HWA CHONG INSTITUTION
JC2 Preliminary Examinations
Higher 2

CANDIDATE NAME		**CT GROUP**	23S7__
CENTRE NUMBER		**INDEX NUMBER**	

BIOLOGY

9744/02

Paper 2 Structured Questions

22 August 2024

Candidates answer on the Question Paper.

2 hours

No Additional Materials are required.

INSTRUCTIONS TO CANDIDATES

There are **six** question booklets (**I** - **VI**) to this paper. Write your **name**, **CT group**, **Centre number and index number** in the spaces provided at the top of this cover page and on the lines provided at the top of the cover pages of Booklets **II, III, IV, V** and **VI.**

There are **eleven** questions.

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

INFORMATION FOR CANDIDATES

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.

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

You are reminded of the need for good English and clear presentation in your answers.

For Examiners' Use	
1	**/ 9**
2	**/ 8**
3	**/ 10**
4	**/ 10**
5	**/ 10**
6	**/ 10**
7	**/ 13**
8	**/ 10**
9	**/ 10**
10	**/ 5**
11	**/ 5**
Total	**/ 100**

This document consists of **25** printed pages.

QUESTION 1

Fig 1.1 shows the amoeba, a unicellular organism that inhabits freshwater ponds. It exhibits characteristic motility.

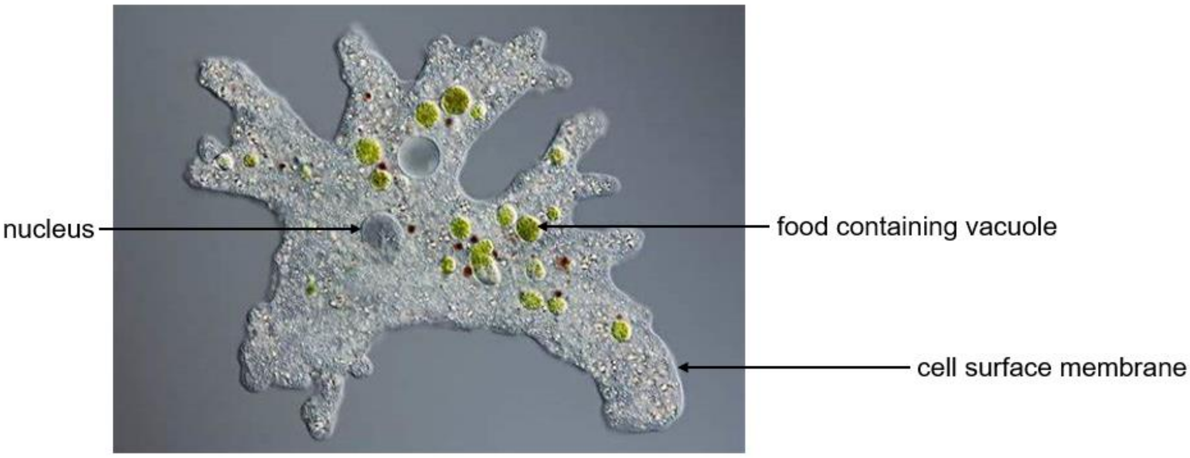


Fig. 1.1

(a) Describe one feature visible in Fig. 1.1 that identifies the amoeba as a eukaryotic organism.

[1]

The amoeba contains structures called contractile vacuoles. They expel excess water from the cell. A contractile vacuole first increases in size, then migrates to and fuses with the cell surface membrane.

Proteins, synthesised using the endomembrane system, are embedded within the membrane of these contractile vacuoles where they pump ions into the lumen of the contractile vacuoles.

(b)(i) Explain how the structure of the contractile vacuole membrane enables it to perform its function.

[4]

(ii) Explain how organelles of the endomembrane system are involved in the synthesis of proteins embedded within the membranes of contractile vacuoles.

[4]

[Total: 9]

QUESTION 2

Keratin is the structural protein in the feathers of birds. Keratin polypeptides are composed of a high proportion of cysteine amino acids, which have sulfur-containing R groups.

Keratin polypeptides form filaments. The two main types of keratin in feathers are α-keratin, which consists of many α-helices, and β-keratin, consisting of many β-pleated sheets.

(a) Keratin can be classified as α-keratin or β-keratin based on a study of protein structure.

Suggest the level of protein structure used to classify a protein as α-keratin or β-keratin.

.... [1]

Feathers are not easily degraded (broken down) because keratin is a very stable protein.

Fig. 2.1 shows the structure of β-keratin in feathers.

