

TEMASEK JUNIOR COLLEGE
2025 JC2 PRELIMINARY EXAMINATION
Higher 2



CANDIDATE
NAME

ANSWERS

CENTRE
NUMBER

S

INDEX
NUMBER

BIOLOGY

9744/03

Paper 3

17 September 2025

2 hours

Candidates answer on the Question Paper.

READ THESE INSTRUCTIONS FIRST

Write your Centre 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 in the Question Paper.

The use of an approved scientific calculator is expected, where appropriate.

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

For Examiner's Use	
1	/ 30
2	/ 10
3	/ 10
4 OR 5	/ 25
Total	/ 75

This document consists of **14** printed pages and **2** blank pages.

[TURN OVER

Section A

Answer **all** questions.

- 1 Myeloid stem cells in the human bone marrow undergo repeated proliferation and differentiation once they receive external signals to produce more white blood cells that are critical in fighting infections from pathogens. Such stem cells will go through cell cycles in different stages and are regulated tightly by various proteins and checkpoints found along the way.

Fig. 1.1 shows the various stages of the cell cycle and how it is regulated at the various checkpoints. The important control points of the cell cycle lie at the end of the G2 phase (G2/M transition), in mitosis (metaphase/anaphase transition) and in G1 phase (restriction point). Controls are shown in both solid and broken arrows.

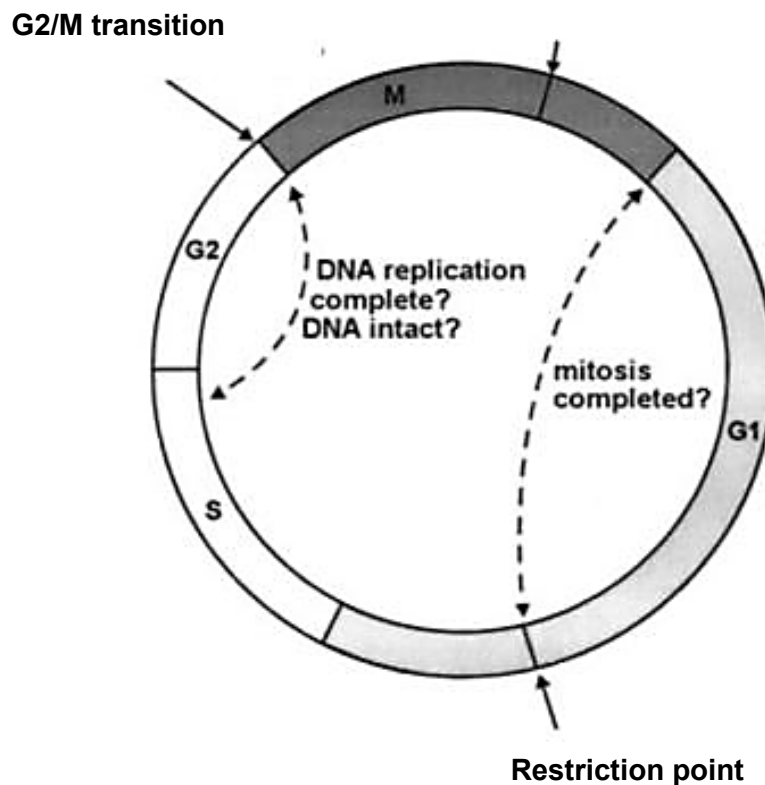


Fig. 1.1

- (a) Describe the function of metaphase/anaphase transition control and how this may prevent the development of cancer. [3]

1. Metaphase/anaphase transition control checks for spindle fibre attachment to kinetochore of chromosomes;
2. Checks that all chromosomes are attached to the spindle fibres in preparation for anaphase;
3. Ensuring that each daughter cell receives a complete set of chromosomes after mitosis is complete (genetic stability);
4. Cell cycle is arrested at metaphase if any chromosomes are not attached to the spindle fibres;
5. Transition into anaphase is prevented until all chromosomes are aligned properly at metaphase;
6. Which may lead to uncontrolled cell division leading to tumour formation.

Spindle fibres are polymers made from tubulin monomers. The removal of tubulin monomers causes spindle fibres to shorten. Scientists investigated the effect of the rate of tubulin removal on the speed of movement of chromatids during mitosis.

Fig. 1.2 shows the results of the investigation.

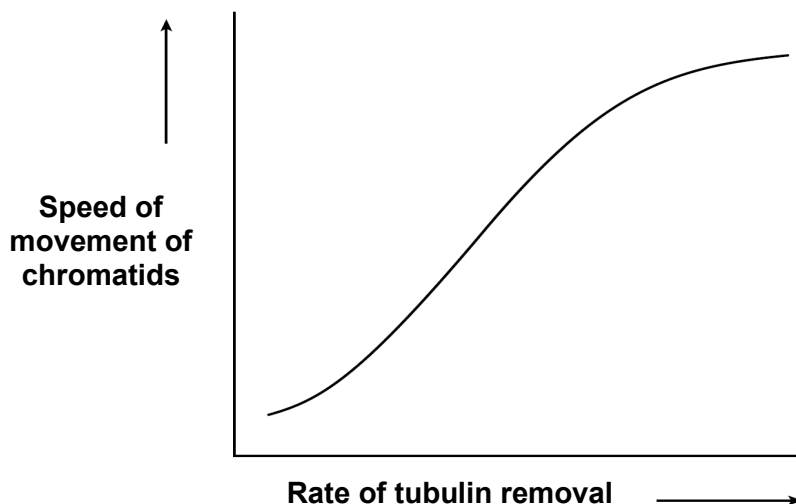


Fig. 1.2

- (b) (i) Describe how these results support the role of spindle fibres in mitosis. [2]
1. As rate of tubulin removal increases, the speed of movement of chromatids also increases until it approaches the maximum speed of movement of chromatids
 2. Suggesting that tubulin removal is required for shortening of spindle fibres to allow separation of sister chromatids to opposite poles of the cells in anaphase of mitosis
- (ii) Paclitaxel, also known as Taxol, is a microtubule structure-stabilizing drug that is commonly used to treat both early-stage breast cancer and advanced, or metastatic breast cancer.

Explain why drugs such as paclitaxel are effective as an anti-cancer therapeutic. [2]

1. During cancer cell division, shortening of microtubules is required to separate sister chromatids to the opposite poles of the cell during anaphase;
2. Presence of paclitaxel prevents shortening of the microtubules during anaphase /affecting arrangement of chromosomes at metaphase plate;
3. This causes the cell cycle to be arrested at metaphase/anaphase transition control checkpoint;
4. Cancer cells unable to proceed to next stage of cell cycle leading to apoptosis of cancer cells.

Chronic myeloid leukemia (CML) is a cancer of the white blood cells. Patients with CML suffer from shortness of breath and have increased risk of infection.

This slow-growing cancer arises from a disorder in the myeloid stem cells found in bone marrow. Myeloid stem cells are responsible for maintaining the red blood cells and white blood cells populations in the body.

CML patients are diagnosed via a complete blood count test, which will identify abnormal numbers of different types of blood cells in a fixed volume of blood.

Fig. 1.3 shows the blood cells in 100 ml of blood from a healthy person and a CML patient.

