H2

ANDERSON SERANGOON JUNIOR COLLEGE
HIGHER 2
ANSWERS

2022 JC2 PRELIMINARY EXAMINATIONS

CANDIDATE NAME	
CLASS	
INDEX NUMBER	

BIOLOGY 9744/02

PAPER 2
SHORT STRUCTURED QUESTIONS

13 SEPTEMBER 2022
TUESDAY

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

2 HOURS

READ THESE INSTRUCTIONS FIRST

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

Answer **all** questions.

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

At the end of the examination, fasten all your work securely together.
The number of marks is given in brackets [ ] at the end of each question or part question.

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

This document consists of **13** printed pages and **1** blank page

Answer **all** the questions.

1 Chitin, the second most abundant organic polymer after cellulose on Earth, is found in the cell walls of fungi and the exoskeleton of insects. Similar to cellulose, chitin is a structural polysaccharide. Chitin consists of N-acetylglucosamine.

Fig. 1.1 shows the structure of chitin.

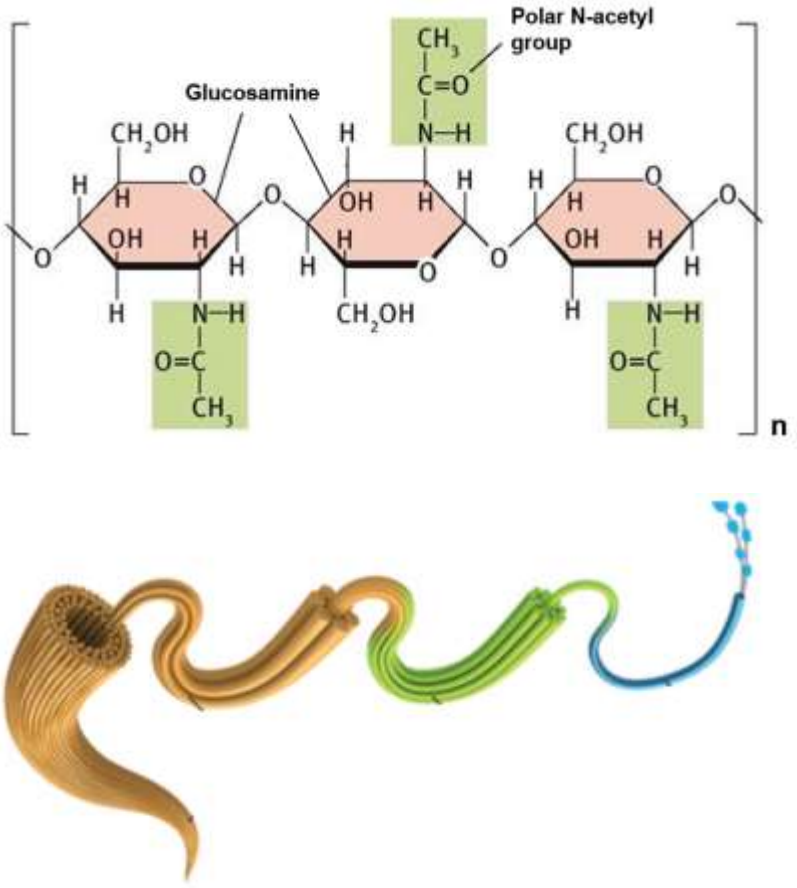


Fig. 1.1

(a) With reference to Fig. 1.1,

(i) name the covalent bond between two monomers in a chitin molecule and describe how this bond is formed.

1. Monomers are linked by **β (1,4) glycosidic bonds;**
2. Which is formed via a **condensation reaction**, with **loss of** 1 **water molecule per bond formed;**
3. between **a hydroxyl/OH group on carbon atom 1 of one N-acetylglucosamine and a hydroxyl/OH group on carbon atom 4 of another N-acetylglucosamine;**
4. **every alternate/successive N-acetylglucosamine monomer has to be rotated by 180°/inverted with respect to one another**, so that the –OH groups on carbon atoms 1 and 4 to line up alongside each other during condensation.

[3]

(ii) explain how the structure and property of chitin are related to its role as a structural polysaccharide in fungi and insects.

1. **Alternate N-acetylglucosamine** in chitin chain is **inverted**/ **rotated 180º** → results in a **straight / linear** chitin chain/molecule, allowing **bundling** of cellulose chains into microfibrils, macrofibrils and fibres;
2. **Polar/hydrophilic –OH groups and/or N-acetyl groups** in chitin chains are **projected outwards** in all directions;
3. This allows extensive **cross-linking** between chitin chains by formation of **interchain hydrogen bonds** between –OH groups and N-acetyl groups across parallel chains;
4. Parallel **straight / linear** chitin chains **bundle**/associate together to form **microfibrils**, which are arranged in larger bundles to form **fibres**/ Parallel chitin chains associate together to form a **fibrous structure;**
5. giving it **high tensile strength;**
6. each chitin chain/molecule is composed of **large number** of N-acetylglucosamine **monomers** → **large** molecule, thus is **insoluble** in water. [4]

(c) Chitinase is an enzyme found in plants. It degrades chitin in fungal cell walls and exoskeletons of insects, protecting the plants against a range of pathogens.

Describe the mode of action of chitinase.

1. Chitinase **lowers activation energy** + any one elaboration below
   1. **physically strains bonds within substrates** to be broken / distorts the substrate;
   2. **Altering charges** on substrates;
   3. active site provides a **favorable microenvironment** for catalysis to occur, eg **hydrophobic micro-environment** for hydrophobic substrates to react;

   max 2 from above
2. [**lock and key hypothesis**] The (**3D conformation** of) **substrate** (e.g., cellulose) is **complementary** to the **active site** of the **enzyme**, thus forming **enzyme-substrate complexes**;
3. [**induced fit** hypothesis] With ref. to **change in 3D conformation** of enzyme for a **better fit/ tighter binding** between substrate and enzyme;
4. Resulting in **hydrolysis of glycosidic bond** between N-acetylglucosamine residues

Note to answer in context, presence of 1 or more than 1 types of substrate

[3]

Easy: 3, Moderate: 5, Challenging: 2 [Total: 10]

2 Fig. 2.1 is an electronmicrograph of a human cell during mitosis.

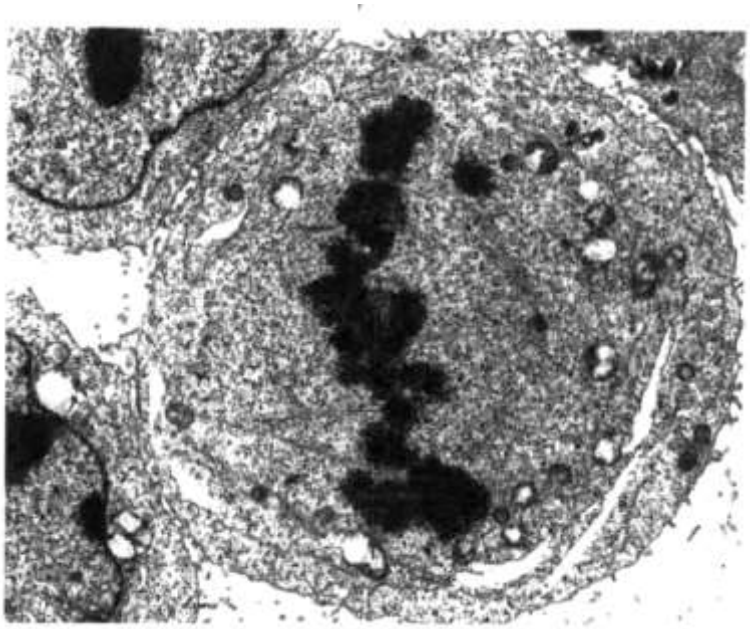


Fig. 2.1

(a) Describe the events that take place in the stage of mitosis **before** that seen in Fig. 2.1.

