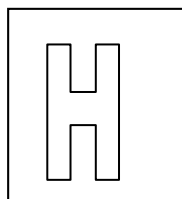


Candidate Name: _____

Class Adm No

--	--



2017 Promotional Examination II Pre-University 2

H1 Biology

8875/02

Paper 2

12 September 2017

2 hours

READ THESE INSTRUCTIONS FIRST

Do not open this booklet until you are told to do so.

Write your Admission number and name on all the work you hand in.
Write in dark blue or black pen on both sides of the paper.
You may use a soft pencil for any diagrams, graphs or rough working.
Do not use staples, paper clips, highlighters, glue or correction fluid.

Answer **all** questions.

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. At the end of the examination, fasten all your work securely together.

For Examiner's Use	
Section A	
1	
2	
3	
Section B	
Total	

This question paper consists of 14 printed pages including 1 blank page.

[Turn over

Answer **all** questions in this section.

1. Measurement of cellular DNA content and the analysis of the cell cycle can be performed by flow cytometry. The DNA content of retinal cells of zebrafish is analysed and Fig. 1.1 show the number of cells at different stages of the cell cycle.

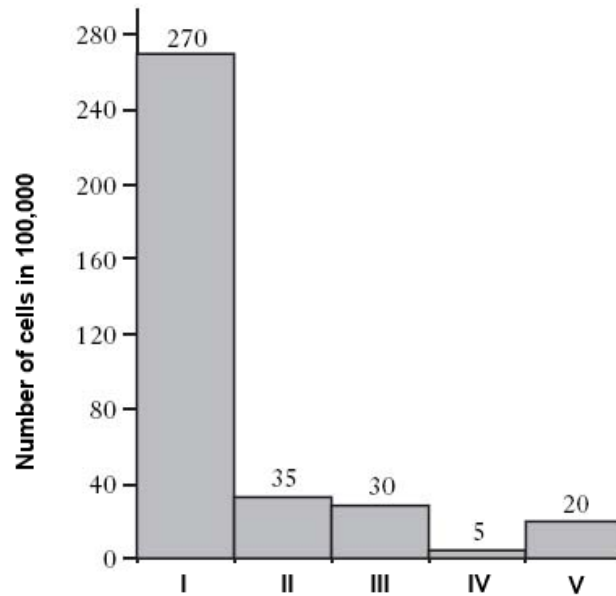


Fig. 1.1

(a)

- (i) Identify which stage (I to V) correspond to interphase.

I

:: for 1 mark, max is 1 mark

- (ii) Suggest a reason for your answer in (a)(i).

Interphase has the longest duration/consist of G1, S and G2 phases, so more cells will be found in the interphase;

; for 1 mark, max is 1 mark

- (iii) Explain the importance of DNA replication before mitosis

DNA replication results in each chromosome consists of 2 genetically identical sister chromatids joined at centromere during prophase and metaphase;

The daughter cells are genetically identical because they receive a copy of exact/same DNA molecule/same number and type of chromosomes;
Maintain genetic stability;

; for 1 mark, max is 2 marks

Fig. 1.2 shows the electronmicrographs of three zebrafish retinal cells (**A** to **C**). Each cell is undergoing a different stage of mitosis.

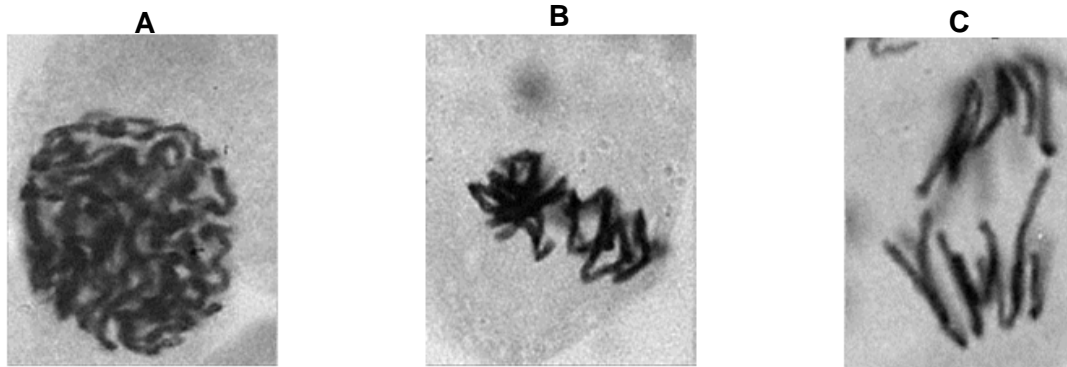


Fig. 1.2

(b)

- (i)** Identify stages of mitosis that cell **A** and **B** is undergoing.

A: prophase;
B: metaphase;
;; for 1 mark, max is 1 mark

1

- (ii)** State the visible features in cell **A** and **B** that enabled your identification in **(b)(i)**.

Stage A
Chromatin fibres condense to become discrete chromosomes, which are visible;
Absence of nuclear membrane/envelope;

Stage B
Chromosomes start to align in a single row/singly at metaphase plate/equator of the spindle;
;; for 1 mark, max is 2 marks

Fig. 1.3 shows the changes in the DNA amount during the meiotic cell cycle of the germ cells in zebrafish.

