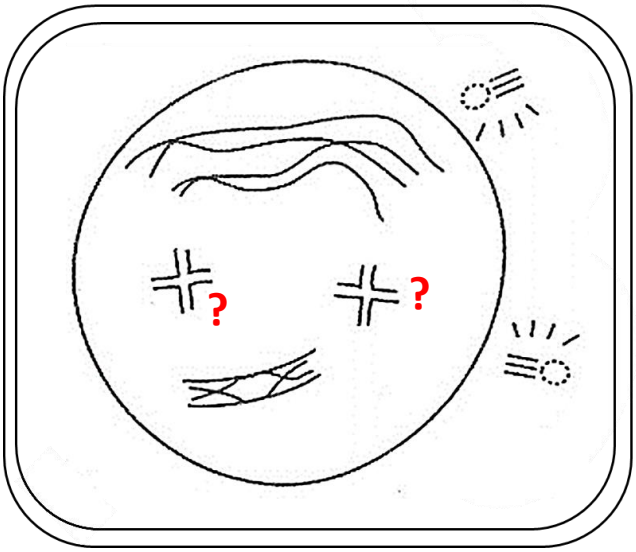
   Example:
   "Calvin cycle starts with ribulose-1,5-bisphosphate (RuBP) and CO_2 which is fixed by rubisco, whereas Krebs cycle starts with oxaloacetate and releases CO_2." (point 1 and 4)

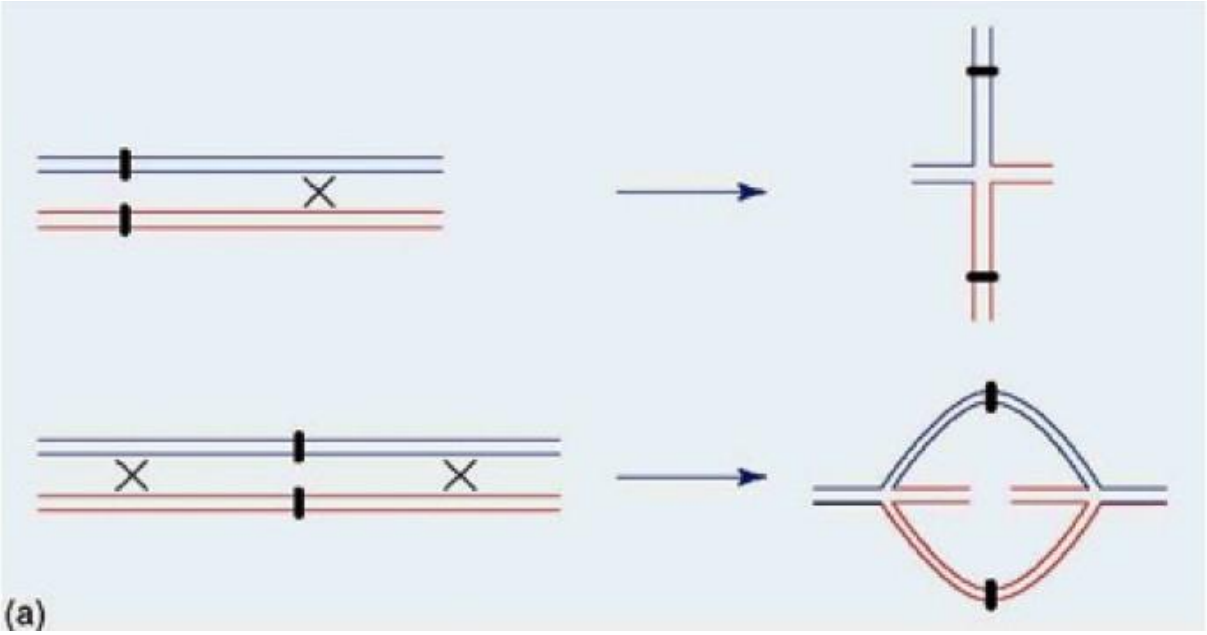
3. Answers such as the presence of stage or products unique to the process are rejected.

   Examples:
   - "CO_2 fixation is present in Calvin cycle but absent in Krebs cycle."
   - "Calvin cycle involves CO_2 but Krebs cycle involves O_2."
   - "Oxaloacetate is present in Krebs cycle but not in Calvin cycle."
   - "NADPH is involved in Calvin cycle, but NADH is involved in Krebs cycle."
   - "Krebs cycle involves 2 cycles whereas Calvin cycle only involves 1 cycle."

[Total: 12]

Just for reference – not for students to memorize





3 The *lac* operon is a section of DNA present in the genome of *Escherichia coli*. The structural genes of the *lac* operon are only fully expressed when the bacteria are exposed to certain conditions.

Fig. 3.1 is a diagram showing the *lac* operon and a nearby region of the *E. coli* genome.

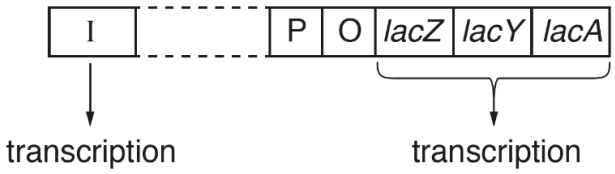


Fig. 3.1

(a) Fig. 3.1 shows how the *lac* operon consists of structural genes and regulatory sequences.

(i) Using Fig. 3.1, **identify** **two** additional structural genes on the *lac* operon, and complete Table 3.1 to **name** each **structural gene** and **its product**. One example has been shown for you. [2]

Table 3.1

structural gene	name of gene product
*lac*Y	*lac* permease
lacZ	**β-galactosidase**
lacA	**β-galactoside transacetylase**

Note:
- **Only the names of genes will be awarded marks.**
- **Many students need to practice the correct spelling for gene product of *lacA* gene.**

(ii) Gene ***I*** is transcribed all the time to produce its protein. This is known as constitutive expression.

Explain why some genes show constitutive expression. [1]

Important reminders:
1. **MUST learn the phrase "genes code for"**
   Reject: "gene produce proteins" or "gene synthesize proteins"
2. **Reject: "expressed all the time" – you have only define the terms without providing the reason.**

1. **These genes code for gene products that are essential components of living cells**
   OR
   the gene products / enzymes / proteins that are coded for are needed all the time

(iii) The product of gene ***I*** has a unique structure that is tied to its specific function on the *lac* operon.

