TEMASEK JUNIOR COLLEGE

2022 JC2 PRELIMINARY EXAMINATION

Higher 2

CANDIDATE NAME									
CENTRE NUMBER	**S**					INDEX NUMBER				

BIOLOGY **9744/02**

Paper 2 Structured Questions **23 AUGUST 2022**

2 hours

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

READ THESE INSTRUCTIONS FIRST

Write your Center number, index number and name in the spaces at the top of this page.
Write in dark blue or black pen.
You may use an HB pencil for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.
DO **NOT** WRITE IN ANY BARCODES.
Answer **all** questions in the spaces provided on the Question Paper.

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

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

For Examiner's Use	
1	**/ 9**
2	**/ 9**
3	**/ 11**
4	**/ 7**
5	**/ 8**

This document consists of **11** printed pages and **1** blank page.

Answer **all** questions**.**

1 Muscle cells are known to store large amounts of glycogen that act as glucose reserves when blood glucose concentration is lower than the homeostatic range.

Fig 1.1 shows an electronmicrograph of a part of a muscle cell.

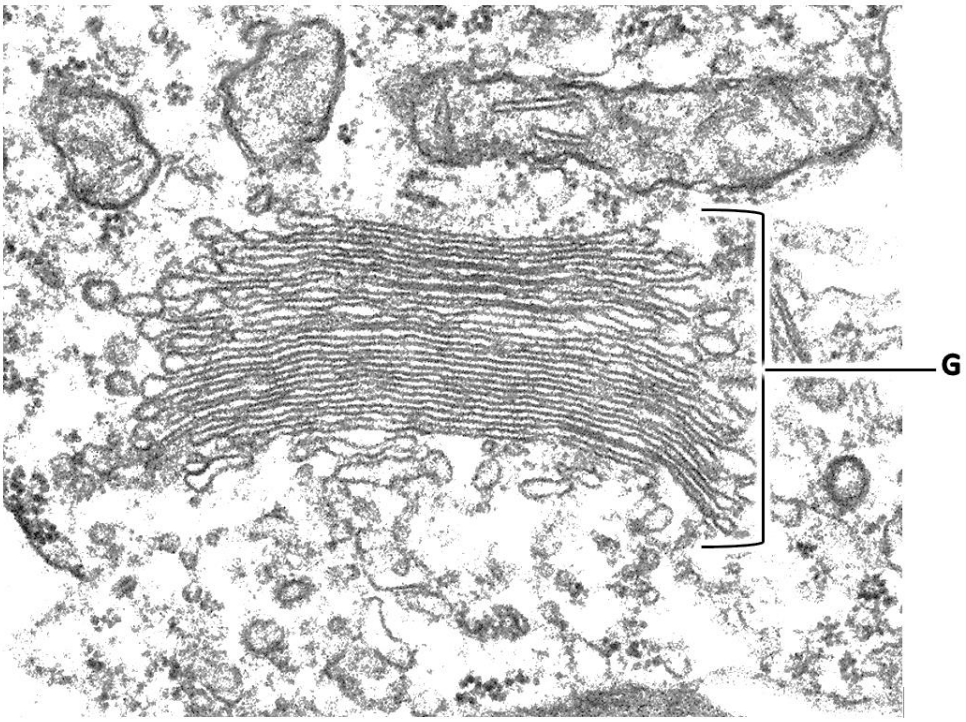


Fig. 1.1

(a) Outline structural features shown in Fig 1.1 that identify **G** as the Golgi body and not the rough endoplasmic reticulum (rER). [2]

Note: There are 2 parts to this question – (1) what distinguishing features of G are, AND (2) why NOT rER, which will require comparison with rER.

1. **G consists of separate / not interconnected flattened, curved membraneous sacs whereas rER consists of flattened sacs connected to one another.**
   ½ m – if no mention of separate vs interconnected

   Marker's comments:
   Many students missed out the word "flattened" in point 1 or only mentioned the word 'cisternae' without describing what it means.

2. **The surface of G is smooth whereas the surface of rER is rough.**
   OR
   Ribosomes absent on G whereas ribosomes present on rER.

AVP: The outer membrane of nucleus envelope is not continuous with G whereas it is continuous with the membrane of rER (idea of continuity with nucleus; R: connected to nucleus).

Max 1 m if no mention / comparison with rER (basically merely stating the features of G and not addressing the second part of the question)

(b) Describe how the function of **G** and rER are linked. [2]

1. Ribosomes located on the surface of rER synthesise polypeptide chains which are inserted into the lumen / both organelles involved in formation of lysosomes / secretory vesicles
2. Polypeptide chains will be packaged into ER vesicles and transported to
   Reminder: it is NOT rER vesicles

3. cis-face of G. (R: golgi)
4. At G, these polypeptide chains will go through chemical modification, sorted and transported / packaged in secretory vesicle. (MUST write chemical modification)
   Most students are unable to write point 4 in full with the necessary details

½ m: proteins / enzymes synthesised at rER, packaged into vesicles at G (Awarded if MP1 and MP4 not awarded)

Fig. 1.2 shows the binding of glucagon to a cell surface receptor.

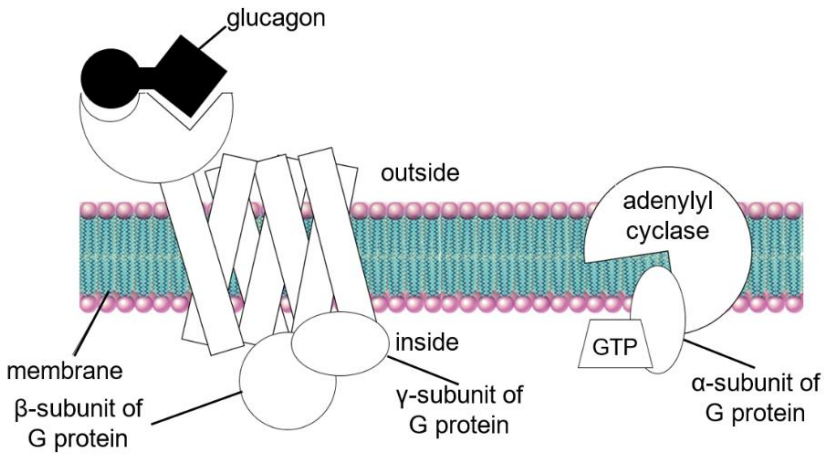


Fig. 1.2

(c) Receptors for some hormones are found within their target cells.

Explain why glucagon receptors are found on the cell surface membranes of target cells and never within the cells. [2]

1. Glucagon cannot enter the cell
   A: cannot pass through the membrane (if MP3 not given)
2. Glucagon is a polar and large molecule
3. Unable to cross the hydrophobic core of the phospholipid bilayer
4. Glucagon receptors have an extracellular ligand-binding site
   R: Glucagon receptors on the extracellular side of the cell
5. Allows for signal to be transduced / passed into the cell without glucagon entering the cell / cellular response to be triggered.

Marker's comments:
Some students focused on the structure of the receptor being hydrophobic (7 alpha-helices) instead of the reason why the receptors have adapted to be found on the cell surface membrane instead of within the cell.

(d) Use Fig. 1.2 to explain how the presence of glucagon is able to trigger a signal transduction pathway inside the target cell. [3]

Note: students are reminded to use their own contextual knowledge to help them interpret the diagram – the diagram is static and some understanding of G protein activation is required to fully answer the question!

1. **Glucagon binds to the extracellular ligand-binding site of the GPCR**
2. **Triggers conformational change and activates GPCR**
   Note: GPCR must be mentioned to be awarded the mark – learn to be specific in your answers.

3. **Inactivated G protein binds to GPCR**
   Note: always remember to mention the change from inactivated to activated.

4. **GTP displaces GDP, activating G protein**
5. **QF: α-subunit of G protein and GTP molecule diffuse / travel / move along cell membrane**
   Note: there is a difference between across and along

6. **Bind to adenylyl cyclase and activates it, triggers signal transduction pathway**
   Note: link back to question – no need to mention PKA and phosphorylation cascade when question asks for triggering of signal transduction pathway (NOT for cellular response)

[Total: 9]

2 Collagen is the most common protein in the human body. It is a fibrous protein which is found in structures such as blood vessels, bones, cartilage, connective tissue, tendons, and skin.

Fig. 2.1

Fig. 2.1 shows a molecular model of collagen.

(a) Describe the primary structure of collagen polypeptide chains and how it contributes to the function of collagen. [3]

1. **Each polypeptide chain has about 1000 amino acid residues**
2. **and consists mainly of repeated glycine-X-Y sequences.**
3. **This repeating organisation contributes to a stable helical structure (secondary structure).**
   Note: students must state that it is the helical structure that is stabilized.

4. **Every third amino acid in the polypeptide is glycine.**
5. **The R-group of glycine is a H atom and is the only R-group that is small enough to fit into the centre of the triple helix.**
6. **This allows close association of the three polypeptide chains.**
   Pay attention to the use of 'triple helix' and 'three polypeptide chains' in MP5 and MP6.

(b) Explain how three collagen polypeptide chains are associated with one another. [2]

Note: This question is asking about the bonds within ONE tropocollagen molecule. Points regarding covalent cross links are not relevant to this question!

1. **Three helical chains wound around each other to form a**
   Note: Many students failed to state that each chain is helical

2. **triple helix.**
3. **The chains are held together by interchain hydrogen bonds**
4. **between the -NH groups of glycine residues on one chain, and the -CO groups of proline residues of adjacent chain.**

Marker's comments:
About half of the cohort also mentioned about glycine being small enough to fit into the centre of the triple helix. This is a key feature of the primary structure (every third amino acid being glycine which allows for close association) and does not directly answer the question on how (bonds) the three chains can come together.

(c) Collagen molecules are built up into fibrils. Each of the lines in the diagram below represents one of the collagen molecules shown in Fig. 2.1.

Complete the diagram to show the location of some possible covalent cross-links between the collagen molecules that make up part of a fibril. [1]

Fig. 2.2

Covalent cross-links at each terminal should be with one chain above and one chain below (at least 1 cross-link shown between chain 1 and 2, chain 2 and 3)

Marker's comment:
Very badly done – please revise location of covalent cross links and clarify any doubts with tutor ASAP.