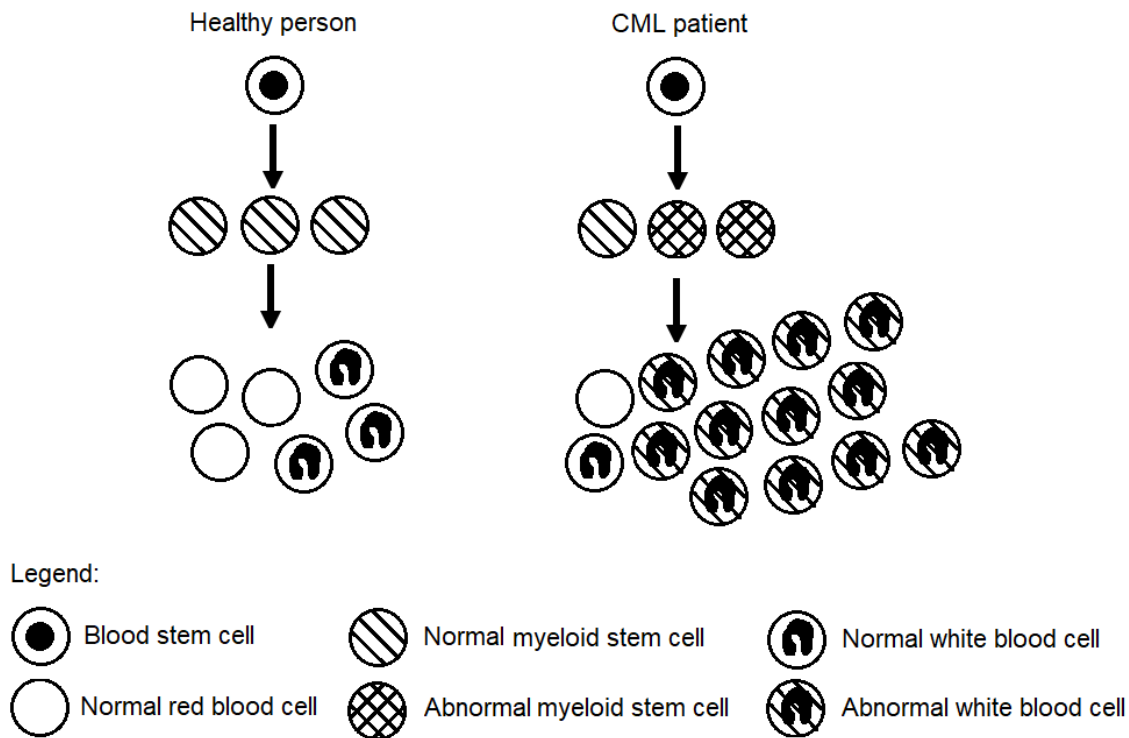


Fig. 1.3

(c) Explain what is meant by cancer.

[3]

1. A disease characterised by uncontrolled cell division;
2. Due to dysregulation of cell cycle checkpoints;
3. And failure to undergo apoptosis (programmed cell death)/ evade cell death;
4. Resulting in formation of mass of cells called tumour;
5. Malignant tumour cells are able to invade other neighbouring tissues;
6. And metastasize by entering bloodstream to other parts of the body.

(d) With reference to Fig. 1.3, explain how abnormal myeloid stem cells change the red blood cells and white blood cells populations.

[4]

1. Abnormal myeloid stem cells undergo uncontrolled cell division;
2. To proliferate to many more blood cells;
3. [QF] Increase from 6 to 14 red and white blood cells compared to normal myeloid stems cells;
4. Abnormal myeloid stem cells differentiate to produce more abnormal white blood cells than red blood cells;
5. [QF] Increase from 0 to 12 abnormal white blood cells;
6. As mutations are passed down from parent cell to daughter cells during mitosis;
7. Abnormal myeloid stem cells also differentiate to produce less red blood cells;
8. [QF] Decrease from 3 to 1 normal red blood cells.

Changes to ABL and BCR genes are normally associated with CML cancer. A genetic study that screens for the presence and length of ABL and BCR genes in specific chromosomes reveal that abnormal myeloid stem cells arise from a mutation event. The mutation results in mutant chromosome 22, also known as the Philadelphia chromosome.

Fig. 1.4 shows the results of the genetic study. Chromosome 2 is known to not carry ABL and BCR genes.

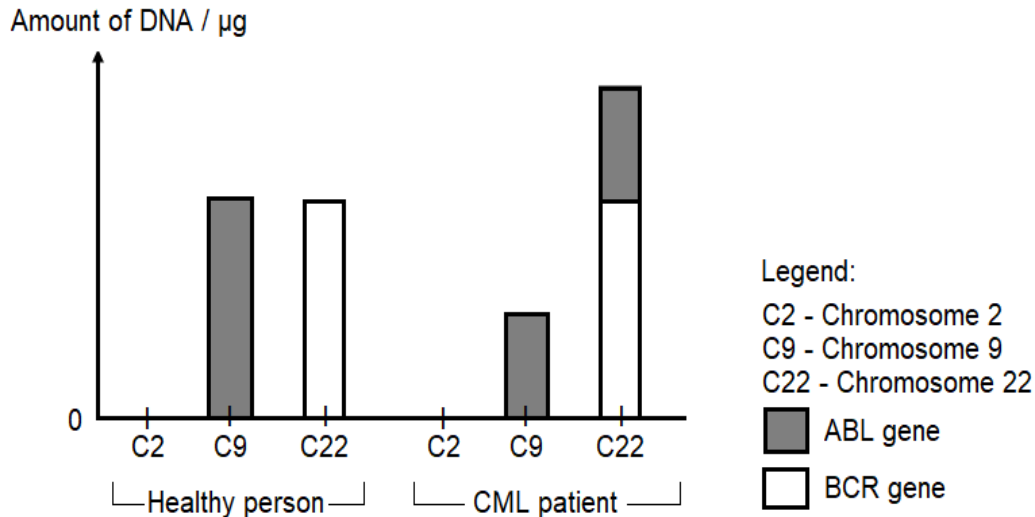


Fig. 1.4

(e) (i) Describe the mutation event that gives rise to Philadelphia chromosome. [1]

1. Chromosomal translocation of part of ABL gene;
2. from chromosome 9 to chromosome 22.

(ii) Suggest the purpose of screening chromosome 2. [1]

Serves as a negative control to eliminate false positives / OWTTE

Further studies revealed that CML patients that have the Philadelphia chromosome express an altered form of tyrosine kinase receptor, known as BCR-ABL. BCR-ABL is a receptor in a cell signaling pathway that stimulates cell growth. BCR-ABL receptor is observed to have a higher than normal level of activity, and abnormality in its ligand-receptor interaction.

(f) (i) Describe how a receptor tyrosine kinase receptor (RTK) such as the BCR-ABL is activated in a cell signalling pathway. [2].

1. Signal molecule binds to ligand binding site on RTK via complementary binding;
2. Dimerisation of both subunits of RTK;
3. Results in activation of tyrosine kinase;
4. Autophosphorylation/cross-phosphorylation of tyrosine residues on tyrosine tails of the other subunits;
5. Activation of tyrosine tails, RTK activated.

- (ii) Suggest how the presence of a Philadelphia chromosome may lead to the development of cancer. [2]

1. Philadelphia chromosome expresses a hyperactive BCR-ABL receptor;
2. Triggering signal transduction in the absence of a ligand molecule;
3. This causes continuous/unregulated signal for cell growth stimulation;
4. Causing overstimulation of cell cycle thus uncontrolled abnormal myeloid stem cell cell division.

In the regulation of cell cycle, roles of proteins such as cyclin-dependent kinases (CDK) and cyclins are involved in allowing cells to progress to the subsequent stages of the cell cycle. For example, the formation of CDK 4-cyclin D complex is required for the completion of S phase in the cell cycle. Without this complex, the cell cycle will be arrested at the G1 phase.