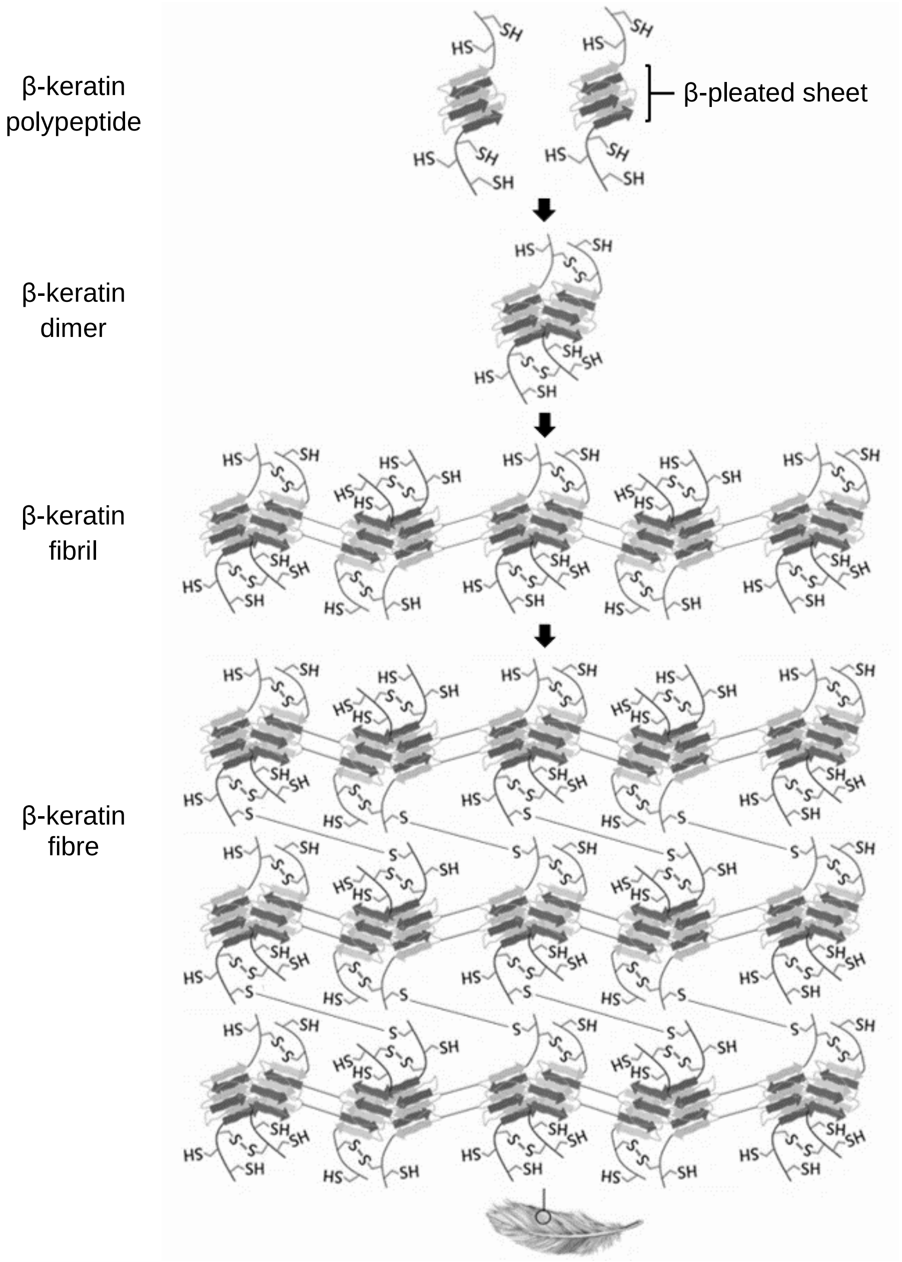


Fig. 2.1

(b) With reference to Fig. 2.1, describe features of keratin structure that contribute to its stability.

....

....

....

....

....

....

....

....

.... [4]

(c) Keratinase is a type of protease that catalyses the hydrolysis of α-keratin and β-keratin. Many proteases are able to hydrolyse more than one type of protein.

Explain why it is possible for a protease to act on different types of protein.

....

....

....

....

....

....

.... [3]

[Total: 8]

QUESTION 3

Fig. 3.1 shows the flow of genetic information from DNA to RNA to polypeptide, according to the central dogma of molecular biology.

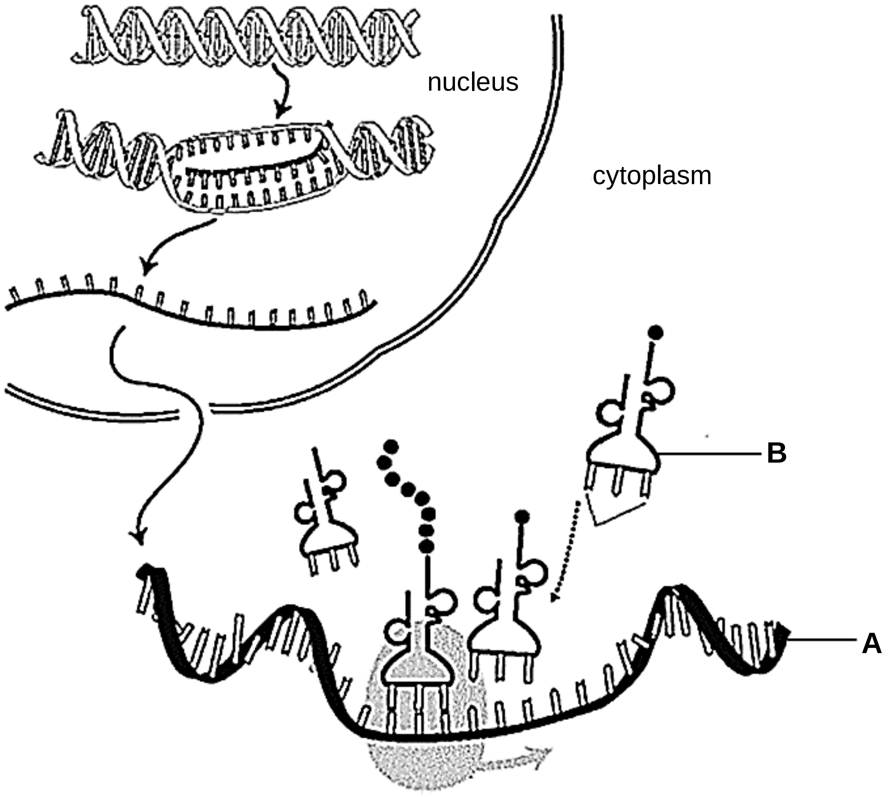


Fig. 3.1

(a)(i) Name molecules **A** and **B**.

A ....

B .... [2]

(ii) With reference to molecules **A** and **B**, discuss the role of hydrogen bonds in translation.

....

....

....

....

.... [2]

Transcription and DNA replication are processes involving polymerisation.

(b) Describe the differences between transcription and DNA replication.

....

....

....

....

....

....

.... [3]

Abacavir is an analogue used in the treatment of some viral diseases. It enters a cell infected by a virus and is metabolised to the analogue carbovir triphosphate.

Fig. 3.2 shows the molecular structure of abacavir and carbovir triphosphate.