1. During **prophase**, **chromatin fibres condense** to become **discrete chromosomes**;
2. **nuclear envelope breaks down/disintegrates;**
3. **nucleolus** gradually **disappears** (reject disintegrate nucleolus);
4. **Centrioles** migrate to **opposite poles** of the cells;
5. The **mitotic spindle** begins to **form** and **spindle fibres** begin to **assemble/extend**.

Reject Interphase events

The majority of candidates were able to identify the correct stage of mitosis.

[3]

(b) The normal diploid number of chromosomes for a human cell, such as that shown Fig. 2.1, is 46.

The cell in Fig. 2.1 has 92 DNA molecules.

Explain the presence of 92 DNA molecules in this cell and why it is important to have this number.

Accounting of 92 ds DNA molecules:

1. **DNA replication** occurs during **S phase of interphase** before mitosis occurs;
2. **each strand** of parental DNA is used as **template** to synthesize a **complementary** DNA strand → **doubling in number of DNA molecules from 46 to 92**;
3. After DNA replication, **each chromosome** consists of **two sister chromatids joined at the centromere;**

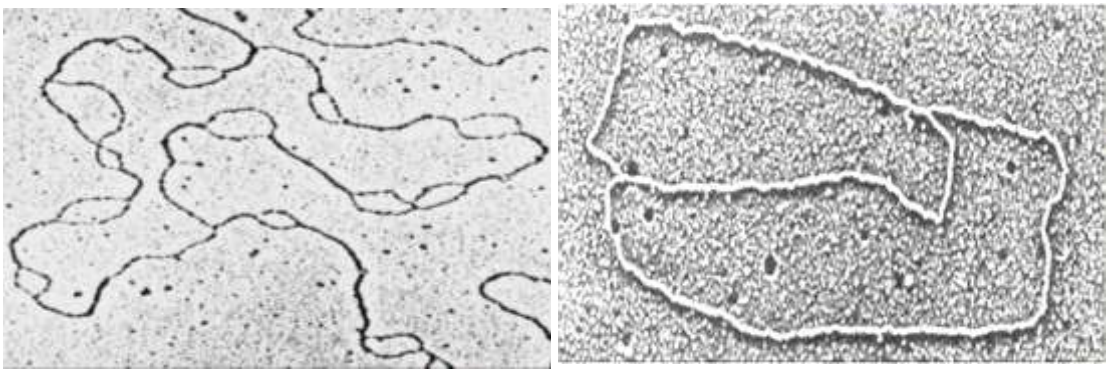
Importance of 92 ds DNA molecules:

1. ensures that after mitosis, **each daughter nucleus** is **genetically identical (same type and number of chromosomes)** to the parent nucleus;
2. for **growth in multicellular organisms(role)**, - increase in the **number of genetically identical cells**, carrying out the **same function;**
3. to **repair tissues by replacement of** (NOT REPAIR cells) **damaged or worn-out cells** with **genetically identical cells**

*Most candidates demonstrated a good understanding of the underlying reason for DNA replication during mitosis, but few complete answers were seen. Details were often missing. Although the information in the question clearly stated **that the context was mitosis, the most common error was for candidates to confuse mitosis with meiosis**. A number of candidates referred to the **formation of haploid gametes and the production of diploid zygotes following fertilisation. (WRONG!)***

[4]

(c) Fig. 2.2 shows DNA replication occurring in a human cell (**A**) and in an *Escherichia coli* (**B**). Diagrams are not shown to scale.



A **B**

Fig. 2.2

(i) State **one** visible difference in the structure of these two DNA molecules during DNA replication and account for this difference.

1. **Single** origin of replication in bacterium but **multiple** origins of replication in mammalian cell; Accept: multiple replication sites / bubbles;
2. **Larger / longer DNA** in **mammalian cell**, thus **multiple Ori R to increase rate of DNA replication**

[2]

(ii) Explain why there is both continuous and discontinuous synthesis of daughter strands during DNA replication.

1. **DNA polymerase** only adds **DNA nucleotides** to the **free 3' end** of the newly synthesized strand/ DNA polymerase synthesize DNA in the **5' to 3' direction**;
2. as the **active site of DNA polymerase** is **complementary** to the **shape of free 3'OH end**;
3. The two **parental/ template** DNA **strands** are **anti-parallel**

[2]

Easy: 3, Moderate: 5, Challenging: 3 [Total: 11]

3 Fig. 3.1 shows a diagram of protein synthesis.

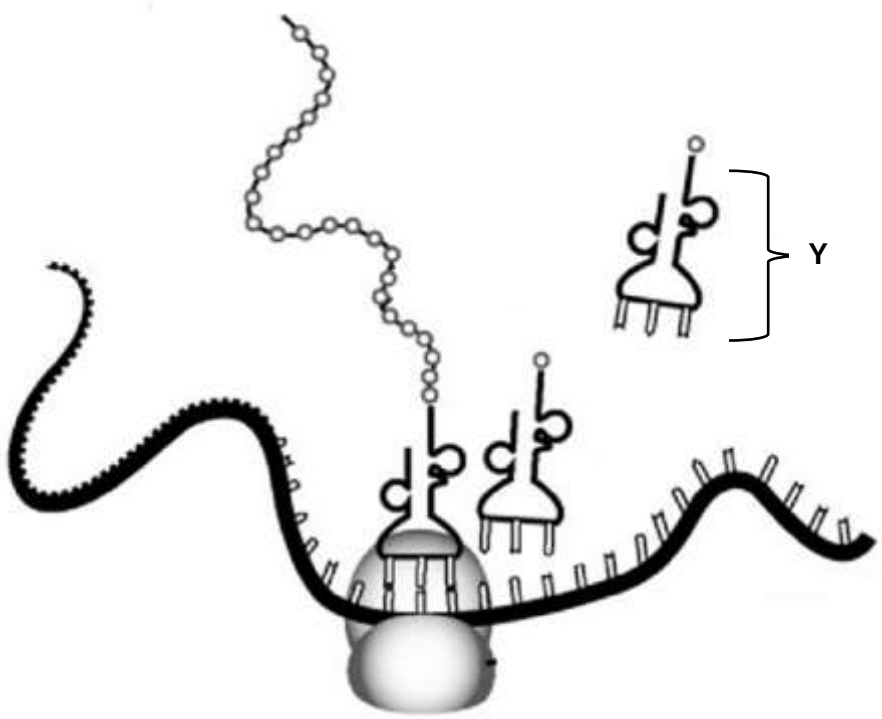


Fig. 3.1

(a) With reference to Fig. 3.1, outline the synthesis of the polypeptide chain from its mRNA.

1. **mRNA is used as a template for translation;**
2. **Anti-codon of aminoacyl tRNA complex** binds to **codons of mRNA** via **complementary base pairing,** at the A (aminoacyl tRNA binding) site;
3. the **growing polypeptide chain from its tRNA** in the **P (peptidyl tRNA binding) site is detached** and then attached to the **amino acid** carried by the **tRNA at the A site;**
4. **Peptidyl transferase** catalyses formation of **peptide bonds between the amino acids;**
5. Ribosome moves along mRNA in **5' to 3' direction until the stop codon (UGA, UAA, UAG)** is reached, releasing polypeptide;

[4]

(b) During protein synthesis in cells of an embryo, all molecules **Y** in Fig.3.1 are observed to be attached to the arginine amino acid instead of lysine.