(d) State three similarities between the structures of collagen and cellulose. [3]

Any three

1. **Both cellulose and collagen are polymers / made up of many monomers.**
2. **Both are formed via condensation reactions between monomers.**
3. **Both contain interchain hydrogen bonds.**
4. **Both contain cross-linking between chains.**
5. **Both serve as structural support as they confer high tensile strength.**
6. **Both are insoluble in water.**

AVP: Fibrous structures / associate to form microfibrils and macrofibrils / fibers
R: Both are straight chains (collagen made of helical polypeptide chains)
R: Both are unbranched (all proteins are unbranched, we only use branched / unbranched when describing carbohydrate structure)

[Total: 9]

3 Fig. 3.1 is a transmission electron micrograph showing parts of two plant cells. The function of the middle lamella is for cell-to-cell adhesion. The middle lamella is composed of a polysaccharide known as pectin.

Pectin interacts with the polysaccharides cellulose and hemicellulose in the cell walls of the plant cells so that the cell walls are held close together, as shown in Fig. 3.1.

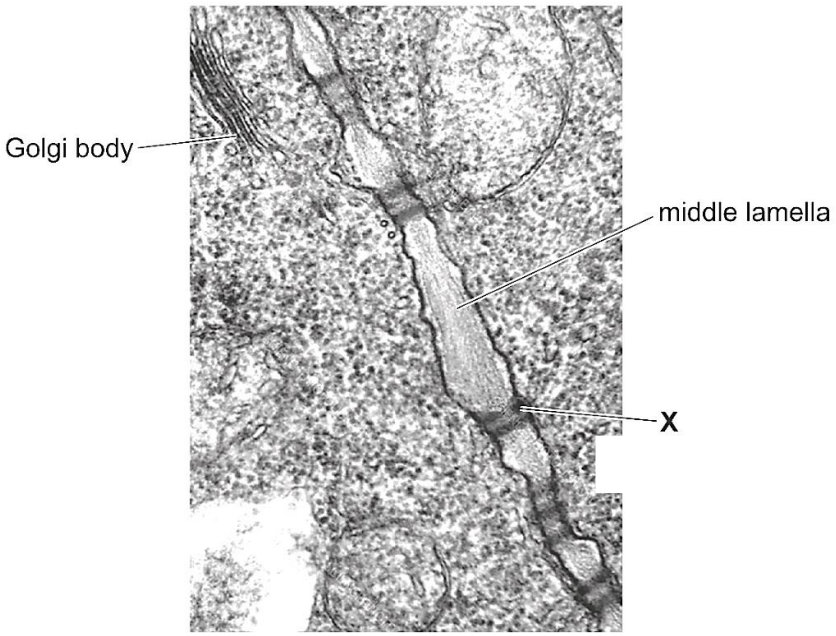


Fig. 3.1

(a) Researchers have discovered that pectin is synthesised within the Golgi body. Golgi vesicles containing pectin are moved to the cell surface membrane for release.

(i) Suggest why researchers would **not** have investigated ribosomes as being the possible location for the synthesis of pectin. [1]

Question is asking: Knowing that pectin is a polysaccharide, why did the researches not investigate ribosome as a potential possible location for the synthesis – not about whether or not there is pectin at ribosomes.

Any one

1. **Proteins are synthesized at ribosomes**
2. **Carbohydrates / polysaccharides not synthesized at ribosomes**
3. **Enzymes required for synthesis of pectin not found in ribosomes**

Note: Please make sure you read through ALL the context and use relevant information in the context. A handful of students wrongly mentioned that pectin is a glycoprotein and can only complete chemical modification at the Golgi.

(ii) Name the mechanism that is used to transport pectin out of the cell. [1]

Exocytosis

Juices that are extracted commercially from fruits can be made less cloudy by the breakdown of the cell wall using the enzymes cellulase, pectinase and xylanase:

- cellulase hydrolyses cellulose
- pectinase hydrolyses pectin
- xylanase hydrolyses hemicellulose

(b) Enzymes work by lowering activation energy. State **one** way in which enzymes lower the activation energy. [1]

1. **The active site serves as a platform for substrates to collide at the correct orientation for chemical reactions to occur.**

2. **The enzyme-substrate complex distorts the bonds in the substrate**
   OR
   In active site, certain bonds in the substrate molecule may be placed under physical stress.

3. **The catalytic amino acids at the active site changes substrate reactivity by:**
   change the charge of the substrate or;
   alter distribution of electrons within bonds of substrate or;
   cause other chemical changes which increase reactivity of substrate.
   R: Change pH of amino acid / substrate (pH should only be used to refer to a solution)

(c) Fig. 3.2 is a graph showing the effect of cellulose concentration on the activity of cellulase.

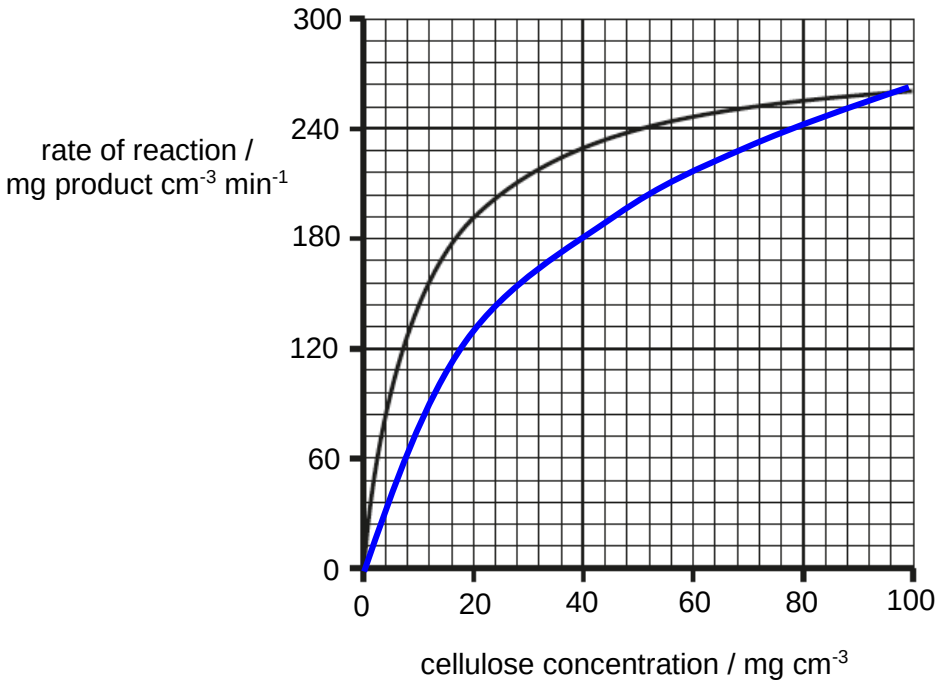


Fig. 3.2

(i) Describe **and** explain the curve shown in Fig. 3.2. [3]

1. **As cellulose concentration increases from 0 mg cm^{-3} to 20 mg cm^{-3}, the rate of reaction increase steeply from 0 mg product cm^{-3} min^{-1} to 192 mg product cm^{-3} min^{-1}**
   [accept if student QF to 16 mg cm^{-3}]

2. **As cellulose concentration increases from 20 mg cm^{-3} to 100 mg cm^{-3}, the rate of reaction increase gradually from 192 mg product cm^{-3} min^{-1} to 262 (A: 260) mg product cm^{-3} min^{-1}**
   ECF: from where QF1 ended to 100 mg cm^{-3} (if QF1 did not end at 16 / 20 mg cm^{-3})

Explanation:

3. **increasing cellulose concentration increases number of effective / successful collision between enzyme and substrate**
   Note: many students missed out "between enzyme and substrate"

4. **More enzyme-substrate complexes formed per unit time**
   Note: idea of RATE must be present to be awarded point 4

5. **At low cellulose concentrations, many active sites, available / not saturated**
   OR
   At higher cellulose concentrations, active sites becoming saturated / most active sites occupied / most active sites not available
   Note: it is the active sites that are saturated, not "The enzymes are saturated". Some students also have difficulties expressing the idea of saturation.

6. **At lower cellulose concentrations, cellulose concentration limiting**
   Or
   At higher cellulose concentrations, enzyme concentration limiting

(ii) Certain chemicals are known to inhibit cellulase. Draw and label on the graph in Fig. 3.2 to show the effects of a competitive inhibitor. [1]

½ m – reach Vmax
½ m – drawn graph below given graph
-1/2 m if drawn graph is not labelled

(d) An investigation was carried out into the effect of ultrasound on the activity of cellulase, pectinase and xylanase used in fruit juice manufacture.

For each enzyme, the effect of ultrasound was compared with no ultrasound on the:

- maximum rate of reaction (Vmax)
- Michaelis-Menten constant (Km)
- catalytic efficiency (Vmax / Km)

Km is obtained by the substrate concentrate which results in ½ Vmax.

Table 3.1 summarises the results. A higher Vmax / Km indicates a higher catalytic efficiency.

Table 3.1

enzyme	method	comparison of Vmax	comparison of Km	Vmax / Km / min^{-1}
cellulase	ultrasound	higher	higher	34
	no ultrasound	lower	lower	29
pectinase	ultrasound	same	lower	945
	no ultrasound	same	higher	759
xylanase	ultrasound	higher	same	146
	no ultrasound	lower	same	125

(i) With reference to Table 3.1, suggest explanations in terms of changes in the interaction between enzyme and substrate when ultrasound is used, for the

lower Km for pectinase [1]

Note:
Km measures affinity of substrate to enzyme. It has nothing to do with rate of effective collision or enzyme-substrate complex formation.
Increase in effective collision will increase Vmax – Vmax did not change for pectinase.