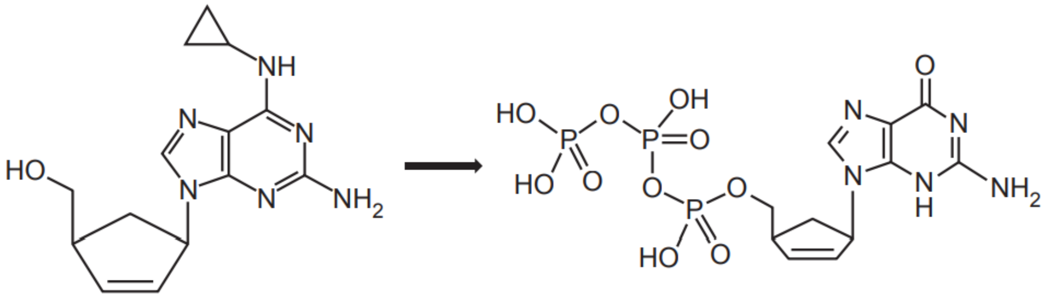


Fig. 3.2

(c) Carbovir triphosphate can be inserted into an elongating polynucleotide chain instead of a nucleotide. This interferes with the action of DNA polymerase during the synthesis of viral DNA.

Explain how carbovir triphosphate may prevent the synthesis of viral DNA.

....

....

....

....

....

....

.... [3]

[Total: 10]

QUESTION 4

Fig. 4.1 shows the structure of a coronavirus, SARS-CoV, which caused the Severe Acute Respiratory Syndrome (SARS). Infection by SARS-CoV causes symptoms resembling influenza that can be deadly.

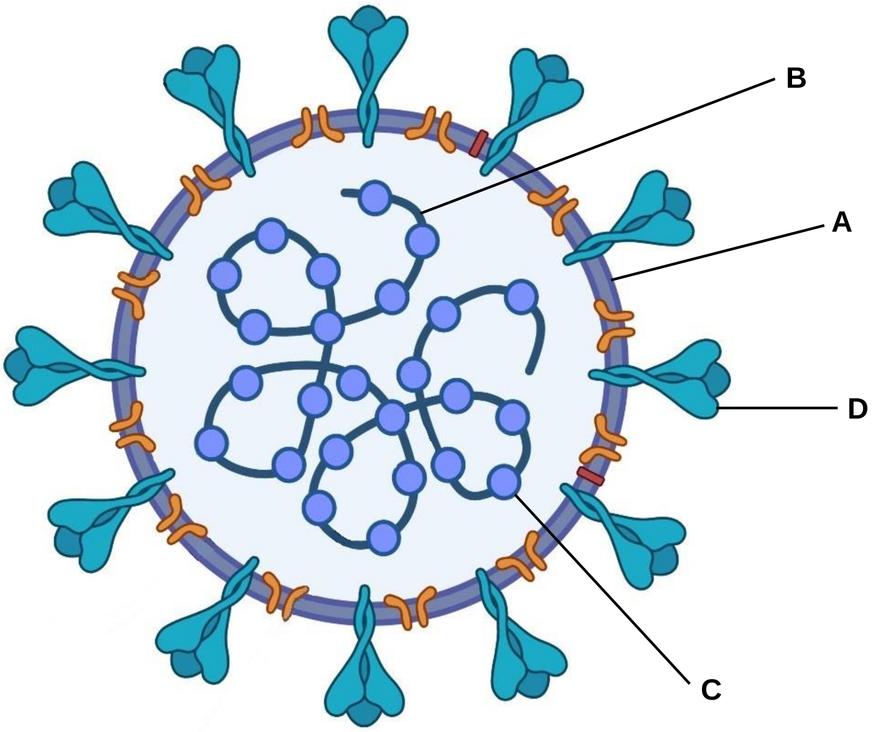


Fig. 4.1

(a) Identify structures **A** to **D**.

A ....

B ....

C ....

D .... [2]

(b) State the origins of structures **A** and **D**.

....

.... [1]

(c) Both coronavirus and influenza virus rely on a similar class of enzyme for their replication processes.

Describe how the coronavirus produces viral progenies after entry into host cells.

[4]

(d) Suggest how a virus such as SARS-CoV can potentially result in outbreak of new viral diseases.

[3]

[Total: 10]

QUESTION 5

Differential gene expression enables eukaryotic cells to synthesise the proteins required for normal function.

(a) Describe how gene expression in eukaryotes can be downregulated at the chromatin level.

....

....

....

....

....

....

.... [3]

Fig. 5.1 shows how a mature mRNA can be reverse-transcribed to form complementary DNA (cDNA), which is subsequently amplified by PCR.

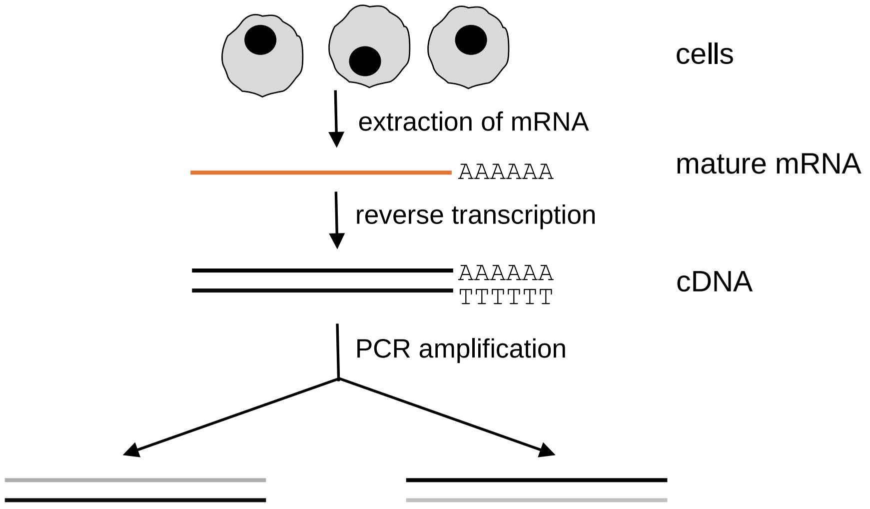


Fig. 5.1

(b) Explain why RNA cannot act as a template for PCR amplification.