Palbociclib is a novel drug with structural similarity to cyclin D was developed to treat CML by targeting cyclin-dependent kinase 4 (CDK 4). Researchers investigated the effect of Palbociclib on the concentrations of CDK 4 – cyclin D complex and free cyclin D.

Fig. 1.5 shows the concentrations of CDK 4-cyclin D complex and free cyclin D in a drug trial involving high dosages of Palbociclib.

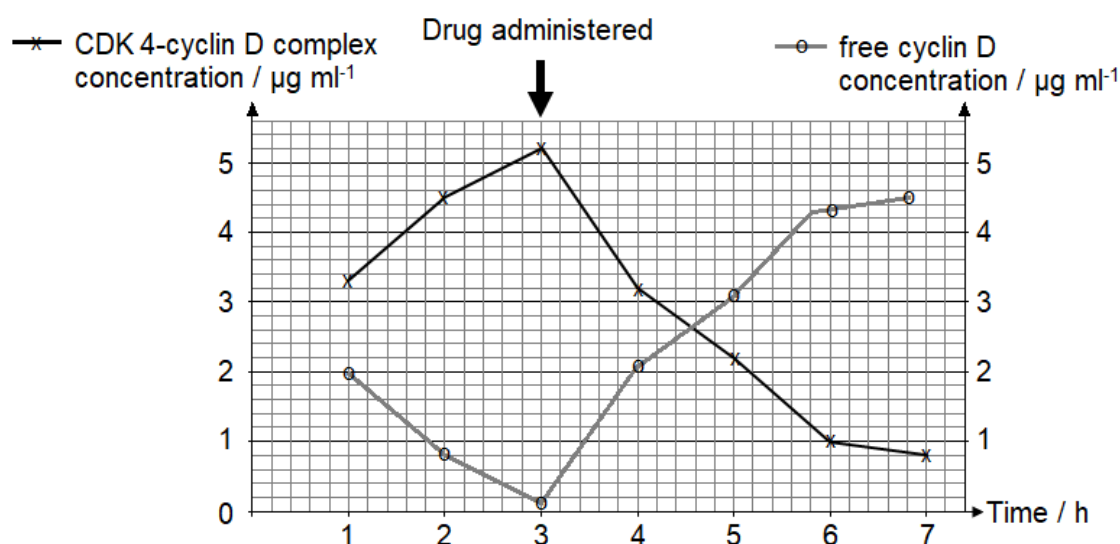


Fig. 1.5

- (g) (i) Describe the changes in the CDK4-cyclin complex and free cyclin. [2]
1. From 1 to 3 hours, gradual increase in CDK 4-cyclin D complex concentration from $3.3 \mu\text{g ml}^{-1}$ to $5.2 \mu\text{g ml}^{-1}$;
 2. However, there is a gradual decrease in free cyclin D concentration from $2.0 \mu\text{g ml}^{-1}$ to $0.1 \mu\text{g ml}^{-1}$;
 3. Upon Palbociclib administration from 3 to 7 hours, steep decrease in CDK 4-cyclin D complex concentration from $5.2 \mu\text{g ml}^{-1}$ to $0.8 \mu\text{g ml}^{-1}$;
 4. However, there is a steep increase in free cyclin D concentration from $0.1 \mu\text{g ml}^{-1}$ to $4.5 \mu\text{g ml}^{-1}$.
- (ii) Explain how Palbociclib could potentially be a therapeutic drug for CML patients. [2]
1. Palbociclib is a competitive inhibitor of CDK 4;
 2. Competes with cyclin D to bind to CDK4 active site;
 3. This delays the completion of S phase, slowing down cell cycle progression;
 4. Reducing the number of abnormal myeloid stem and white blood cells in CML patients.

Upon further investigation, the researchers concluded that Palbociclib is not suited for use in cancer treatment.

(iii) Suggest why Palbociclib may not be suitable for use in cancer treatment.

[1]

Palbociclib is non-specific in targeting cancer cells, thus will also reduce division of normal cells

Two genes, *CCND1* and *CCND2*, encode cyclin D proteins that play crucial role in regulation of cell cycle progression, particularly during the G1 phase. The two genes are located on different chromosomes are responsible for the synthesis of cyclin D that forms complexes with CDK 4.

To examine whether differences in the expression level of *CCND1* and *CCND2* influence the formation of the CDK4 – cyclin D complexes, reverse transcription polymerase chain reaction (RT-PCR) was carried out on adult hair follicular cells from two patients (Patient A and B). The resultant RT-PCR product was analysed by gel electrophoresis.

Fig. 1.6 shows the results of the gel electrophoresis.

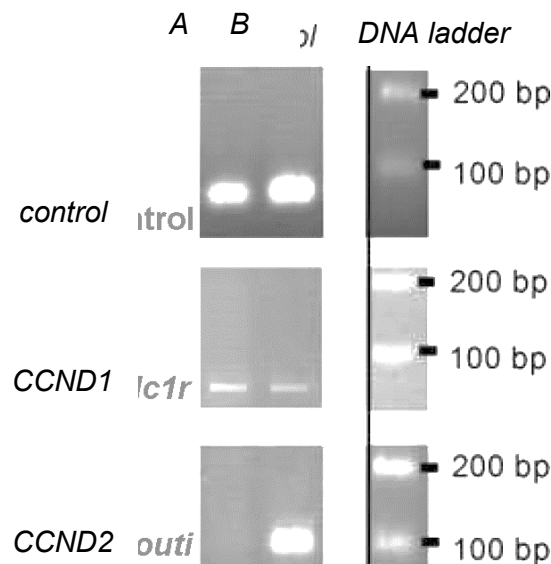


Fig. 1.6

(h) With reference to Fig. 1.6,

(i) outline the principle of gel electrophoresis;

[2]

1. separates DNA fragments by size / length;

Any 1

2. smaller DNA fragments move faster towards positively-charged pole + lower position of 100bp band compared with 200bp band;

3. similar/ same sized DNA fragments move at the same speed + CCND1 bands in both patients A and B are the same size/ CCND2 fragment is approximately 100bp;

4. thickness/ brightness of band reflects relative quantity of DNA + more control DNA in Patient B than in Patient A/ approximately same amount of CCND1 in both Patient A and B;

[TURN OVER

(ii) describe the expression level of *CCND1* and *CCND2*;

[2]

1. *CCND1* is expressed in both Patients A and B;
2. *CCND2* is expressed only in Patient B and not in Patient A;

(j) RT-PCR is a laboratory technique combining reverse transcription of RNA into DNA and amplification of specific DNA targets using polymerase chain reaction. The technique is carried out on mRNA samples isolated from cells.

Suggest one advantage of RT-PCR compared to conventional PCR.

[1]

1. RT-PCR can provide information on spatial expression (location) patterns
2. RT-PCR can provide information on temporal gene expression (time) patterns, as only genes are expressed as mRNA will be amplified;
3. Can show different levels of expression

[Total: 30]

- 2 A certain dominant disease in humans occurs when there are more than 40 repeats of the triplet sequence 'CGG' in a particular gene.

Fig. 2.1 shows an example of one strand of the diseased allele. (CGG)₄₅ represents 45 repeats of the triplet sequence 'CGG'.

