NATIONAL JUNIOR COLLEGE, SINGAPORE
Senior High 2
Preliminary Examination
Higher 2

CANDIDATE NAME			
BIOLOGY CLASS	2bi2_____	REGISTRATION NUMBER	

Biology

9744/02

Paper 2: Structured Questions

24 August 2023

Candidates answer on the Question Paper.

2 hours

No Additional Materials are required.

READ THESE INSTRUCTIONS FIRST

Write your name, Biology class and registration number on all the work you hand in.
Write in dark blue or black pen.
You may use an HB for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.

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

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

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

For Examiner's Use	
1	/10
2	/9
3	/11
4	/11
5	/9
6	/12
7	/10
8	/8
9	/10
10	/5
11	/5
Total	/100

This document consists of **27** printed pages and **1** blank page.

Section A

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

1 Triglycerides are transported via lipoproteins such as low-density lipoproteins (LDL). LDL are taken up by target cells as shown in Fig. 1.1.

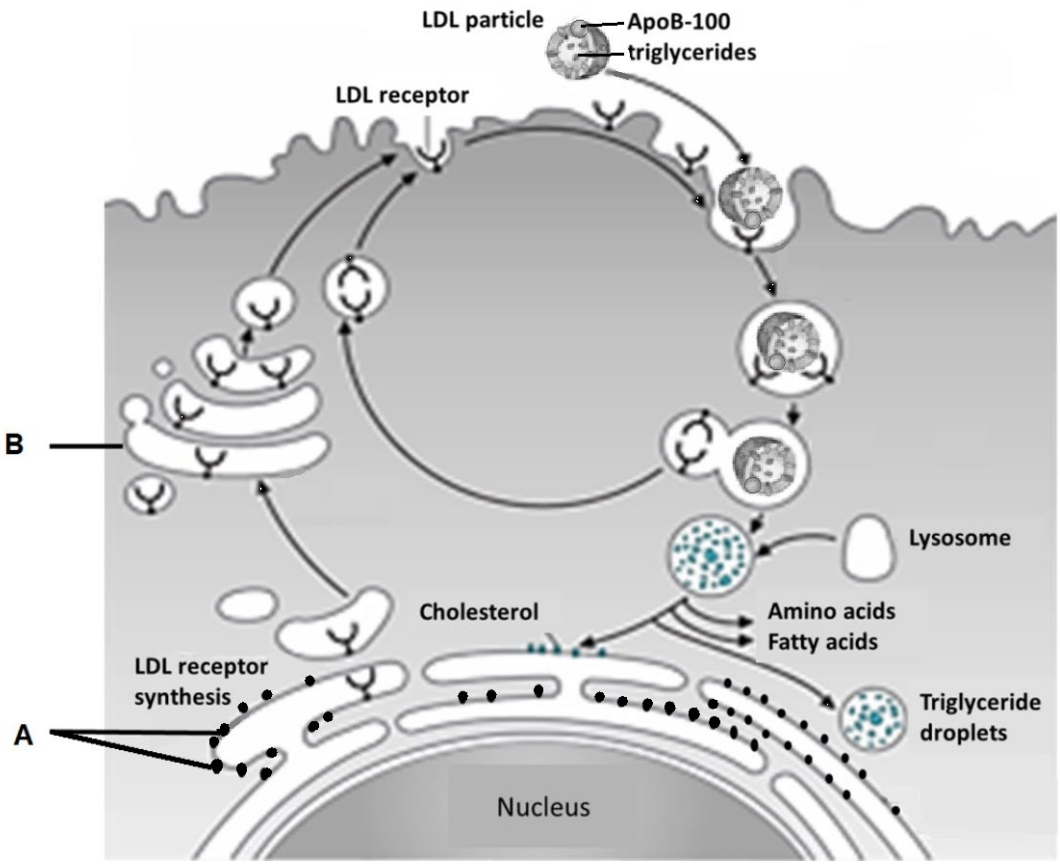

Fig. 1.1

(a) Name the structures labelled **A** in Fig. 1.1.

Ribosomes; [1]

(b) Explain the roles of **B** in the synthesis of LDL receptor.

chemically modifies the LDL receptors (e.g. glycosylation);

packages LDL receptors the into transport vesicles to be **targeted** to the plasma membrane for insertion into membrane;

[2]

(c) With reference to Fig. 1.1, describe how an LDL particle is taken up by a target cell.

Ligands on LDP particle **bind to LDL receptor** on surface of target cell;

Target cell forms an **invagination** of the cell surface membrane;

An **endosome / vesicle** containing the LDL particle is formed within the cell;

[3]

Lipoproteins are made up of proteins and lipids. Their function is to transport cholesterol, triglycerides, and other lipids in the bloodstream.

Fig. 1.2 represents the structure of a lipoprotein.

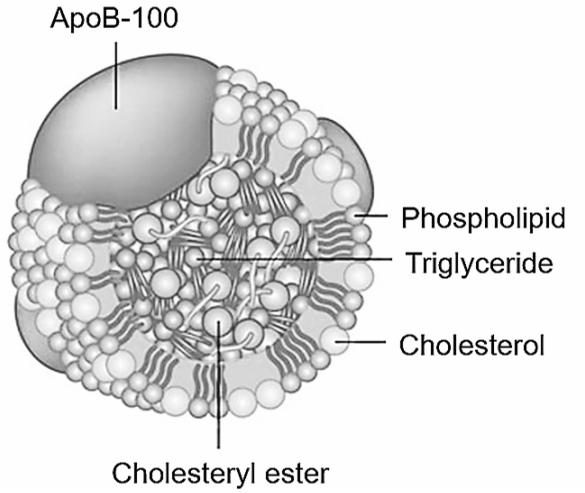

Fig. 1.2

(d) **(i)** With reference to Fig. 1.2, describe the arrangement of phospholipids in lipoproteins.

Phospholipids are arranged in a **monolayer / single layer**;

Hydrophobic hydrocarbon tails face **inwards** while the **hydrophilic** phosphate heads face **outwards**;

[2]

(ii) Suggest why lipoproteins are needed to transport cholesterol, triglycerides, and other lipids in the bloodstream.