....

....

....

....

.... [2]

Genetic diseases can arise from gene mutations, resulting in abnormal gene expression in an individual. To investigate genetic diseases, gene expression profiles of healthy and diseased individuals can be compared. To generate a gene expression profile, cDNA from an individual can be subjected to gel electrophoresis and nucleic acid hybridisation.

Fig 5.2 shows the gene expression profiles of healthy and diseased individuals for genetic diseases **X** and **Y**.

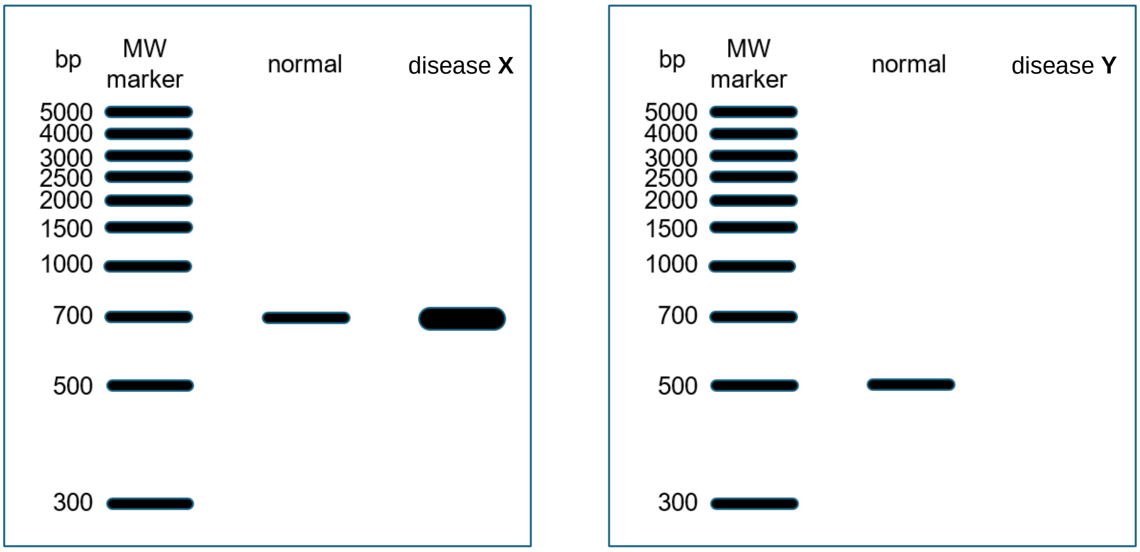


Fig 5.2

(c) With reference to Fig. 5.2, outline how gel electrophoresis and nucleic acid hybridisation can be used to investigate the nature of genetic diseases **X** and **Y**.

....

....

....

....

....

....

....

....

.... [4]

(d) Suggest why comparison of the gene expression profiles of healthy and diseased individuals might be insufficient to help researchers understand the nature of the disease.

....

.... [1]

[Total: 10]

QUESTION 6

There are three checkpoints in a cell cycle, G_1, G_2 and M.

(a) Describe how dysregulation of any of these checkpoints may lead to cancer.

....

....

....

....

.... [2]

Hepatocellular carcinoma (HCC) is the most common type of liver cancer. Mutations in the *Telomerase Reverse Transcriptase (TERT)* promoter, while not found in healthy or cirrhotic tissue, are one of the first indicators of malignant transformation. These mutations arise in dysplastic nodules, which consists of abnormal cells.

Fig. 6.1 shows the progression of HCC, with the number of mutations increasing over time. Stages **A**, **B**, **C**, **D** and **E** represent different points in the development of HCC.

- Percentage of cells with mutation in the *TERT* promoter increases with the progression of HCC.
- Mutation of *TP53* were observed in late-stage HCC, affecting the function of p53.
- Other mutations of tumour suppressor genes, *ARID1*, *RB1*, and the protooncogene *CTNNB1* were also observed in late-stage disease HCC.