5' CAGTATGCA ----- (CGG)₄₅ ----- ATGCGTAAT 3'

Fig. 2.1

- (a) With reference to Fig. 2.1, state the sequence of the complementary strand. [1] – HAE, E

3' GTCATACGT ----- (GCC)₄₅ ----- TACGCATTA 5'

Markers comment:

1. Most candidates are able to write the complementary sequence. Please remember to include the directions, 5' and 3'
2. Also please note that question is asking for complementary strand NOT mRNA.

- (b) Describe a mutation that can give rise to a variable number of repeats in an allele. [2]

– 1 KU 1 HAE, 1 E 1 M

1. Insertion mutation
2. of variable number of GCC / CGG nucleotides / gene segments

or

1. Duplication mutation
2. of triplet sequence of GCC / CGG nucleotides / gene segments

Markers comment:

1. Most candidates are able to identify the type of mutation, but unable to get full credit, because did not quote sequence (GCC)
2. Note that candidates should not extend answers to transcription and translation, e.g. giving rise to mutant protein / non-functional protein as question DID NOT ask for such prediction/impact on protein. – Read Question and understand the requirement)
3. Reject gene amplification – more for genes that will be transcribe and translated.

A genetic counsellor was tasked to determine if the child of two individuals (Individual A and B) was at risk of inheriting this disease. After obtaining the DNA of both individuals and all their immediate family members, the researcher ran the DNA through gel electrophoresis but **obtained a smear**.

- (c) Explain briefly how the researcher can **obtain distinct bands corresponding to the gene of interest from the gel electrophoresis results**. [2] – 1 KU 1

HAE, 2 M

1. Perform a Southern Blot with
2. Radioactive probes that are complementary to sequences of the gene of interest

Markers comment:

1. **Reject PCR or RE digestion as question asked “obtained a smear...” “obtain distinct bands corresponding to the gene of interest from the gel electrophoresis results” - > strongly pointed to a step to follow up from Gel E.**
2. **Note, it is very important to include “radioactive”, the probes must be radioactive so that researchers can observe the dark distinct bands after autoradiography.**

(d) Suggest the significance of obtaining the DNA samples of the immediate family members.

[1] – HAE, D

Better investigate the inheritance patterns of the gene / OWTTE
AVP

Markers comment:

1. To determine probability of child inheriting the disease – 1/2m
2. To determine if sex-linked (without mentioning autosomal) – 1/2m
3. Answers that mentioned DNA sequences between family members are similar = no marks as this does not answer the “significance”.

Fig. 2.2 shows the outline of a pedigree for the disease described above for all individuals and a representation of a gel showing the bands that contain the gene of interest.

The DNA corresponding to each individual is directly below his or her place in the pedigree.

A dotted line is also drawn in the gel representation to indicate the position of any bands that contain DNA fragments with 40 repeats of the triplet sequence ‘CGG’.

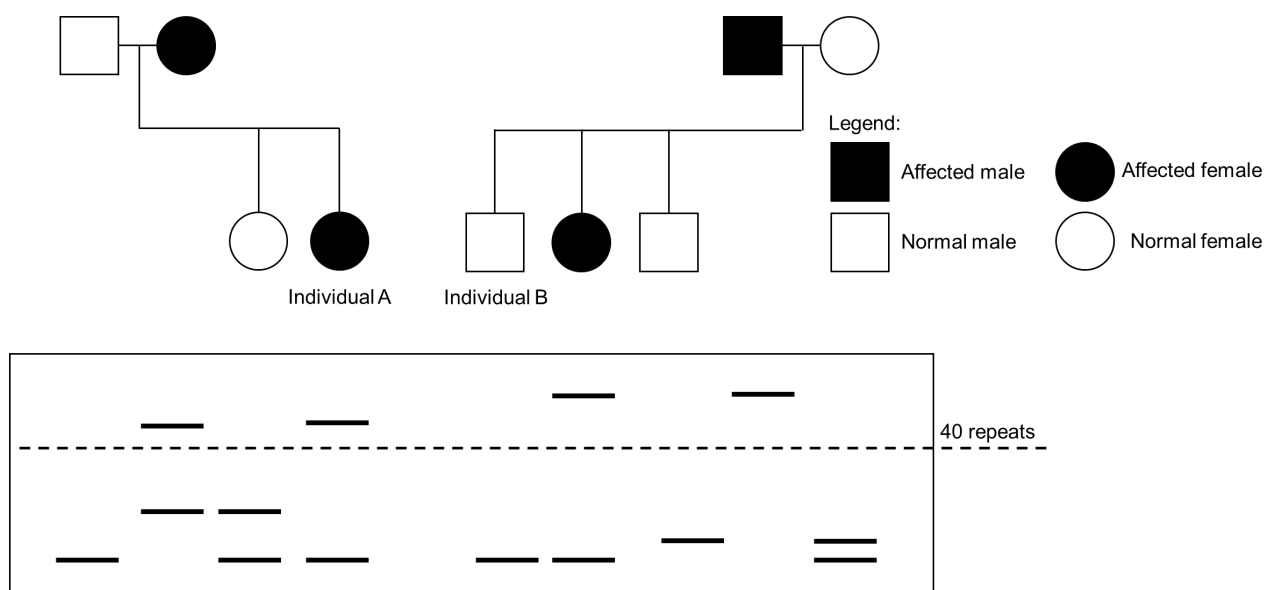


Fig. 2.2

(e) (i) Based on the information provided in this question, deduce if the gene of interest is found on an autosome or sex chromosome.

[1] – HAE, M

Sex chromosome

(ii) Explain your answer to (e)(i).

[2] – 2 HAE, 1

E 1 D

1. All males only have 1 band present while all females have 2 bands present
2. which corresponds to males having 1 X chromosome / heterogametic and females have 2 X chromosomes / homogametic

[TURN OVER]

OR

3. All daughters have the same band as their fathers
4. corresponds to fathers passing down their X chromosome to their daughters.

Markers comment:

1. Most candidates are able to determine sex-linked. Also able to explain in terms of affected father passing the alleles to daughters, resulting in affected daughters.
2. Many gave more than one explanation of the inheritance. Good.
3. But Question requires candidates to link to the banding patterns.
4. Breakdown of marks: 1m for banding patterns, 1m for theory explanation. See model answer.
5. Candidates who identify wrongly as autosomal – most common mistake is did not read that the allele that cause the disease is dominant.

(iii) Hence, state the probability of the child of individuals A and B inheriting the disease.
[1] – HAE, E

0.5

Markers comment:

1. Most candidates are able to answer correctly.
2. Most common mistake, candidates misread question and gave the two different probabilities of Individual A and B being affected.

[Total: 10]

North America is home to diverse migratory bird species that travel long distances between their breeding grounds in the north and wintering grounds in the south. One such migratory bird species is the American robin, a widespread bird across North America. During the winter season, the robins will migrate from the northern region of Canada to the southern region to seek for their food source – caterpillars.

Over the years, climate changes have affected the population of American robins, affecting their migration pattern and possibly impacting their survival.

Figure 3.1 below shows the average global temperature over the years.