Describe how the product of gene ***I*** binds to region O of the *lac* operon. [2]

Important reminders:
1. **Many students misread the question / focused on the wrong concepts and provided detail description of the conditions that cause the lac repressor to change to an active conformation.**
2. **Students should try to use the phrase "recognize and bind"**
3. **The lac repressor is NOT considered a transcription factor – prokaryotes do not have transcription factors.**

1. **The product of gene *I* is a lac repressor.**
2. **Lac repressor with an active conformation binds to operator.**
   It contains a DNA-binding domain, Reject: "DNA-binding site"
3. **which recognises and binds to the operator / Region O.**
4. **This is because the shape of the DNA-binding domain of the lac repressor is complementary to the shape of the nucleotide sequences in region O / lac operator.**
   Reject: "complementary base-pairing" because lac repressor is a protein. Complementary base-pairing only takes place when nuclei binds to nuclei acid.

(b) When the *E.coli* are exposed to certain conditions, the *lac* operon will synthesise some enzymes. These are described as inducible enzymes.

(i) **Explain** what is meant by an *inducible enzyme*. [2]

Important reminders:
1. **Number with a circle ② ⇒ 1 mark**
2. **The abbreviations:**
   WF: wrong focus
   WCAE: wrong cause and effect
   EB: encoded by
   CFB: coded for by
   IO: inducible operon
3. **Reject: inducer binds to inducible enzymes.**
   Many students confused inducible enzymes with the lac repressor!
4. **Some students confused catabolic reactions with anabolic reactions.**

1. **An inducible enzyme is encoded by inducible operons / coded by inducible genes of inducible operon**
2. **The synthesis of inducible enzyme is induced by the presence of its inducer / lactose / allolactose. (R: substance in the environment)**
3. **Presence of inducer allows for the transcription of the *lac* operon structural inducible genes.**
4. **An inducible enzyme usually function in catabolic pathways, where a nutrient is broken down to simpler molecules.**

(ii) Apart from the presence/absence of lactose, the levels of glucose present in the external environment also affects the expression of the *lac* operon.

Explain how low levels of glucose affect the expression of the *lac* operon. [3]

Important reminders:

1. **It is not necessary to spell out cAMP.**
2. **Must spell CAP once.**
3. **Bacteria does not have transcription factors which bind to promoter to form transcription initiation complex.**
4. **Lactose is not mentioned – no need to include in your answer**

1. **When glucose levels in the cell is low, there is an increase in the concentration of cAMP.**
2. **cAMP is able to bind to the allosteric site on the Catabolite Activator Protein (CAP).**
3. **CAP will assume its active conformation and bind to the CAP-binding site upstream of the *lac* promoter.**
4. **The attachment of CAP bends the DNA molecule (R: bends the lac operon), which makes it easier for RNA polymerase to bind to the *lac* promoter.**
   Reject: no marks if students included transcription factors
5. **Therefore, the *lac* operon genes are transcribed at a high rate,**
6. **Producing enzymes required for the hydrolysis of lactose / lac permease, β-galactosidase and β-galactoside transacetylase**
7. **This is a form of positive control. (BONUS)**

(iii) The unphosphorylated form of a protein, $EIIA^{GLC}$, is able to interact with *lac* permease and inactivate it. ⇒ **cannot transport lactose**

Suggest the effect of $EIIA^{GLC}$ on the expression of the *lac* operon even when lactose is present in the external environment. [2]

Important reminders:

1. **Must answer directly – when lactose cannot be transported into the cell. Do NOT describe what should take place if lactose can be transported in.**
2. **Some students confused operator with operon.**

1. ***Lac* permease will be unable to transport lactose from the external environment into the cell.**
   Note: Do not use the term "diffuse"
   Reason: The movement of lactose into the bacteria cell is a very complex process. Therefore the term "transport" is used.
2. **Therefore, allolactose will not be formed and does not bind to the lac repressor.**
3. **The lac repressor will remain in its active conformation, bound to the *lac* operator.**
4. **RNA polymerase is unable to bind to the *lac* promoter to transcribe the structural genes of the *lac* operon.**
   OR
   This causes the *lac* operon to be switched off.

(c) The prokaryotic genome is different from the eukaryotic genome in many different ways.

With reference to structural organization, state **two differences** between the prokaryote and eukaryote genome, other than the presence of operons. [2]

Important reminders:

1. **Students MUST read the question and highlight important considerations.**
2. **Must focus on structural organization NOT the process of transcription or translation.**
3. **Must not compare structural organization related to operons.**
   Reject: 1 promoter controlling many structural genes vs 1 promoter control one gene.
4. **For differences – students must use the term "whereas" or "while" to connect 2 contrasting statements.**
5. **Must be point to point (PTP) differences.**
6. **Must write complete phrase or sentence.**
7. **MUST use the term "DNA" when you are describing DNA. Do NOT use the term Genome.**
8. **Reject reference to enhancer & silencer. There are DNA sequences in the prokaryotes which also have similar functions. Similary for Pribnow box.**

	FEATURE	PROKARYOTIC GENOME	EUKARYOTIC GENOME
1	Ploidy	**Only one set of chromosomes / haploid**	**2 set of chromosomes / Diploid**
2	Number of chromosomes	**One**	**May be more than one**
3	Size and complexity of genome	**Smaller** and **simpler**	**Larger** and **more complex**
4	Structure of chromosome	Double stranded **circular DNA**	Double stranded **linear DNA**
5	Number of origin of replication	**Single origin** of **replication**	**Multiple origins** of **replication**
6	Presence of histone proteins	Histones are **absent**. Instead, **nucleoid-associated proteins** facilitate the **folding** of **DNA**	**DNA** is bound to **histone proteins**, which facilitate folding
7	Presence of centromeres	**No centromeres** in the **DNA**	**Presence** of **centromere** (a **constricted** region of **repetitive** sequences)
8	Presence of telomeres	**Telomeres absent** in the **DNA**	**Telomere present**
9	Introns	**Introns absent**: Each gene is a continuous coding sequence	**Introns present** between coding sequences (called exons) in each gene.

[Total: 14]

4 A diagram of a chromosome from a dividing cell is shown in Fig. 4.1.

Fig. 4.1

(a) Before a cell divides, DNA replication takes place via semi-conservative replication.