(i) Suggest how the attachment of the wrong amino acid, arginine, to molecule **Y** may arise.

1. Errors during (amino activation stage) involving aminoacyl tRNA synthetases;
2. Ref. possible mutation in the **gene/DNA/base** sequence for the (lysine) aminoacyl tRNA synthetases,
3. resulting in **altered 3D conformation** of active site which is now **complementary** (in shape) to the amino acid arginine or the corresponding tRNA with anticodon for arginine

Reject mutation of tRNA gene

[2]

(ii) Suggest and explain the effect of attachment of the wrong amino acid, arginine, to molecule **Y** on the embryo.

1. ref. altered **primary sequence** of polypeptides (all lysine replaced by arginine) and folding of polypeptides to **tertiary structure** / 3D conformation is affected;
2. ref. **non-functional proteins** made in cells
3. [compulsory point] ref. possible disruption of metabolic processes in the **cell** / cells might die easily, **embryo cannot further develop** into a fetus [3]

Easy: 2, Moderate: 4, Challenging: 3 [Total: 9]

4 The building blocks of anterior (head) – posterior (tail) axis patterning in *Drosophila* embryo (fertilised egg) are laid out during egg cell formation. Four genes (*hunchback, caudal, bicoid*, *nanos*) are responsible for the polarity of the egg cell and then of the subsequent embryo. mRNA molecules of these four genes were found to be distributed along the anterior-posterior axis of the developing egg cell as shown in Fig. 4.1.

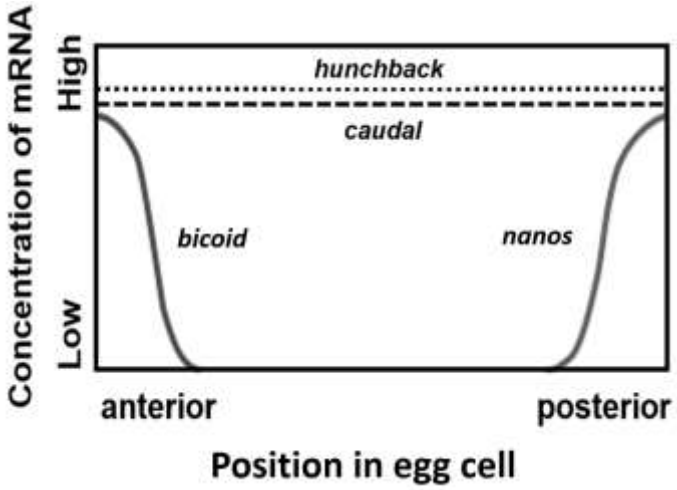


Fig. 4.1

(a) With reference to Fig 4.1,

(i) explain the types of chromatin modifications that may be carried out on the *hunchback* and *caudal* genes. [4]

1. **Histone acetylation/ Adding of acetyl groups to histones** catalysed by **histone acetyl transferase**;
2. **positive charges removed** on histones leads to less electrostatic attraction / reduced affinity between histones and negatively charged DNA;
3. **DNA demethylation / removal of methyl groups** from DNA catalysed by **DNA methyl transferase;**
4. Histone demethylation

5. idea of more DNA unwinding from histones / loosening of chromatin packaging/ to form **euchromatin** → Idea of **greater accessibility of RNA polymerase and transcription factors to the promoter** sequences/ Idea

of loosely condensed chromatin facilitate assembly of general transcription factors and RNA polymerase at the promoter (to form transcription initiation complex);

6. (compulsory point) Idea of upregulation of transcription / genes become transcriptionally active → **high** levels / concentrations of mRNA observed for both *hunchback* and *caudal* genes;

[4]

(ii) The length of *hunchback* and *caudal* mRNA in the cytoplasm is shorter than the *hunchback* and *caudal* primary mRNA in the nucleus.

Describe what happens to the *hunchback* and *caudal* mRNA in the nucleus before they enter the cytoplasm.

- **Small nuclear Ribonuclear Proteins (snRNPs)** made up of **proteins** and **small nuclear RNA** associate with other proteins to bind at **splice sites at each end of an intron** (of a pre-mRNA), forming a **spliceosome**;
- A lariat structure (the intron looped structure) forms and spliceosome **cuts / cleaves / excise** at both ends of an intron
- to release the intron which is rapidly degraded by nucleases;
- exons flanking intron are **spliced** together via **phosphodiester bonds** formation to form **mature mRNA** with **continuous coding sequence**

[3]

(iii) mRNAs in cells are very unstable, having short half-lives of not more than 30 minutes. Explain how the *hunchback* and *caudal* mRNA levels are maintained within the cell.

- (post-transcriptional control) addition of **5' cap** and **3' polyA tail** and to prevent digestion of mRNA by exonucleases;
- (translational control) Idea of **increasing** the length of **3' polyA tail** / **long** 3'polyA tail of the mRNA to increase half life;
- (translational control) Binding of certain proteins/inhibitors/hormones which can slow down / block degradation of mRNA (by exonucleases);

[2]

(b) The corresponding protein concentrations of the four genes were measured in the early stages of development of the *Drosophila* embryo as shown in Fig. 4.2.

It was found that bicoid and nanos proteins act as repressors to block the translation of *caudal* and *hunchback* mRNA respectively.

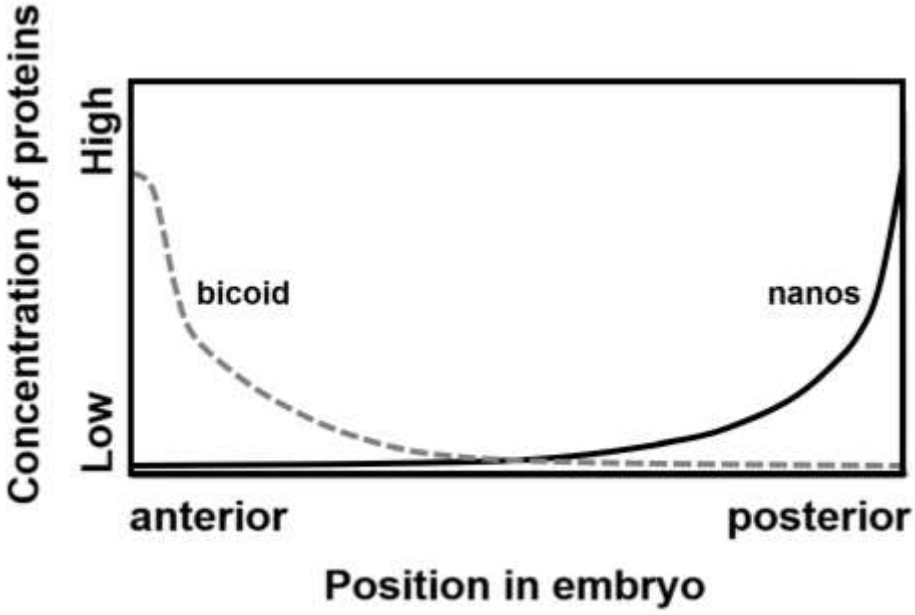
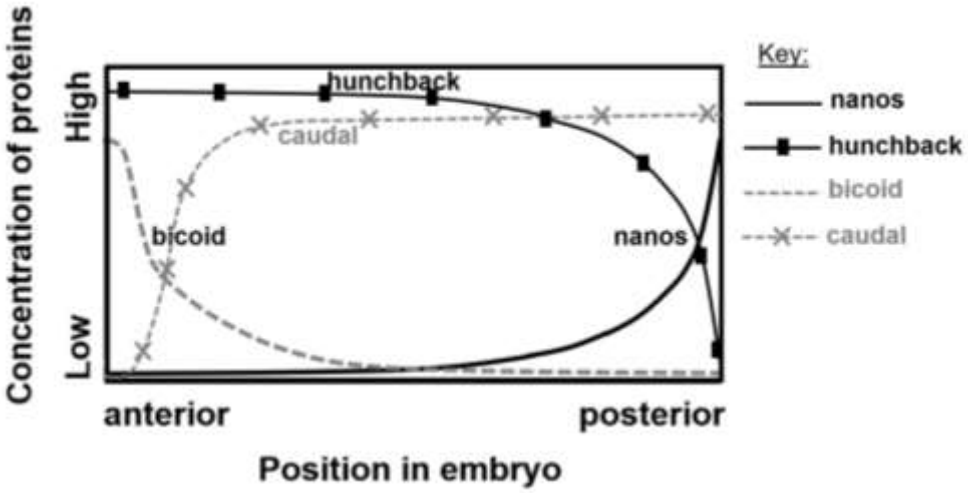


Fig. 4.2

Sketch **one** graph on Fig. 4.2, to represent the concentration of hunchback protein.