1. **ultrasound changed shape of active site to be more complementary to shape of substrate**

2. **makes the active site bind more easily to substrate**
   OR
   ultrasound increases affinity of enzyme for substrate
   Note: some students wrote the wrong substrate – be careful when the context can be overwhelming.

higher Vmax for xylanase [1]

1. **ultrasound increases rate of successful collision between enzyme and substrate**
   OR
   may lower activation energy more than normal;
   OR
   may change substrate for easier hydrolysis

2. **more enzyme-substrate complexes formed per unit time**

(ii) Explain whether the data shown in Table 3.1 supports the recommendation that ultrasound can be used in the manufacture of fruit juices. [2]

1. **Yes [1]**
2. **For all enzymes, there is an increase in catalytic efficiency**
   R: increase in Vmax/Km (context stated what a high Vmax/Km indicates – students should be using that information in their explanation)

   QF any two enzymes
3. **Vmax / Km for cellulase increased from 29 to 34 min^{-1}**
   Vmax / Km for pectinase increased from 759 to 945 min^{-1}
   Vmax / Km for xylanase increased from 125 to 146 min^{-1}
   (R: Vmax increased)

Marker's comments:
Many students had difficulty figuring out what the table heading (Vmax/Km/min^{-1}) meant and just copied the heading wholesale when quoting figures. Careful analysis of the information given should make it clear that the units for QF should be min^{-1}.

[Total: 11]

4 Stem cells are found in all tissues of the body.

(a) Describe how myeloid stem cells differ from red blood cells. [2]

Reminder to students that the word "differs" implies the need to do point to point comparison where necessary.

Any two

1. **Myeloid stem cells can self-renew for long periods whereas red blood cells have a finite life span.**
2. **Myeloid stem cells can divide by mitosis whereas red blood cells are unable to.**
   R: undergo mitosis (Undergo mitosis to do what? Purpose of mitosis needs to be clear)

3. **Myeloid stem cells are unspecialised whereas red blood cells have a specialised function to transport oxygen (1/2 m – no mention of function of RBC).**
4. **Myeloid stem cells can differentiate [1/2] to give rise to different types of blood cells [1/2] whereas red blood cells do not have the ability to.**
5. **Myeloid stem cells have nucleus whereas red blood cells do not have a nucleus.**

(b) Two common examples of stem cells are embryonic stem cells and zygotic stem cells. When comparing embryonic stem cells and zygotic stem cells, two features can be considered:

- the number of genes permanently switched off
- the range of cell types that each can produce

Fill in Table 4.1 to show the differences between embryonic and zygotic stem cells. [3]

Table 4.1

	number of genes permanently switched off *Indicate more/less*	range of cell types that each can produce *Indicate more/less*	potency
embryonic stem cell	**More**	**Less**	**Pluripotent**
zygotic stem cell	**Less**	**More**	**Totipotent**

½ mark per field

Note: since ESC have lower potency, more genes that allow for potency will be switched off.

[3]

(c) Scientists are hoping to be able to use embryonic stem cells to help repair nerve, muscle, or glandular damage in adults. Embryonic stem cells are extracted 4-5 days after fertilization, when the embryo consists of 50 to 150 cells.

Suggest **two** ethical considerations regarding the use of embryonic stem cells. [2]

1. **Embryo is killed / destroyed. [1/2]**
2. **Some may consider embryos to have the same rights as a living person, consider the moral status of embryos. [1/2]**
   a. **Some religious groups consider the embryo to be a living person. [1/2]**
   or
   b. **Using embryonic stem cells for research is as good as killing lives. [1/2]**

3. **If rights of the embryo are ignored it could lead to: [1/2]**
   a. **disrespect for the value of human life. [1/2]**
   or
   b. **de-sensitisation to the destruction of human life. [1/2]**

***AVP: Any one* [1]**

- **Donor stem cells may be rejected by patient's immune system.**
- **The implanted stem cells may become cancerous.**
- **The stem cells could be contaminated by viruses, which could harm health.**
- **Treatment could potentially be costly, only available to the rich.**
- **For treatments which involve gene editing of stem cell, this may result in attempts to change human traits not related with disease.**

[Total: 7]

5 Vector-borne diseases are one of the leading causes of infections globally. The dengue virus is one such virus that requires a vector, *Aedes aegypti* mosquito, to transmit the virus from one human host to another.

Fig. 5.1 shows the predicted changes in the land area suitable for dengue in 3 regions – Americas, Africa and Asia. The lines depict the maximum and minimum value with the symbol indicating the mean value.

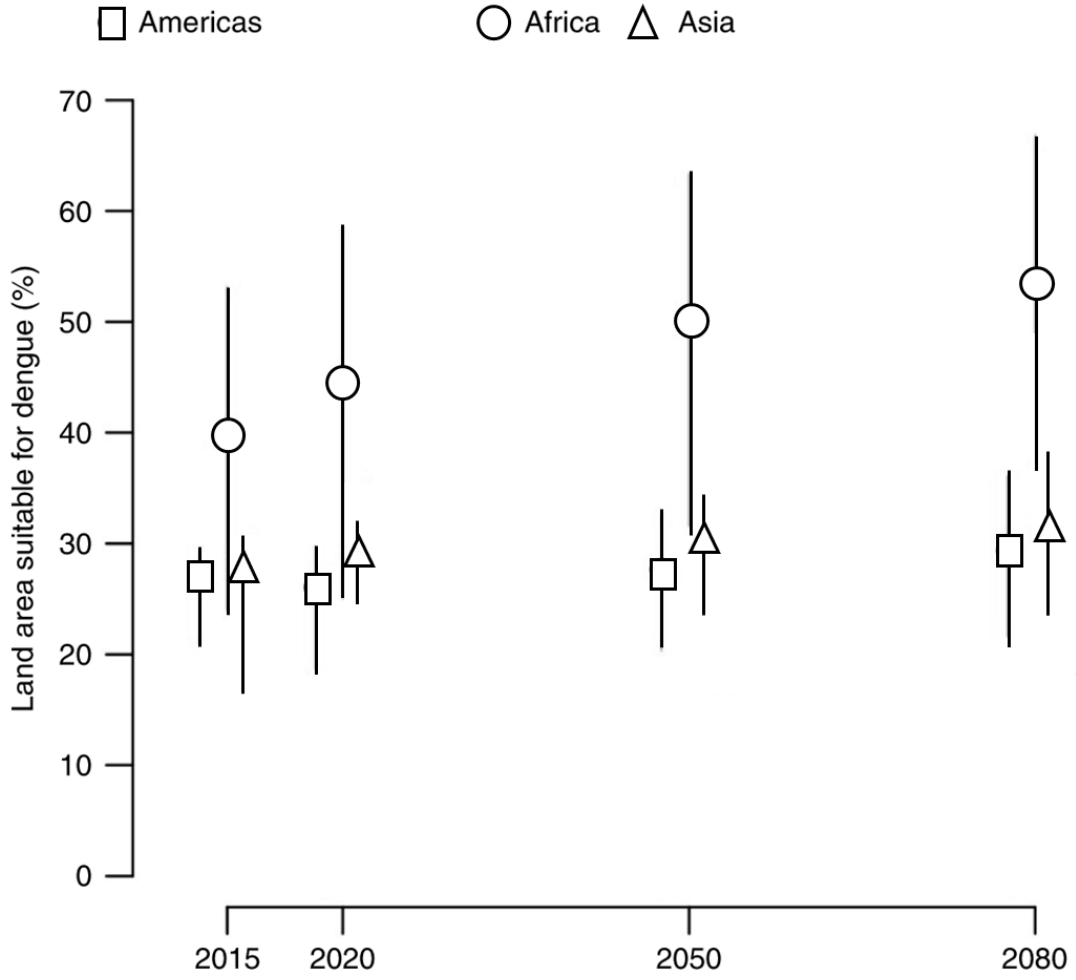


Fig. 5.1

(a) Comment on the predicted change in land area suitable for dengue as the years increase. [2]

"Comment" requires students to state trends and important observations / points of interest from the Figure. There is no need to evaluate / discuss / justify / explain!

1. **Overall, as the year increases from 2015 to 2080, the land area suitable for dengue increases. [1] (-1/2 m if no QF of year throughout answer)**
2. **QF (any one region) [1/2]**
   Note: QF must be consistent – either compare mean only or maximum value only

3. **The region with the largest predicted increase is Africa [1/2]**
   OR
   Asia and America showed the least increase [1/2]
   OR
   Land area suitable in America reduced in 2020 before increasing from 2020 to 2080. [1/2]

Marker's comments:
Many students stated that the change in land area for Asia and Americas remained relatively constant. This is wrong. There is an increase, albeit slight. There is also no fluctuation since fluctuations imply several ups and downs in the graph.

Some students incorrectly compared mean and minimum value across different continents which would give rise to unfair comparisons.

Students are reminded to use as much data as provided (i.e. from 2015 to 2080) instead of picking data (i.e. only comparing 2015 to 2020 or 2020 to 2080)

(b) Describe the life cycle of an *Aedes aegypti* mosquito. [2]

1. **After successful mating, pregnant female mosquito lays eggs in stagnant pools of freshwater.**
   Note: many students forgot to state that the pools have to be freshwater.

2. **Once eggs come into contact with water, they hatch to larvae within 24 to 48 hours.**
3. **Larva develops in water and within 7 to 10 days, enters the pupal stage.**
4. **Pupa continue to develop for 2 to 3 days before emerging as an adult mosquito.**

Marker's comments:
Many students were not confident with the duration of each stage – please revise the details. If students wrote Aedes aegypti without underline, no marks were deducted this time. Please be mindful in future examinations.

(c) Using your knowledge on global warming, discuss how dengue may potentially spread beyond the tropics. [3]

Note: command word is "how" – many students spent first 3 – 4 lines discussing WHY the temperatures would rise which was the wrong focus.

A number of students also discussed how the mosquito life cycle and viral reproductive cycle changes with increased temperature which would be appropriate if the question was "explain how an increase in temperature can result in higher dengue transmission rate".

The focus of this question is "spreading beyond the tropics" which is answered in point 1!