Triglycerides are **hydrophobic** in nature and cannot interact with the aqueous medium in the blood;

Ref. to phospholipids as amphipathic;

Their **tails interact with triglycerides** within its interior and its **heads interact with the aqueous medium** in the blood;

[2]

[Total: 10]

2 Collagen serves as the main structural protein in various connective tissues in animals. These tissues include bone cartilage, blood vessels, gum, and skin.

(a) Describe the primary structure of collagen.

Primary structure refers **repeating Gly-X-Y** triplet amino acid sequence joined together by peptide bonds;

X is usually proline and Y is usually hydroxyproline;

Ref. to every third amino acid in the polypeptide sequence is glycine;

[2]

(b) Explain how the structure of collagen differs from cellulose.

Collagen	Cellulose
▪ Collagen is a polymer made up of **amino acids.**	▪ Cellulose is a polymer made up of **β-glucose monomers.**
▪ Compose of **three repeat units** of amino acids.	▪ Compose of **one repeat unit** of glucose. (only β-glucose)
▪ Monomers of collagen (amino acids) are linked via **peptide bonds**.	▪ Monomers of cellulose (β-glucose) are linked via **glycosidic bonds**.
▪ Collagen is composed of **three helical polypeptide chains** twisted together to form a **triple helix / tropocollagen.**	▪ Cellulose chain is made up of **a single straight and unbranched chain** of β-glucose polymer.
▪ **Inter-chain H-bonding** maintains the stability of **within** a single triple helix / tropocollagen. ▪ H-bonding is between **-C=O groups of proline residues on one chain and –NH groups of glycine residues on an adjacent polypeptide chain**.	▪ Inter-chain H-bonding maintains the stability **between parallel chains of cellulose molecules** → this **cross-linking** by hydrogen bonds form **microfibrils**. ▪ H-bonding is between **OH / hydroxyl groups attached to carbon atom 3 on one chain and carbon atom 6 on a β-glucose on an adjacent chain**.
▪ Each tropocollagen **crosslinks** with a neighbouring tropocollagen running parallel to it → via **covalent bonds** on adjacent tropocollagen forming **collagen fibrils**	▪ **No covalent cross-links** exist between the cellulose microfibrils.

[3]

Fig 2.1 show the main steps involved in the synthesis and assembly of collagen.

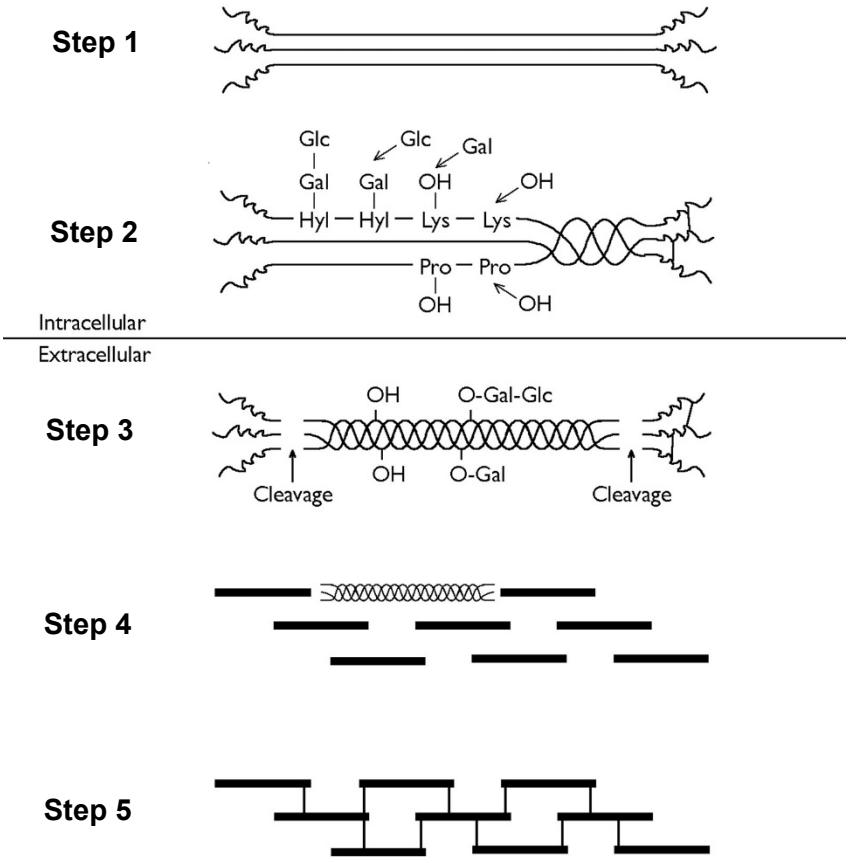

Fig 2.1

(c) Suggest why the assembly of collagen takes place outside the cell.

Cleaving of the ends of the tropocollagen before assembly into collagen fibres is performed by **enzymes found only outside** of the cell;

Collagen molecule is **too large to pass through the cell surface membrane** and has to be assembled outside the cell;

Assembly of collagen outside the cell allows **alignment of microfibrils** / formation of bonds between the microfibrils;

[2]

(d) Vitamin C is necessary in aiding the hydroxylation of amino acids to form hydroxyproline and hydroxylysine in **Step 2**. A deficiency in Vitamin C can lead to scurvy, a disease associated with symptoms such as loss of teeth and easy bruising.

Suggest why vitamin C deficiency can lead to scurvy.

Hydroxylation / addition of OH groups on proline or lysine allow for formation of hydrogen bonds to further stabilize tropocollagen structure;

It also allows for formation of covalent bonds between tropocollagen molecules forming collagen fibril;

As a result, basic units of tropocollagen slide against each other as they are unable to form stable bundles of collagen fibres;

leading to low tensile strength of collagen, thus causing scurvy;

[2]

[Total: 9]

3 In eukaryotes, transcription of a gene produces RNA transcripts that must be successfully processed before they can be exported out of the nucleus into the cytoplasm for translation. This process is illustrated in Fig. 3.1.