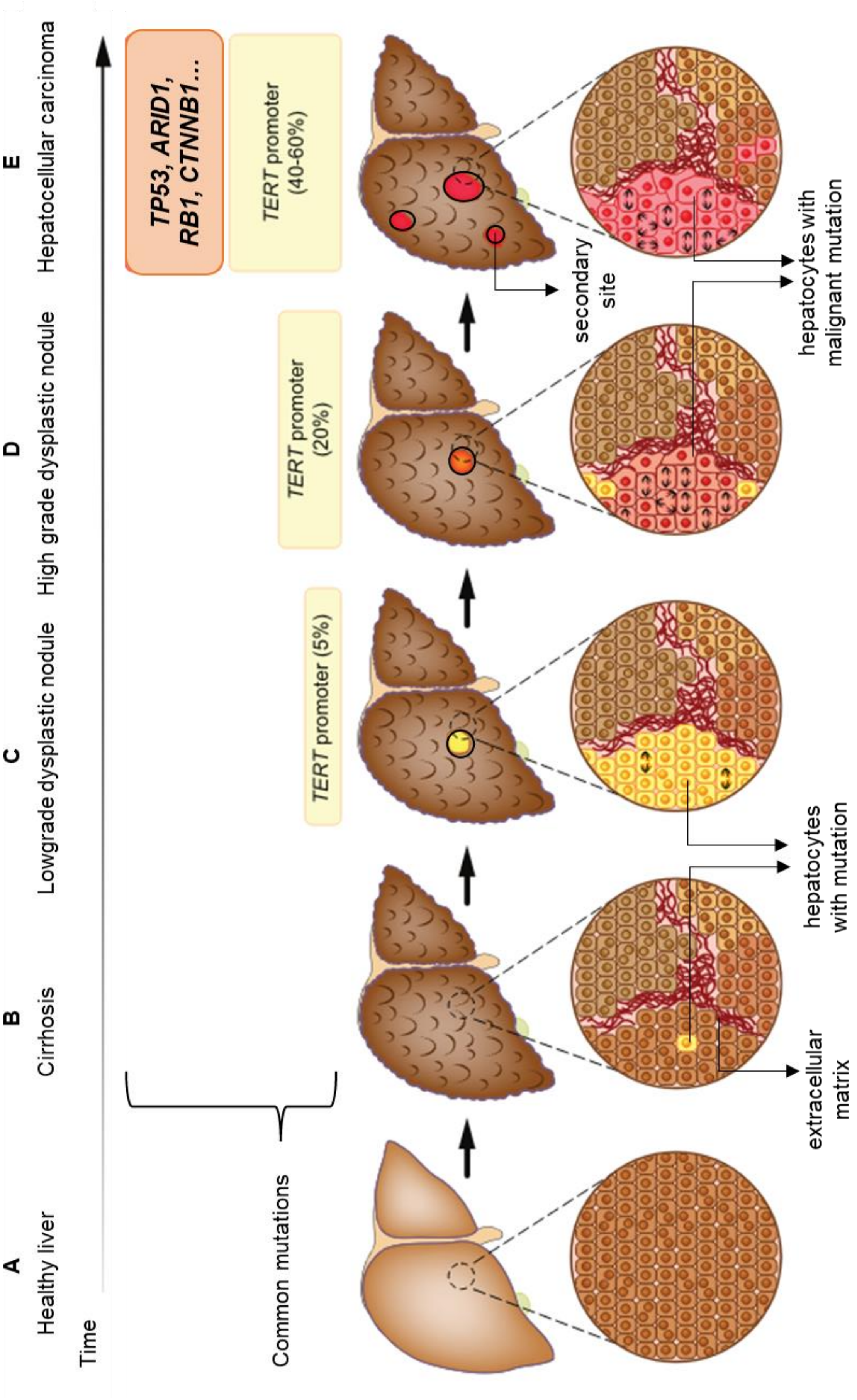

Time
A
Healthy liver
B
Cirrhosis
C
Lowgrade dysplastic nodule
D
High grade dysplastic nodule
E
Hepatocellular carcinoma
Common mutations
TERT promoter (5%)
TERT promoter (20%)
TERT promoter (40-60%)
TP53, ARID1, RB1, CTNNB1…
extracellular matrix
hepatocytes with mutation
secondary site
hepatocytes with malignant mutation

Fig. 6.1

(b) With reference to Fig. 6.1, explain why HCC development is a multi-step process.

[5]

(c) Outline the differences between the malignant cells in Stage **E**, with the cells in Stage **C** in Fig. 6.1.

[2]

(d) Chronic hepatitis B virus (HBV) and hepatitis C virus (HCV) infection are the most important causes of HCC, but other factors can also increase the risk of HCC.

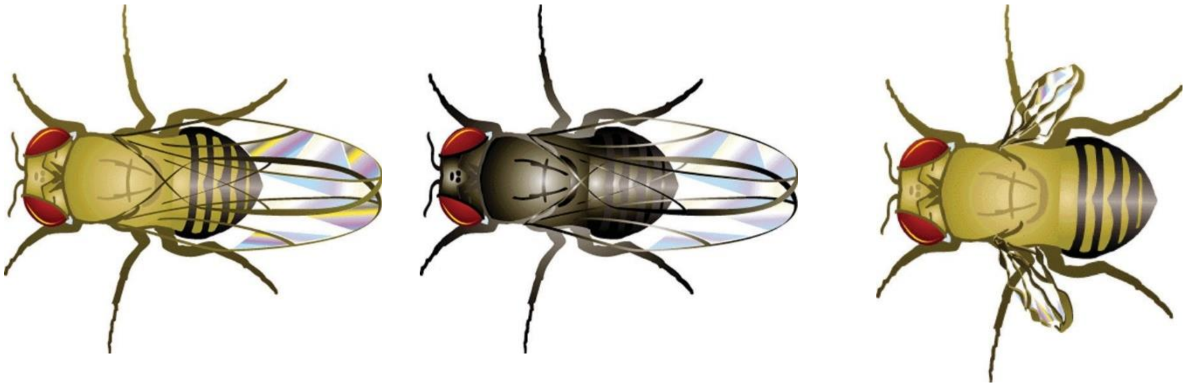
Identify one causative factor that may lead to HCC.

[1]

[Total: 10]

QUESTION 7

The fruit fly, *Drosophila melanogaster*, has autosomal genes for body colour and wing shape. A fly with normal features is called a wild type. It has a striped body and its wings are longer than its abdomen. There are mutant variations such as an ebony-coloured body or vestigial wings. These three types of fly are shown in Fig. 7.1.



wild type ebony body vestigial wing

Fig. 7.1

Wild type features are coded for by dominant alleles, **A** for wild type body and **B** for wild type wings.

When a researcher crossed two pure-breeding fruit flies with different phenotypes, the resultant F_1 generation are all wild types.

(a) State what is meant by the term *autosomal* in this context.

....

.... [1]

The F_1 wild types were then test crossed with fruit flies with ebony bodies and vestigial wings. Table 7.1 shows the number of offspring of each phenotype obtained in the test cross.

Table 7.1

phenotype	observed number	expected number
wild type body and wild type wings	842	
wild type body and vestigial wings	2768	
ebony body and wild type wings	2843	
ebony body and vestigial wings	855	

(b)(i) With reference to the observed test cross results in Table 7.1, deduce the phenotypes of the two pure-breeding fruit flies used to produce the F_1 generation.

1 ....

2 .... [2]

(ii) Explain your answers to **(b)(i)**.

....

....

....

....

.... [2]

(iii) Draw a genetic diagram to show the observed test cross results in Table 7.1.