[1]



Easy: 4, Moderate: 4, Challenging: 2 [Total: 10]

5 Fig. 5.1 shows the main structural features of the influenza virus.

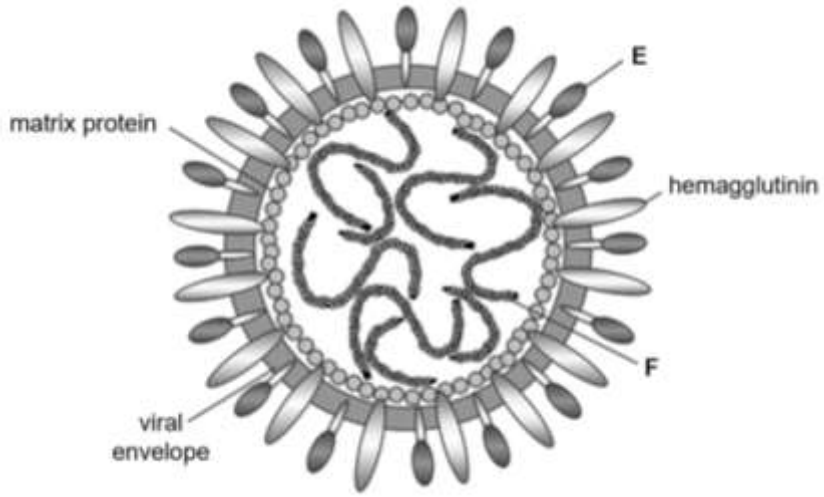


Fig. 5.1

(a) Explain the role of **E** and **F** in the influenza virus.

E ……..

……..…

……..

F ……..

……..…

……..

- **E** is neuraminidase
- Neuraminidase *facilitates the release* of newly formed virus from the infected host cell by cleaving the *sialic acid receptors*. (answers from 2013prelims AJ P2Q2a)

- **F** is ss (-) RNA

Max 1 from the following

- Comprises of genes for viral proteins (give at least one example such as RNA dependent RNA polymerase)
- Template for the synthesis of complementary (+) RNA which are used for translation by host cell ribosomes into viral proteins in cytoplasm/ templates for making new copies of the ssRNA (-) genome in the nucleus

[4]

The sub-types of the influenza **A** virus that infect birds, human and pigs in one area of the world in recent times are shown in the Table 5.1 below.

Table 5.1

<table>
<tr><td rowspan="2">time period</td><td colspan="3">influenza A virus sub-types present</td></tr>
<tr><td>birds</td><td>humans</td><td>pigs</td></tr>
<tr><td>1918 – 1957</td><td rowspan="3">show any one of the H1 – H16 antigens combined with any one of the N1 – N9 antigens</td><td>H1N1</td><td rowspan="2">H1N1</td></tr>
<tr><td>1958 – 1970</td><td>H2N2</td></tr>
<tr><td>1971 to present day</td><td>H3N2
H1N1</td><td>H3N2
H2N3</td></tr>
</table>

(b) Using the data in Fig. 5.1, two students, each has different claims that described how influenza **A** is a danger to human health in this area of the world.

(i) Student **X** claimed that “Antigenic drift of influenza human virus such as H3N2 would lead to vaccines that target hemagglutinin glycoprotein being less effective.”

Put a tick (√) in one box to indicate whether or not this statement is true.

Give a reason for your answer.

true ☐ false ☐

Reason …..…….

…….. [3]

- True
- (Antigenic drift) **Caused by accumulations of mutations** in the **haemagglutinin gene → Change shape/conformation/configuration** of H1 haemagglutinin glycoprotein
- mutated H1 protein is **more complementary in shape** to/ is **able to better fit or bind to** receptors containing sialic acid found on the surface of human host cells/ not complementary to antigen binding site of antibodies produced by memory plasma cells
- Gene evolves under the **selection pressure** of virus-specific antibody stimulated from the vaccine.

(ii) Student **Y** claimed that “Antigenic shift of influenza virus is happening within humans, by combining H2N2 from older people with H1N1 or H3N2.”

Put a tick (√) in one box to indicate whether or not this statement is true.

Give a reason for your answer.

true ☐ false ☐

Reasoning ……

…….. [3]

- *False*
- *For antigenic shift to happen, different strain of virus need to infect the same host cell in the same organism (not just same species).*
- *Influenza pandemic wave caused by H2N2 did not happen in the same time period as H1N1 or H3N2.*
- *Influenza does not integrate its genome and stay dormant in the host cell (so the H2N2 virus did not stay in the same host when H1N1 or H3N2 infect the human host).*

Easy: 3 , Moderate: 5, Challenging: 2 [Total: 10]

6 Wing pattern in the butterfly species *Heliconius melpomene* is controlled by genes on autosomal chromosomes.

The gene for banding pattern on the upper wing has two alleles:

- a dominant allele coding for a full band
- a recessive allele coding for a broken band.

The gene for ray pattern on the lower wing has two alleles:

- a dominant allele coding for rays
- a recessive allele coding for no rays.

Scientists crossed a butterfly that was homozygous dominant for both genes with a butterfly that was homozygous recessive for both genes. The scientists wanted to check whether the phenotypic ratio for offspring in the F2 generation agreed with the expected phenotypic ratio of 9 : 3 : 3 : 1.

The results of these genetic crosses are shown in Fig. 6.1.