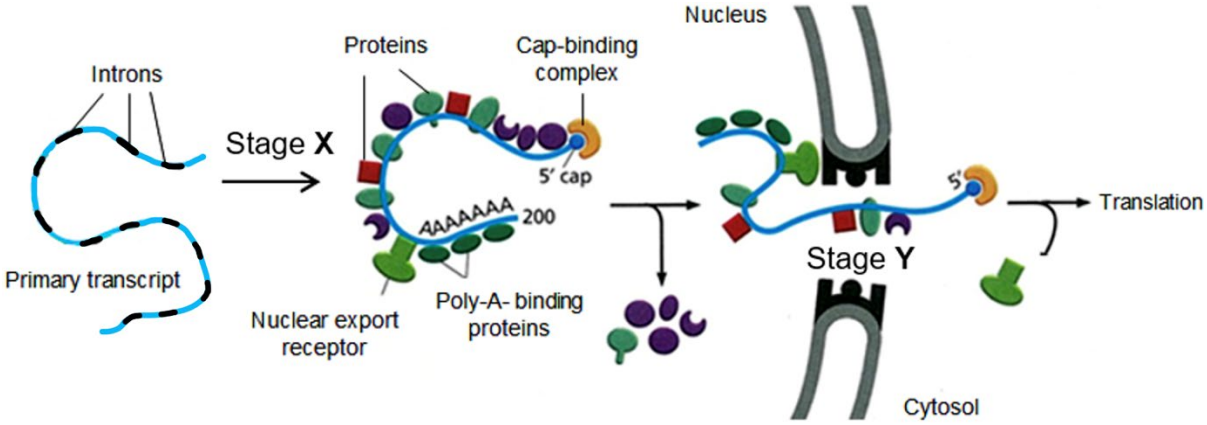

Fig. 3.1

(a) With reference to Fig. 3.1,

(i) describe the process occurring at stage **X** that results in the formation of a continuous coding sequence in mRNA.

RNA **splicing** carried out by the **spliceosome**;

Introns are excised/removed and **exons are ligated/spliced/joined** to each other to form a mature mRNA molecule;

[2]

(ii) suggest why the cap-binding complex and poly-A-binding proteins are essential for stage **Y**.

Proteins are recognised by nuclear pore which facilitate the export of mRNA;

To ensure that the mRNA is **stable** for export into the cytoplasm; [1]

(b) Describe **three** differences between eukaryotic and prokaryotic translation.

In prokaryotes small ribosomal subunit recognises and binds to the **Shine-Dalgarno sequence** on the mRNA, while in eukaryotes it recognises and binds to the **5' cap**;

In prokaryotes the initiator amino-acyl-tRNA is **fMet-tRNA**, while in eukaryotes the initiator amino-acyl-tRNA is **Met-tRNA** / ref to first amino acid added;

Prokaryotic translation uses **polycistronic mRNA** as a template, while eukaryotic translation uses **monocistronic mRNA**;

Prokaryotic ribosomes are **70S** while eukaryotic ribosomes are **80S**;

[3]

(c) The development of a mouse, from a fertilised egg into an adult, is regulated by variations in DNA methylation. Fig. 3.2 shows the developmental stages of a mouse with corresponding levels of DNA methylation. **R**, **S** and **T** represent the zygote, inner cell mass of blastocyst, and embryo respectively.

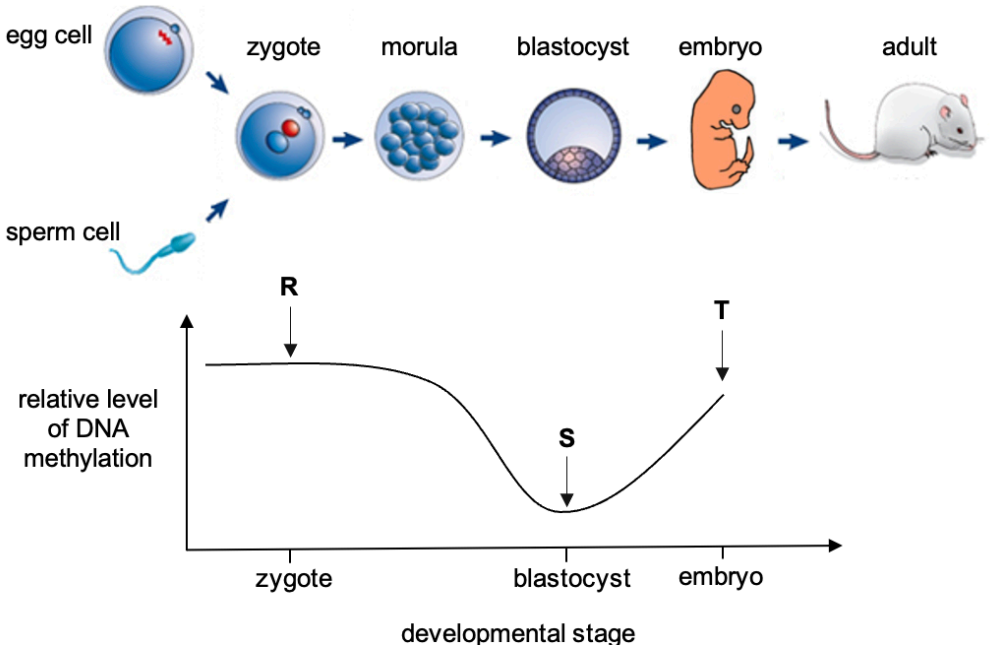

Fig. 3.2

(i) State the level of potency of the inner cell mass of blastocyst.

Pluripotent; [1]

(ii) With reference to Fig. 3.2, suggest reasons for the different relative levels of DNA methylation at **R**, **S** and **T**.

Zygote **inherits the DNA methylation from the egg and sperm cells** which are specialised cells with high levels of DNA methylation resulting in high DNA methylation at R;

During the development of blastocyst from zygote, demethylation of DNA occurs in order **to reprogramme the cell / dedifferentiate / achieve high level of potency / allow all genes to be accessible for transcription**, leading to the decrease in DNA methylation from R to S;

During embryo development, stem cells in the blastocyst differentiate into specialised cells, resulting in **silencing of genes that are not required for their functions**, hence increasing the DNA methylation from S to T;

[3]

(iii) Although the inner cell mass of blastocyst has low levels of DNA methylation, many genes are not transcribed.

Suggest how the levels of transcription is kept low in blastocyst.