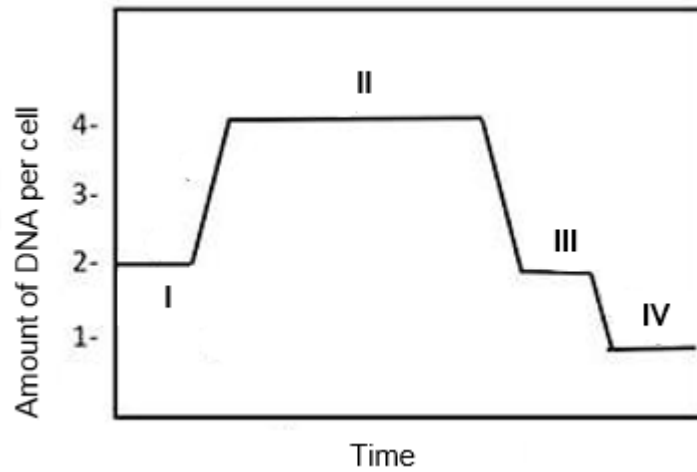


Fig. 1.3

(c) With reference to Fig. 1.3, explain the changes in DNA amount from stage II to IV.

Stage II correspond to meiosis I while Stage III correspond to meiosis II;
The amount of DNA in each cell remain constant during meiosis I and II because the germ cell has not divided/cytokinesis has not occurred, which occur at the end of meiosis I and II;

; for 1 mark, max is 1 mark

The amount of DNA in each cell is halved at the end of meiosis I due to the separation of the homologous chromosomes during anaphase I;

The amount of DNA in each cell is halved again at the end of meiosis II due to the separation of chromatids during anaphase II;

; for 1 mark, max is 2 marks

[Total: 10]

2. In recent years, numerous biochemical and genetic studies have demonstrated that peptide signalling plays a greater than anticipated role in various aspects of plant growth and development. A substantial proportion of these plant peptides are secretory and act as local signals mediating cell-to-cell communication.

Fig 2.1 and Fig. 2.2 show two different membrane-bound organelles found in shoot apical meristematic cells.

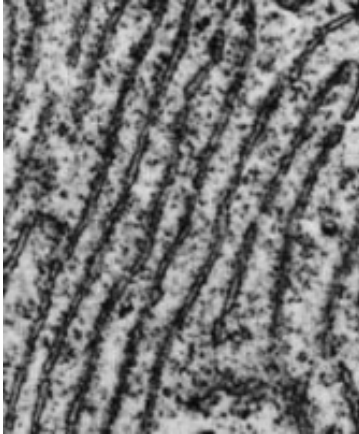


Fig 2.1



Fig. 2.2

- (a) Describe how the two organelles in Fig 2.1 and Fig. 2.2 work together in the production and secretion of plant peptides.

The bound/fixed ribosomes on the rough endoplasmic reticulum synthesise polypeptides/translation, which enters the RER lumen to be modified and folded;
Transport vesicles containing the proteins bud off from the RER and fuse with the cis face of the golgi apparatus;
 GA is involved in chemical modification for e.g. glycosylation, sorting and packaging of the proteins;
Secretory vesicles bud off from the trans face of the GA;
 Fuse with the cell surface membrane to release the plant peptides via exocytosis;

; for 1 mark, max is 3 marks

[3]

Fig. 2.3 shows the process of protein synthesis that takes place on the organelle shown in Fig. 2.1.

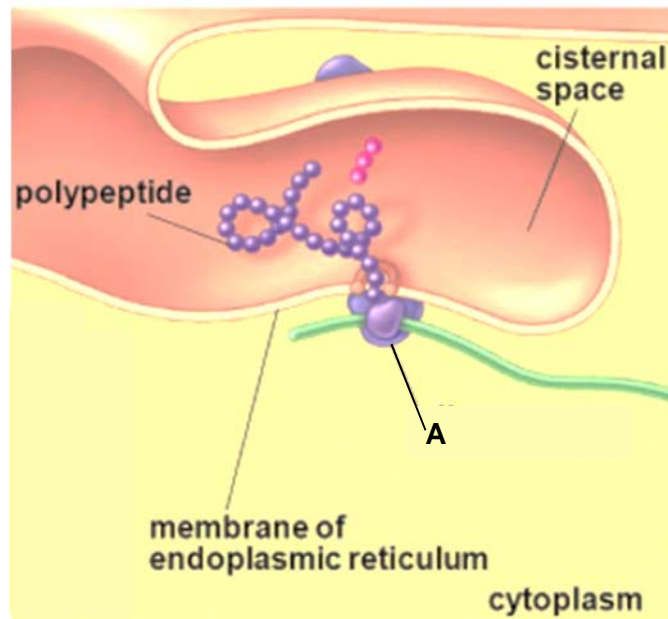


Fig. 2.3

(b) Describe how the structure of **A** is adapted to its role in the process shown in Fig. 2.3.