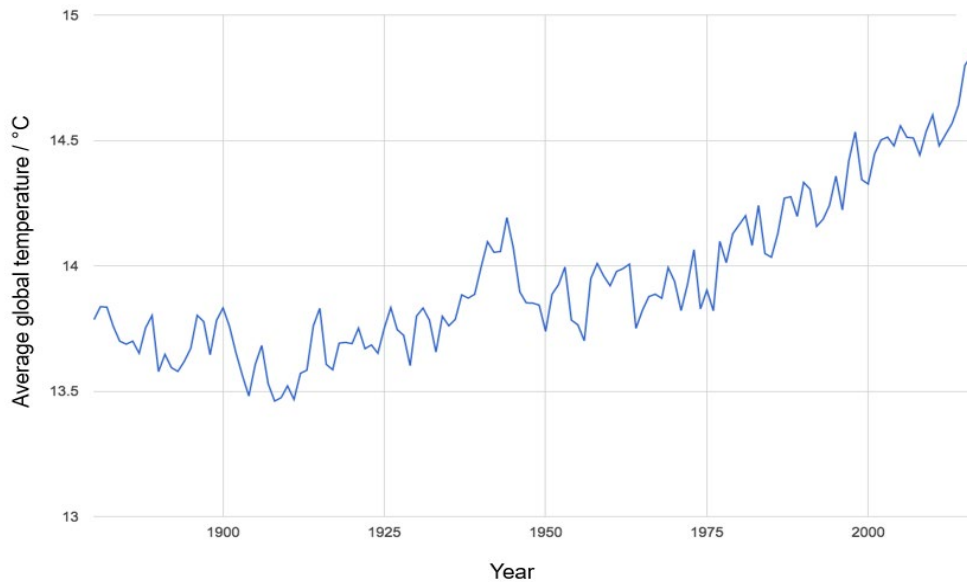


Figure 3.1

Figure 3.2 shows the migration period of the robins from north Canada to south Canada in 1950 and 2000 while Figure 3.3 shows the period where there is great abundance of caterpillars in south Canada in 1950 and 2000.

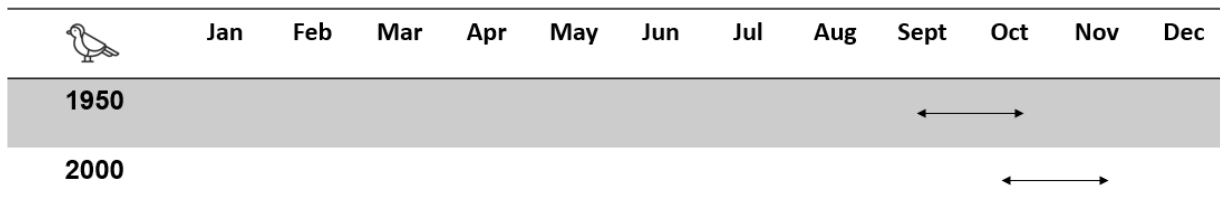


Figure 3.2

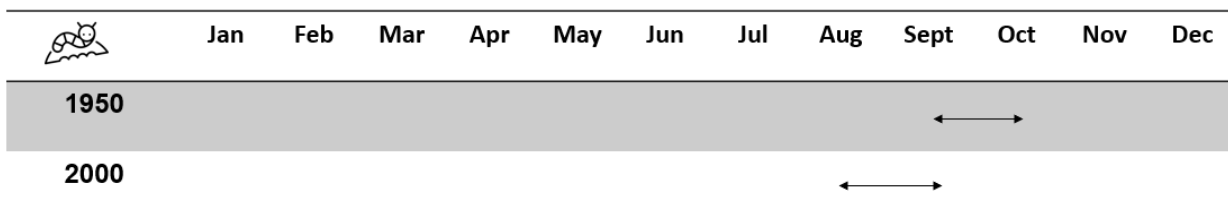


Figure 3.3

Climate change has been said to affect the American robins migratory phenology.

(a) Suggest what is meant by the term “phenology”. [1] – HAE, D

- Phenology refers to the timing of events over the annual cycle of animals. / OWTTE

Markers comment:

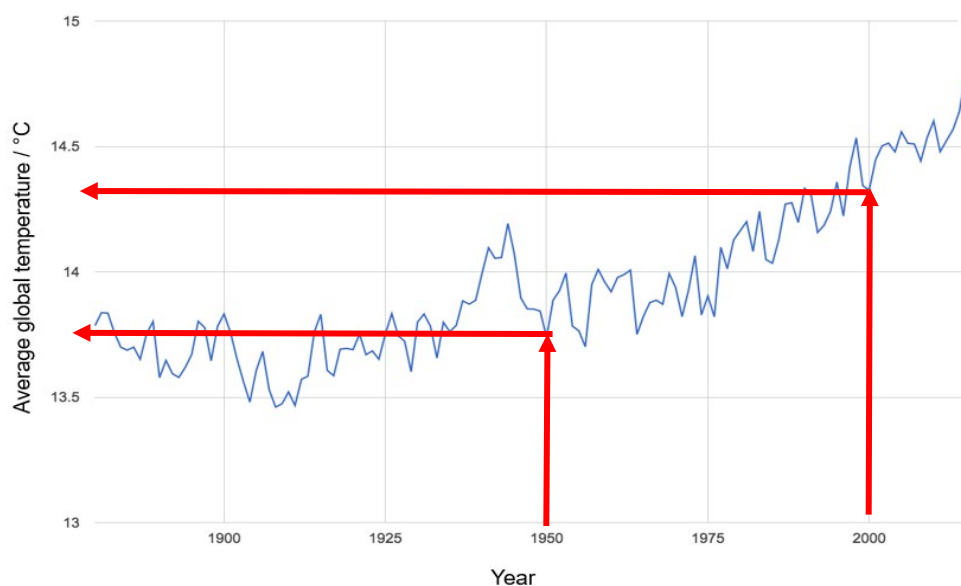
- Most candidates are unable to gain full credit.
- Note this is a new term, NOT Phenotype.
- Question context is on time period and pattern.

(b) With reference to Fig. 3.1 and 3.2, describe and explain how climate change has caused the change in the migration pattern. [3] – HAE, 2E 1D

- QF:** As years increased from 1950-2000, there was an increase in global average temperature from 13.75 to 14.75.
- QF:** The migration of the robin was delayed from September to October in 1950 to October to November in 2000.
- Explain:** This can be due to warmer winter / delayed winter which delayed the departure of the robin from north Canada

Markers comment:

- Most candidates are able to gain FULL credit.
- Well attempted! Keep it up! QF is good. Interpretation of data is accurate.
- But note some candidates still quote values wrongly, e.g. 14.8 for year 2000, see below, is definitely too far off. Please use ruler and make sure your ruler is perpendicular to the side of the paper.



(c) Suggest why caterpillars are found in abundance earlier in the year in 2000 as compared to 1950, as shown in Figure 3.3. [2] – 1 KU 1 HAE, 2 M

1. The increase in global temperature can increase the metabolic rate of the insect. (@increased temperatures resulting increased enzymatic activities – only 1/2m)
2. This can result in the shortening of developmental time of the insect, resulting in caterpillars emerging from the egg much earlier / faster time to complete life cycle. (OWTTE)

Markers comment:

1. Reject caterpillars are in abundance due to lack of predators (robins flew in only later). Note that even in 1950, prior to Sept, there was also no predators, yet, caterpillars were able to grow into abundance in Sept.
2. Thus the change in temp. must be affecting the life cycle of the caterpillars rather than the environment.