Ref to absence of activator proteins / presence of repressor proteins;

Ref to low expression of general transcription factors e.g. TATA binding protein [1]

[Total: 11]

4 Influenza and COVID-19 are both contagious respiratory diseases caused by different viruses. COVID-19 is caused by infection with a coronavirus, SARS-CoV-2, first identified in 2019. Flu is caused by infection with an influenza virus.

Fig. 4.1 shows the structure of the SARS-CoV-2.

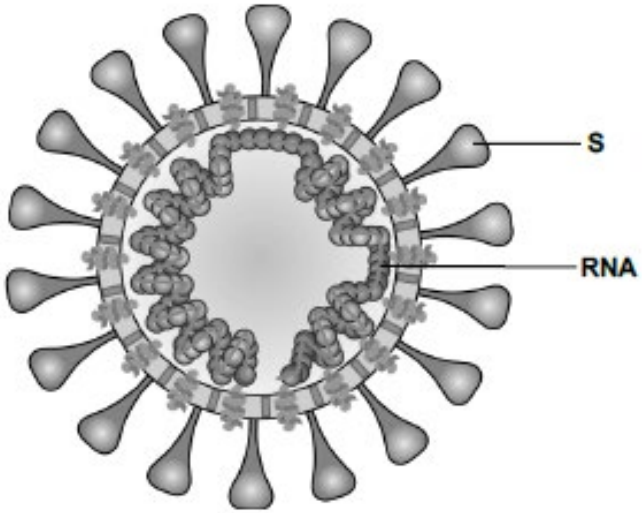

Fig. 4.1

(a) Compare the structures of SARS-CoV-2 and influenza virus.

[2]

(b) Both influenza virus and SARS-CoV-2 have viral genes coding for viral RNA polymerases.

Explain why such genes coding for viral RNA polymerase are needed by these viruses despite the availability of host RNA polymerases.

[2]

The subtypes of the influenza virus that infect birds, human and pigs in one area of the world in recent times are shown in the Table 4.1 below.

Table 4.1

time period	influenza virus subtypes present	
	humans	pigs
1918-1957	H1N1	H1N1
1958-1970	H2N2	
1971-present day	H3N2 H1N1	H3N2 H2N3

(c) Based on the above information, discuss the plausibility that an antigenic shift of the influenza virus can occur from H2N2 combining with H1N1 or H3N2 in present human populations.

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..... [3]

(d) Fig. 4.2 shows the structure of haemagglutinin (HA) of the influenza virus. The numbers in Fig. 4.2 indicate the positions of amino acids that are frequently changed.

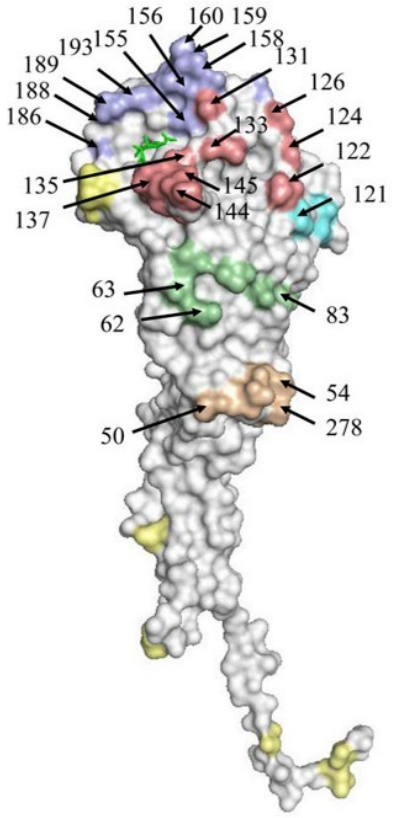

Fig. 4.2

(i) Based on your knowledge on the reproductive cycle of influenza, explain why amino acids in HA are frequently changed.

.....

.....

.....

.....

.....

.....

..... [3]

(ii) Suggest why such frequent changes is a significant burden on the economy.

.....

..... [1]

[Total: 11]

5 In bacteria, the synthesis of amino acid tryptophan is regulated by a repressible operon, *trp* operon.

(a) Explain the term repressible operon.

A repressible operon is a system of enzymes whose **transcription is usually on** but **can be repressed / inhibited** when a molecule (co-represssor) binds allosterically to a regulatory protein;

It generally functions in **anabolic pathways** that synthesise essential end-products from precursors.

[2]

Bacteria cells can take up tryptophan from their surroundings. When external supply of tryptophan is high, transcription of genes in the *trp* operon is repressed.

(b) Explain how the *trp* operon is repressed in the presence of high tryptophan supply.

Tryptophan will bind to and **activate Trp repressor**;

Active Trp repressor **binds to the operator of Trp operon**;

This **prevents RNA polymerase** from **binding** and/or **initiating transcription**;

[2]

In an experiment, bacteria strain **A** and bacteria strain **B** were mixed together. Strain **A** has the *trp* operon but lacks the *lac* operon. Strain **B** has the *lac* operon but lacks the *trp* operon. Mixing of the two strains of bacteria resulted in bacteria strain **C** containing a fusion of *trp* and *lac* operon. This experiment is illustrated in Fig 5.1.