Small ribosomal subunit able to recognise and bind to 5' end/start codon on mRNA to initiate translation;
 Large ribosomal subunit contains A site, P site and E site;
 P site contains the initiator tRNA/tRNA with the growing polypeptide chain attached;
 A site is for the binding of incoming aminoacyl-tRNA;
 E site is for tRNA to be released from ribosome;
 Attachment of large ribosomal subunit holds the translation initiation complex in place;
 Large ribosomal subunit contains peptidyl transferase + to catalyse formation of peptide bonds between amino acids;

; for 1 mark, max is 3 marks

[3]

Fig. 2.4 shows the role of tRNA in the process of protein translation while Fig. 2.5 shows the genetic code in terms of the mRNA codons sequence.

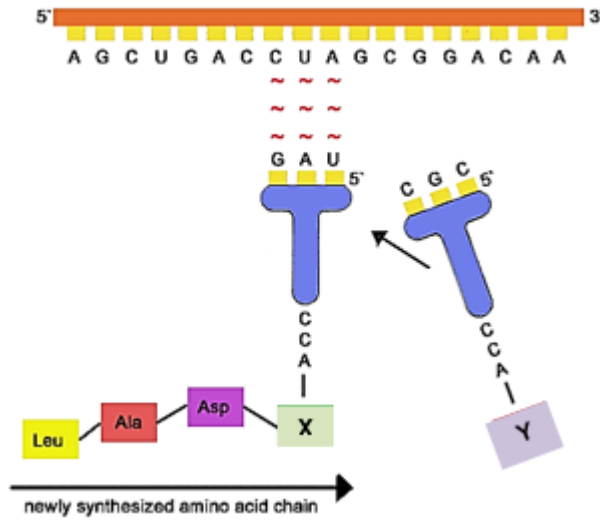


Fig. 2.4

		Second Letter					
		U	C	A	G		
1st letter	U	UUU Phe UUC UUA Leu UUG	UCU Ser UCC UCA UCG	UAU Tyr UAC UAA Stop UAG Stop	UGU Cys UGC UGA Stop UGG Trp	3rd letter	U C A G
	C	CUU Leu CUC CUA CUG	CCU Pro CCC CCA CCG	CAU His CAC CAA Gln CAG	CGU Arg CGC CGA CGG		U C A G
	A	AUU Ile AUC AUA Met AUG	ACU Thr ACC ACA ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG		U C A G
	G	GUU Val GUC GUA GUG	GCU Ala GCC GCA GCG	GAU Asp GAC GAA Glu GAG	GGU Gly GGC GGA GGG		U C A G

Fig. 2.5

(c) With reference to Fig. 2.4 and Fig. 2.5, identify amino acid X and Y.

X: ... X: leucine;
Y: ... Y: Alanine;
Y: ... ; for 1 mark

[1]

The palisade mesophyll cells of plant contain numerous chloroplasts. Fig. 2.6 shows an electron-micrograph of a chloroplast in plant cell.

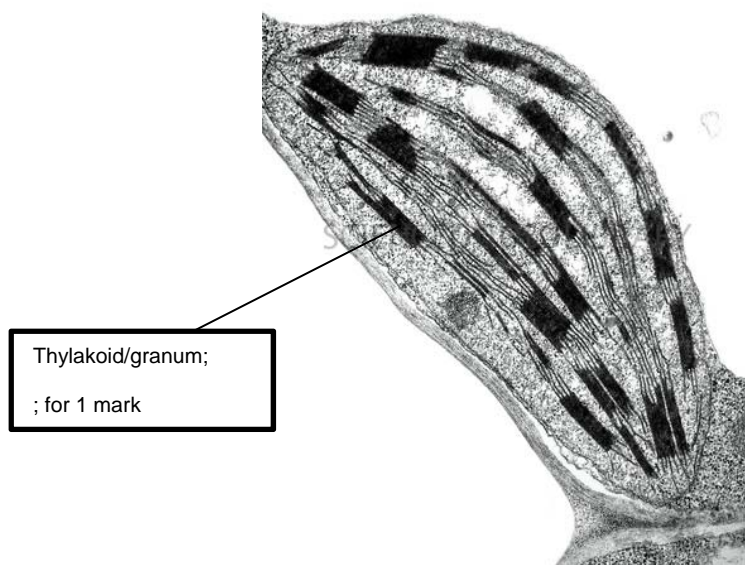


Fig. 2.6

(d) Draw an arrow and labelled the structure where light-dependent reactions occurs in the chloroplast. **[1]**

The rate of decolourisation of DCPIP in the Hill Reaction is a measure of the rate of the light-dependent stages of photosynthesis. DCPIP, a blue dye, acts as an electron acceptor and becomes colourless when reduced, allowing any reducing agent produced by the chloroplasts to be detected.

A suspension of chloroplasts was made by grinding fresh leaves in buffer solution and centrifuging the mixture. Tubes were then prepared and treated in the following way and the results of this investigation is shown in Table 2.1.

Table 2.1

Tubes	Content	Condition	Colour	
			Start	After 15 min
A	3 cm ³ chloroplast suspension 8 cm ³ DCPIP	Illuminated strongly	Blue-green	Green
B	3 cm ³ buffer solution 8 cm ³ DCPIP	Illuminated strongly	Blue	Blue
C	3 cm ³ chloroplast suspension 8 cm ³ DCPIP	Left in the dark	Blue-green	Blue-green

(e) Using your knowledge of light-dependent reactions, account for the results shown in Table 2.1.