[4]

(c)(i) Calculate the expected number of each phenotype if the two genes were on **different** autosomes. Write your answers in Table 7.1. [1]

(ii) A chi-squared (χ^2) test was carried out to compare the observed results with the results that would be expected from a dihybrid cross involving genes on different autosomes.

The value of χ^2 = 2097.836.

Table 7.2 shows the critical values for the χ^2 distribution.

Table 7.2

degrees of freedom	***p* value**		
	0.05	**0.01**	**0.001**
1	3.841	6.635	10.828
2	5.991	9.210	13.816
3	7.815	11.345	16.266
4	9.488	13.277	18.467

Explain how the value of χ^2 and Table 7.2 can be used to assess the significance of the difference between the observed results and the expected numbers in Table 7.1.

....

....

....

....

....

....

.... [3]

[Total: 13]

QUESTION 8

Fig. 8.1 is a transmission electron micrograph of part of a chloroplast.

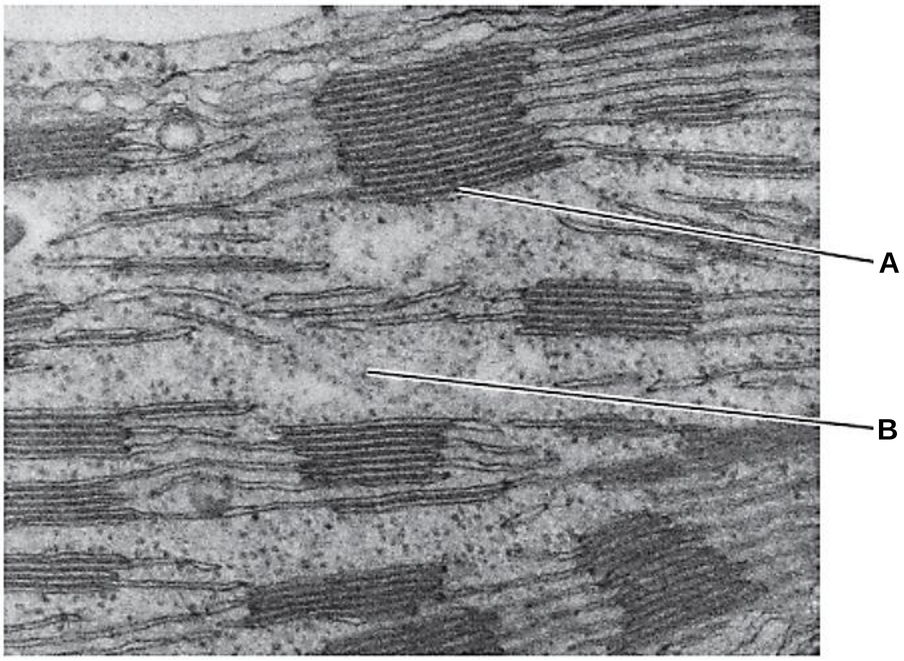


Fig. 8.1

(a) Table 8.1 shows some substrates and products involved in photosynthesis.

Use letter **A** or letter **B** from Fig. 8.1 to complete Table 8.1 to show the location where the substrates or products are used or produced.

Table 8.1

substrate or product	**location**
oxygen produced	....
carbon dioxide used	....
reduced NADP used	....
hexose produced	....

[2]

The regeneration of ribulose bisphosphate (RuBP) in the Calvin cycle is known to limit the rate of photosynthesis.

Sedoheptulose-1,7-bisphosphatase (SBPase) is an enzyme that controls the rate of regeneration of RuBP in the Calvin cycle. SBPase is coded for by the gene *SBPase*.

In an experiment, wheat plants were genetically modified to make more SBPase by introducing the *SBPase* gene from another plant species. The resulting genetically modified (GM) wheat plants were named Sox4.

- Wild type plants (not GM) and Sox4 plants were grown.
- A leaf from the wild type plant was placed in a sealed glass vessel.
- The carbon dioxide (CO_2) concentration in the vessel was increased so that the intercellular air spaces also had an increase in CO_2 concentration.
- All other environmental conditions were kept constant.
- The CO_2 fixation rate was measured for the leaf.
- The experiment was repeated with a leaf from a Sox4 plant.

Fig. 8.2 shows the rate of CO_2 fixation by the leaves of the wild type plants and Sox4 plants when the intercellular air space CO_2 concentration was increased.