State **two** ways how DNA replication differs from transcription. [2]

Important reminders:

1. **Students MUST use comparative term "whereas" or "while" to connect the 2 contrasting statements.**
   Reject: if students use "and" or "comma"
   E.g. The enzyme used in DNA replication is DNA polymerase while the enzyme used in transcription is RNA polymerase.
2. **MUST write "D" & "R" clearly.**
3. **Reject any differences where students just list all the different proteins.**
4. **Some students confused transcription with translation.**

	FEATURE	DNA REPLICATION	TRANSCRIPTION
1	Enzyme involved	DNA polymerase	RNA polymerase
2	Raw materials	Deoxyribonucleotides	Ribonucleotides
3	Template	Both strands of DNA molecule	Only template strand of the DNA
4	Base pairing	Adenine with thymine and vice versa Cytosine with guanine and vice versa Reject : if students only mention thymine in DNA	Adenine on DNA with uracil on RNA Thymine on DNA with adenine on RNA Cytosine with guanine and vice versa
5	Proofreading property on enzyme involved	DNA polymerase carry out 3' to 5' exonuclease on daughter strand, ensuring precise complementary base pairing / proofreading of daughter strand	RNA polymerase does not carry out 3' to 5' exonuclease proofreading of RNA transcript.
6	Product(s)	2 DNA molecules Reject : 2 strands OR daughter strand	mRNA, tRNA or rRNA
7	Products destination	Products remain in the nucleus.	All products leave nucleus via nuclear pore
8	Enzymes involved in unwinding DNA	Helicase	RNA polymerase
9	Requirement of primers	DNA polymerase require primers to start the process of DNA replication	RNA polymerase does not require primers to start the process of transcription
10	Start site	DNA replication starts at the origin of replication	Transcription starts at the promoter

(b) A dividing cell is at risk of losing genetic material each time DNA replication occurs.

(i) On Fig. 4.1, **add** a label line and the letter G to show the location on the chromosome of an area that helps to prevent the loss of genes. [1]

Important reminders:

1. **Students should put a tick next to the mark once they have answered a question – so as not to leave any such questions answered.**

1. **Draw a label line (not bracket) [1/2]**
2. **Point to one end of the chromosome & label G [1/2]**
   Reject: if student pointing further into the 1st shaded region.

(ii) **Briefly describe** one **other** function of this region of the chromosome. [1]

Any ONE:

1. **Telomeres bind to proteins (shelterin) that protect the chromosomal ends from joining to other chromosomes and from degradation / prevent apoptosis of cells**
   Note:
   - **Must write "bind proteins" to the mark (all or nothing)**
   - **Too many students wrote that telomeres prevent chromosomes from joining together – this is WRONG!**
   - **Reject: "degradation by RNase" – this enzyme hydrolyse RNA not DNA.**

2. **Length of telomeres determines life span of cells.**
   - **Reject: determines half-life of chromosomes or half-life of cells**

3. **In cells where telomerase enzyme is present - telomeres provides the recognition site for telomerase to recognise and bind to lengthen DNA**
   - **Reject: removes end-replication problem.**

(c) The chromosome shown in Fig. 4.1 consists of one long DNA molecule associated with histone proteins.

Name one stage of mitosis in which a chromosome would have the same general structure as the chromosome shown in Fig. 4.1. [1]

Note : MUST be a stage AFTER sister chromatids have separated.

- **Anaphase OR telophase**

(d) **Name** the stage in the cell cycle during which the cell divides to produce two genetically identical daughter cells. [1]

- **Cytokinesis**

The enzyme telomerase ensures that telomeres do not shorten after DNA is replicated.

Fig. 4.2 shows a specific region of a DNA molecule during replication. DNA polymerase cannot attach to the region labelled X, so it cannot complete the synthesis of the new strand without the action of telomerase.

Telomerase synthesises additional lengths of DNA that are added to the telomere. These additional lengths are used by DNA polymerase to complete the process of replication.

Fig. 4.3 is an enlarged view of region X to show the action of the enzyme telomerase.

Fig. 4.2

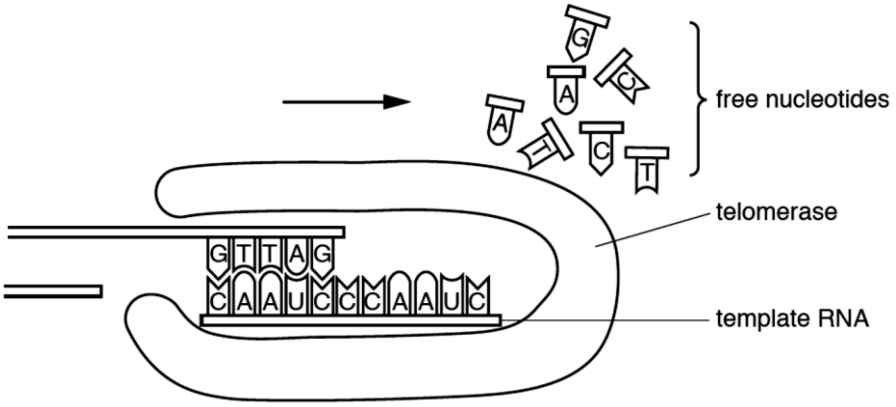


Fig. 4.3

(e) With reference to Fig. 4.2 and Fig. 4.3, **explain how** a molecule of telomerase synthesizes additional lengths of DNA. [4]

Important reminders:

1. **Students MUST INCLUDE information from BOTH figures in their answers (QF).**
2. **Many students did not mention active site (AS)**
3. **Students must not confuse ribonucleotides with deoxyribonucleotides.**
4. **Formation of hydrogen bonds between complementary bases do NOT require enzymes. These are not covalent bonds. Just attraction between chemical groups.**

1. Telomerase enzyme has a short length of RNA CAAUCCCAAUC in its active site
OR
1a. Telomerase enzyme has a short length of RNA in active site
1b. QF : CAAUCCCAAUC

2. This RNA has a sequence complementary to telomere DNA sequence GTTAG
OR
2a. RNA has a sequence complementary to telomere DNA
2b. QF : GTTAG

3. Telomerase recognises and binds to telomere at region X / quote whole sequence of X
OR
3a. Telomerase recognises and binds to telomere
3b. QF : region X

4. The RNA acts as a template to extend 3' end of the telomere DNA.

5. **This process is known as reverse transcription / telomerase acts as reverse transcriptase**

6. **Free DNA nucleotides base pairs with RNA template**
   Note: these are not ribonucleotides.