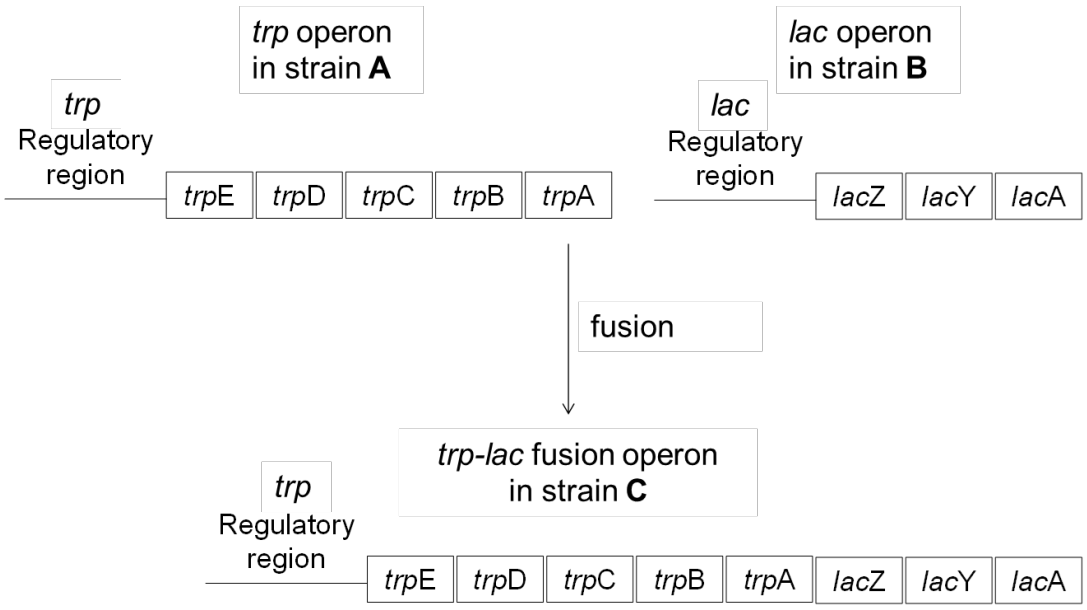

Fig 5.1

(c) Suggest, with reason, the condition(s) needed for β-galactosidase to be expressed in bacteria strain **C**.

Only when **tryptophan is absent**;

Fusion of trp and lac operon means that the genes in the lac operon are now under the control of the regulatory region of the trp operon;

In the absence of tryptophan, the **repressor is inactive** and is therefore **unable to bind to the operator**.

RNA polymerase is able to bind to the promoter and **transcribe** lacZ genes that encode **β-galactosidase**;

[3]

(d) Experiments were performed to determine how the two operons become fused. It was found that bacteria strain **C** contains a Fertility factor.

Explain why there is insufficient evidence to conclude that conjugation resulted in the fusion of the two operons.

Bacteria strains A and/or B **already possess F factor**;

Horizontal gene transfer could also be due to **transformation / transduction**;

[2]

[Total: 9]

6 In domestic cats, fur colour is controlled by several genes.

The gene for melanin production is located on the X chromosome. This gene has two alleles, allele **B** codes for eumelanin resulting in black fur, and allele **O** codes for phaeomelanin resulting in orange fur. These two alleles are codominant so a heterozygous cat will have fur with patches of black and orange colours, known as a tortoiseshell. Male cats rarely have tortoiseshell colour.

Another gene known as the white masking gene is located on a different chromosome. The allele **W** prevents normal development of melanocytes (pigment-producing cells). This results in cats with entirely white fur regardless of the alleles for melanin. Note that these white cats are not albino.

(a) State the name for this type of interaction between gene loci.

(Dominant) **epistasis**; [1]

(b) A female cat with black fur mates with a male cat with white fur, and one of the kittens produced has tortoiseshell fur.

Using appropriate symbols, draw a genetic diagram to explain the result of the cross.

Parental generation

Parental phenotypes	Black fur female	x	Male, white fur male
Parental genotypes	X^BX^Bww	x	X^OYWw
After meiosis, gametes produced	X^Bw	x	X^OW, X^Ow, YW, Yw

Random fertilisation

F_1 generation

F_1 Genotypic ratio: 1 X^BX^OWw : 1 X^BX^Oww : 1 X^BYWw : 1 X^BYww

F_1 Phenotypic ratio	1 White fur female	:	1 Tortoiseshell female	:	1 White fur male	:	1 Black fur amke

Parental genotype + phenotype + gametes;

F1 genotypes;

Relate F1 genotypes to phenotypes;

F1 phenotypic ratio;

[4]

Another gene, piebald spotting, determines the occurrence of patches of white fur. Cats which are homozygous recessive (**ss**) for this gene do not have any patches of white, while cats with at least one dominant **S** allele will have patches of white.

A female cat with black fur and white spots mates with a black fur male and produced four kittens. Fig. 6.1 shows the pedigree of this family of cats and their phenotypes.

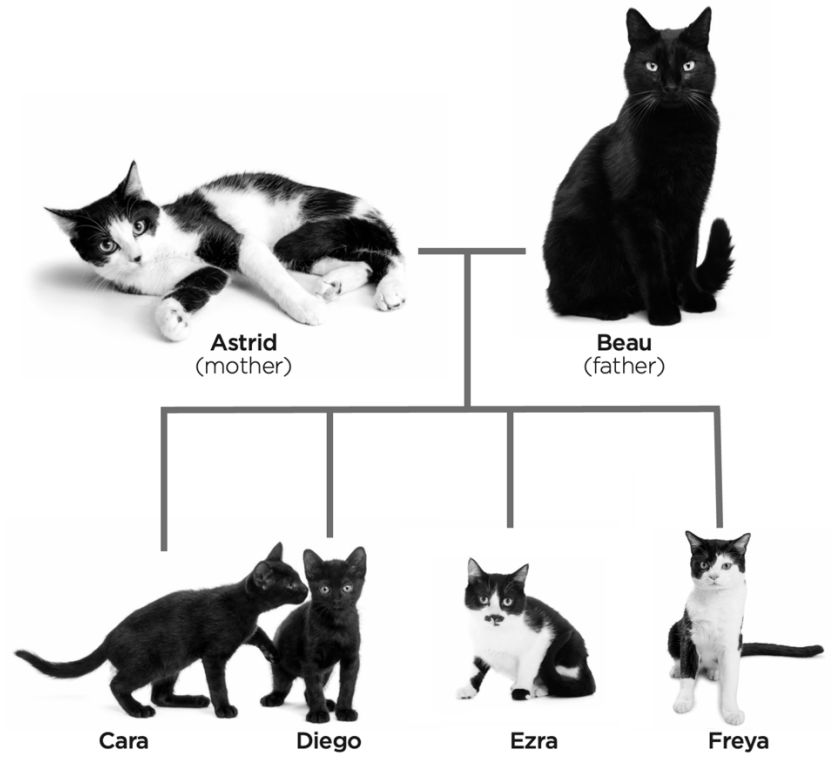

Fig. 6.1

The DNA from each of the cats were isolated and PCR was performed to amplify the piebald spotting gene. The PCR products were separated by gel electrophoresis and the results are shown in Fig. 6.2.

Fig. 6.2

(c) Explain the main principles that allow gel electrophoresis to separate DNA fragments.