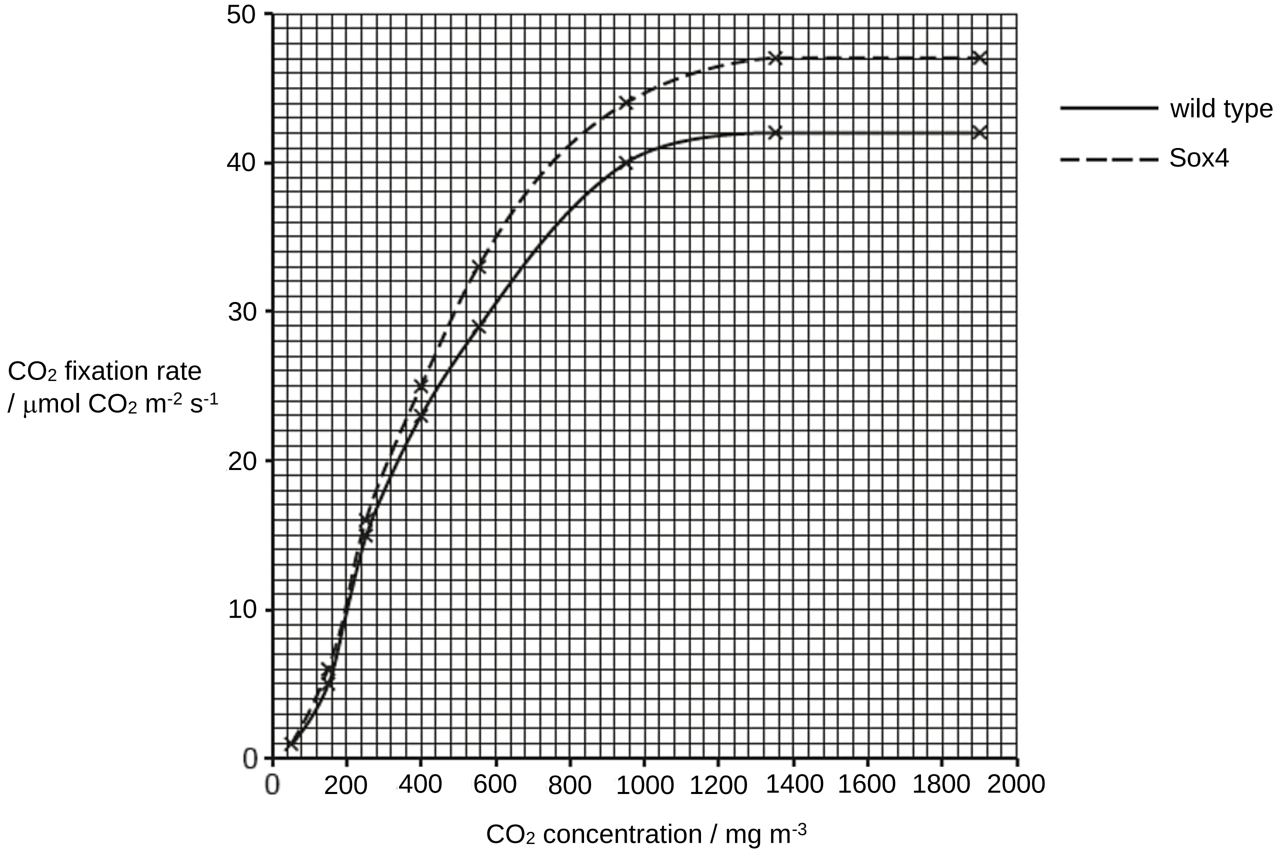


Fig. 8.2

(b) With reference to Fig. 8.2,

(i) describe **and** explain the effect of CO_2 concentration on the rate of CO_2 fixation shown by the **wild type** plants.

....

....

....

....

....

....

....

....

.... [4]

(ii) suggest explanations for the differences in the rate of CO_2 fixation between wild type plants and Sox4 plants.

....

....

....

....

....

....

.... [3]

(c) Research has shown that the mean plant biomass of Sox4 plants is 37% higher compared with wild type plants.

Suggest why Sox4 plants has a higher mean plant biomass compared with wild type plants.

....

.... [1]

[Total: 10]

QUESTION 9

A subspecies is a genetically distinct population within a species that has some phenotypic differences from the rest of the species, but is not yet reproductively isolated.

Nine subspecies of the tiger, *Panthera tigris*, have been identified. Six of these subspecies are found on mainland Asia. Three of the subspecies originate from the Sunda Islands. These islands include Bali, Java and the large island of Sumatra.

Fig. 9.1 shows these three islands.

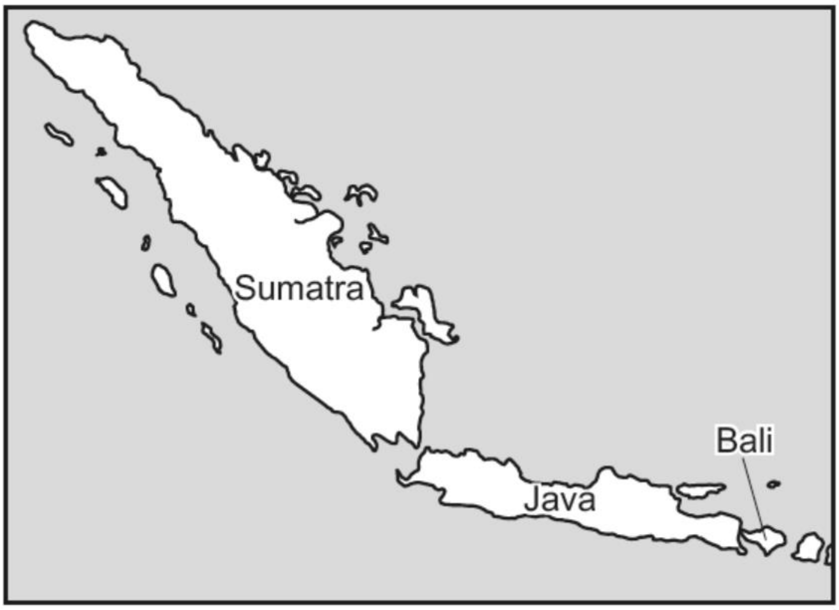


Fig. 9.1

- The Bali tiger, *Panthera tigris balica* (*P. t. balica*), became extinct in the 20th Century. The Bali tiger was found only on the island of Bali.
- The Javan tiger, *P. t. sondaica*, became extinct in the 20th Century. The Javan tiger was found only on the island of Java.
- The Sumatran tiger, *P. t. sumatrae*, lives only on Sumatra and is the closest living relative of Bali and Javan tigers.

20 000 years ago land bridges temporarily connected the Sunda Islands.

A recent study carried out a genetic analysis of the nine subspecies of tiger. Specific sections of mitochondrial DNA (mtDNA) that are useful in studies of evolution were amplified using PCR and compared to assess their evolutionary history.

- The source of DNA for the extinct subspecies came from museum specimens.
- mtDNA was extracted and polymerase chain reaction (PCR) carried out using primers based on specific sections of tiger mtDNA.
- The mtDNA sections for the three island subspecies were genetically distinct from the other six mainland subspecies.
- The mtDNA sections for the three island subspecies were all found to be very similar.

(a) Explain how the three subspecies of tiger on the Sunda Islands formed.

[4]

(b) Explain why specific primers were used for the tiger mtDNA sections.