7. **telomerase catalyse formation of phosphodiester bond between nucleotides.**
   Reject: hydrogen bonds

8. **Telomerase moves to the right.**

(f) Telomerase is not present in prokaryotic cells.

Suggest why prokaryotes do **not** have telomerase. [1]

Important reminders:

1. **Do NOT confuse cells with DNA.**
2. **Some students are confused that bacteria do not carry out DNA replication. ☹**
3. **½ mark if student wrote "do not have end replication problem or DNA is not shortened"**

1. **Prokaryotes have circular DNA ;**

2. **Prokaryotes do not have telomeres ;**

3. **Prokaryotes DNA has no free ends**

4. **Absence of telomerase gene**
   Reject: If students stated that the telomerase gene is not activated
   Reason: the gene is absent in prokaryotes.

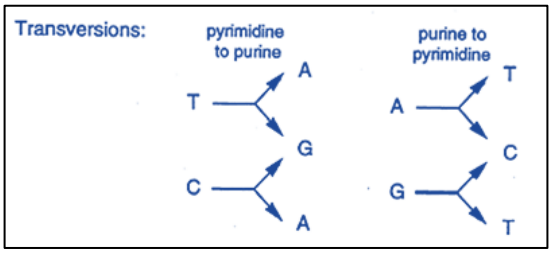
(g) Lung cancer can be caused by carcinogens. Benzopyrene, a compound found in tar from tobacco smoke is known to interfere with DNA replication.

It brings about gene mutation via transversion mutation or transition mutation. Both cause the newly synthesised strand to have an incorrect base.

(i) A transversion mutation is when a pyrimidine is used in the newly synthesised strand instead of a purine, or the other way round. **[purine instead of pyrimidine]**

For your reference:

Note:
MUST know :
1. **Purines: Adenine, Guanine**
2. **Pyrimidines: Cytosine, Thymine**



Name the **two** possible bases that could be used instead of cytosine in a transversion mutation. [1]

Important reminders:

1. **The mutation is at the DNA level – uracil should not be a possible answer!**
2. **Cytosine is a pyrimidine – therefore your answer must list purines.**
3. **Must spell out in full.**

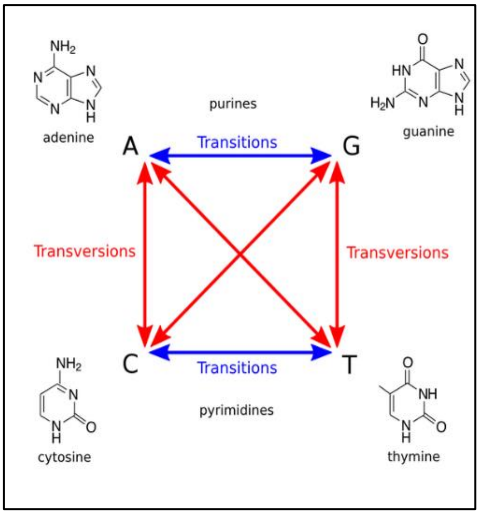
1. **adenine and**
2. **guanine ;**

(ii) A transition mutation is when a purine is replaced by an incorrect purine or a pyrimidine is replaced by an incorrect pyrimidine.

Suggest why transversion mutations are less likely to occur than transition mutations. [2]

Note:
- **MUST KNOW:**
- **Purine: 2 rings**
- **Pyrimidine: 1 ring**
- **Purine always base-pair with pyrimidine**

- **Wrong reasoning when students consider the chance of occurrence based on the total number of bases in pyrimidines vs purines.**
- **Wrong focus when students consider the chance of occurrence based on number of hydrogen bonds.**



1. **purines have two rings and pyrimidines have one ring ;**

2. **(a) purine base-pairs with pyrimidine to**
   (b) maintain constant width between 2 DNA strands
   Note : Reject constant length

3. **two purines or two pyrimidines change / distort the double helix constant width in a transversion event**

4. **so transversion event more likely to be detected by DNA polymerase during DNA repair mechanism and remove wrong nucleotide**

(iii) It has been observed that the carcinogens in cigarette smoke can also cause the deletion of a nucleotide base from the promoter of a gene.

State the role of the promoter in a gene. [1]

- **Specifies transcription start site** on the template strand of DNA.
  OR
- **RNA polymerase** and **general transcription factors** bind to promoter to **initiate transcription**

(iv) The methylation of tumour suppressor genes can cause loss of function mutation driving a cell to become cancerous.

Describe how the promoter of tumour suppressor genes becomes methylated. [2]

1. **Attachment of methyl groups ($-CH_3$) to DNA bases.**

2. **Added to cytosine linked by a phosphodiester bond to a guanine nucleotide / CpG site**

3. **Enzyme involved: DNA methyltransferase**

4. **Basal transcription factors and RNA polymerase cannot recognise and bind to promoter / not accessible to promoter**

The process of protein synthesis takes place in both cancerous and non-cancerous cells. Many types of nucleic acids are involved in the process.

(h) **State one** way in which the structure of DNA differs from the structure of messenger RNA. [1]

Reject any differences that does not refer to structure

Any one

Feature	DNA	RNA
1. Monomer	▪ deoxyribonucleotide.	▪ ribonucleotide.
	Reject: DNA nucleotides VS RNA nucleotides, because it is just repeating stating the terms DNA & RNA.	
2. Sugar	▪ deoxyribose sugar	▪ ribose sugar
3. Nitrogenous bases	▪ Adenine ▪ Thymine ▪ Cytosine ▪ Guanine	▪ Adenine ▪ Uracil ▪ Cytosine ▪ Guanine
	Note : No marks given if students only mention thymine verses uracil	
4. Number of strand	▪ It is usually double-stranded	▪ It is usually single-stranded
5. Types	▪ 1 form as a double helix	▪ It exist at least in 3 forms: – Mrna – tRNA – rRNA
6. Length OR	▪ Longer	▪ Shorter
7. Size	▪ It is a large molecule.	It is a smaller molecule than DNA

(i) At the start of translation, amino acid activation takes place whereby an amino acid attaches to its specific tRNA molecule. This process requires an enzyme, aminoacyl tRNA synthetase.