1. **Previously non-endemic / not suitable areas may become suitable [1]**
2. **Increase in temperature**
3. **to fall within favourable temperature range**
4. **Spread of mosquitoes to higher latitudes**
5. **as they are now able to survive**

As of 30 April 2022, Singapore reported 6, 642 dengue cases with an increase of 3, 298 cases since 4 April 2022.

(d) Suggest **one** possible intervention that can be used to control the rise of dengue cases. [1]

Any one (vector control)

1. **Mosquito traps**
   R: Gravitrap ONLY – must explain what Gravitrap does.

2. **Reduce mosquito breeding habitats [1/2]**
3. **(must state e.g. – flipping of buckets, breaking up hardened soil etc.) [1/2]**
   Note: many students only stated the "clearing of stagnant pools of freshwater" without explaining WHY that was necessary.

4. **Introducing sterile male mosquitoes OWTTE (re: Project Wolbachia)**

5. **Prevent mosquito bites [1/2]**
6. **Wear long sleeves / mosquito net / mosquito repellent [1/2]**

[Total: 8]

6 When a cell replicates it goes through a series of events as shown in Fig. 6.1. Four points in the cell cycle are labelled **A**, **B**, **C** and **D**.

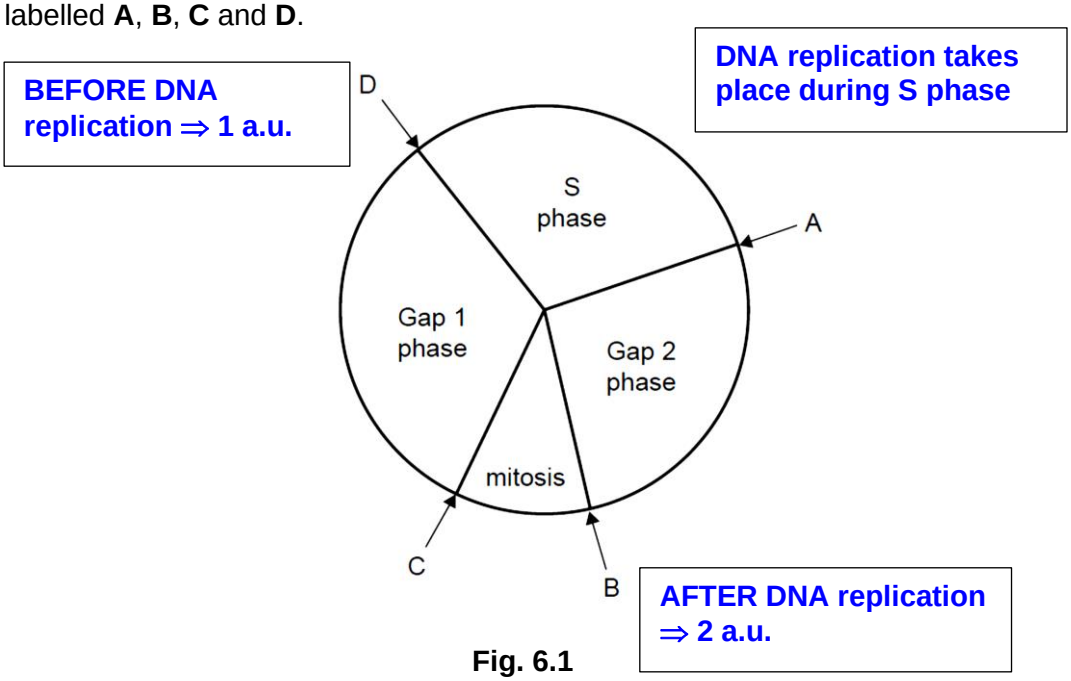


Fig. 6.1

(a) Given that two cells are formed as a result of replication, a cell must replicate its DNA during the cycle. The relative amount of DNA in a non-dividing cell is 1 arbitrary units.

Using crosses, mark on the graph in Fig. 6.2 the relative amount of DNA per cell present at each of the stage **B** and **D** of the cell cycle. [2]

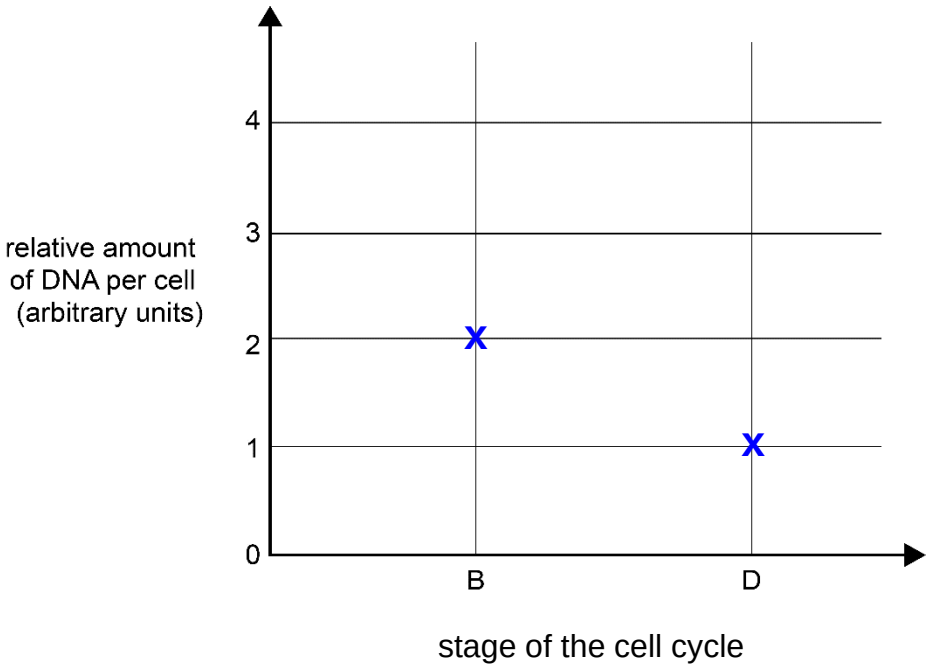


Fig. 6.2

(b) **Explain why** the daughter strands are synthesized in opposite directions during DNA synthesis. [2]

Important reminder:

1. **Abbreviation**
   AP: Anti-parallel
   T.S.: Template Strand
   ES: Existing Strand

2. **Do NOT confuse DNA strand with DNA molecule**
3. **Do NOT write:**
   ✕ "daughter strands are identical"
   ✕ "daughter strand is identical to parental strand" or
   ✕ "sequence of daughter strand same as parental strand"
   Reason:
   ✓ daughter strands are complementary to each other
   ✓ daughter strands are complementary to parental strand
   ✓ 2 daughter DNA molecules are identical

Must have marking point 1 and any 3 others.

1. **The two parental strands are anti-parallel.**
   Note: students must not refer to parental strand anti-parallel to daughter strand

2. **DNA polymerase reads the template strand in the 3' to 5' direction**
   OR
   DNA polymerase can only synthesise daughter strands in the 5' to 3' direction.

3. **DNA polymerase can only add deoxyribonucleotides to free 3'-OH end of an existing strand.**
   Note: students MUST state "-OH" and "existing strand" to get the mark

4. **Leading strand is synthesized towards replication fork**
5. **Lagging strand is synthesized as Okazaki fragments away from replication fork before they are joined together by DNA ligase.**

(c) The enzyme that catalyses the replication of DNA also checks for errors in the process and corrects them. This makes sure that the cells produced in mitosis are genetically identical.

Explain why checking for errors and correcting them is necessary. [3]

1. **This ensures that the correct nucleotide is base-paired with the template strand / incorrect nucleotide is removed by DNA polymerase and replaced with correct nucleotide.**

2. **Errors result in mutations / specify mutation**

3. **If corrected, the nucleotide sequence remains the same / nucleotide sequence will change if not corrected**

4. **There will not be change in amino acids in the protein / primary structure**
5. **Will not result in change the 3-D conformation of proteins**
6. **Will not result in non-functional proteins**

7. **Will not result in mutation of proto-oncogene gene or tumour suppressor gene could cause a cell to divide uncontrollably**

[Total: 7]

7 In bacteria, genes may be organised into operons. The *trp* operon consists of genes that encode five enzymes involved in the synthesis of tryptophan (trp). The *trp* operon and its regulatory gene are shown in Fig. 7.1.

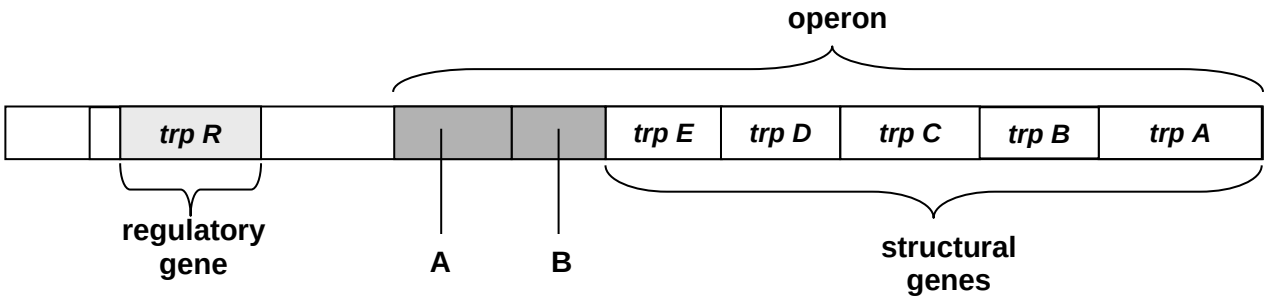


Fig. 7.1

(a) **Name** the structures labelled **A** and **B** in Fig. 7.1. [2]

A promoter

B operator

(b) **State** whether the *trp* operon is a repressible or an inducible operon. [1]

- **Repressible operon**

Different operons in the bacteria encode different types of enzymes.