(d) Comment on how changes shown in Fig. 3.2 and Fig. 3.3 can impact the American robins. [4] – 1
KU 3 HAE, 2 M 2 D

1. The robins migrate later while the caterpillars are in abundance earlier. / do not overlap (OWTTE)
 2. This results in the lack of food source for robins as they arrive at south Canada
 3. The lack of food source can result in reduced ability of robins to survive and reproduce (need to link to inability to reproduce)
 4. Robins might need to fly further south to find a region with food source
 5. Robins might need to find other food sources in the region in order to survive
- (Points 4 and 5 – relating to behaviour of robin)
 AVP

[1] – relating robin migration to caterpillar abundance period

[1] – lack of food source

[1] – reduced survive and reproduce

[1] – change in robin's behaviour

Markers comment:

1. Candidates were able to gain credit for points 1 and 2 but not 3 onwards.
2. Most stopped at “resulting in death/ decreased population” without stating inability to reproduce.
3. Also most candidates relate to natural selection – leading to speciation etc which is not possible to happen within 50 years (1950 – 2000). Thus not accepted.
4. Generally candidates need to achieve greater clarity in concepts to understand which concepts can be applied or cannot be applied to a given novel context.

- 4 (a) In 1665, Robert Hooke discovered cells using one of the first microscopes ever invented. Subsequently, the biologists Matthias Schleiden and Theodor Schwann summarised a large number of observations by themselves and others.

Their conclusions have come to be known as the cell theory and forms the foundation for understanding the reproduction and growth of all organisms.

Using a named example, **describe the cell theory** and discuss **how** we can determine if an **unknown entity** is a cell. [10]

Cell Theory [max 5]

1. The cell is the smallest, most basic unit of life that carries out all the essential processes of life such as metabolism and inheritance.
Note: most responses were missing the second half of this point on “all essential processes”.
2. All living organisms are made up of cells.
3. All cells arise from pre-existing cells by cell division.

4. Named example of eukaryotic cell and its features (presence of nucleus, ribosomes, mitochondria, can divide by mitosis)

[1] – Named example (4N)

[1] – Feature (4F)

5. Named example of prokaryotic cell and its features (presence of nucleoid region, ribosomes, can divide by binary fission)

[1] – Named example (5N)

[1] – Feature (5F)

Note: Question asked for “named example” – simply stating eukaryotic / prokaryotic cell is insufficient to get credit for named example.

Determination of unknown entity (must cover at least 2 categories)

Microscope observations

6. Look for plasma membrane / cell wall
7. Look for nucleus structure / nucleoid region
8. Look for other organelles such as ribosomes and/or mitochondria
[1/2] if no examples of organelles provided

Note: - ½ if response did not indicate method (microscopy) to use to look for MP6, 7, 8

Chemical composition tests

Note: 1 mark for stating type of molecule (with specific example) + 1 mark for stating method

9. Detect nucleic acid [1] using PCR amplification [1] (accept if students state DNA / RNA)
10. Detect metabolic enzymes such as ATP synthase / presence of proteins
11. through biuret test
12. Detect peptidoglycan cell wall
13. Through gram-staining

Functional tests**14. Check for respiration or photosynthesis**

Note: [1/2] for generic use of word 'metabolism'

15. through checking for oxygen uptake, release of carbon dioxide, reactions under light

(Accept any other plausible methods)

16. Check if can divide / reproduce under the right conditions without a host / other cells given glucose or other growth medium

Note: [1/2] for 'reproduce on its own'

QWC:

P – appropriate paragraphing

Q – address both parts of the questions (must cover at least 2 categories for determination)

General comments:

1. Many candidates included viruses in their response as 'named examples' – how do viruses answer the question? They are neither living nor non-living.
2. There were a sizable number of responses that also mentioned endosymbiont theory as a named example? Not sure how this answers the question too. Possible misconception? Please approach your STs if unsure why it is not accepted.

(b) Describe how **complementarity** between biomolecules enable eukaryotic cells to **carry out their diverse functions**. [15]

Question analysis:

1. What is complementarity? List some examples here. What are the roles of these examples, where do they occur? What is the significance of such interaction?
 1. Complementary shape;
 2. Complementary base pairing;
2. What functions rely on complementarity? What biomolecules are involved in these functions?

max 5 m for each category

Category	Description
Transport protein + molecule to be transported (T)	1. A <u>transport protein</u> has a <u>binding site complementary in shape</u> to shape of <u>molecule</u>, [1] 2. Allows for <u>transport</u> of <u>molecules</u> into and out of <u>organelles</u> / <u>cells</u> / <u>compartments</u> via <u>facilitated diffusion</u> / <u>active transport</u> [1] Examples: [1 each] 3. Channel protein e.g. aquaporin specific for water 4. Carrier protein e.g. glucose transporter 5. Pump e.g. proton pump 6. Protein complex e.g. nuclear pore specific for nucleotides, exit of pre-mRNA, entry of ribosomal proteins, exit of ribosomal subunits 7. ATP synthase recognise H⁺ can diffuse through its channel to form ATP from ADP and Pi;

Category	Description
Enzyme + substrates (E)	<u>Enzyme active site</u> is complementary in shape to shape of <u>substrate</u>; [1] <u>Enzyme active site</u> is complementary in shape to shape of <u>competitive inhibitor</u>. [1] Examples: [1 for name of enzyme and substrate] [1 for reaction catalyzed] <u>DNA polymerase</u> – active site shape complementary to shape of <u>deoxyribonucleotides</u>; - catalyses <u>formation of phosphodiester bonds</u> between <u>adjacent DNA nucleotides</u> to synthesise new strand (DNA replication); <u>DNA ligase</u> – active site shape complementary to shape of <u>DNA fragments</u>; <u>forms a phosphodiester bond between two DNA fragments/ sealing nick</u>; <u>RNA polymerase</u> – active site shape complementary to shape of <u>ribonucleotides</u>; - and catalyses <u>formation of phosphodiester bonds</u> between <u>adjacent RNA nucleotides</u> of newly synthesised strand; <u>Amino acyl tRNA synthetase</u> – active site shape complementary to an <u>amino acid</u> and <u>tRNA</u> molecule; - and <u>catalyses formation of ester bond</u> between <u>tRNA</u> and <u>specific amino acid</u>; <u>Peptidyl transferase</u> – active site shape complementary to <u>shape of growing polypeptide chain</u> and <u>incoming amino acids</u>; - form <u>peptide bonds</u> between <u>amino acids</u>; <u>NADP⁺ reductase</u> – active shape complementary to shape of <u>NADP⁺</u> - reduces <u>NADP⁺ to NADPH</u> in the final step of electron transport chain in photophosphorylation; <i>AVP any other enzyme</i>
Protein + DNA (PD)	- Proteins have <u>DNA binding domains</u> that are complementary in shape to shape of <u>specific DNA sequence</u>; [1] Examples: Note: [1] – named protein and DNA interaction + [1] – function <u>TATA binding protein</u> – <u>TATA box</u>; <u>Recruiting general transcription factors</u> and <u>RNA polymerase</u>; <u>RNA polymerase</u> – <u>promoter</u> sequence; <u>Initiating RNA synthesis/transcription</u>; <u>Activators</u> – specific <u>enhancer</u> sequences; - to <u>increase frequency of transcription</u>; / <u>promoting assembly of transcription initiation complex</u>; <u>Repressors</u> – specific <u>silencers</u> sequences - to <u>decrease frequency of transcription</u>/ <u>inhibiting assembly of transcription initiation complex</u>; <i>AVP any other named interaction</i>