Separates DNA fragments based on **molecular weight**;

DNA fragments are loaded in a well of agarose gel nearer to the negative electrode;

DNA is negatively charged and will be attracted to the positive electrode;

DNA fragments of lower molecular mass will move faster compared to higher molecular mass creating bands of different distance moved per unit time;

[3]

(d) With reference to Fig. 6.1 and Fig. 6.2,

(i) state the genotype of Astrid (mother) for all three genes.

X^BX^BwwSs ; [1]

(ii) explain which band corresponds to the allele for white patches.

Larger/Top band corresponds to the allele for white patches;

Only cats with white patches have the larger/top band;

Cats without white patches only has the shorter/bottom band;

Since cats without white patches are homozygous recessive, it means that the shorter/bottom band is the recessive allele which does not result in white patches;

[3]

[Total: 12]

7 Krebs cycle is a stage in aerobic respiration where acetyl-CoA is oxidised through a series of reactions. Electron carriers, reduced NAD and reduced FAD, are produced from these reactions. These electron carriers are used to generate ATP through oxidative phosphorylation.

(a) State the precise location in a cell where Krebs Cycle occurs.

Mitochondrial matrix; [1]

(b) Describe how reduced NAD and reduced FAD can be used to generate ATP through oxidative phosphorylation.

Reduced NAD and reduced FAD are **oxidised to release electrons** into the **electron transport chain (ETC)**;

As the **electrons are passed down the ETC**, the energy released by the electrons is used to **pump protons**;

Across the **inner membrane**, from the **matrix** into the **intermembrane space**;

Proton gradient generated in in the intermembrane space contributes to **chemiosmosis**;

Where the movement of protons across the membrane via **ATP synthase** leads to the **synthesis of ATP**;

[4]

There is another metabolic pathway that can bypass some reactions in Krebs cycle. This pathway is called glyoxylate cycle as shown in Fig. 7.1.

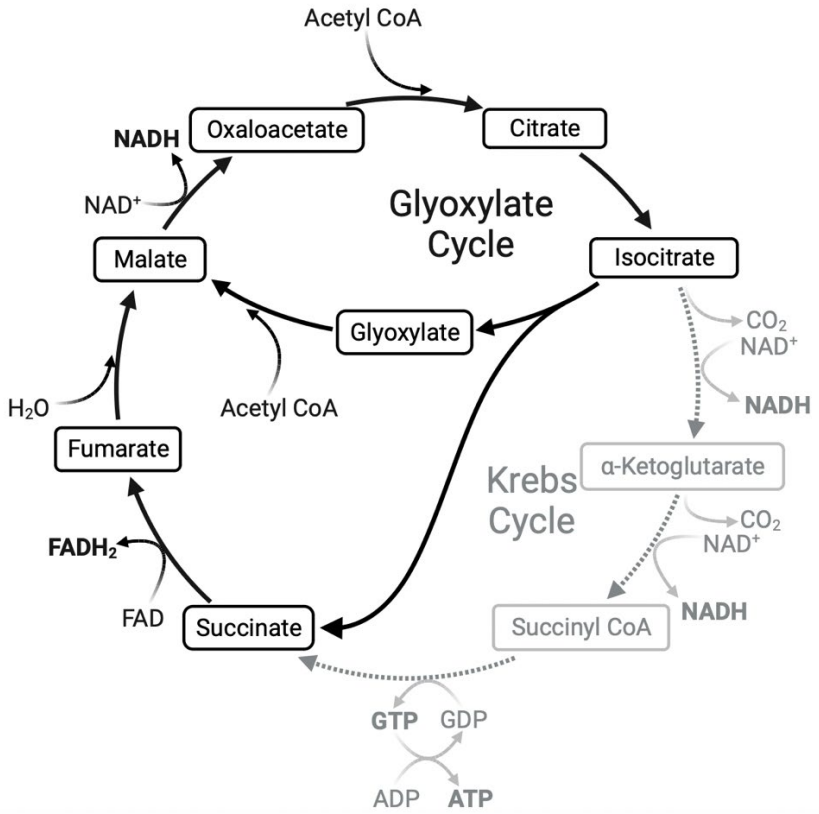

Fig 7.1

(c) Compare the efficiency of ATP production between Krebs and glyoxylate cycles when **2** molecules of acetyl-CoA enter each cycle. Show your workings.

Assume that 1 molecule of reduced NAD is converted into 3 ATP and 1 molecule of reduced FAD is converted into 2 ATP during oxidative phosphorylation.

For Krebs cycle:
Per 2 acetyl-CoA that enters the Krebs cycle
6 NADH produced x 3 = 18 ATP (converted in oxidative phosphorylation)
2 $FADH_2$ produced x 2 = 4 ATP (converted in oxidative phosphorylation)
2 ATP produced (substrate-level phosphorylation)

Total number of ATP= 18 + 4 + 2 = **24 ATP;**

Number of ATP molecules = ……

For glyoxylate cycle:

Per 2 acetyl-CoA that enters the glyoxylate cycle
2 NADH produced x 3 = 6 ATP (converted in oxidative phosphorylation)
1 $FADH_2$ produced x 2 = 2 ATP (converted in oxidative phosphorylation)

Total number of ATP= 3 + 2 = **8 ATP;**

Number of ATP molecules = ……

Compare the efficiency of ATP production between both cycles.

Krebs cycle is 3 times **more efficient** / **produces more ATP** as compared to the glyoxylate cycle;

[3]

(d) Oxaloacetate is an intermediate of both Krebs and glyoxylate cycles and is needed for amino acids synthesis.

Although Krebs cycle generates more ATP, glyoxylate cycle is preferred over Krebs cycle during seed germination for plant growth.

Suggest why glyoxylate cycle is preferred over Krebs cycle during seed germination.

Two molecules of oxaloacetate are produced **per glyoxylate cycle**;

While only **one molecule of oxaloacetate** is produced **per Krebs cycle**;

Seed germination requires **high level of protein synthesis**;

[2]

[Total: 10]

8 Odorant receptors are found on sensory neurons. Binding of odorants to their respective receptors triggers signal transduction pathways, resulting in the perception of smells.

Fig. 8.1 shows the binding of an odorant to its receptor and its resulting signalling pathway.