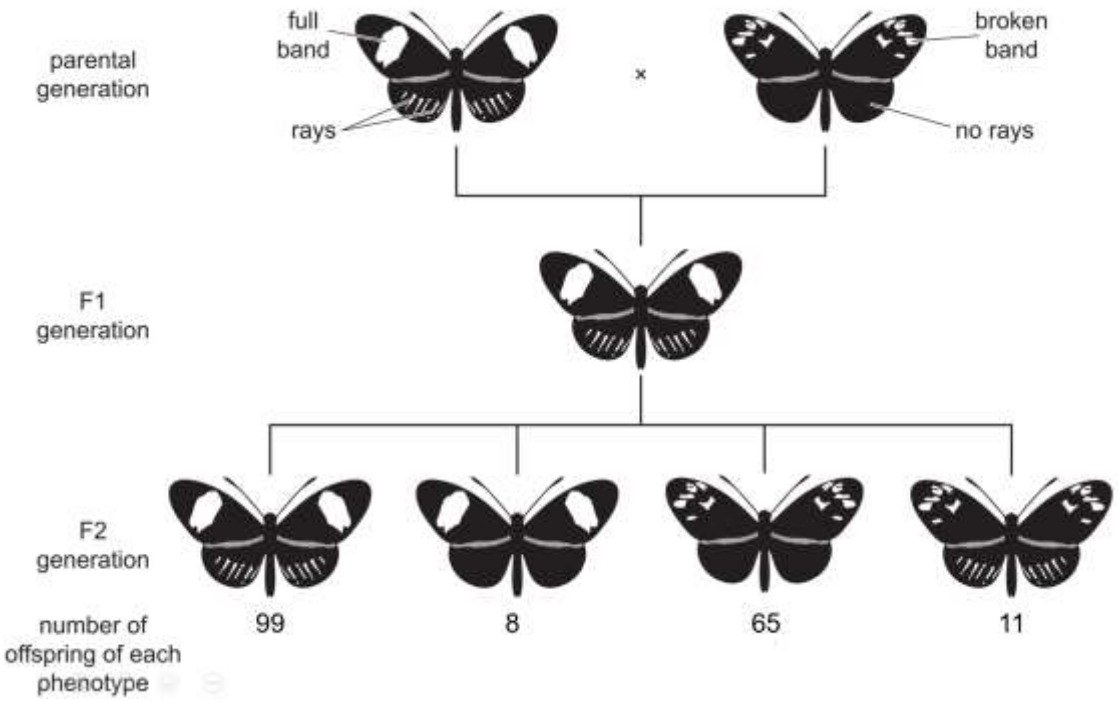


Fig. 6.1

(a) Draw a genetic diagram to explain these results.

5 Marking points (any 4), parental, F1 and F2 must be drawn
- Parental & F1 and F2 phenotype/genotype (drawn with linked genes) +legend
- All Gametes + circles (can ecf if not drawn with linked genes).
- Identified recombinant gametes and parental gametes in gametes produced in F1
- Cross / Punnett Square with correct gametes (gametes circled)
- Expected/observed offspring genotype and observed phenotypic numbers

[5]

(b) Two varieties of *Heliconius* butterflies, both pure-breeding for white wings, were crossed.

All the F1 generation progeny produced orange wings.
The F1 butterflies were then crossed.

In the F2 generation, 145 butterflies had orange wings and 111 butterflies had white wings. The control of wing colour is an example of epistasis resulting in a ratio that is close to 9:7.

Explain the term epistasis in this context.

- (define) Epistasis is a form of gene interaction in which a gene at one locus alters the phenotypic expression of a gene at a second locus;
- 2 copies of recessive alleles at either gene locus A and/or B is sufficient to prevent phenotypic expression of the dominant allele of the other (hypostatic) gene/ aa is epistatic to BB and Bb and bb is epistatic to AA and Aa
- e.g. allele A of one gene codes for a functional enzyme A, which converts the yellow precursor into a yellow intermediate. Allele B of another gene codes for enzyme B, which converts the yellow intermediate into the orange pigment;
- Genotype aa masks genotype BB and Bb. Thus lack of functional enzyme A in pea plant will result in white flowers despite presence of functional enzyme B/ When the organism is homozygous recessive (aa) at the gene locus A/a and/or homozygous recessive (bb) at the gene locus B/b, the phenotype of yellow wingis observed regardless of whether there is a dominant allele present at the other gene locus A/a and/ or B/b respectively.
- Accept other labels other than A and B [3]

(c) The genus *Heliconius* contains more than 40 species of brightly patterned butterflies.

Researchers have investigated in the laboratory how one species, *Heliconius heurippa*, could have developed as a separate species. The phenotype of *H. heurippa* is intermediate between that of two other species, *H. cydno* and *H. melpomene* as it contains DNA from the two parent species as a result of hybridisation.

Laboratory breeding experiments showed that:

- matings between *H. cydno* and *H. melpomene* (parent species) produce fertile hybrid offspring
- controlled matings of the hybrids produces individuals identical in appearance to *H. heurippa* within three generations
- hybrid butterflies prefer to mate with each other, rather than with individuals of either of the parent species.

In the wild,

- the genus *Heliconius* butterflies taste unpleasant to predators such as birds.
- the bright colours on the wings of the butterflies act as warnings so that birds avoid eating them. Therefore, this pattern provides a selective advantage.
- *Heliconius* hybrids occur in small numbers and have patterns that do not resemble the established warning pattern of either parent species. These hybrids have a selective disadvantage.

The researchers thought that, because the hybrid butterflies preferred to mate with each other, this could make speciation more likely to occur.

Suggest why *H. heurippa* are still not regarded as a separate species in the wild.
1 hybrids, are eaten/ die thus fail to survive and reproduce (accept reproduce/ reject survive only) ; reject just lifting from the passage that they have selective disadvantage
2 hybrid gene pool not maintained because not enough individual to interbreed; [2]

Easy: 3 , Moderate: 4, Challenging: 3 [Total: 10]

7 Pancreatic cancer is an almost universally lethal disease.

Many genes are involved in the development of pancreatic cancer. Table 7.1 shows four of these genes.

Table 7.1

genes	genetic changes observed
P	homozygous deletion
Q	hypermethylation of the gene promoter
R	substitution in codon 56
S	amplification of gene

(a) Using the data in Table 7.1, identify an oncogene and a mutated tumour suppressor gene. Explain your answer.

(i) oncogene

- Gene R;
- (mutation → effect on protein) relates substitution to a gain of function mutation as one copy is sufficient to produce a hyperactive/ constitutively active protein that sends signals to the nucleus to stimulate cell division;

Or

- Gene S;
- relates amplification of gene to a gain of function mutation as multiple copies of the gene / greater number of protein products present that will drive the cell towards cell division/ cause dysregulation in cell cycle control/ uncontrolled cell division;

[2]

(ii) mutated tumour suppressor gene

- Gene P
- relates homozygous deletion to a loss of function mutation. Both copies of the alleles for the gene has to be lost for the proteins that regulate the cell cycle control not to be produced;

Or

- Gene Q;
- relates hypermethylation of the gene promoter to a loss of function mutation as it will lead to the gene being silenced hence no protein products that control cell division are produced;

[2]

(b) Fig. 7.1 shows where the restriction enzyme *EcoRI* cuts within the two different alleles of gene **R**, the sizes of the fragments produced and the regions that bind to two probes, **Y** and **Z**.

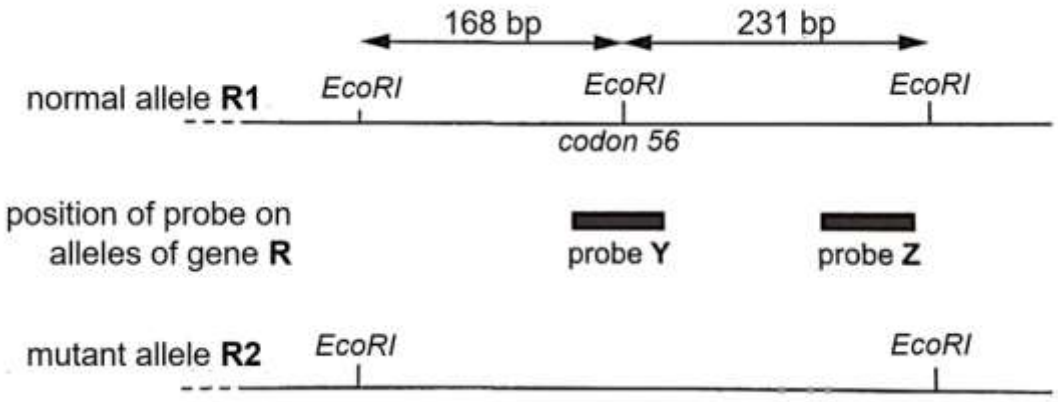


Fig. 7.1

(i) With reference to Fig. 7.1, explain how the two alleles of gene **R** can be distinguished using gel electrophoresis and detected by probe **Y**.