DCPIP acts like final hydrogen ion/electron acceptor/NADP+ in non-cyclic photophosphorylation/light-dependent reactions;

; for 1 mark, max is 1 mark

Tube A: When light and chloroplast suspension are present, photo-excited electrons from water/PSII/PSI;

Electrons are passed along the electron transport chain to reduce DCPIP;

There is light-dependent reactions + decolourising/changing it from blue to colourless, solution turn green due to the colour of chloroplast/chlorophyll;

; for 1 mark. max is 1 mark

However, when tube C is placed in the dark/absence of light, DCPIP remained blue, indicating that it is not being reduced, thus no photoactivation in the dark;

; for 1 mark. max is 1 mark

Tube B is a control and shows that DCPIP is reduced and decolourised by the photoactivation/non-cyclic photophosphorylation/light-dependent reactions in the chloroplast suspension;

; for 1 mark, max is 1 mark

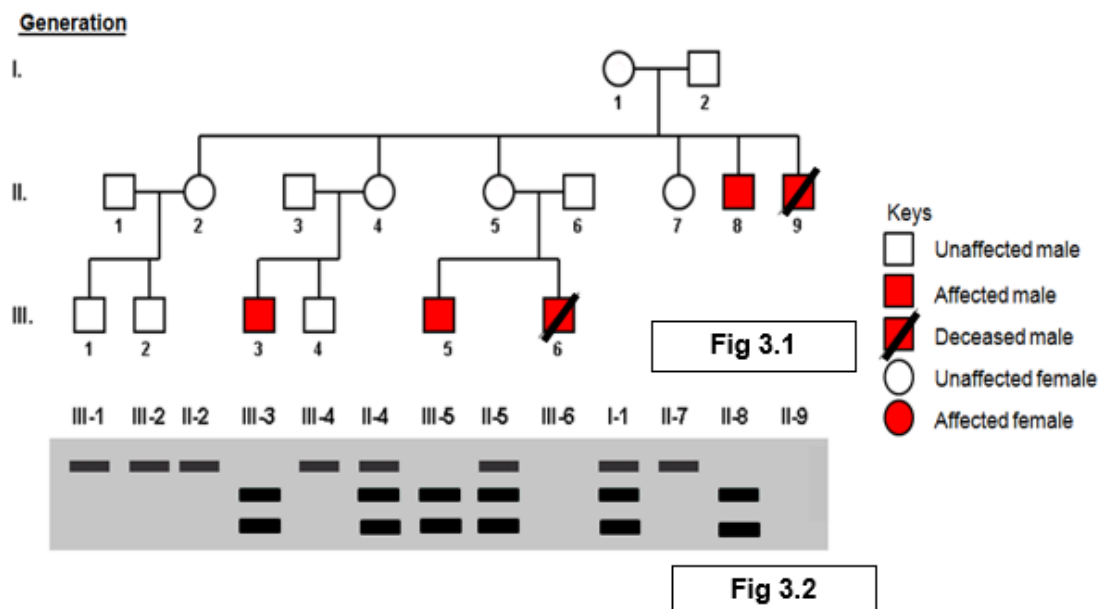
.....
.....[4]

[Total: 12]

3. Haemophilia A, also called factor VIII (FVIII) deficiency or classic haemophilia, is a genetic disorder caused by missing or defective factor VIII, a clotting protein. This genetic disorder is characterised by episodes of internal and external bleeding in affected individuals.

According to the United States Centers for Disease Control and Prevention, haemophilia occurs in approximately 1 in 5,000 live births. There are about 20,000 people with haemophilia in the United States. All races and ethnic groups are affected.

Fig. 3.1 shows a pedigree of a family with history of haemophilia A. The FVIII gene was first isolated from each individual using Polymerase Chain Reaction (PCR). The PCR products were then digested using restriction enzymes and the resulting fragments separated by gel electrophoresis. Fig. 3.2 shows the results of the gel electrophoresis for some of the individuals.



- (a) With reference to Fig. 3.1 and Fig. 3.2, state two pieces of evidence that confirm that haemophilia A is an X-linked recessive disorder.

X-linked because:

More males affected than females;

Or

Phenotypically normal female/mother unaffected by the disorder/carrier females, only affected sons and daughters not affected + e.g.:

I-1 not affected/carrier/heterozygous, II-8 and II-9 are affected while II-2, II-4, II-5 and II-7 unaffected;

Or

II-4 not affected/carrier/heterozygous, III-3 affected;

Or

II-5 unaffected/carrier/heterozygous but III-5 and III-6 are affected;

; for 1 mark, max is 1 mark

Recessive because:

Identification of which band correspond to mutant and normal allele;

Phenotypically normal parents can produce an affected child + e.g.

I-1 and I-2 gives rise to II-8 and II-9;

II-3 and II-4 gives rise to III-3;

II-5 and II-6 gives rise to III-5 and III-6;

; for 1 mark, max is 1 mark

Individual II-3 and II-4 do not exhibit the symptoms of haemophilia A and they are heterozygous for both blood type A and B respectively. III-3, who is the son of II-3 and II-4, suffers from haemophilia A and has a blood type is AB.

- (b) With reference to Fig. 3.1 and Fig. 3.2, construct a genetic cross diagram to explain how II-3 and II-4 can result in a child with haemophilia A and blood type AB.