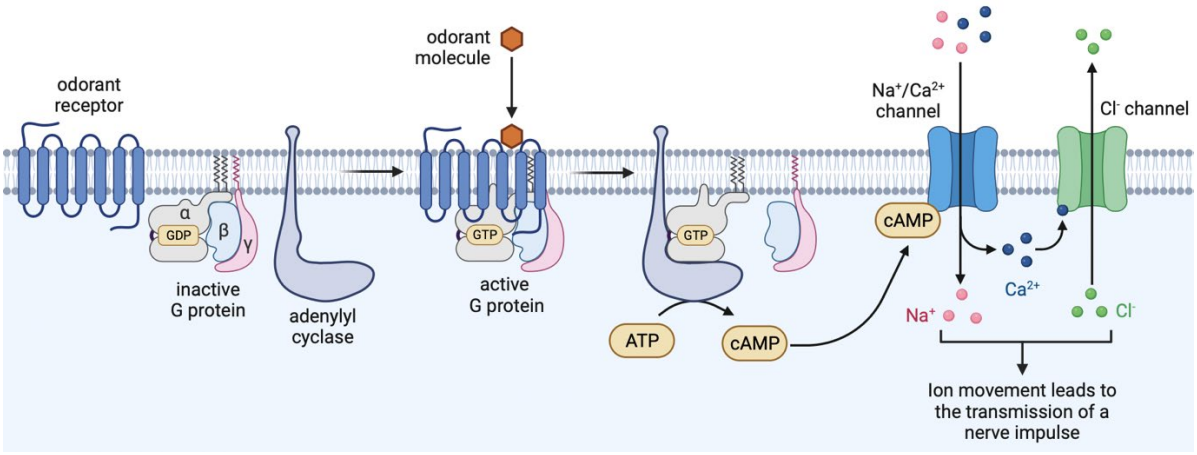

Fig. 8.1

(a) With reference to Fig. 8.1,

(i) describe how the binding of an odorant molecule to the odorant receptor results in the activation of G-proteins.

[3]

(ii) explain how the initial signal is amplified via signal transduction.

[2]

Olfactory fatigue is a temporary condition where the sense of smell becomes less sensitive after prolonged exposure to a specific scent. This phenomenon is due to the desensitisation of the odorant receptor.

Fig. 8.2 shows a desensitised odorant receptor.

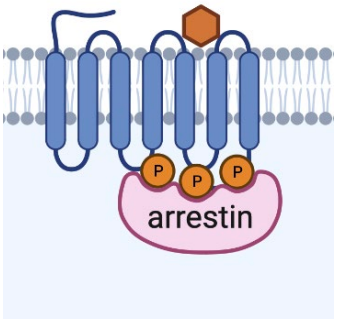

Fig. 8.2

(b) With reference to Fig. 8.2, suggest how an odorant receptor becomes desensitised.

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..... [2]

(c) In the perfume industry, buyers are instructed to inhale the smell of coffee beans in between the testing of perfume samples to recover from olfactory fatigue.

Suggest a mechanism by which the inhalation of coffee beans may achieve recovery from olfactory fatigue.

.....

..... [1]

[Total: 8]

9 Two subspecies of reindeer, *Rangifer tarandus*, live in North America. Members of the different subspecies belong to the same species, but they have some morphological differences and are found in different geographical locations.

Fig. 9.1 shows the two subspecies of reindeer in their respective habitats.

southern woodland subspecies,

R. tarandus caribou

northern barren ground subspecies,

R. tarandus groenlandicus

Fig. 9.1

(a) During the last ice age, an ice sheet separated southern and northern populations of *R. tarandus* in North America.

With reference to Fig. 9.1, explain how this ice sheet resulted in the formation of two different subspecies of *R. tarandus*.

Ref to **geographical isolation** leading to allopatric (sub)speciation;

Ref to **disruption of gene flow / no interbreeding** between the southern and northern populations of *R. tarandus*;

Ref to **different selection pressures** in different environments;

Ref to different traits provide **selective advantages** in the different environments;

E.g. dark fur colour are selected for in the woodlands while light fur colour are selected for in the barren ground as these colours allows reindeers to camouflage in their respective environment, protecting them against predators;*

Ref to each population of *R. tarandus* **accumulate mutations independently**;

[4]

(b) A mixed population consisting of individuals from both subspecies now occupies the area previously covered by the ice sheet.

(i) Explain why *R. tarandus caribou* and *R. tarandus groenlandicus* are consider the same species.

The differences accumulated in the two populations are **not sufficient to cause reproductive isolation** / individuals of the populations of *R. tarandus caribou* and *R. tarandus groenlandicus* can **interbreed**;

The offspring produced from interbreeding is **viable and fertile**, hence they are considered as the same species under the Biological Species Concept;

[2]

(ii) Evaluate the ability of this mixed population compared to the pure subspecies populations to adapt to increasing temperatures from climate change.

Hybrid populations have **more genetic variation**;

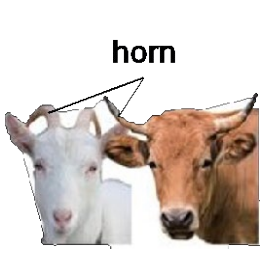
As the gene pool of hybrid populations would contain **genes / mutations / alleles are from both subspecies**;

Hybrid populations are more likely to have **alleles for warmer temperatures** and hence have **selective advantage** when temperatures increase;

[2]

(c) Reindeer belong to a suborder Ruminantia, which are the only group of mammals with cranial appendages, also known as headgear. Table 9.1 shows the different headgear morphologies of different ruminant families.

Table. 9.1

family	 Antilocapridae	 Giraffidae	 Cervidae	 Bovidae
headgear structure	bone covered by skin, hair, and a keratinous sheath	bone covered by skin and hair	regenerable bone covered by skin, hair	bone covered by skin, hair, and a keratinous sheath

With reference to Table 9.1, explain how the structure of headgears provides evidence to support the theory of evolution.