Explain why a particular amino acid needs to be linked to a specific tRNA molecule. [2]

1. **tRNA carries a (a) specific amino acid to the (b) ribosome during translation**
2. **anti-codon of tRNA forms complementary base pairs with codons on the mRNA**
3. **which allows for correct sequencing of amino acids on the polypeptide chain.**

(j) Ribosomes are required for protein synthesis.

State **two** functions of ribosomes in protein synthesis. [2]
Reject : Ribosomes are the sites of protein synthesis – mentioned in the question.

ANY TWO

1. **For (a) translation of mRNA codons into (b) amino acid sequence.**
2. **To hold tRNA and mRNA in close proximity**
3. **Allow anticodons of amino acyl tRNA complexes to bind to complementary codons on mRNA**
4. **to ensure correct matching of codon and anti-codon pairs for accuracy of protein synthesis**
   OR
   to ensure (a) correct sequence of (b) amino acids joined together in the polypeptide chain
5. **Site of peptide bond formation catalyzed by peptidyl transferase on the large ribosomal subunit.**

(k) Suggest **one** possible effect of gene mutation in the cell during the synthesis of proteins. [1]

Important reminders:

1. **Focus is on effects of gene mutation, NOT types of gene mutation**
2. **Stating "nonsense mutation", "silent mutation" & "frameshift mutation" is incomplete regarding the effect during synthesis of protein.**
3. **Reject: "results in a different protein"**
   Reason: A non-functional protein is NOT a different protein.

Any one

1. **A non-functional protein is produced**
2. **change in primary structure / amino acid sequence, of polypeptide / protein ;**
3. **A truncated protein is produced**

[Total: 23]

SECTION C: STRUCTURED QUESTIONS

Comments / Feedback

1. **Candidates are advised to start a new essay answer on a fresh page instead of starting the part b on the same page as the end of part a.**
2. **Candidates are also advised to**

5 **(a)** Describe the process of oxidative phosphorylation and state ways it is different from photophosphorylation [13]

Oxidative phosphorylation – MAX 6 marks

1. **NADH and $FADH_2$ donate electrons**
2. **to electron carriers of electron transport chain (ETC).**
3. **Electrons are passed down electron carriers of decreasing energy levels.**
4. **Electrons are then passed to final electron acceptor O_2 to form water.**

5. **Energy released from flow of electrons is used to pump H^+**
6. **from matrix into intermembrane space (across inner mitochondrial membrane).**
7. **This creates a steep proton gradient.**

8. **Diffusion of H^+ from intermembrane space into matrix down concentration gradient**
9. **Mention of: hydrophilic channel of stalked particle**
10. **releases energy which is coupled/linked to ATP synthesis.**
11. **This is catalysed by ATP synthase.**
12. **Mention of: Chemiosmosis.**

13. **Oxidation of 1 NADH yields 3 ATP; oxidation of 1 $FADH_2$ yields 2 ATP.**
(Note: Do not mention "1 NADH releases 3 ATP")
14. **Hence, oxidative phosphorylation yields a total of 34 ATP per glucose.**

Differences – MAX 6 marks
1 mark per difference

Features	Photophosphorylation	Oxidative phosphorylation
D1. Location	• **Thylakoid** of **chloroplasts**	• **Inner mitochondrial membrane**
D2. Source of electrons	• [Non-cyclic] **Water** • [Cyclic] **PS I** R: special chlorophyll a	• **NADH** • **$FADH_2$**
D3. Final electron acceptor	• [Non-cyclic] **$NADP^+$** R: NADPH or NADP • [Cyclic] **PS I**	• **O_2**
D4. Products formed	• **NADPH (and ATP)** • **(O_2 by-product)**	• **H_2O (and ATP)**
D5. Requirement of light energy	• **Yes, during photolysis of water and photoactivation.**	• **No**
D6. Source of energy	• **Light**	• **Oxidation of glucose**

D7. Direction of H^+ pumped to generate steep proton gradient	• **Pumped from stroma to thylakoid space.**	• **Pumped from matrix to intermembrane space.**
D8. Direction of H^+ diffusion to synthesize ATP	• **Diffusion from thylakoid space to stroma.**	• **Diffusion from intermembrane space to matrix.**

QWC [1]
Paragraphing + both parts of the question (process + differences) are addressed.

Comments / Feedback

3. **Candidates are advised to start a new essay answer on a fresh page instead of starting the part b on the same page as the end of part a.**

4. **The question was generally well done especially for the description of oxidative phosphorylation with many scripts capped at the max 6 marks.**

   The comparison was slightly weaker with some invalid / superficial points (e.g., chloroplast vs mitochondrion, no. of ETC, type of cells, etc).

5. **Candidates should also be mindful of their phrasing in answering the question.**

   Incorrect phrasing: Photophosphorylation contains photosystems…
   Correct phrasing: Photophosphorylation involves photosystems in absorbing light energy…

   If the question is asking for the differences between chloroplast vs mitochondrion, it is correct to mention that chloroplast contains photosystems (embedded in the thylakoid membranes) which are not found in mitochondria.

(b) With named examples, describe the different roles of proteins in the eukaryotic cell. [12]

Enzymatic (MAX: 6m) (Annotate with E)

E1. Helicase

a. Binds to parental DNA strands at the Origin of Replication (ORI),
   Note: Many students left this point out.
b. and disrupts hydrogen bonds between complementary base pairs, **[MUST HAVE]**
   Reject: Distort hydrogen bonds
   Reason: [Note Terminology] Distortion does not equate to the fact that the hydrogen bonds are broken, which is necessary to separate the parental DNA strands.
c. to unwind the double helix,
   Reject: uncoil
d. and unzip / separate the two parental DNA strands.

E2. Primase

Note: [Use Precise terminology]
Some students wrongly name the enzyme as “RNA Primase”

a. Synthesises RNA primers from free ribonucleotides via complementary base pairing
b. in the provide 3’OH group
c. using the parental strand as a template.

E3. DNA polymerase

a. Catalyses the formation of phosphodiester bonds between adjacent deoxyribonucleotides, **[MUST HAVE]**
b. by reading the bases on the parental strand in the 3' → 5' direction,
c. and synthesizing the daughter strand in the 5' → 3' direction.
d. Proofreads the newly synthesised daughter strand.