Let X^H be the allele on the X-chromosome that code for normal blood clotting factor

Let X^h be the allele on the X-chromosome that codes for the defective blood clotting factor

Let I^A be the allele coding for blood type A

Let I^B be the allele coding for blood type B

Let I^O be the allele coding for blood type O

Parental phenotype	Male, unaffected				Female, unaffected			
Parental genotype	$X^H Y I^A I^O$				$X^H X^h I^B I^O$			
Gamete	$\textcircled{X^H I^A}$ $\textcircled{X^H I^O}$ $\textcircled{Y I^A}$ $\textcircled{Y I^O}$				$\textcircled{X^H I^B}$ $\textcircled{X^H I^O}$ $\textcircled{X^h I^B}$ $\textcircled{X^h I^O}$			
Punette's square		$X^H I^B$	$X^H I^O$	$X^h I^B$	$X^h I^O$			
	$X^H I^A$	$X^H X^H I^A I^B$ Female, normal, blood type AB	$X^H X^H I^A I^O$ Female, normal, blood type A	$X^H X^h I^A I^B$ Female, normal, blood type AB	$X^H X^h I^A I^O$ Female, normal, blood type A			
	$X^H I^O$	$X^H X^H I^B I^O$ Female, normal, blood type B	$X^H X^H I^O I^O$ Female, normal, blood type O	$X^H X^h I^B I^O$ Female, normal, blood type B	$X^H X^h I^O I^O$ Female, normal, blood type O			
	$Y I^A$	$X^H Y I^A I^B$ Male, normal, blood type AB	$X^H Y I^A I^O$ Male, normal, blood type A	$X^h Y I^A I^B$ Male, affected, blood type AB	$X^h Y I^A I^O$ Male, affected, blood type A			
	$Y I^O$	$X^H Y I^B I^O$ Male, normal, blood type B	$X^H Y I^O I^O$ Male, normal, blood type O	$X^h Y I^B I^O$ Male, affected, blood type B	$X^h Y I^O I^O$ Male, affected, blood type O			
F1 genotype	$X^H X^H I^A I^B$, $X^H X^h I^A I^B$	$X^H X^H I^A I^O$, $X^H X^h I^A I^O$	$X^H X^H I^B I^O$, $X^H X^h I^B I^O$	$X^H X^H I^O I^O$, $X^H X^h I^O I^O$	$X^H Y I^A I^B$, $X^H Y I^A I^O$	$X^H Y I^B I^O$, $X^H Y I^O I^O$	$X^h Y I^A I^B$, $X^h Y I^A I^O$	$X^h Y I^B I^O$, $X^h Y I^O I^O$
F1 phenotype	Female, normal, blood type AB	Female, normal, blood type A	Female, normal, blood type B	Female, normal, blood type O	Male, normal, blood type AB	Male, normal, blood type A	Male, normal, blood type B	Male, normal, blood type O
F1 genotype	$X^h Y I^A I^B$ $X^h Y I^A I^O$		$X^h Y I^B I^O$		$X^h Y I^O I^O$			
F1 phenotype	Male, affected, blood type AB		Male, affected, blood type A		Male, affected, blood type B		Male, affected, blood type O	
Phenotypic ratio	Female, Normal, Blood type AB 2 :	Female, normal, blood type A 2 :	Female, normal, blood type B 2 :	Female, normal, blood type O 2 :	Male, normal, blood type AB 1 :	Male, normal, blood type A 1 :		
	Male, normal, blood type B 1 :	Male, normal, blood type O 1 :	Male, affected, blood type AB 1 :	Male, affected, blood type A 1 :	Male, affected, blood type B 1 :	Male, affected, blood type O 1		

Correct parental phenotypes and genotypes;

Correct gametes drawn;

Correct punette's square drawn including phenotypes;

Correct F1 phenotypes and genotypes;

Correct phenotypic ratio

[5]
[Total: 7]

4. MRSA is a variety of *Staphylococcus aureus*. It is difficult to treat infections caused by this type of bacteria because it is resistant to methicillin and to some other antibiotics. As a result, some patients who are already very ill may die if they become infected with MRSA.

(a) Describe how natural selection makes MRSA resistant to the commonly used antibiotics.

Pre-existing genetic variations in the bacterial population due to random mutations;
Antibiotic resistant gene / allele already existing in gene pool of bacterial population;
Selection pressure of antibiotic/methicillin being exerted on bacterial population;
 Resistant bacteria are at the selective advantage and are able to survive and reproduce to pass down the allele for antibiotic resistance to their offspring;
 Or
 Non-resistant bacteria are selected against and cannot survive and reproduce to pass down the allele for antibiotic resistance to their offspring;

 Over time, frequency of antibiotic resistance allele in the bacterial population increases;
 As a result, the population of resistant bacteria increases. Thus, make MRSA resistant to the commonly used antibiotics;

 ; for 1 mark, max is 4 marks

...
...
...
...
...

.....[4]

Antibiotic resistance genes have been employed widely in recombinant DNA technology to produce transgenic bacteria containing human genes.

To produce insulin for medical uses, human insulin genes are transferred into bacteria. Plasmids containing two antibiotic resistance genes, one coding for resistance to tetracycline and one for resistance to ampicillin, are used to carry out this transfer.