They all share the same **bony outgrowth covered by skin and hair** as their headgear, which suggests that they originated from a **common ancestor** in the Pecora lineage;

The headgear of each family have **different coverings and branching structures** which shows modifications from the common ancestor;

[2]

[Total: 10]

10 Fig. 10.1 shows the immune response upon an infection of the lungs with *Mycobacterium tuberculosis*.

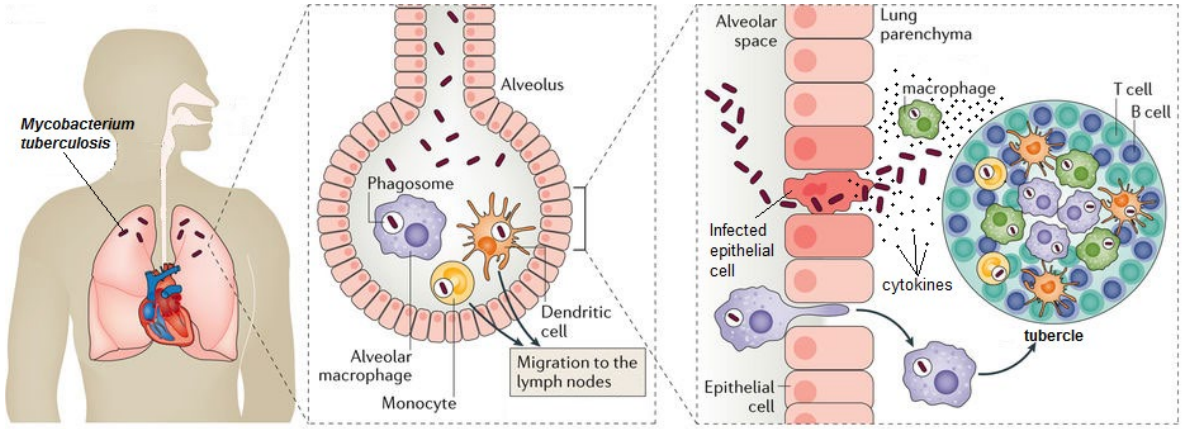


Fig. 10.1

(a) State the mode of transmission by *M. tuberculosis.*

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[1]

(b) With reference to Fig. 10.1, describe the immune response to *M. tuberculosis*.

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[3]

(c) Suggest why it is challenging to treat tuberculosis by antibiotics.

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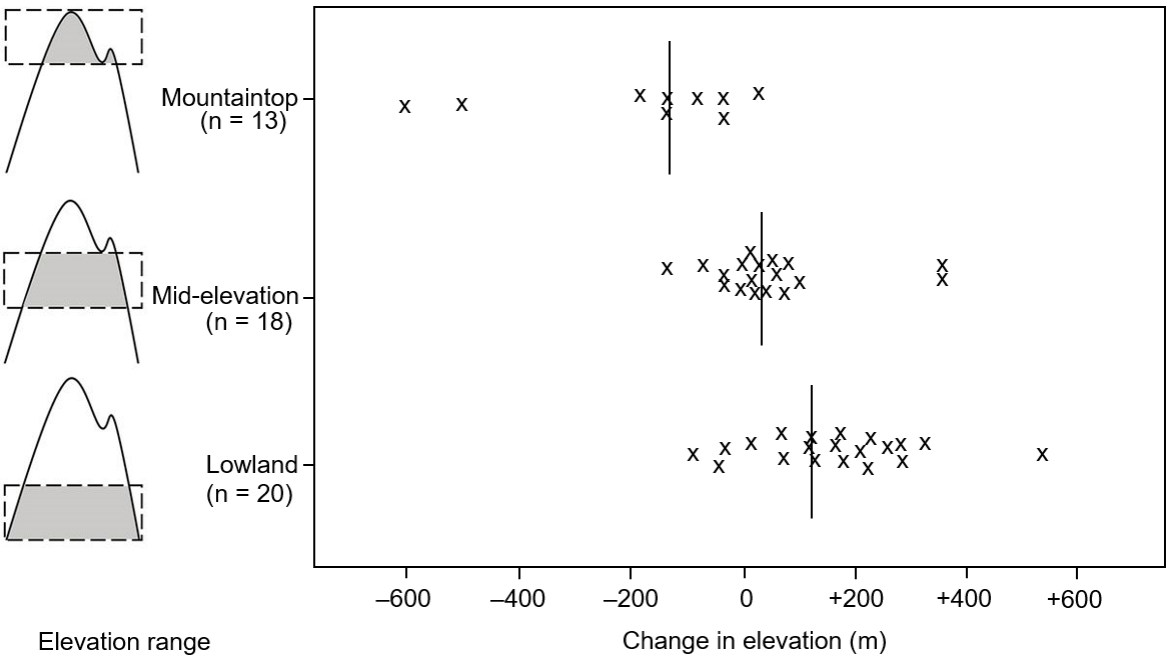
[1]

[Total: 5]

11 The response to increasing temperature from climate change may differ between species. One response is to migrate to a different elevation.

Researchers studied 51 species in Malaysia over a 10-year period to assess the impact of increasing temperature on their habitat range on a mountain.

Fig. 10.1 shows the change in elevation of each species' habitat after the 10-year study.



Key

n - number of species originally present at that elevation range

x - data point for change in elevation for one species after the 10-year study

vertical line (I) - the average change at that elevation range

Fig. 11.1

(a) Describe and explain the effects of increasing temperature on the change in elevation for species living at lowland and mid-elevation.

Lowland: Range of about **-180m to +530m**. Most of the data points indicate a **positive change** in elevation after 10 years / average of about **+100m**;

Mid-elevation: Range of about **-160m to +350m**. Most of the data points indicate a **no or slight change** in elevation after 10 years / average of about **+20m**;

As temperature rises, species from lowland will likely shift to higher elevations where **temperatures are cooler** to stay within their ideal range of environmental conditions;

Species for mid-elevation range may not shift as much because the increase in temperature still falls **within the range which the species can tolerate**;

[3]

(b) Suggest two reasons why species living at mountaintop migrate to a lower elevation as a result of climate change.

Climate change may lead to the decline of food sources or preferred habitats at higher elevations. Thus species move to lower elevations where resources are still available;

Melting snow caps and altered precipitation patterns due to climate change can affect the availability of water sources at high altitudes. Species may now thrive in lower elevations where more water is available;

As species from lower altitude shift to higher elevations, there may be increased competition for limited resources (eg. food, mates, and nesting sites). Animals at higher altitudes may choose to migrate to lower areas where competition is less intense;

[2]

[Total: 5]