(c) **State one** difference between a repressible enzyme and an inducible enzyme. [1]

Important reminder:

1. **Be careful with the use of terms and phrasing**
2. **Enzymes do NOT code for genes**
3. **Students confused repressible enzyme with repressor**

Any one:

1. **Inducible enzymes are encoded by genes of inducible operons while repressible enzymes are encoded by genes of repressible operons**

2. **Inducible enzymes usually function in catabolic pathways which break a nutrient down to simpler molecules while repressible enzymes usually function in anabolic pathways which synthesize essential end products from raw materials (precursors).**

3. **The synthesis of inducible enzymes are induced by the presence of their inducer e.g. allolactose while the synthesis of repressible enzymes is repressed by the presence of the end product (tryptophan) of the pathway.**

4. **Inducible enzymes are usually absent when inducer is absent while repressible enzymes are always present unless the end product (tryptophan) of their pathway is available.**

(d) Table 7.1 indicates the activity levels of five functional enzymes **E**, **D**, **C**, **B** and **A** found in different strains of bacteria cells. Each mutant strain is the result of a single base-pair substitution in a control element of the *trp* operon.

These bacteria were grown in either the presence or absence of tryptophan (trp).

Table 7.1

	Activity level of enzymes / arbitrary units							
	Wild-type		Mutant strain **1**		Mutant strain **2**		Mutant strain **3**	
Enzymes	trp absent	trp present	trp absent	trp present	trp absent	trp present	trp absent	trp present
E	700	0	700	700	700	0	0	0
D	700	0	700	700	0	0	0	0
C	700	0	700	700	700	0	0	0
B	700	0	700	700	700	0	0	0
A	700	0	700	700	700	0	0	0

(i) **Identify** and **explain** which mutant strain has a phenotype that is consistent with a loss-of-function mutation in the *trp* ***R*** gene. [3]

Important reminder:

1. **Abbreviations:**
   NF: None functional
   NBO: Not Bind to Operator

2. **Focus of the question: loss of function mutation of *trp R* gene**

3. **Must answer directly and address what is affected due to non-functional repressor**

4. **MUST QF – read the heading of the table!**
5. **Do NOT confuse level of enzyme activity with amount of enzyme produced.**

6. **Do NOT confuse RNA polymerase with DNA polymerase**
7. **Do NOT confuse operator with operon**

1. **Mutant strain 1 [1]**
   Note: It cannot be strain 3 because no enzyme activity recorded. It means that the enzymes were not produced.

2. **QF: Mutant strain 1 shows activity level of enzymes of 700a.u. whether tryptophan is present or absent** / when **tryptophan** is **present**.
3. **This indicates that non-functional repressors are produced due to loss of function mutation**
   Note: Do NOT state "no repressor synthesized or cannot be synthesized"

4. **Even if tryptophan is present, binding of tryptophan to repressor does not take place**
5. **so repressor does not bind to operator**

(ii) **State where** in the *trp* operon, the loss-of-function mutation has occurred in mutant strain 3. [1]

- **Trp promoter / Promoter of the trp operon**

Reason: there was no enzyme activity ⇒ enzymes not synthesized by bacteria

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

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

Important reminder:

1. **There is a need to mention DNA for some of the differences otherwise it will be totally wrong description – when the answer is not presented in a table format**

FEATURE	PROKARYOTIC GENOME	EUKARYOTIC GENOME
Ploidy	**Only one set**	**Diploid**
Number of chromosomes	**One**	**May be more than one**
Size and complexity of genome	**Smaller** and **simpler**	**Larger** and **more complex**
Structure of chromosome	Double stranded **circular DNA**	Double stranded **linear DNA**
Number of origin of replication	**Single origin** of replication	**Multiple origins** of replication
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
Presence of centromeres	**No centromeres** in the **DNA**	Presence of **centromere** (a **constricted** region of **repetitive** sequences)
Presence of telomeres	**Telomeres absent** since **DNA** is circular	**Telomere** (**repetitive** sequences) present at the top of **DNA**
Introns	**Introns absent**: Each gene is a **continuous coding** sequence	**Introns present** between **coding** sequences (called **exons**) in each gene.

[Total: 10]

8 Fig. 8.1 shows the structure of the influenza virus.

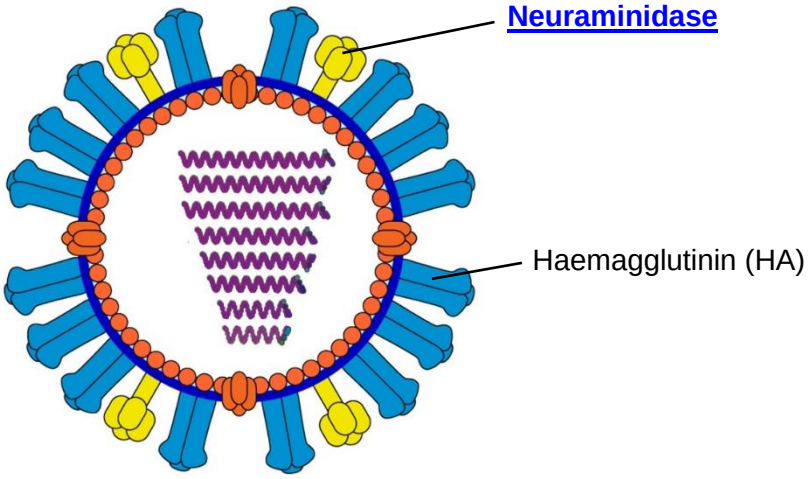


Fig. 8.1

(a) **Name** the other glycoprotein spike on Fig. 8.1. [1]

(b) **State how** viruses challenge the cell theory and concepts of what is considered living. [2]

Important reminder:

1. **The focus of the question is on how it challenge ⇒ meaning that you need to explain why it is not considered a cell or why it is not living.**
2. **"virus can mutate / evolve" does not apply to this question.**

Max 1

C1 Cells are the smallest unit of life,
C2 all cells come from pre-existing cells,
C3 living organisms are composed of cells;;

Max 1/2

4 They are non-cellular / do NOT have a cell structure
OR
5 They do NOT have organelles or cellular components like nucleus, ribosomes, cytoplasm
Reject: "lack membrane-bound organelles"
Reason: this could imply that the virus have organelles which are not membrane-bound. This is the case for bacteria which do not have membrane-bound organelles but have organelles which are not membrane-bound (e.g ribosomes).
OR
6 Cannot carry out own metabolism or cannot produce ATP
Reject: "do not have metabolic machinery"
Reason: it is too vague
OR
7 Cannot make their own proteins

Max 1/2

8 Can only reproduce using host cell organelles such as ribosomes and Golgi body and host enzymes / within host cell
OR
9 Can only acquire and use energy in host cell
Reject: "survive in the host cell"
Reason: it is not even considered a living cell

Fig. 8.2 shows the structure of HA and positions of amino acid where changes are frequently observed in antigenic variants of the virus.

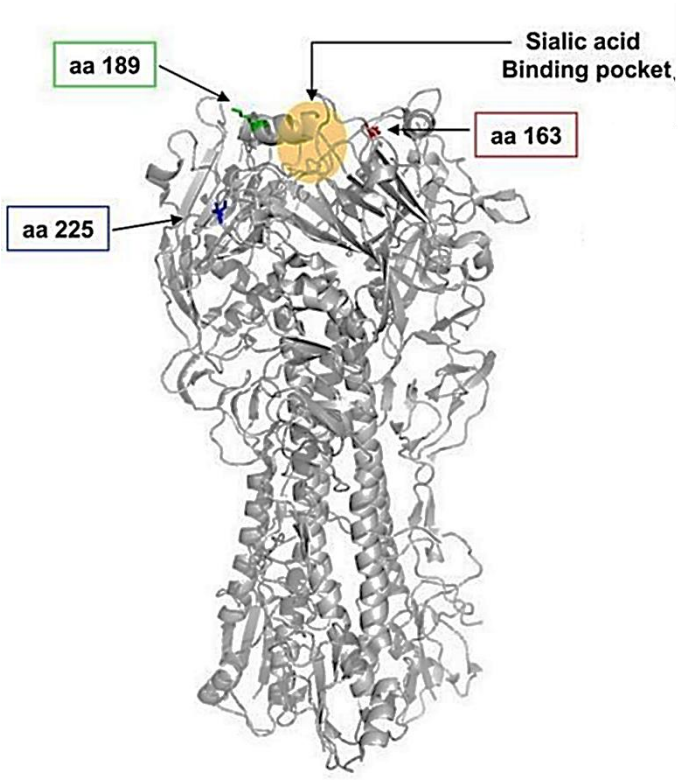


Fig 8.2

(c) (i) **Identify** the type of antigenic change that resulted in the variants. [1]

Antigenic drift

Note:

Mutation → drift

Recombination of RNA segments → shift

(ii) **Explain how** the features of the virus contribute to these antigenic changes. [2]

1. **RNA-dependent RNA polymerase lacks proof-reading ability**
2. **Error in replication of viral RNA**

   Reject: "viral genome"

   Reason: It is too vague.

   Important reminder: ALWAYS state viral RNA or viral DNA instead of viral genome if the genome is known.

3. **Fast / high rate of replication of the virus**
4. **Accumulate more mutations;**

(c) **Contrast** the replication of genetic material between influenza and HIV. [2]

Important reminder:

1. **"Contrast" refers to differences, do not include similarities.**
2. **Focus on the replication of genetic material, not just comparing type of nucleic acid.**
3. **Must use the correct terms.**
4. **Must be clear about the process.**

INFLUENZA

(-) RNA as template
↓ replication
(+) RNA
↓ replication
(-) RNA

Both steps catalysed by
RNA-dependent RNA polymerase

HIV

(+) RNA as template
Reverse transcriptase ↓ reverse transcription
ss cDNA
Reverse transcriptase ↓ replication
ds DNA
RNA polymerase ↓ transcription
(+) RNA

Any two

Point of comparison	Influenza	HIV
Enzyme involved	**RNA Dependent RNA Polymerase**	**Reverse transcriptase** & **RNA Polymerase**
Template used at the start	**Negative single-stranded RNA**	**Positive single-stranded RNA**
Process of how viral genome is replicated	(-) RNA acts as template to form (+) RNA which is then used as a template to form (-)RNA	(+) RNA acts as template to form double stranded viral DNA. One strand will then be used to form (+) RNA Note: must start from (+)RNA to get the marks for this part
Product formed at the end	**Negative single-stranded RNA**	**Positive single-stranded RNA**

Either template or product – to be awarded marks

Apart from antigenic variants, the emergence of new strains of influenza pose challenges to public health.