[2]

(c) Suggest **and** explain **one** characteristic of mtDNA that makes it more useful than using nuclear DNA to provide evidence of evolution.

[2]

(d) Suggest **two** reasons why *P. t. balica* and *P. t. sondaica* became extinct.

[2]

[Total: 10]

QUESTION 10

(a) Explain why *Mycobacterium tuberculosis* (MTB) is only detected at later stages of infection.

....

....

....

....

.... [2]

Infection by MTB can be determined in the laboratories by detecting antibody and interferon-γ (IFN- γ) in the blood throughout the infection as shown by Fig. 10.1. The bracketed regions indicate when it is possible to detect a response using the antibody and IFN- γ blood tests. IFN- γ is a cytokine.

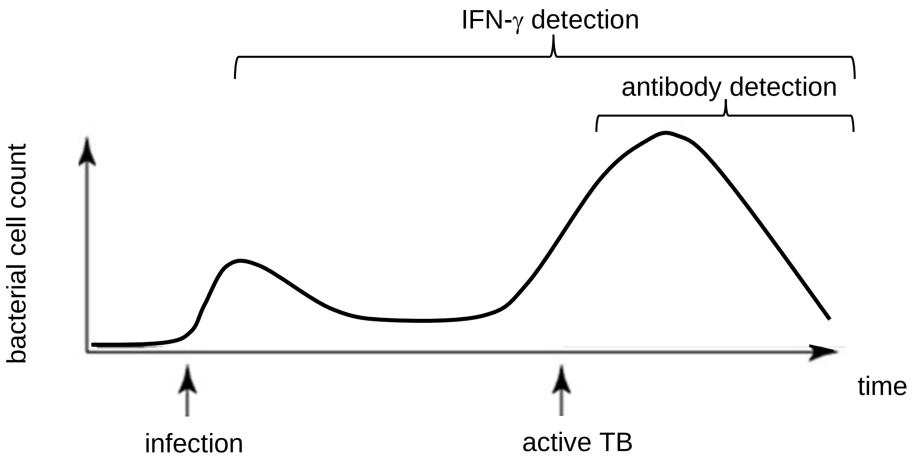


Fig. 10.1

(b) (i) With reference to Fig. 10.1, explain why MTB-specific antibody responses are usually undetectable during the early phase of infection, but detectable as the infection progresses to active TB.

....

....

....

....

.... [2]

(ii) Suggest why IFN- γ would be a better indicator for identification of individuals at risk of developing active contagious TB.

....

.... [1]

[Total: 5]

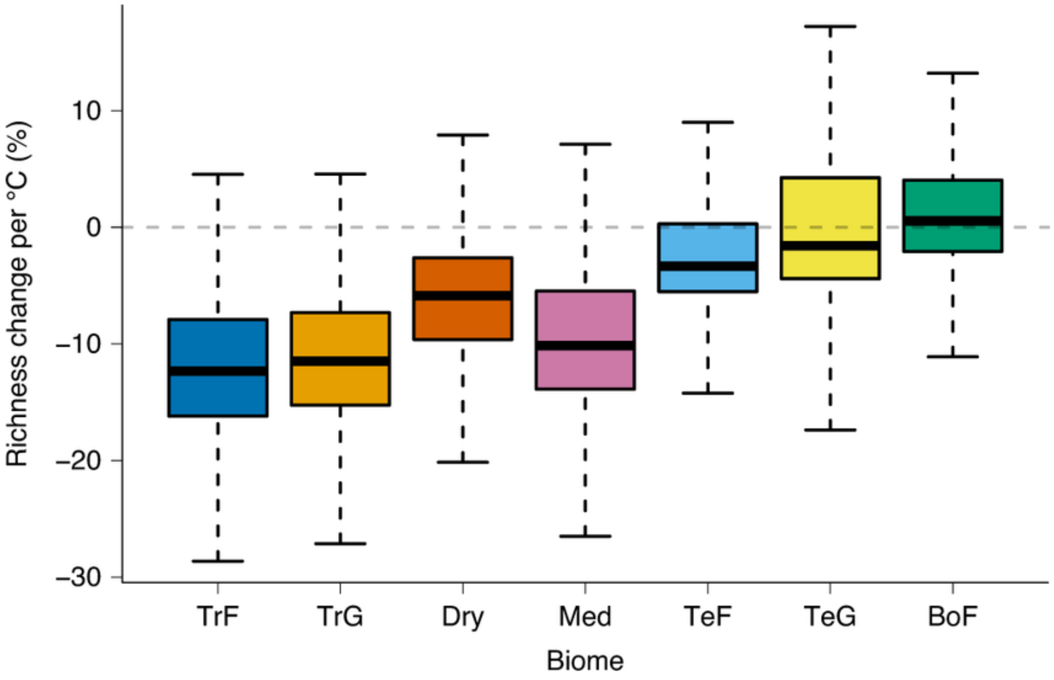
QUESTION 11

Global biodiversity is undergoing rapid declines, driven in large part by changes to land use and climate.

Fig. 11.1 shows the results of a study on the predicted sensitivity of biodiversity to climate change across biomes as illustrated by using boxplots, which are visual representations comparing the distribution of datasets. The results show the predicted percentage change in vertebrate species richness for each °C of climate warming expected.

A boxplot consists of:

- the box that represents the data distribution through their quartiles, consisting of lower (25), median (50) and upper (75)
- the whiskers extending beyond the box that represent the two extreme quartiles, lower (0) and upper (100)



key:

TrF:	tropical forest
TrG:	tropical grasslands
Dry:	drylands
Med:	mediterranean
TeF:	temperate forest
TeG:	temperate grasslands
BoF:	boreal forest

Fig. 11.1

(a) With reference to Fig. 11.1, compare the effects of climate warming on the biodiversity in tropical and temperate regions.

....

....

....

....

....

....

.... [3]

(b) Suggest possible reasons for the difference in **(a)**.

....

....

....

....

.... [2]

[Total: 5]

--- END OF PAPER---