Table 4.1 shows the actions of four different restriction enzymes, which might be used in the production of a recombinant DNA molecule, and the source of these enzymes.

Table 4.1

Organism	Restriction enzyme	Target DNA sequences (cleavage sites shown by arrow linings)
<i>Escherichia coli</i> RY 13	<i>EcoRI</i>	5' G <u>↑</u> A A T T C 3' 3' C T T A A <u>↓</u> G 5'
<i>Bacillus amyloliquefaciens</i>	<i>BamHI</i>	5' G <u>↑</u> G A T C C 3' 3' C C T A G <u>↓</u> G 5'
<i>Providencia stuartii</i>	<i>PstI</i>	5' C T G C A <u>↑</u> G 3' 3' G <u>↓</u> A C G T C 5'
<i>Haemophilus influenzae</i>	<i>HindII</i>	5' G T Py <u>↑</u> Pu A C 3' 3' C A Pu <u>↓</u> Py T G 5'

- (b) With reference to Table 4.1, explain why *EcoRI*, *BamHI* and *PstI* are more suitable for use in the cloning of human insulin gene than *HindII*.

EcoRI, *BamHI* and *PstI* make staggered cuts in DNA to produce sticky ends on the human insulin gene and plasmid;
Upon mixing together, the insulin gene and the plasmid can then annealed through complementary base-pairing via hydrogen bond formation;

; for 1 mark, max is 1 mark

HindII produces blunt ends;

Decrease efficiency/require additional steps of producing recombinant DNA molecules as linker DNA must be added for reannealing of the gene of interest and vector;

HindII has restriction site/sequence that is not specific, may cut at multiple sites/another antibiotic resistant gene;

HindII restriction site is not specific hence it may cut the plasmid at multiple locations, the gene of interest could be inserted into multiple locations/sites in the plasmid;

; for 1 mark, max is 1 mark

After the fragments of human DNA and the cut plasmids were mixed together, several types of plasmid were formed. The different types of plasmid are shown in Fig 4.1.

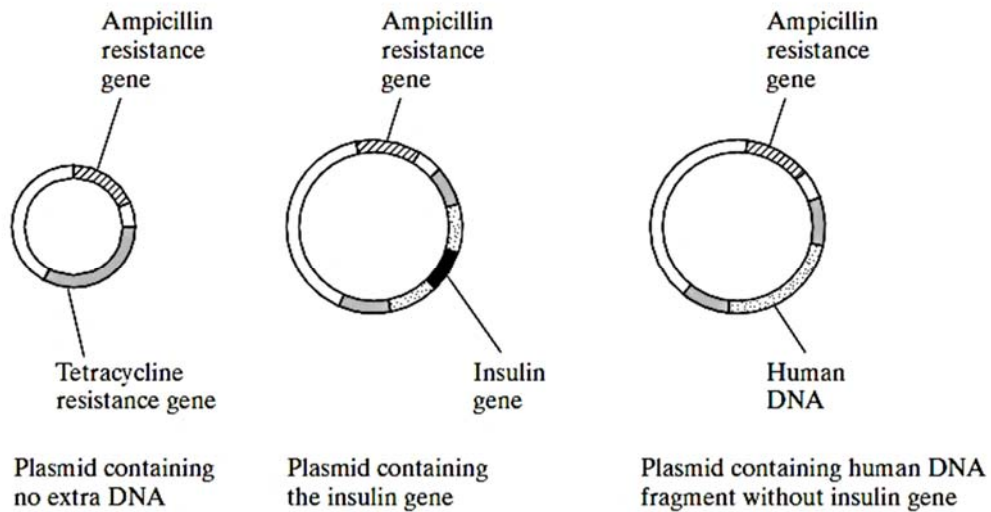


Fig 4.1

- (c) State another property of the plasmid not shown in Fig. 4.1 that enables it to be used as a cloning vector.

Origin of replication;
Multiple cloning site/restriction sites;

.....[1]

: for 1 mark, max is 1 mark

- (d) Explain how it is possible to distinguish between bacteria, which have taken up a plasmid with human DNA and those, which have taken up a plasmid without any extra DNA.

- Plate the bacteria on nutrient agar plate containing ampicillin;
Only bacteria that have taken up the plasmid/both reannealed and recombinant plasmids can survive due to the presence of ampicillin resistance gene;
- Using pad/velvet surface to transfer bacteria via replica plating onto a nutrient agar plate containing tetracycline;
For bacteria with human DNA, tetracycline gene is disrupted by insertion of the human DNA, and is no longer functional;
- Comparing the colonies on the agar plate with ampicillin and those colonies growing on agar plate with tetracycline;

; for 1 mark, max is 3 marks

- Bacteria with human DNA grow on agar plate with ampicillin but are killed by tetracycline on agar plate containing tetracycline;
- Bacteria with no extra DNA in plasmid/reannealed plasmid can survive on agar plate containing tetracycline;

; for 1 mark, max is 1 mark

[Total: 11]

Section B

Answer **one** question.

Write your answers on the separate answer paper provided.

Your answers should be illustrated by large, clearly labelled diagrams, where appropriate.

Your answers must be in continuous prose, where appropriate.