Fig. 8.3 shows the sources of the eight RNA segments in a novel virus **Q** as a result of an organism being infected with two different strains of the influenza virus. In 1957, the novel virus **Q** caused an influenza pandemic, known as the Asian influenza, in human populations.

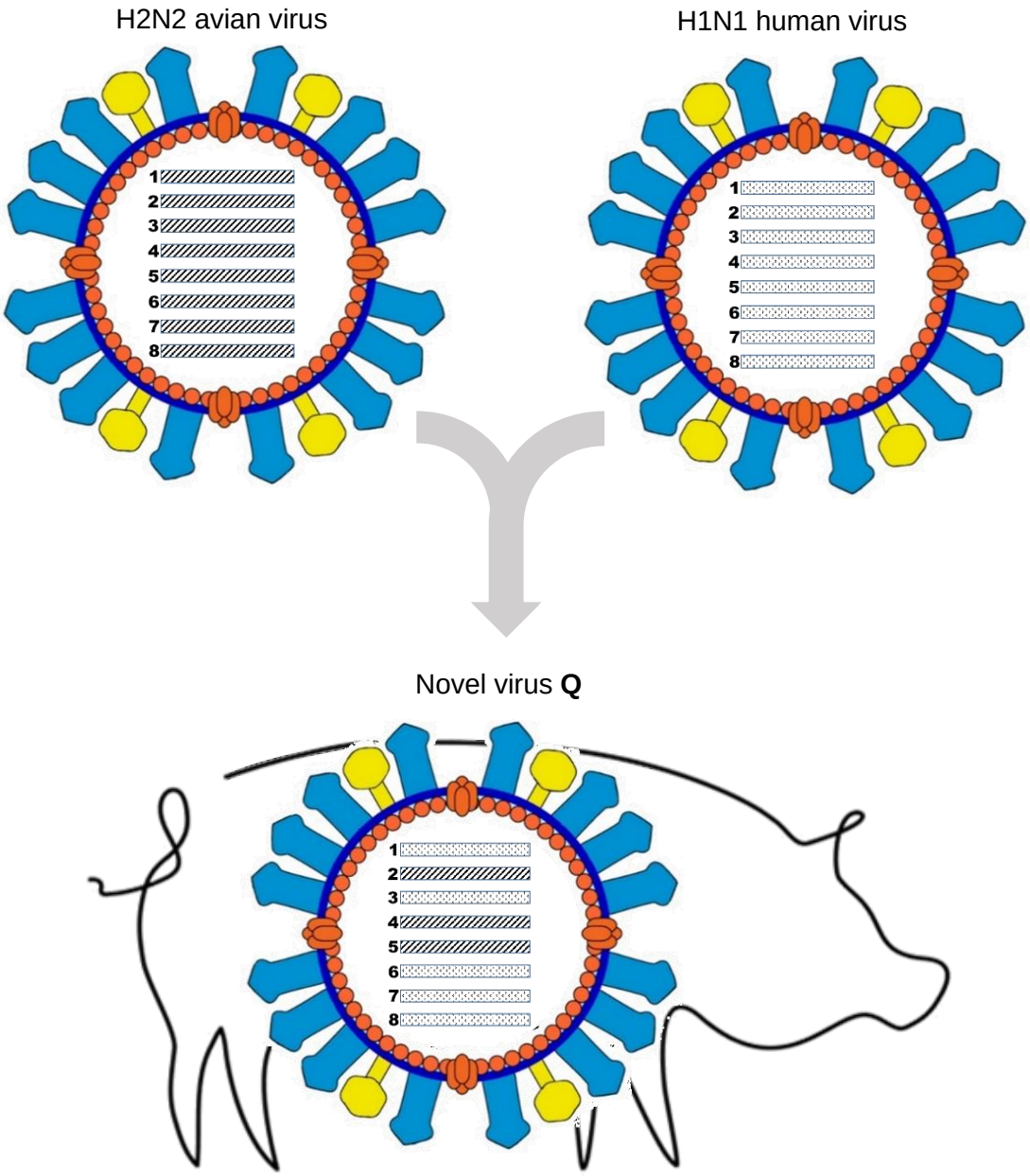


Fig. 8.3

(e) With reference to Fig. 8.3,

(i) **explain how** the new combinations of RNA segments in virus **Q** could have occurred; [3]

Important reminder:

1. **Abbreviations**
   A.S.: Antigenic Shift
   R.A.: Random Assembly
   S.C.: Same Cell

2. **Must name each virus completely at least once.**

1. **Caused by antigenic shift**
2. **Two genetically different strains of viruses co-infected the same cell in the pig.**
   Reject: in the same organism
   Reject: in the human

3. **QF: H2N2 avian virus and H1N1 human virus**
   This marking point is given if "2 genetically different strains" stated in pt 2 and viruses are named in pt 6
4. **When influenza virus Q formed, there was random assembly of eight viral RNA segments, with a new combination of viral RNA segments.**
5. **QF: The RNA segments 2, 4 and 5 were derived from H2N2 avian virus,**
6. **QF: while the RNA segments 1, 3, 6, 7, 8 were derived from the H1N1 human virus**
   Reject: RNA fragment
   Reject: bands
   Reject: RNA strands / strains

(ii) **suggest why** most people in 1957 were susceptible to influenza caused by the new virus. [2]

Important reminder:

1. **Do not write "B & T cells cannot recognize and bind to the new virus"**
   Reason: there will be naïve B & naïve T cells with receptors that will recognize new antigen
   ➔ We fall sick because it takes time for body to mount primary immune response
2. **Reject: "less able to recognize and bind"**
3. **Reject: "lack of response"**

1. **New combination of RNA segments causes changes the combinations / 3D conformation of HA & NA / glycoprotein spikes**
   Reject: viral antigens

2. **Allows virus to bind recognise and bind effectively to receptors on the respiratory epithelial cells**
3. **Do not have antibodies that recognise and bind to HA & NA of the new virus. [1]**
4. **Do not have memory B cells that recognise and bind to HA & NA of the new virus. [1]**
   Reject: "evade memory cells"

5. **It takes time to mount a primary immune response**
6. **Immune system / immune cells have not encountered novel virus**
7. **Lack immunity or lack secondary immune response**

[Total: 13]

9 **(a)** In the Labrador Retriever breed of dogs, the development of coat colour is determined by two genes on separate autosomes. Gene **B** has two alleles. The dominant **B** allele produces black coat while recessive **b** allele produces brown coat. On another chromosome, the dominant allele **E** of another gene **E** is required to deposit the black pigment, melanin, in the coat.

Two black Labrador retrievers from the same generation were mated several times and the following offspring ratio was obtained:

black coat	9
brown coat	3
white coat	4

(i) **State** the type of epistasis that controls the expression of coat colour. [1]
Recessive epistasis

(ii) **State** the epistatic gene and the hypostatic gene. [2]
Important Reminder:
1. Do not confuse gene and allele

epistatic gene **Gene E (reject if student stated "e" only)**

hypostatic gene **Gene B**

(b) A group of scientists decided to study the inheritance of flower colour and plant height in another plant species.

They carried out a cross between a heterozygous tall, yellow-flowered plant with a homozygous recessive dwarf, white-flowered plant and obtained a large number of offspring. Table 9.1 shows the results.

Table 9.1

phenotype	number of offspring
tall, yellow-flowered plant	78
tall, white-flowered plant	22
dwarf, yellow-flowered plant	20
dwarf, white-flowered plant	80

(i) Assuming there is no linkage, **state** the expected phenotypic ratio of the offspring in Table 9.1. [1]
Important Reminder:
1. For this question, it is acceptable to just write the numbers without stating the phenotypes because they are of equal number.

1 tall yellow-flowered plant : 1 tall white-flowered plant : 1 dwarf yellow-flowered plant : 1 dwarf white-flowered plant

(ii) To determine if the difference between the expected numbers and observed numbers were statistically significant, the scientists conducted a chi-squared test.

Suggest why a chi-square test was conducted instead of a *t*-test. [1]

Important reminder:

1. **Do not state what is present or what information is provided or not provided.**
2. **Reject: "means and standard deviation not provided" or "observed and expected data provided"**
3. **Must mention the name of at least one test**

1. **x^2 test is conducted to compare between the expected and observed results whereas**
2. **t-test compares the means of two samples**

(c) The calculated χ^2 value obtained was 67.36.

Table 9.2

	probability, p				
degrees of freedom	**0.10**	**0.05**	**0.02**	**0.01**	**0.001**
1	2.71	3.84	5.41	6.64	10.83
2	4.61	5.99	7.82	9.21	13.82
3	6.25	7.82	9.84	11.35	16.27
4	7.78	9.49	11.67	13.28	18.47

Using the table of probabilities shown in Table 9.2,

(i) **state** what conclusion may be drawn from the calculated χ^2 value obtained; [2]

1. **For 3 degrees of freedom,**
2. **The calculated x^2 value of 67.36 is more than 7.82.**
3. **Therefore, the p-value is less than 0.05.**
4. **The deviation / difference is statistically significant and not due to chance.**

Many students left out "not due to chance" (NDC)

Reject: "it is statistically significant"

Reason: must mention either deviation or difference is statistically significant

(ii) **explain** the observed phenotypic ratio in Table 9.1. [2]

Important Reminder:

1. **Do not confuse gene and allele**
2. **Reject: recombinant alleles / recombinant genes – no such thing**
3. **Do not confuse sex-linked with genes being linked / on the same chromosome.**
4. **Abbreviaton**
   IT: Inherited Together
   LN: Large Number
   SN: Small Number
5. **MUST write "crossing between homologous chromosome," not just "crossing over"**

1. **The genes for flower colour and plant height are on the same chromosome / linked**
2. **and are inherited together resulting in large number of offspring with parental phenotypes**

3. **Small number of offspring with recombinant phenotypes due to**
4. **crossing over between homologous chromosomes that occurs during prophase I**
   Reject if students did not write "homologous chromosomes"

[Total: 9]

10 Huntington's disease is a genetic condition that leads to a loss in brain function. The gene involved contains a section of DNA with many repeats of the base sequence CAG.