- ***Eco*RI** is used to **cut DNA** to generate **restriction fragments**
- DNA fragments were **separated** by **size** via **gel electrophoresis** under a influence of a **direct current**
- Substitution at codon 56 results in a loss of restriction site in mutant allele R2
- (allele) R1: has 3 *EcoRI* restriction sites, hence will generate two fragments of 168 kb and 231b(
- allele) R2: has 2 restriction sites/ hence will result in one fragment of 399kb

[4]

(ii) On the Fig. 7.2 below, draw the positions and label the sizes of the DNA fragments of an heterozygous individual if probe **Z** would to be used instead.

- Two fragments, One at 399bp close to the well, and another at 231 closer to 200bp band.
- Correct size label

[2]

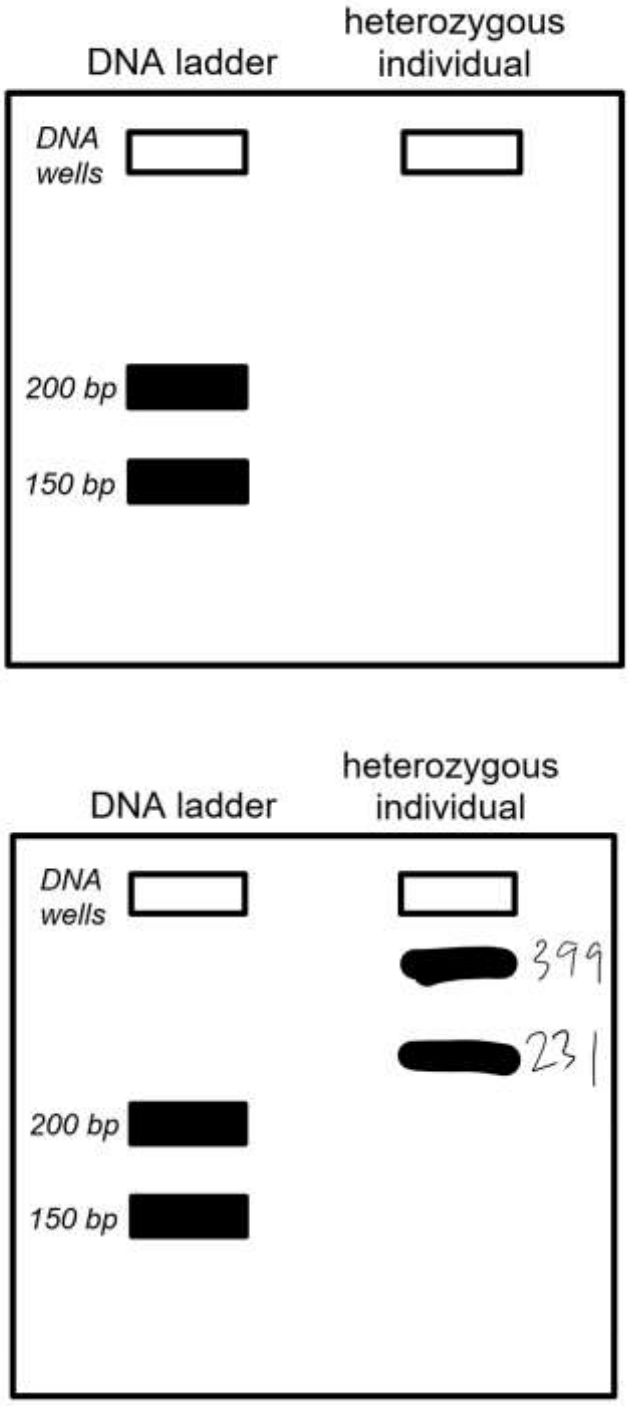


Fig. 7.2

Easy: 2, Moderate: 5, Challenging: 3 [Total: 10]

8 Red algae are multicellular photosynthetic eukaryotes that contain phycoerythrin. Phycoerythrin is a photosynthetic pigment.

Fig. 8.1 shows:

- the absorption spectrum of phycoerythrin
- the action spectrum of red algae.

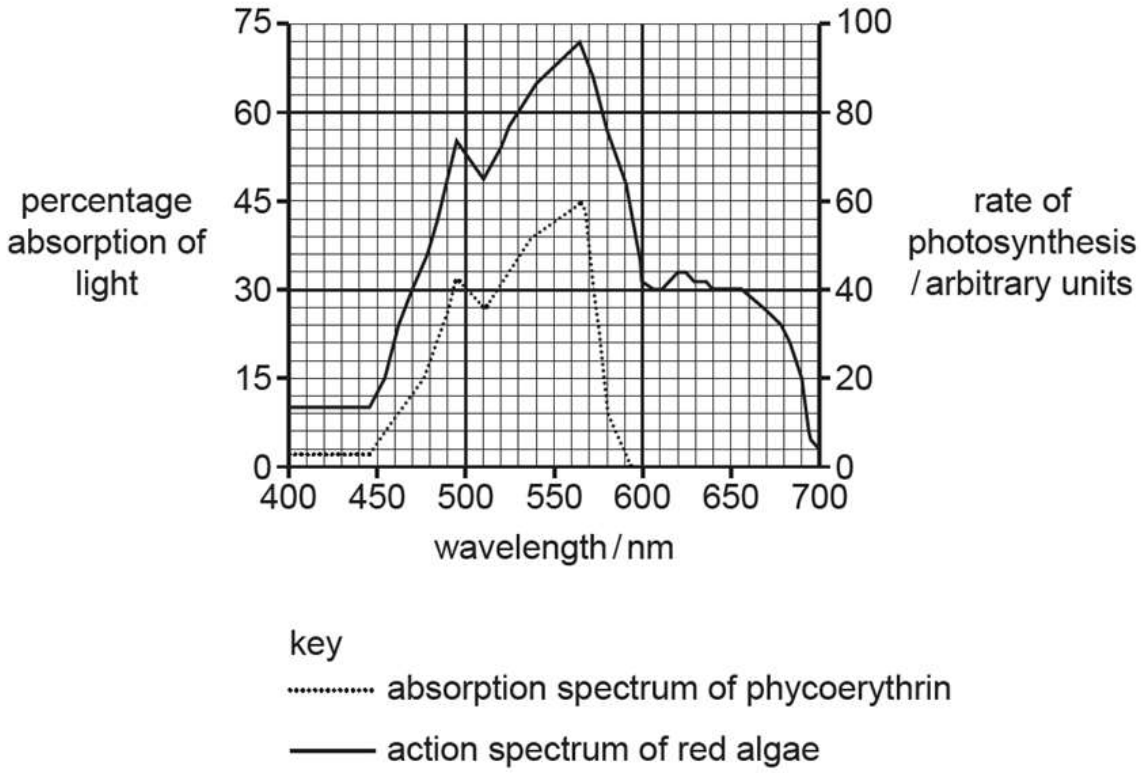


Fig. 8.1

(a) **(i)** With reference to Fig. 8.1, state the wavelength of peak absorption by phycoerythrin.
565nm

[1]

(ii) Explain how the data in Fig. 8.1 show that phycoerythrin is **not** the only photosynthetic pigment in red algae.

1. phycoerythrin does not absorb light between 590–700 (nm) **;**

2. (but) photosynthesis still takes place (between 590–700 nm) with rate of photosynthesis in the range of 4-44 arbitrary units

[2]

(iii) Phycoerythrin is **not** the primary pigment (pigment in reaction centre) for photosynthesis in red algae.