Your answers must be set out in sections **(a)**, **(b)** etc., as indicated in the question.

5.

(a) Compare the structure and role of deoxyribonucleic acid and ribonucleic acid. [6]

Feature	DNA	RNA
Similarities:		
<ul style="list-style-type: none">Both contain <u>nucleotide monomers</u> that is made up of <u>nitrogenous base</u>, <u>pentose sugar</u> and a <u>phosphate group</u>;Both are <u>polynucleotides</u> and can form <u>complementary base pairing</u> between C-G and A-T(DNA) or A-U (RNA);In complementary base-pairing for both DNA and RNA, same <u>number of H-bonds</u> form between C-G and A-T / A-U;Same <u>phosphodiester bonds</u> joining the adjacent nucleotides/sugar-phosphate backbone;		
; for 1 mark, Max is 2 marks		
Differences:		
Type of nucleotide monomer	Deoxyribonucleotide;	Ribonucleotide;
Type of pentose sugar	Deoxyribose;	Ribose;
Type of nitrogenous bases	Adenine, guanine, cytosine and thymine;	Adenine, guanine, cytosine and uracil;
Ratio of nitrogenous bases	<u>Ratio</u> of adenine to thymine, and cytosine to guanine is <u>1:1</u> for all DNA molecules;	Ratio of adenine to uracil, and cytosine to guanine <u>varies/differs</u> from one RNA molecule to another;
Structure	With the exception of the DNA in some viruses, DNA is always <u>double helix/double-stranded/2 polynucleotide chains</u> ;	With the exception of the RNA in some viruses, RNA is always <u>single-stranded/one polynucleotide chain</u> ;
Types of molecules	There is only one type of DNA;	There are three types of RNA, namely mRNA, rRNA and tRNA;
Size	Large molecule with more nucleotides;	Relatively small molecule with fewer nucleotide;
Role	A template for <u>DNA replication</u> and <u>transcription</u> ;	mRNA: A <u>template for protein synthesis/translation</u> ; Or tRNA: form complementary base pair with <u>codons on mRNA</u> to bring the corresponding activated <u>amino acids</u> to the <u>ribosome/for translation</u> elongation; Or rRNA: complex with protein to become <u>ribosomal subunits/ribosome</u> ;
;; for 1 mark, max is 4 marks		

(b) Using named examples, explain how anatomical, embryological and molecular homology supports Darwin's theory of natural selection. [7]

- Anatomy, embryological and molecular homology provide evidences supporting evolution as a process of modifying the characteristics present in an ancestral organism by natural selection in its descendants over time;

Anatomical homology (max 2m)

- An example of an anatomical homology is that of the number and arrangement of bones in the forelimbs of mammals/ pentadactyl limb of mammals;
 - The forelimbs of all mammals, including humans, cats, whales and bats, show the same arrangement of bones from the shoulder to the tips of the digits, even though these appendages have very different functions: lifting, walking, swimming and flying;
 - Similarity is due to their descent from a common ancestor with the same basic structural plan that has been modified to allow the forelimb to adapt to a certain method of locomotion in a particular environment;
- OR

- Vestigial structures which are reduced or non-functional but shows homology to functioning structures in other species;
- such as appendix in human, pelvis and leg bones of snakes;
- Reflect descent with modification from a shared/common ancestor;
- when structure loses function as the selection pressure that selects for it is no longer present;

Embryological homology (max 2m)

- The embryological development of all vertebrates share remarkable similarities;
- All vertebrates embryos share the presence of a post anal tail / pharyngeal pouches / 2-chambered heart/segmented myotomes [mention at least 2 traits];
- Pharyngeal pouches in mammalian embryos are the equivalent/similar to gills in fish embryos at early developmental stages;
- become parts of the ears and throat in humans and other mammals and gills in fishes;

Or

- 2-chambered heart is retained in fish but develops into 3-chambered heart in amphibians and 4-chambered heart in mammals;
- Similarities during early embryonic development in different vertebrate species can be explained if they descended from a common ancestor/;

Molecular homology (max 2m)

- All forms of life use the same genetic language of DNA and RNA/genetic code is universal. ;
- Likely that all species descended from common ancestors that used the same genetic code;
- Closely related species have more similar DNA/RNA/amino acid sequences in the homologous genes / proteins;
- Differences are a result of accumulated DNA mutations as descendants evolve independently/evolve along different lineages;
- Similarity in nucleotide base sequences is seen in both coding regions but also non-coding region of the DNA genome;

(c) Using named examples, discuss the importance of genetic engineering in solving the global demand for food. [7]

- Increase yield by genetically modifying food crops that will result in decreased losses caused by pesticides, fungal infestation, viruses, bacterial infection and pests;

Introduction of genes that code for proteins that confer insecticidal resistance

- Example: Genetically engineered crop plants that express the Bt-toxin gene from the bacteria *Bacillus thuringiensis* produce Bt-toxin protein which kills insect larvae feeding on the plant;

Introduction of genes that code for proteins that confer herbicidal resistance

- Example: Genetically engineered crop plants that are resistant to herbicides by introducing the herbicide/glyphosate resistance gene;
- When herbicide is applied to the field, the weeds are eliminated but not the herbicide resistance crop plants;