E4. DNA Ligase

a. Seals the nicks/gap in the DNA by catalysing the formation of phosphodiester bonds between DNA fragments.

Note: Many students wrote incompletely (ie only wrote "seal nicks"). You must mention the main function of the enzyme in catalysing the formation of phosphodiester bonds.

E5. DNA topoisomerase

a. Catalyses the removal of DNA supercoils.

E6. RNA polymerase

a. Catalyses the formation of phosphodiester bonds between adjacent ribonucleotides, **[MUST HAVE]**
b. by reading the bases on the template strand in the 3' → 5' direction,
c. and synthesizing the mRNA strand in the 5' → 3' direction.
d. Unwinds the DNA helix by breaking hydrogen bonds between complementary base pairs.

E7. Telomerase

a. Catalyses the lengthening of telomeres

Reject: lengthening of DNA
Reason: Vague. Which part of the DNA?
Reject: lengthen template strand
Reason: there is only 1 template strand in the process of lengthening telomeres, and this is the RNA component of telomerase.

b. by catalysing the formation of phosphodiester bonds between adjacent deoxyribonucleotides.

Max 2 marks for these

E8. Proteases (Accept: **Trypsin**, **Chymotrypsin**, **Pepsin**, **Proteasome**)

a. Catalyses the breaking down of proteins.

E9. Glycosidases

a. Catalyses the breaking down of carbohydrates.

E10. Lipases

a. Catalyses the breaking down of lipids.

E11. Nucleases (Accept: **RNase**, **exonuclease**) **(1m)**

e. Catalyses the breaking down of nucleic acids.

E12. Amylase

a. Catalyses the hydrolysis of starch to maltose.

E13. Maltase

a. Catalyses the hydrolysis of maltose to glucose.

E14. Cellulase

a. Catalyses the hydrolysis of cellulose to glucose.

(Note: marks from E8 to E14 to capped at 2m)

E15. ATP synthase

a. Catalyses ATP synthesis.

E16. Cellulose synthase

a. Catalyses the synthesis of cellulose microfibrils.

E17. Kinase

a. Phosphorylates glucose to glucose-6-phosphate (G6P).
b. Phosphorylates fructose-6-phosphate to fructose-1,6-bisphosphate.
c. Phosphorylates 1,3-bisphosphoglycerate to 3-phosphoglycerate.
d. Phosphorylates 3-phosphoglycerate to pyruvate.

E18. Isomerase

a. Isomerises glucose-6-phosphate to fructose-6-phosphate (F6P).

E19. Aldolase

a. Cleaves fructose-1,6-bisphosphate to glyceraldehyde-3-phosphate and dihydroxyacetone phosphate.

E20. Lactate Dehydrogenase

a. Pyruvate reduced to form lactate during anaerobic respiration.

E21. Pyruvate dehydrogenase

a. Catalyses oxidative decarboxylation of pyruvate to acetate.

E29. Pyruvate decarboxylase

a. Catalyses the decarboxylation of pyruvate to ethanal / acetaldehyde.

E30. Alcohol dehydrogenase

a. Catalyses the reduction of ethanal / acetaldehyde to ethanol,

E31. $NADP^+$ reductase

a. Catalyses the reduction of final electron acceptor $NADP^+$ to NADPH.

E32. Rubisco (**Ribulose-1,5-bisphosphate carboxylase oxygenase**) **(2m)**

a. Catalyses carbon fixation
b. that incorporates CO_2 with RuBP
c. to form 2 molecules of glycerate-3-phosphate.

E33. Spliceosome

a. Cuts at splice sites to release / excise introns,
b. and join / splice exons together,

E34. Peptidyl transferase

a. Catalyses the formation of peptide bonds between adjacent amino acids
b. on the large ribosomal subunit / “P site” of large subunit.

E35. Aminoacyl-tRNA synthetase

a. Catalyses the attachment of a specific amino acid to its specific tRNA
b. to form an aminoacyl-tRNA complex.

Note: some students confused between the peptidyl transferase and aminoacyl- tRNA synthetase.

E36. DNA methyltransferase

a. Catalyses the addition of methyl groups to DNA bases. .

E37. Histone acetyltransferase

a. Catalyses the addition of acetyl groups to certain amino acids of histone proteins.

E38. Histone deacetylase

a. Catalyses the removal of acetyl groups from amino acids of histone proteins.

E39. Cyclin-dependent kinases

a. Activated by cyclins to
b. phosphorylate target proteins in the cell.

Support / Structural (MAX: 4m) (Annotate with S)

S40. Nuclear lamina
a. Network of protein filaments that maintains the shape of the nucleus.

S41. Nuclear matrix
a. A network of protein fibres that help to organise the DNA with the nuclear lamina.

S42. Histone proteins
a. Associates with DNA (A: coil around DNA) to form chromatin
b. for DNA packing into the nucleus.

S43. Ribosomal proteins Reject: Ribosomes
a. Combines with rRNA to form the large and small ribosomal subunits.

S44. Intermediate filaments
a. Provide structural support / Serves as scaffold for the cell and nucleus.
b. Anchorage of nucleus and organelles.
c. Formation of nuclear lamina.

S45. Collagen
a. Major component of connective tissue to provide strength and resilience to tissues.

Note: Quite many students gave details on the structure. This is not applicable to the question requirements.

S46. Keratin
a. Provide structural support for hair, hoofs and feathers.

S47. Fibroin
a. Results in silk having high tensile strength.

S48. Kinetochore
a. Binds to DNA at the centromere,
b. for spindle fibres / microtubules to attach to.

S49. Single-strand binding proteins
a. Stabilise the unwound DNA helix,
b. and prevent rewinding of the double helix.

S50. Shelterin / Telomere caps
a. Binds to the ends of the telomeres to form telomere caps,
b. enabling the 3' protruding ends to loop back and tuck the single-stranded end into the DNA, forming a t-loop. (Accept idea; OWTTE)

Transport (MAX: 4m) (Annotate with T)

T51. Nuclear pore / nuclear pore complex
a. Controls the movement of water-soluble substances between the nucleus and cytoplasm.
b. Allows for the entry of free ribonucleotides, RNA polymerase and transcription factors for transcription.
c. Allows for the exit of mature mRNA and tRNA to the cytoplasm for translation.