Suggest the role of phycoerythrin in photosynthesis in red algae.

1. accessory pigment **;**

2. absorbs light (energy) / photons of light and) and passes it to, primary pigment / reaction centre / chlorophyll *a* **;**

3. **via transfer light <u>energy</u>** from one pigment molecule to another (in the light harvesting complex) through **excitation of electrons**

[2]

(b) The rate of photosynthesis is affected by factors other than wavelength of light. These factors may act as limiting factors. A student investigated the effect of limiting factors on rate of photosynthesis by measuring the volume of oxygen released from a plant.

(i) Explain what is meant by the term limiting factor and state an example of a limiting factor in photosynthesis.

<u>Explain</u>
(process / photosynthesis, affected by more than one factor)
1. rate is limited by the factor nearest its minimum value/ **in short supply** reaction.
2. It is the factor which **directly affects** a process (rate of a reaction) if its **quantity is changed**.

<u>State</u>
Light intensity/ temperature/ carbon dioxide concentration

Reject wavelength of light/ merely saying light [3]

(ii) Explain why the volume of oxygen released from a plant does not give a true rate of photosynthesis.
1. Idea of Volume is a **net** volume of oxygen / amount released during photosynthesis minus amount taken in during respiration / volume measured is lower than the actual released during photosynthesis
2. Because oxygen is used as a **final electron acceptor** (at the end of the electron transport)
3. during **oxidative phosphorylation** in respiration

[2]

Easy: 5, Moderate: 5, Challenging: 0 [Total: 10]

9 **(a)** Fig 9.1 shows the arrangement of bones in the pentadactyl forelimbs of four vertebrates. This is used by many people to provide evidence for evolution.

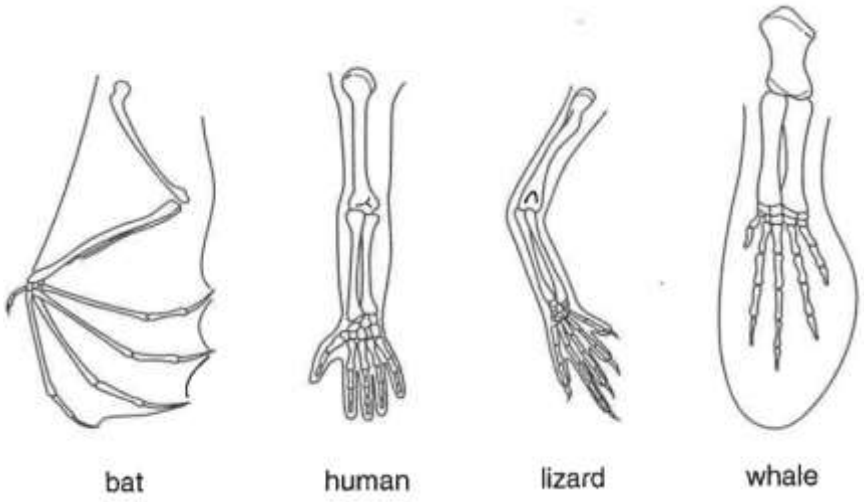


Fig. 9.1

(i) State the term used to describe the relationship between structures such as those in Fig. 9.1.

1. **Homology**

(ii) Explain how the relationship between the structures in Fig. 9.1 provides evidence to support the theory of evolution.

1. Although the forelimbs had **different functions (for instance grasping for humans and swimming for whales),** they have the **same arrangement of bones;**
2. they were likely to have **originated from a common ancestor;**
3. and had been **modified over time in descendent species** through **natural selection,** suggesting **descent with modification.**

*Candidates were expected to **relate their answer to the structures shown in Fig. 9.1**. Many candidates were able to say that **although the forelimbs had different functions** (often stated) they basically **have the same arrangement** (frequently described). Therefore they were likely to have **originated from a common ancestor and had been modified over time**.*

[3]

(b) There are many different species of lizards. Three of these species, *Liolaemus fabiani, L. molinai* and *L. multicolor*, are thought to be closely related.

Samples of these three species were collected from the Andes range in Western South America. The base sequences of four regions of DNA of each species were sequenced.

The percentage difference in the base sequences in *L. molinai and L. multicolor,* compared to the sequences in *L. fabiani,* was calculated. The results are shown in Table 9.1.

Table 9.1

DNA region	Lizard species	Percentage difference in base sequence from that of *L. fabiani* / %
Non-coding region 1	*L. molinai*	4.8
	L. multicolor	4.4
Non-coding region 2	*L. molinai*	8.1
	L. multicolor	7.3
Coding region 1	*L. molinai*	2.1
	L. multicolor	2.0
Coding region 2	*L. molinai*	1.9
	L. multicolor	1.7

(i) Using the evidence from the non-coding regions in Table 9.1, explain why *L. fabiani* may be more closely related to *L. multicolor* than to *L. molinai*.

1. The percentage of divergence of base sequence of *L. multicolor* from *L. fabiani* is **less compared** to divergence of *L. molinai* from *L. fabiani* for **both non-coding region 1 & 2**;
   Quote data : For region 1, the difference between *L. multicolor from L. fabiani* is **4.4%** while the difference from *L. molinai* is **4.8%.** Or region 2, the difference between *L. multicolor from L. fabiani* is **7.3%** while the difference from *L. molinai* is **8.1%.**
2. This means that *L. multicolor from L. fabiani* **share a more recent common ancestor** / **diverge from a common ancestor more recently;**
3. As a result, there was less time to **accumulate mutations/ fewer mutations** observed in the DNA sequences. [2]

(ii) The coding region 1 and 2 in Table 9.1 were measured by analysing *cytochrome c* gene.

Suggest why the *cytochrome c* gene is used to measure changes in DNA sequences in closely related species.

1. *cytochrome c* gene, is **essential** for aerobic respiration/ essential cellular functions;
2. therefore, **present in all / expressed in all cells of** the three species → serves as a good **basis for comparison;**
3. *cytochrome* c gene sequences **changes very slowly** → useful for studying divergence that occurred a long time ago + quote data;
4. cytochrome c gene is found on **mitochondria DNA**, so changes in DNA sequences are passed down the maternal line → does not undergo [2]

recombination (crossing-over and independent assortment). Any differences between mtDNA sequences show only the mutations accumulated since divergence from a common ancestor.

(c) State the importance of variation in the coding regions for evolution to occur.

1. It may result in formation of new alleles which codes for new phenotype / gene product (May confer selective advantage to the organism OR May allow better adaptation to the environment) in the event of sudden/ drastic change;
2. It increases variation in the population allowing natural selection to operate

[2]

Easy: 3 , Moderate: 5, Challenging: 2 [Total: 10]

10 Fig 10.1 shows an antigen presenting cell (APC) presenting an antigen from a pathogen such as a virus, to a cytotoxic T cell.

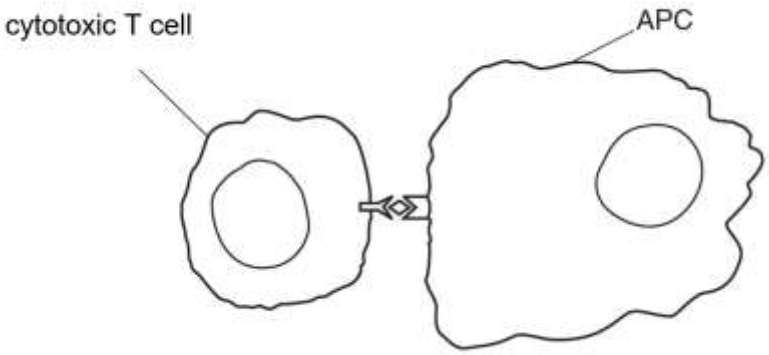


Fig. 10.1

(a) Using Fig. 10.1, describe how presentation of an antigens by APC will lead to the elimination of the pathogen.