Category	Description
Protein + protein (PP)	1. Proteins have <u>protein binding domains</u> that are <u>complementary in shape</u> to other <u>protein</u> molecules; Examples: 2. Protein binding domain of specific transcription factors interact with general transcription factors
Base pairing (BP)	1. <u>Purine</u> complementary base pairs with a <u>pyrimidine</u> base; 2. <u>Adenine base pairs with thymine</u> and <u>guanine pairs with cytosine in DNA</u> by complementary base pairing; 3. <u>Adenine base pairs with uracil</u> and <u>guanine pairs with cytosine in RNA</u> by complementary base pairing; Examples: 4. <u>Semi-conservative DNA replication</u> using one <u>DNA template strand</u> to synthesise a complementary <u>daughter DNA strand</u>; 5. <u>Transcription</u> using <u>DNA template</u> strand to synthesise <u>RNA</u>; 6. <u>Spliceosome</u> has <u>snRNA</u> which recognises <u>splice sites on RNA</u> to carry out splicing; 7. <u>Translation</u> involves complementary base-pairing between <u>codon</u> of mRNA and <u>anticodon</u> on tRNA; 8. <u>Telomerase</u> has a <u>template RNA</u> which is complementary to the <u>3' overhang</u> of telomeres, allowing the elongation of telomeres; <i>AVP stability of DNA double helix</i>
Ligand + receptor (LR)	1. <u>Ligand</u> has a <u>complementary shape</u> to shape of <u>ligand binding site</u> of <u>receptor</u> molecules; 2. in order to <u>transmit signal into cell</u> when specific molecules (ligands) bind to them; Examples: 3. Cell surface receptors: has an <u>extracellular ligand-binding site</u> binding to hydrophilic <u>ligand</u>; 4. <u>Binding of ligand</u> causes <u>conformational change</u> in <u>intracellular domain</u> of receptor; 5. (Name) <u>GPCR</u>: 6. Ligand binding to GPCR causes <u>conformational change</u> in intracellular domain of receptor allowing it to bind to and <u>activate G protein</u>; 7. (Name) <u>RTK</u>: 8. Ligand binding to RTK causes <u>dimerisation</u> and <u>conformational change</u> in intracellular domain of receptor, leading to 9. <u>activation of tyrosine kinase</u> for <u>autophosphorylation</u>;
Immune system (IS)	1. e.g. Neutrophils recognise pathogens and carry out phagocytosis; 2. CD4 T cell has MHC II receptor that recognizes and binds to antigens presented on antigen presenting cells / naïve B cells 3. CD8 T cell has MHC I receptor that recognizes and binds to abnormal proteins presented on infected cells 4. B cell has B cell receptor that recognizes and binds to specific antigens and/or cytokines 5. Helps to trigger cell proliferation and differentiation of naïve T cells (5T) / B cells (5B); 6. Antibodies have shape of antigen binding site that is complementary to shape of antigens; 7. Fc region of antibodies can be recognised by Fc receptors on neutrophils / natural killer cells, 8. (<i>Function</i>) Antibodies functions to neutralise pathogens / toxin / opsonisation
QWC: 3 different categories	

General comments:

1. Must state method of complementary (Complementary shape? BP?) and the regions involved.

2. Double check question focus – quite a number of candidates misread and discussed roles of biomolecules instead.

(a) There are many methods to classify organisms.

Describe some methods and explain their limitations.

Any 2 of 1 - 3

(a) Type of Classification	(b) Definition [1]	(c) Limitations [1]
1. Biological	Living things classified based on shared characteristics/structural similarities into hierarchical levels (taxa) Levels: Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species Highest level is the domains, lowest level is the species. Lower levels have fewer members than higher levels but their members share more similarities.	Organisms with similar structures do not share a common ancestor, as similar characteristics are not homologous but analogous. Does not take into consideration the evolutionary origin (or ancestry) of the characteristics.
2. Phylogenetic	Organisms with many similar characteristics tend to share a common ancestor. Evolutionary relationships can be established by the degree of similarities. Species are grouped into evolutionary categories and show divergence of ancestral forms.	Only shared homologous characteristics are used in phylogeny since they are derived from a common ancestor. Common ancestor(s) are also presented in the evolutionary/phylogenetic trees.
3. Molecular	Molecular data (e.g. DNA and amino acid sequences) are aligned and compared The greater the similarity in the DNA or amino acid sequences, the more closely related the species are to each other the more recently they branched from their common ancestor	Amino acid sequence does not reflect all differences in DNA nucleotide sequences. Genetic code is degenerate. More than one codon may code for the same amino acid. In eukaryotes, differences in the intron sequences will not be detected because only exons in the mature mRNA are reverse transcribed to produce the complementary DNA sequences.

Any 3 of 4 - 8

For each pt 2 marks must have (a), (b) & (c)

(sp) A species is the basic unit of classification, all members of a particular species have similar features that distinguish them from members of other species

(a) Species Concept	(b) Definition [1]	(c) Limitations [1]
4. Biological	Members of the same species which are able to interbreed with each other to produce viable and fertile offspring/reproductively compatible .	It cannot be applied to organisms (e.g. bacteria, certain protists, fungi, plants and animals) that only carry out asexual reproduction. It cannot be applied to fossils. Certain species can interbreed with each other.
5. Morphological	Members of the same species are identical based on measurable physical (morphological) features (e.g. body shape and other structural features).	Morphology of members of the same species (e.g. male and female individuals, different stages of life cycle) may be very different. Members of different species may look similar due to convergent evolution. Difficult to determine the differences in a morphological trait that exhibits continuous variation (e.g. color, length, etc) due to subjectivity. Deciding the number and type of morphological traits to compare in order to determine if two groups of organisms are considered as different species is also subjective.
6. Ecological	Members of the same species share the same ecological niche, live in the same type of habitat / environment, and have similar roles within the environment Usually compete with each other for the same resources (e.g. food, habitat, etc).	Although each species has an ecological niche, there may be different species that occupy similar ecological niche. Different populations of a species could occupy an ecological niche that may vary slightly under certain situations. Many animals are elusive and determining their niches can be time-consuming and difficult.
7. Genetic	Members of the same species share are genetically similar and share a common gene pool .	It is difficult to determine how much difference in DNA sequence is enough to constitute separate species. Obtaining DNA samples from the organism directly may be very

	It is based on similarities and differences of DNA sequences of mitochondrial and nuclear DNA.	difficult if the organism is elusive / hard to capture . DNA samples taken from a living organism may be contaminated with the DNA of parasites living on or in an organism.
8. Phylogenetic	Members of the same species share a common ancestor considering evolutionary relationships (i.e. common ancestry / shared evolutionary history) among organisms. Obtained by comparing its physical characteristics , its molecular sequences with those of other organisms, as well as from fossil records .	As multiple evidences need to be gathered and processed, it is time-consuming and difficult . Accuracy of the phylogenetic tree is dependent on the availability, diversity and accuracy of the source data. Lack of fossil evidence makes it difficult to determine the most recent common ancestor of a species.

QWC:

In paragraphs for each of the classification & species concept

Satisfy both classifications and species concepts (at least 1 of each)

General comments:

1. Most students were only able to obtain a maximum of 6 marks from stating speciation concepts.
2. Reminder that we can also classify species based on biological classification (kingdom, class etc.) which is based on shared characteristics AND phylogeny which is based on evolutionary relationships (see learning outcomes below)

(i) define biological classification as the organisation of species according to shared characteristics and describe how evolutionary relationship is established

(k) define phylogeny as the organisation of species to show their evolutionary relationships

- (b) With named examples, explain how anatomical and molecular homology support Darwin's theory of evolution on descent with modification. [15]

Evolution Definition (ED) (max 2)

1. All organisms share a common ancestor.
2. New forms of organisms develop from pre-existing ones over time.
3. This involves the passing of heritable traits through generations but these traits were modified over time due to genetic changes.