T52. Porins / Channel Protein
a. Transport water soluble molecules (A: polar molecules / charged ions) across the phospholipid bilayer
b. via facilitated diffusion.

T53. Carrier Protein / proton pump
a. Transports molecules / ions across the phospholipid bilayer
b. from a region of lower concentration to a region of higher concentration
c. via active transport.

T54. Stalked particles
a. Contains a hydrophilic channel for H^+ ions to diffuse

b. from intermembrane space into matrix OR thylakoid space into stroma.

Comment: Some students were mixed up on the direction of movement of H^+

c. This releases energy, which is coupled to ATP synthesis.

T55. Electron carriers

a. Electron is passed down electron carriers of decreasing energy levels. **[MUST HAVE]**
b. Energy released from flow of electrons is used to pump H^+ ions
c. from matrix into intermembrane space OR stroma into thylakoid space
d. to create a steep proton gradient.

T56. Microtubules

a. Enables intracellular transport of organelles, vesicles and other cellular components.
b. Form the spindle fibres required to separate chromosomes / chromatids during nuclear division.
c. Guide cellulose synthase in the synthesis of the cellulose cell wall.
d. Form the basal body of flagella and cilia.

T57. Actin Filaments / Microfilaments

a. Transport substances across plasma membrane.
b. Form the microvilli.
c. Form pseudopodia.
d. Contraction of muscle cells.
e. Involved in cytoplasmic streaming.

T58. Aquaporin

a. Transports water molecules through hydrophilic channel across the phospholipid bilayer
b. via osmosis

T59. Haemoglobin

a. Transport of oxygen.

Note: Quite many students gave details on the structure. This is not applicable to the question requirements.

T60. Lipoproteins

a. Transport of cholesterol in the blood.

Hormonal (MAX: 2m) (Annotate with H)

H61. Insulin

a. Act on muscle / liver cells
b. to increase permeability of cells to glucose.
c. This increases the uptake of glucose into the cells,
d. reducing blood glucose levels. **[MUST HAVE]**

H62. Glucagon

a. Act on muscle / liver cells
b. to increase conversion of glycogen to glucose.
c. This increases blood glucose level.

Note: Many students did not specify how blood glucose level was changed. A generalised statement that blood glucose level was regulated is considered as vague.

Communication between and within cells (MAX: 4m) (Annotate with C)

C63. G-protein Coupled Receptors (GPCR)

a. Receives the signal from the extracellular domain and relays into the cell,
b. through the binding of specific ligands at the extracellular ligand binding site,
c. which triggers a conformational change of the GPCR, activating the GPCR.

C64. G protein

a. Couples with GPCR.
b. Activated G protein relays signals within the cell,
c. resulting in a cellular response.

C65. Ras protein

a. Relays a signal from a receptor on the plasma membrane to the nucleus
b. via a cascade of protein kinases,

C66. Growth Factors (Accept: **Platelet-derived growth factors**, **epidermal growth factors**)

a. Binds to cell surface receptors on the cell membrane,
b. triggering a phosphorspliceosoylation cascade by the protein kinases,
c. stimulating cell division.

Reject: stimulate growth of the organism.
Reason: context of the question is on the eukaryotic cell.

C67. Glycoproteins on the cell surface membrane

a. Binds to other proteins/glycoproteins/glycolipids of other cells during cell-cell recognition.
b. Binds to adjacent/neighbouring cell in the correct orientation during cell-cell adhesion.
c. Act as receptors involved in cell-cell recognition.

Note: Many students just listed cell-cell recognition, cell-cell adhesion, cell-cell recognition without elaborating how → the 'How' helps to describe the function more fully.

Regulate Transcription (MAX: 3m) (Annotate with TC)

TC68. General / Basal Transcription Factors

a. Position RNA polymerase correctly at the promoter. **[MUST HAVE]**
b. Aid in the formation of the transcription initiation complex at the promoter.
c. Help in separating the 2 strands of DNA to allow transcription to begin.
d. Help release RNA polymerase from promoter once transcription has started.

TC69. TATA-Binding protein

a. Recognises and binds to the TATA box.
b. Distorts the DNA, causing the helix to partially unwind, placing strain on the two DNA strands.

TC70. Transcriptional activators

a. Bind to enhancers
b. to make it easier for RNA polymerase and general transcription factors to bind to DNA
c. thus increasing the rate of transcription.

TC71. Transcriptional repressors

a. Bind to silencers
b. to slow down or stop transcription.

TC72. DNA bending protein

a. Bends DNA,
b. bringing activators bound to enhancer in contact with proteins.

Regulate Translation (MAX: 1m) (Annotate with TL)

TL73. Translation initiation factors

a. Promote proper binding of small ribosomal subunit to 5' end of mRNA.
b. Promote movement of small ribosomal subunit to start codon.
c. Promote binding of initiator aminoacyl-tRNA complex to start codon.
d. Promote joining of large ribosomal subunit.

TL74. Poly(A)-binding protein

a. Binds to poly(A) tail to promote translation.

TL75. Translational repressors

a. Binds to 5' cap / 5' UTR / poly(A) tail to prevent binding of small ribosomal subunit to 5' cap.

Protection (MAX: 2m) (Annotate with P)

P76. Fibrinogen / Thrombin
a. for the clotting of blood.

P77. Antibodies
a. neutralisation of toxin secreted by viruses or bacteria
b. opsonisationof foreign antigens
c. activation of complement system
d. antibody-dependent cell-mediated cytotoxicity

Storage (MAX: 2m) (Annotate with K)

K78. Ferritin
a. Stores iron in the liver.

K79. Myoglobin
a. Stores oxygen in skeletal muscle cells

Others (MAX: 8m) (Annotate with O)

O80. Photosystems
a. Contains photosynthetic pigments
b. which absorb light energy from 400nm to 700nm,
c. leading to photoactivation of special chlorophyll a.

O81. Release factors
a. Recognises and binds to stop codon at "A" site,
b. stopping polypeptide synthesis / leading to dissociation of ribosomal subunits / ribosome.

O82. Ubiquitin
a. Identifies the protein for degradation by proteasome.