Activation of cytotoxic T cells (max 2)

1. (Epitope of) antigen (peptide) on the **cell surface** of APC bind to the **T cell receptor** of a (naive) cytotoxic T cell
2. via **complementary shape**
3. Naïve T cells divide via **mitosis**/ undergo **clonal expansion** and **differentiate** into effector/ activated cytotoxic T cells

Action of cytotoxic T cells (at least 1)

4. T cell receptor on cytotoxic T cells binds to infected cells displaying corresponding antigen via complementary shape
   (no need to look out for complementary shape if already mentioned in MP2)
5. Cytotoxic T cells kill infected cells via **apoptosis** through release of **perforin** and/or **granzymes**

[3]

(b) State **two** differences between artificial active immunity and natural passive immunity.

Difference between artificial and natural immunity…….

artificial active	natural passive
deliberate / AW **A** from medical staff	**or** not deliberate / from mother / in breast milk / across placenta ;
vaccine / (foreign) antigens in injection	**or** antibodies passed on ;

Difference between active and passive immunity…….

immune response	**or** no immune response ;
antibodies / memory cells produced	**or** no, antibodies / memory cells produced ;
longer lasting	**or** short-lived ;
protection not immediate	**or** immediate protection ;

[2]

Easy: 2, Moderate: 3, Challenging: 0 [Total: 5]

11 Plant biodiversity varies throughout the world and is dependent on many factors, particularly climate.

Fig. 11.1 shows the relationship between the number of plant genera and the mean annual rainfall in seven countries.

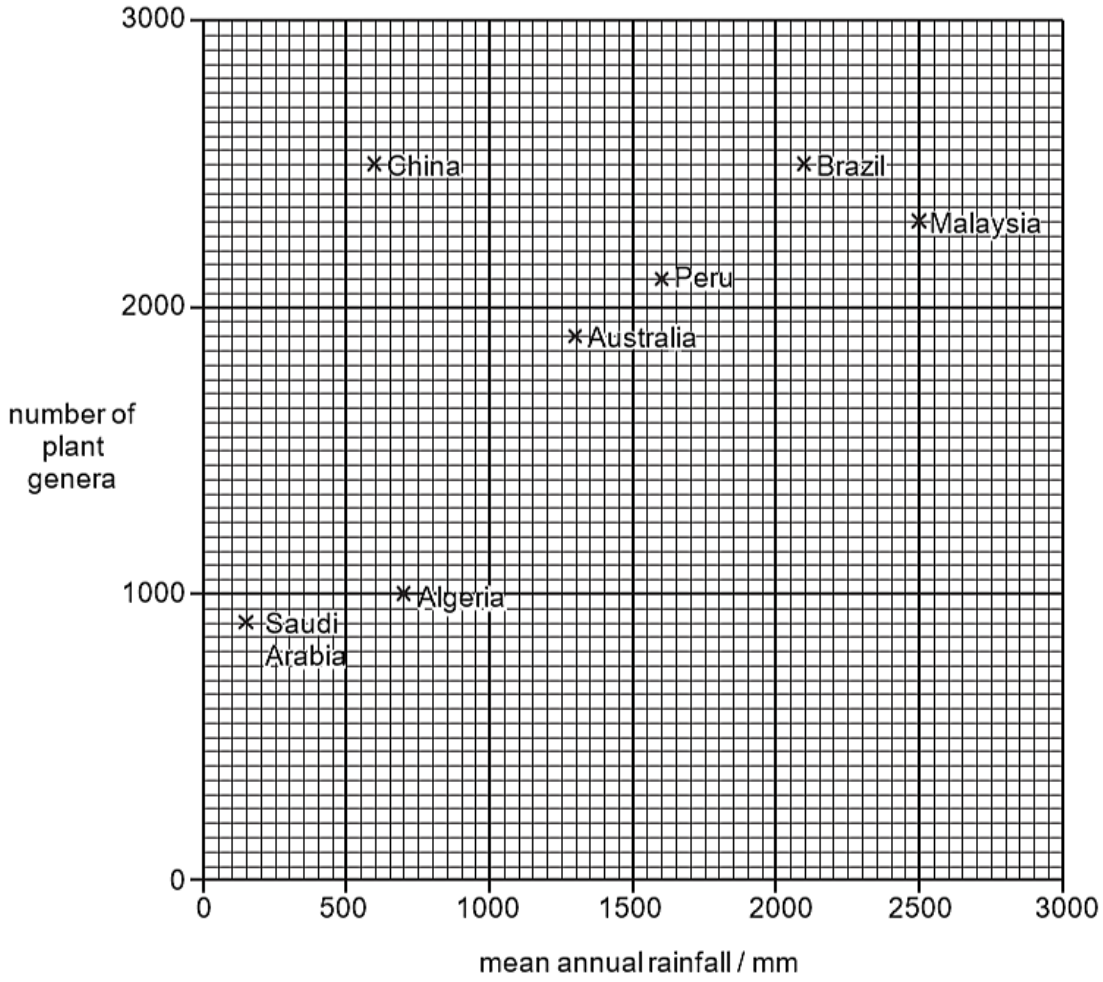


Fig. 11.1

(a) **(i)** Describe the relationship between the number of plant genera and the mean annual rainfall in these seven countries.

- *Ref to overall trend (i.e. positive correlation) / number of plant genera increases as mean annual rainfall increases*
- *Ref to paired figures (i.e. genera number and mean annual rainfall in 2 named countries showing the trend) correctly quoted with units*
  - *Saudi Arabia with lowest mean annual rainfall of with 150mm has lowest number of plant genera at 900*
  - *Algeria with higher mean annual rainfall of 700mm also has higher number of plant genera at 1000*
  - *Australia with higher mean annual rainfall of 1300mm also has higher number of plant genera at 1900*
  - *Peru with higher mean annual rainfall of 1600mm also has higher number of plant genera at 2100*
  - *Brazil with higher mean annual rainfall of 2100mm also has higher number of plant genera at 2500*

- *Malaysia with higher mean annual rainfall of 2500mm also has higher number of plant genera at 2300*
- *Ref to China not fitting the trend as she has low mean annual rainfall of 600mm but has high number of plant genera at 2500 (accept Malaysia as anomaly)*

[2]

(ii) Global warming has led to changes in rainfall in many parts of the world**.**

Explain how changes in rainfall can decrease plant biodiversity.

- *Ref to increase / decrease in rainfall result in increased incidence of flooding / drought, shorter / longer rainy season*
- *Ref to relevant consequence on plants (e.g. plant wilting from loss of water /stomata closure/ loss in cell turgidity/ decrease in photosynthetic pigments/ decrease in Rubisco/ plant rotting from waterlogged roots / plants infected by pests and pathogens)*

[2]

(b) The Millennium Seed Bank is located in the United Kingdom. So far it has successfully stored seeds from 10% of the world's wild plant species.

Suggest **one** benefit to humans of conserving plant species.

may be of use in the future

- *(may produce) biomedicines / AW*
- *resources (for humans) e.g. wood for building / fibres for clothes / fuel / food / agriculture*
- *maintain, gene pool / genetic diversity*
- *to maintain stability in ecosystems*
- *aesthetic reasons*
- *(eco)tourism*

[1]

Easy: 2, Moderate: 2, Challenging: 1 [Total: 5]