Introduction of genes that code for proteins that confer viral resistance;

- E.g., tobacco plant can be made resistant to the tobacco mosaic virus by expressing the coat protein gene of a virus;

Introduction of genes that code for growth hormones;

- Example: The Atlantic salmon has been genetically modified by the addition of a growth hormone gene from a Pacific Chinook salmon and an active promoter from an ocean pout placed upstream of the growth hormone gene;
- The insertion of the growth hormone gene results in faster growth rate and yield of the salmon, thereby increasing the supply of salmon;

Introduction of genes that delayed ripening

- Flavr Savr tomatoes are engineered to include a gene for antisense mRNA to polygalacturonase gene to reduce expression of polygalacturonase;
- This will result in delayed ripening allowing crops to be stored for longer period of time;

AVP;

; for 1 mark, max is 7 marks

6.

(a) Relate the structure of haemoglobin to its function in animals.

[6]

HAEMOGLOBIN	
Structure	Function
Presence of <u>non-polar amino acids</u> , formation of a <u>hydrophobic cleft</u> , containing a haem binding site/region;	This provides a <u>hydrophobic</u> environment for the <u>haem group</u> to function;
Each subunit/polypeptide bears <u>one haem prosthetic group containing Fe²⁺ ion</u> ; Each haem group contains an <u>Fe²⁺ ion</u> within a porphyrin ring;	<u>Fe²⁺ ion</u> is able to <u>bind/combine reversibly</u> to <u>oxygen</u> accounting for the oxygen-transporting ability of haemoglobin;
Each haemoglobin molecule carries 4 prosthetic haem group;	Each molecule can bind to/transport <u>4 oxygen molecules</u> . This increases the oxygen-carrying capacity of red blood cell;
<u>Amino acid residues</u> found on the <u>surface</u> are generally <u>hydrophilic/polar</u> ;	This allows haemoglobin to be a <u>soluble globular protein</u> in <u>aqueous medium</u> ;
Binding of oxygen to 1 of the 4 subunits resulting in <u>conformational changes</u> in the remaining subunits/polypeptides;	This allows the other subunits to more <u>readily bind</u> to oxygen; Or Reference to cooperativity;

; for 1 mark, max is 3 marks

Structure and function must be correctly matched to be awarded the mark

(b) Explain the small yield of ATP produced by anaerobic respiration in mammals. [6]

Oxygen is the final electron acceptor of electron transport chain;No oxygen means no movement of electron along ETC, no oxidative phosphorylation, no Krebs cycle and link reactions;Oxidative phosphorylation produces 34 ATP per glucose molecules;

; for 1 mark, max is 2 marks

Incomplete/partial oxidation of glucose during anaerobic respiration in the absence of oxygen;During glycolysis, 1 molecule of glucose is broken down to 2 molecules of pyruvate;Glycolysis produces net yield of 2 ATP only and 2 reduced NAD/NADH per glucose molecule;ATP production during glycolysis occur via substrate level phosphorylation;No ATP is produced during lactate fermentation;During lactate fermentation, pyruvate will be reduced to lactate by lactate dehydrogenase;Reduced NAD/NADH is needed during lactate fermentation and NAD⁺ is regenerated so that glycolysis can continue to occur;

; for 1 mark, max is 4 marks

(c) Restriction digest is usually performed prior to agarose gel electrophoresis.

With reference to the principles of gel electrophoresis, discuss why the incubation time for restriction digest of the plasmid DNA is important in obtaining accurate results from gel electrophoresis. [8]

- DNA molecules are negatively charged due to the presence of negatively charged phosphate groups;
- When placed in an agarose gel with an electric current passing through it, DNA molecules will move towards the positive electrode/anode;
- Movement/migration of DNA molecules towards the positive electrode is impeded by agarose gel;
- The agarose gel forms a cross-linked matrix and functions as a 'molecular sieve' as the matrix forms little pores through which DNA must travel;
- DNA molecules will be separated into bands according to size/molecular mass and shape;
- Larger DNA molecules have more difficulty/encounter more resistance moving through the pores of the agarose gel;
- The larger DNA molecules move/migrate through the agarose gel at a slower rate/vice versa;
- Supercoiled DNA migrates the fastest, followed by the linear DNA. Circular DNA migrates the slowest;

; for 1 mark, max is 4 marks

- If the duration of restriction digestion is too long, it may result in the restriction enzymes cutting at unspecific sequences of the plasmid other than at the restriction sites;
- This affects the reliability and accuracy of the results as more fragments will be generated and more bands will be observed after gel electrophoresis;
- The fragments will also be smaller in size and will encounter less resistance, thus the band positions will be found closer to the anode;
- If the duration of restriction digestion is too short, it may result in the incomplete restriction digestion of the DNA;
- This affects the reliability and accuracy of the results as the total number of fragments will be lesser than actual, and fewer bands will be observed after gel electrophoresis;
- The plasmid may not be completely cut, resulting in circular DNA with 1 strand cut at 1 place;
- This leads a higher band position than usual as circular DNA encounter more resistance than linear DNA;
- Some plasmids may not be cut at all and may undergo supercoiling;
- This leads to lower band position than usual as supercoiled plasmid encounter the lesser resistance than linear DNA.

; for 1 mark, max is 4 marks