O83. Cyclins
a. Activate cyclin-dependent kinases,
b. thereby helping to control progression from one stage of the cell cycle to the next. (Accept: idea of cell cycle to proceed to next stage)

O84. p53 protein
a. Plays an important role at the G_1 checkpoint of cell division
b. by monitoring the integrity of DNA sequence. **[MUST HAVE]**
c. It activates the transcription of various genes which produces special DNA repair enzymes to repair the damage. **(R: activate DNA repair enzymes)**
d. Activates the cell's suicide pathway (apoptosis) if damage cannot be repaired.

O85 . Small ribonucleoproteins (**snRNPs**)
a. Contains snRNA
b. which recognises and binds to splice sites at each end of an intron via complementary base pairing.

Reject

ER signal peptide: because it is not a protein
Hydrolytic enzymes: not specific
Receptors: not specific
Active site/ allosteric site of viruses: no such thing

QWC:
1. Paragraph
2. Covers at least 4 different functions

6 DNA is a hereditary material which contains thousands of genes which code for proteins that control cell function. DNA must be replicated and passed to daughter cells.

(a) Describe the process of DNA replication. [12]

1. **Helicase binds to DNA molecule at the origin of replication,**
2. **and disrupts hydrogen bonds between complementary base pairs,**
3. **Helicase separates/unzips parental strands.**
4. **Single-strand binding proteins stabilize the unwound helix and prevent rewinding of double helix.**
5. **A replication bubble with two Y-shaped replication forks are formed.**
6. **Replication proceeds in BOTH directions from the origin until the entire DNA molecule is replicated.**
7. **Primase synthesises RNA primer using free ribonucleotides (RNA) in the 5'→3' direction.**
   This occurs via complementary base pairing with the parental strand which acts as a template.
8. **DNA polymerase reads template strand in the 3'→5' direction**
9. **and synthesizes daughter strand in the 5'→3' direction**
10. **Free deoxyribonucleotides complementary base pairs with template strand**
11. **Adenine base pairs with thymine**
12. **Cytosine base pairs with guanine**
13. **Phosphodiester bonds are formed between adjacent deoxyribonucleotides via condensation reactions.**
14. **DNA polymerase also proofreads the daughter strand.**
15. **If a nucleotide in the daughter strand is wrongly paired with template, the DNA polymerase will remove and replace with correct nucleotide.**
16. **Since the 2 parental strands are anti-parallel,**
17. **the 2 daughter strands are synthesized in the opposite direction by DNA polymerases.**
18. **Leading strand is synthesized continuously towards the replication fork.**

DNA polymerase adds new nucleotides in the 5' →3' direction without any breaks

19. **Lagging strand is synthesized discontinuously as Okazaki fragments away from the replication fork.**
20. **As helicase separates DNA strands at the replication fork to expose the DNA templates, new primers will be synthesised by primase.**
21. **Another DNA polymerase replaces the RNA primers with deoxyribonucleotides.**
22. **DNA ligase seals the gaps (nicks) between the Okazaki fragments by catalysing the formation of phosphodiester bonds between them.**
23. **At the end, two DNA molecules are formed.**
24. **each DNA molecule consists of 1 parental strand AND 1 daughter strand, which will wind to form a double helix.**

QWC – 1 mark

1) **paragraph**
2) **Correct flow (sequence of events)**

(b) Describe how ribonucleic acids are involved in the flow of information from DNA to proteins. [13]

1. **RNAs (i.e., mRNA, rRNA and tRNA) are synthesised in nucleus via transcription**
2. **rRNA synthesised in nucleolus via transcription.** (must mention "transcription" at least once in pt 1 or 2)
3. **RNAs are complementary to template strand of genes / DNA templates.**
4. **RNA is transported from nucleus to cytoplasm through nuclear pores.**

mRNA

5. **mRNA carry genetic information from nucleus to ribosomes (either free or bound) in the cytoplasm for translation to occur.**
6. **mRNA serves as a template for translation** (must mention "translation" at least once in pt 4 or 5)
7. **which is read by ribosome for the synthesis of a polypeptide.**

8. **Each codon in the mRNA codes for an amino acid.**
9. **The sequence of codons on mRNA is translated,**
10. **resulting in a specific amino acid sequence of polypeptide / that specifies order in which amino acids are joined to form a polypeptide chain.**

11. **Codons on mRNA are complementary to anticodons on tRNA**
12. **They base-pair by hydrogen bonds.**

Note: Point 11-12 overlaps with tRNA

13. **mRNA also contains start codon to ensure that translation begins / initiates at the correct point.**
14. **Mention of: AUG**
15. **mRNA also contains stop codon to ensure that translation ends / terminates at the correct point.**
16. **Mention of any e.g.: UAA, UGA or UAG**

rRNA

17. **rRNA combines with ribosomal proteins**
18. **to form the large subunit and small subunit of ribosomes.**

19. **Within small subunit of ribosome, rRNA binds mRNA**
20. **to ensure translation starts at the correct location on the mRNA.**
    OR
    to align / orientates / position mRNA within the sites in the ribosome for complementary base pairing with tRNA.

21. **Within large subunit of ribosome, rRNA forms binding sites (or E, P, A sites) for tRNA.** (linked to point 28)
22. **Part of rRNA has peptidyl transferase activity / forms the enzyme, peptidyl transferase.**
23. **to catalyse formation of peptide bonds between adjacent amino acids.**

tRNA

24. **tRNA carries a specific amino acid to the ribosome during translation.**
25. **The 3' end with CCA nucleotides serves as a site of attachment for specific amino acid.**

26. **tRNA has a specific 3D conformation / clover-leaf structure**
27. **allows for interaction with aminoacyl-tRNA synthetase**
28. **and large ribosomal subunit.** (linked to point 21)

snRNA

29. **Small nuclear RNA in snRNPs**
30. **recognize and bind to splice sites at the ends of introns**
31. **during the formation of spliceosome.**
32. **Excise introns and splice exons**
33. **to form a continuous coding sequence in mature mRNA for translation**

QWC [1]

1. **Separate paragraphs**
2. **Includes at least two ribonucleic acids.**

Marker's comments / feedback:

1. **The most common error of answering this question was to describe the process of transcription or/and translation instead of addressing each RNA separately.**

2. **Note that rRNA genes code for rRNA and not ribosomal proteins.**

3. **Candidates can simply write the different types of RNA as mRNA, rRNA and tRNA in their ESQ answer. However, in STQs where the question is to "name the molecule", candidates should spell out in full (e.g., messenger ribonucleic acid and not mRNA).**