Homology Definition (HD)

1. Refers to **similarity in characteristics** resulting from a **shared / common ancestry**.

Note: no candidate wrote the definition of homology.

Anatomical Homology (max 3)

2. Structures having **similarity of evolutionary origin** (i.e. inherited from shared / common ancestor)
3. **Not necessarily similar function**, structures may perform different functions, Limbs are used for different functions (e.g. grasping, walking, swimming and flying).
4. Due to **divergent evolution** - evolution of **dissimilar features** (as of structure or behavior) in **closely related** populations, species or evolutionary lineages of common ancestry.
5. **Greater the number of homologous structures** between two species, the **closer the two species are related** (evolutionary relatedness between species)

Examples: Either 6 – 11 or 12 – 19

- [1] – name
 [1] – description of example
 [1] – state how example shows 'descend'
 [1] – state how example shows 'modification'

Note: for responses with incomplete elaboration of named examples, a maximum of 3 marks is given for this section.

Name

6. **E.g.: .Pentadactyl Limbs**

Description

7. **Five digit plan at the end of the limb** found in **all tetrapods** (animals with four limbs).
8. Limbs of humans, cats, whales, bats and other mammals have the same internal skeletal structure with similar **arrangement of bones and five digits at the end of the limb**.

'descend'

9. **Five-digit stage** is observed in the **embryo stage** of the animal.
10. Shows that **all tetrapods descended from a common ancestor with pentadactyl limbs**.

'modification'

11. The basic structure of the pentadactyl limb was **modified for different functions** in different animals because of **adaptations to different selection pressures in their environments** via natural selection

OR

[TURN OVER

Name12. **E.g.: Vestigial Structures**Description

13. Vestigial structures are **remnants of once developed and functional structures** in ancestors but are less important for survival now.

14. E.g. hind limbs in whales, pelvic bones and hind limbs in pythons, human tail bones (coccyx)

'descend'

15. Organisms with vestigial structures **share a common ancestor** with other species in which the structure is still functional.

16. E.g. modern whales descended from a carnivorous, tetrapod terrestrial ancestor, snakes descended from lizards.

17. As the structures are **no longer beneficial** for the organism's survival they **no longer confer a selective advantage**.

'modification'

18. This is driven by **natural selection** which favoured individuals with **smaller or non-functional structures** over time.

19. Example: Hind limbs were a hindrance to the locomotion of modern whales and snakes. Hence, natural selection favored individuals with reduced hind limbs. Over time, the structure became vestigial.

Molecular Homology (max 3)

20. Refers to **similarities in DNA sequence and/or amino acid sequences** in different organisms.

21. **Common genes / homologous DNA sequences** are found in **different organisms** (e.g. humans, fruit flies, bacteria, yeast, etc).

22. Share significant **sequence homology** and when expressed, produce **proteins** that have **same function** in all organisms that possess them

23. **Nucleotide sequences** in ancestral genes were modified due to **accumulation of mutations** that occurred over many generations that were selected for;

24. The **greater the similarity** in the **DNA or amino acid sequences**, the **more closely related** the species are to each other, the **more recently** they branched from their common ancestor

Examples: Either 25 – 27 or 28 – 31

- [1] – name
- [1] – description of example
- [1] – state how example shows 'descend'
- [1] – state how example shows 'modification'

Note: for responses with incomplete elaboration of named examples, a maximum of 3 marks is given for this section.

Name

25. E.g. **Cytochrome b gene**

Description

26. Found in all aerobic eukaryotes, codes for a protein that is part of the electron transport chain

'descend'

27. Since homologous genes (e.g. **cytochrome b gene**) are found in all eukaryotes, this implies that they **are related through descent from a common ancestor**.

'modification'

28. The cytochrome b gene differs slightly in nucleotide sequence in different species of eukaryotes due to mutations.

OR

Name

29. E.g. **haemoglobin** (found in all animals)

Description

30. Amino acid sequence of the beta chain of haemoglobin of 'descend' **humans, gorillas and gibbons** shows **great similarities reflecting the common ancestry of the different primate groups**.

'modification'

31. **Number of amino acid differences shows that humans are more related to gorillas than to gibbons.**

32. The **universal genetic code**, used in the translation of mRNA to polypeptide chains by all organisms supports the idea of common ancestry.

QWC:

In clear paragraphs defining the homologies with one detailed example provided for each type of homology

General comments:

1. This question was VERY badly attempted.
2. The first question to ask: What is Darwin's Theory of Evolution? What is homology? What are anatomical and molecular homologies?
3. There were many responses that confused anatomy homology with analogous structures... These are 2 different areas altogether.
4. Similarly, there were several responses that confused molecular homology with molecular methods of determining evolutionary relationships.
5. Common examples that were given include (a) Galapagos finches, (2) fossils.
6. Galapagos finches are not valid examples here – they demonstrate natural selection, speciation and adaptive radiation but they do not show how homology provides evidence for Darwin's theory.
7. While fossils are evidences, that is not within the scope of the question.
8. From this question, it is clear that many of us are still very unsure / uncertain about the D&E concepts and we are simply regurgitation without putting much thought into the significance of what we are memorising / the nuances of the concepts. Please revise.

DEFINITION

1. **Homology** refers to **similar characteristics** (anatomical or molecular) found in **different species** due to **common ancestry**;

ANATOMICAL HOMOLOGY (max 7m)

2. Organisms with **anatomical homology** have **anatomical (A: morphological) structures** such as bones, organs and gross structural features that they **share with a common ancestor** and thus supports Darwin's theory of descent with modification;
3. Named e.g.: **pentadactyl limb*** structure in forelimbs;
4. of all **tetrapods/humans, cats, whales** (or any valid e.g. where they state a few organisms or a group of organisms);
5. Forelimbs have **same arrangement of bones** but have **different functions** and superficially look different;
6. e.g. **legs for walking** in cats, **flippers for swimming** in whales (any two e.g.);
7. 5 digit pentadactyl limb structure in common ancestor was altered by **natural selection/different selection pressures** in different organisms to suit **specialised functions/environments**, resulting in variations of the pentadactyl limb structure;
8. Anatomically homologous structures that are **greatly reduced in size / have little to no function** as they were **selected against**;
9. are called **vestigial structures***;
10. Organisms with vestigial structures **share common ancestry** with organisms in which the **structure is still functional** and thus supports Darwin's theory of descent with modification.
11. Named e.g.
Hind limbs (femur) / hips (pelvic bones) in whales are reduced to **small bones** (i.e. vestigial structures) as they are no longer beneficial to whales which swim. However, their presence in whales **suggest common ancestry with tetrapods** (terrestrial ancestors with four legs);
Appendix in humans is also a vestigial structure as it is **reduced** from cecum of its **primate ancestors** which was involved in digestion of plant material. Thus, presence of appendix in humans, **suggests common ancestry with primates**;
 Fossil records: modification of homologous structures with time

MOLECULAR HOMOLOGY

12. Organisms with **molecular homology** have **similar DNA, RNA & amino acid* sequences** as they **share a common ancestor** that had these molecules;
13. Named e.g. **cytochrome C/ p53 / haemoglobin** are homologous genes;
14. **Homologous genes** share significant **sequence homology** and when expressed, produce **proteins** that have **same function** in all organisms that possess them and thus supports Darwin's theory of descent with modification;
15. **Nucleotide sequences** in ancestral genes were modified due to **accumulation of mutations** that occurred over many generations that were selected for;
16. The **greater the sequence similarity** between homologous genes, the **more closely related** the 2 species are;