Fig. 10.1 shows a segment of an allele with 4 CAG repeats.

---------- C A G C A G C A G C A G ----------
---------- G T C G T C G T C G T C ----------

Fig. 10.1

The number of these repeats determines if an allele of this gene will cause Huntington's disease.

- An allele with 40 or more CAG repeats will cause Huntington's disease.
- An allele with 36 – 39 CAG repeats may cause Huntington's disease.
- An allele with fewer than 36 CAG repeats will not cause Huntington's disease.

Fig. 10.2 shows the age at which a sample of patients with Huntington's disease first developed symptoms and the number of CAG repeats in the allele causing Huntington's disease in each patient.

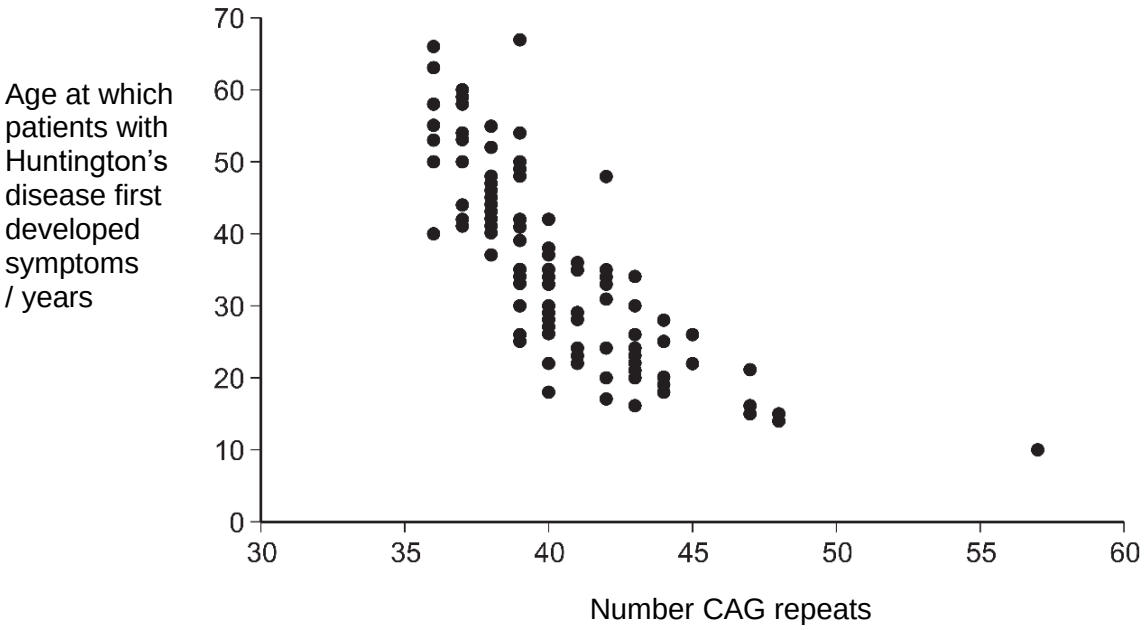


Fig. 10.2

(a) People can be tested to determine if they have an allele of this gene with more than 36 CAG repeats. Some doctors suggest that the results can be used to predict the age at which someone will develop Huntington's disease.

Using the information in Fig. 10.2,

(i) **evaluate** the doctors' suggestion; [2]

Important Reminder:

1. **The focus is whether the data can be used to predict – not meant to confirm whether Huntington's disease will develop or not**

2. **Based on data given – risk of having disease is not associated with age, it is determined by number of CAG repeats.**
   Some students seemed to conclude that as person gets older, chance of developing disease is higher – these students did not take note of the independent variable.

3. **MUST state INDEPENDENT VARIABLE 1ST (number of CAG repeats) in QF**
4. **MUST write CAG in upper case**

1. **Number of CAG repeats is not an accurate prediction.**
   Note: MUST clearly state this in your answer.

2. **Although there is a general trend og increase of CAG repeats from 35 to 57, there seems to be decrease from 68 to 10 years of age at which patients first developed symptoms,**

3. **there is a wide range in age of onset for each CAG repeat e.g. 39 CAG repeats, first symptoms appear range from 68 to 25 yrs old [1]**
   OR
4. **also the large overlap of age of onset e.g. 39 CAG repeats first symptoms appear from 65 to 25 yrs old which overlap with 42 CAG repeats which range from 49 to 19 yrs old. [1]**

5. **Other factors may be involved in age of onset**

(ii) **suggest why** the disease allele is passed on in the human population even though Huntington's disease is always fatal. [1]

Reminder:

1. **Many students did not take note of the fact that the disease tends to develop later in life.**

1. **Symptoms appear later in life**
2. **so individuals already have children and passed on the allele**

(b) Scientists took DNA samples from three individuals, **J**, **K** and **L**. They used PCR to produce many copies of the piece of DNA containing the CAG repeats of each person. Table 10.1 shows the size of fragments based on number of CAG repeats.

Table 10.1

number of cag repeats	size of fragment produced / bp
60	180
39	117
36	108
26	78
15	45

(i) **State** one advantage and one limitation of PCR. [2]

Important Reminders:

1. **Abbreviation**
   SA: Small Amount
   LA: Large Amount
   A: Automated
   ACC: Accurately
2. **Use precise terms**

Any one advantage

1. **A specific process that amplifies only the desired DNA sequence.**
2. **PCR is accurate enough to allow target DNA sequence to be amplified for DNA analysis.**
3. **A cell-free method of DNA replication.**
4. **Very sensitive; a desired sequence from a single DNA molecule / small amount can be amplified to produce an extremely large number of DNA molecules**
   Reject: only small segment / short sequence can be amplified
5. **Fast and easy to use; and the process is automated.**

Any one limitation

1. **Only a short DNA sequence can be accurately amplified.**
2. **DNA target sequence must be known in order to design DNA primers for successful amplification.**
3. **If the DNA mixture is contaminated with DNA from other sources, amplification of unwanted DNA may also take place.**
4. **PCR products cannot be used in the cloning of genes, because the error rate of *Taq* DNA polymerase is too high.**
   Reject: mutation
   Reject: cloning of cells / organisms

They separated the DNA fragments by gel electrophoresis. A radioactively labelled probe was then used and Fig. 10.3 shows the results after autoradiography. The bands show the DNA fragments that contain the CAG repeats.

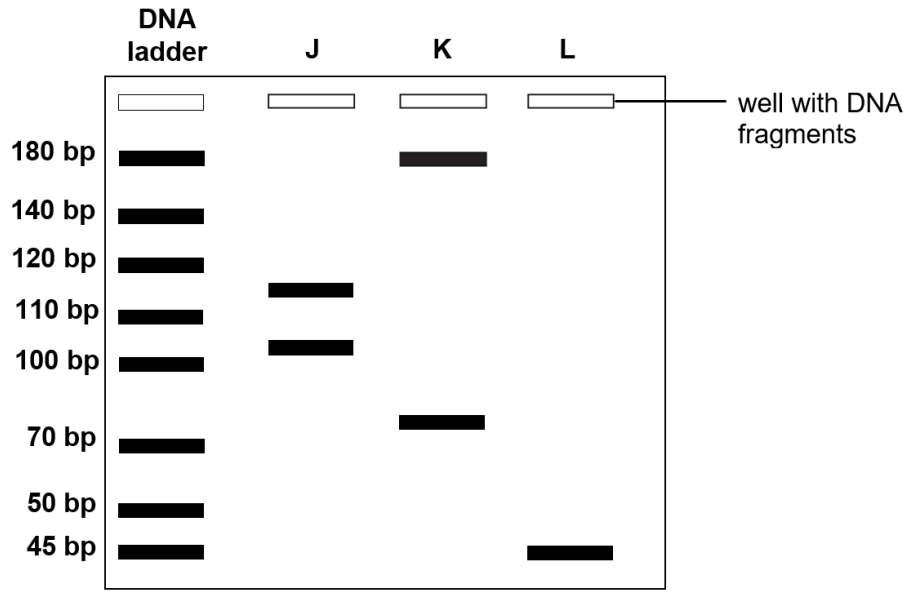


Fig. 10.3

(ii) Only one of these individual developed Huntington's disease. **Identify** the individual and **explain** your answer. [2]

1. **Person K**

2. **The band at 180 bp position**
3. **has the most number of CAG of 60 repeats**
4. **as 40 or more CAG repeats will develop disease**

(iii) Two bands are usually seen for each person tested. **Explain why** only one band was seen for individual **L**. [2]

Important Reminders:

1. **Must be careful of phrasing**
2. **Reject: DNA digested results in 1 fragment**
   Reason: Any DNA that is digest will result in many fragments. You can only refer to number of fragments obtained if you are referring to an allele being digested (refer to tutorial, previous tests & exams)
3. **For this question: Do not need to refer to restriction enzyme or restriction sites since the information is not provided**
   - ➔ **Instead, students need to make use of the data on CAG repeats to figure explain size of fragment**
4. **The CAG repeats are identified through the use of radioactive probe**
5. **Reject: the other band is missing because the fragment was too small and moved out of the gel**
   Reason: the use of tracking dye will ensure this does not happen

1. **Person L is homozygous for normal condition**
2. **with normal allele on each homologous chromosome.**
3. **QF: Normal allele has 15 CAG repeats**
4. **QF: Since the radioactive probe hybridises to only one fragment, only one band at 45 bp position is visualised**

[Total: 9]

11 Relationships between different primates can be found by comparing their proteins and DNA.

The proteins of different species can be compared using immunological techniques. The protein albumin obtained from a human was injected into a rabbit. The rabbit produced antibodies against the human albumin.

These antibodies were extracted from the rabbit and then added to samples of albumin obtained from four different animal species. Precipitation occurs when antibodies bind to albumin. The amount of precipitate produced in each sample was then measured and shown in Table 11.1.

Table 11.1

species from which albumin was obtained	amount of precipitate / arbitrary units
Rat	23
Chimpanzee	96
Marmoset	65
Trout	11

(a) **Comment** on what the results suggest about the evolutionary relationship between humans and the other species. [2]

Important Reminders:

- **MUST QF!**
- **Must refer to all species but many students just mention chimpanzee and trout.**
- **No need to explain.**

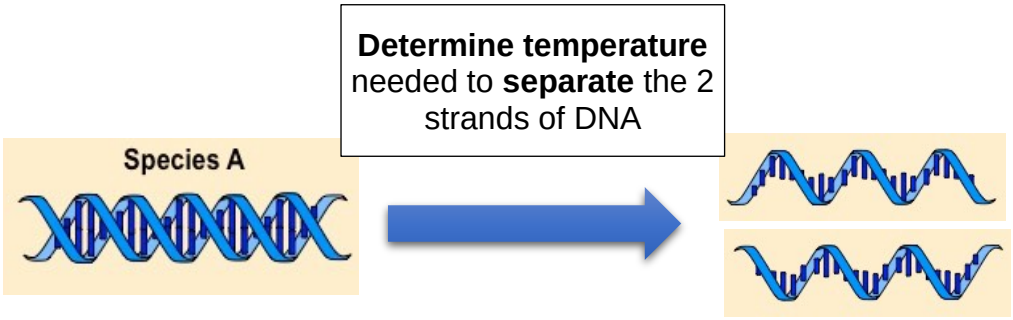
1. **Human is most closely related to chimpanzee, followed by marmoset, rat and least closely related to trout;**

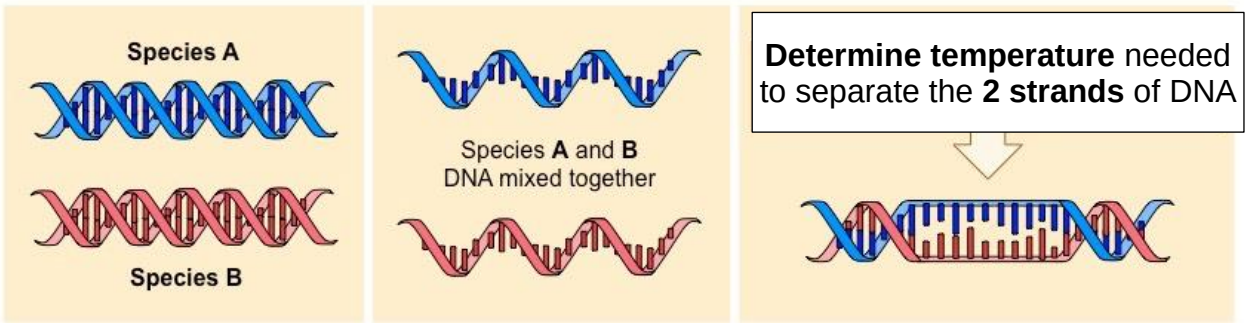
2. **QF: Amount of precipitate formed with chimpanzee is the highest at 96a.u., followed by marmoset (65a.u), than rat (23a.u.) and lowest is trout at 11a.u.**

Scientists also used DNA hybridisation to determine the evolutionary relationships between five species of primate. The separation temperature is the temperature at which a molecule of double-stranded DNA separates into two single strands.

The scientists first recorded the mean separation temperature of DNA in which both strands were from the same species. The scientists then recorded the mean decrease in separation temperature of DNA in which one of the strands was from another species. Their results are shown in Table 11.2.

Explanation regarding the experiment:





Decrease in separation temperature is obtained via:

Temperature needed to separate 2 DNA strands of species A minus temperature needed to separate 2 DNA strand of species A from species B

⇒ small decrease means that the 2 temperatures are very similar

⇒ large decrease means that the 2 temperatures are very different
⇒ the 2nd temperature is much lower
⇒ the other species is NOT closely related
⇒ very few complementary bases & few H-bonds

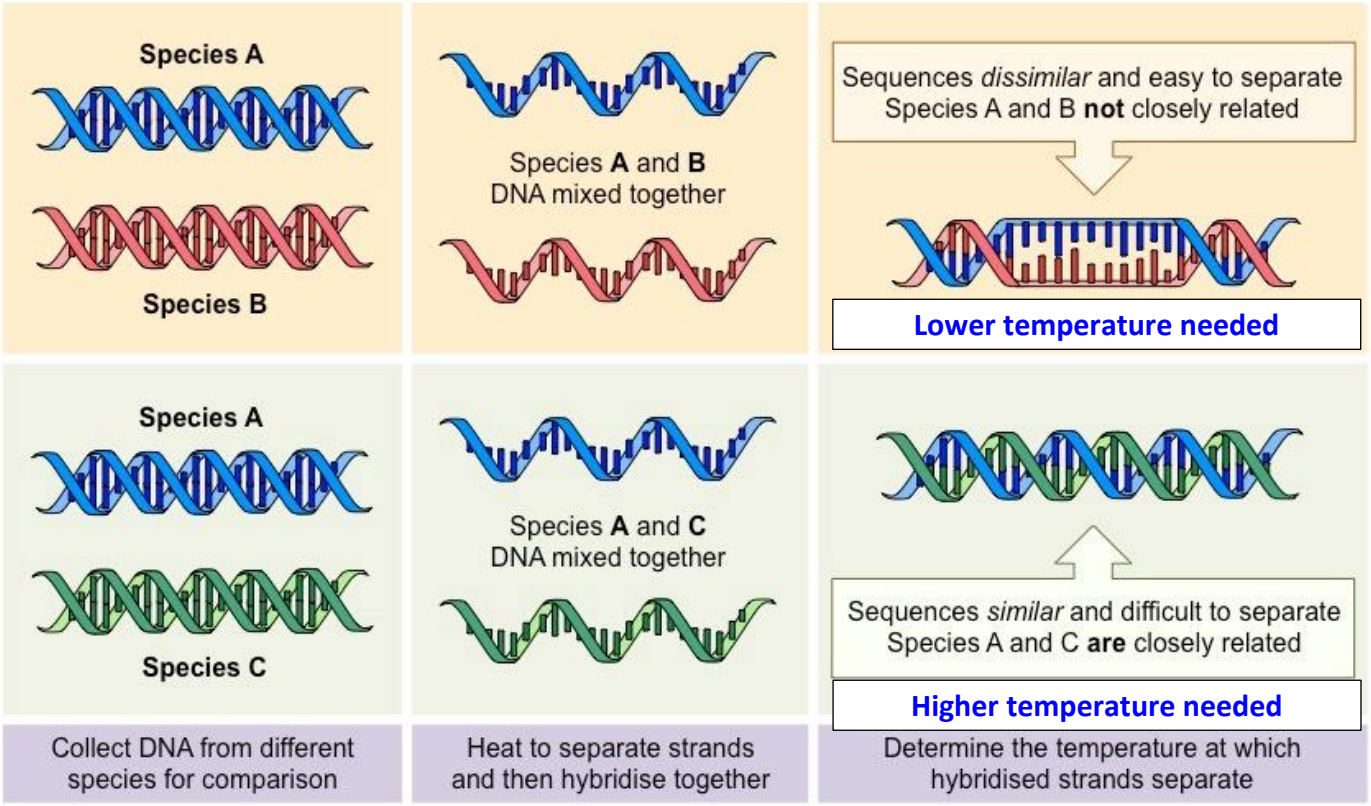


Table 11.2

primate	mean decrease in separation temperature / °c				
	Human	Chimpanzee	Gorilla	Orang-utan	Gibbon
Human					
Chimpanzee	1.7				
Gorilla	2.3	2.3			
Orang-utan	3.6	3.6	3.5		
Gibbon	4.8	4.8	4.7	4.9	

(b) When the scientists first recorded the mean separation temperature of DNA in which both strands were from the same species, differences in the separation temperature were observed.

Suggest why this is so. [1]

- **Individuals within same species have different alleles / different base sequences / different mutations / different combinations of bases / introns**

Reject: if students refer to different species
Note: since the data is an average value, it meant that more than one reading was collected during the experiment

(c) With reference to Table 11.2,

(i) **explain if** the data suggests that gibbons are most distantly related to humans; [3]

Important Reminders:

1. **Wrong focus: trying to figure out how the 2 species are more distantly related**
2. **Focus of Qn: evolutionary relationship pf gibbons with humans compared to other species with human**
3. **If student focused on gibbons and orangutans – max ½ mark for marking points 1 & 2.**

1. **Yes [1]**

2. **There is largest / highest decrease in mean separation temperature of 4.8 ºC compared to the other species**

3. **Sequences are less similar / greater differences in the base sequence**

4. **This means that there are fewer complementary bases between the DNA strand from human compared to gibbon.**

5. **Fewer hydrogen bonds present, so less energy needed to separate the strands.**
   Reject: more time need to break bond

(ii) The scientists assumed that the decreases in separation temperatures are directly proportional to the time since the evolutionary lines of these primates separated.

Gorillas are thought to have separated from orang-utans 20 million years ago. Use this information to **calculate** how long ago the evolutionary lines of humans and chimpanzees separated.

Show your working.

Important Reminders:

1. **MUST write clear statements – look at the space given & number of marks**
2. **MUST have clear indication that 3.5 ºC correlates to 20 million years**
3. **Do NOT round up to 9.71 million years to 10 million – the increase is too great in terms of millions!**
4. **The use of "k" is unclear – this is not a math paper**

Working

- **3.5 ºC correlates to 20 million years [1/2]**
- **For 1 ºC = 20,000 000 ÷ 3.5 = 5.7 million years or 5,714 286 million years [1/2]**
- **Humans and chimpanzees would have separated = 1.7 X 5.7 = 9.69 million years [1/2]**

  Or
  (1.7 ÷ 3.5) X 20 million years = 9.71 [1/2][1/2]

9.69 OR 9.71 [1/2] million years [2]

[Total: 8]

End of Paper 2