H

NANYANG JUNIOR COLLEGE
JC 2 MID YEAR EXAMINATION
Higher 1

CANDIDATE NAME

CLASS

BIOLOGY

8875/02

Paper 2 Core Paper

29 June 2016

Additional Materials: Answer Paper

2 hours

READ THESE INSTRUCTIONS FIRST

Write your Centre number, index number and name on all the work you hand in.
Write in dark blue or black pen.
You may use an HB pencil for any diagrams or graphs.
Do not use staples, paper clips, glue or correction fluid.
DO **NOT** WRITE IN ANY BARCODES.

Section A

Answer **all** questions.

Section B

Answer **one** question.

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 [1at the end of each question or part question.

For Examiner's Use	
Section A	
1	**7**
2	**11**
3	**9**
4	**13**
5 or 6	**20**
Total	

This document consists of **10** printed pages and **0** blank page.

Section A

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

1 Many microorganisms can digest cellulose by using a group of enzymes collectively known as cellulases. Cellobiose is the disaccharide produced during cellulose digestion.

The cellulase known as β-glucosidase completes the digestion of cellulose by hydrolysing the cellobiose molecule to produce two β-glucose molecules.

(a) Draw the ring structure of one β-glucose molecule in the space provided.

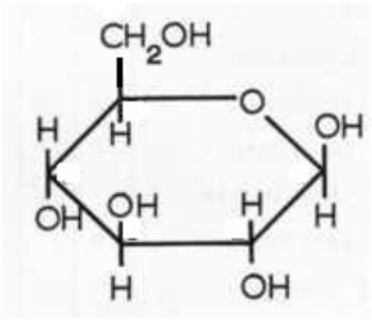


diagram A

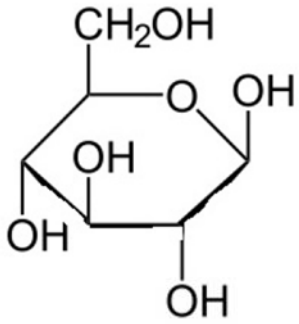


diagram B

if incorrect (e.g. If one or more H missing from the ring in diagram A ***or*** *if an H added to diagram B ring) allow one mark if:*

- hexose ring with oxygen shown in correct position and
- CH_2OH group in correct position and

OH groups of ring in correct position.

[1]

(b) β-glucosidase was extracted from two different bacteria, *Agrobacterium tumefaciens* and *Thermotoga maritima*.

Fig. 1.1 shows the results of an investigation into the effect of temperature between 0 °C and 100 °C, on the activity of each enzyme.

- **L** represents the lowest temperature at which activity of each enzyme was detected.
- **H** represents the highest temperature at which activity of each enzyme was detected.

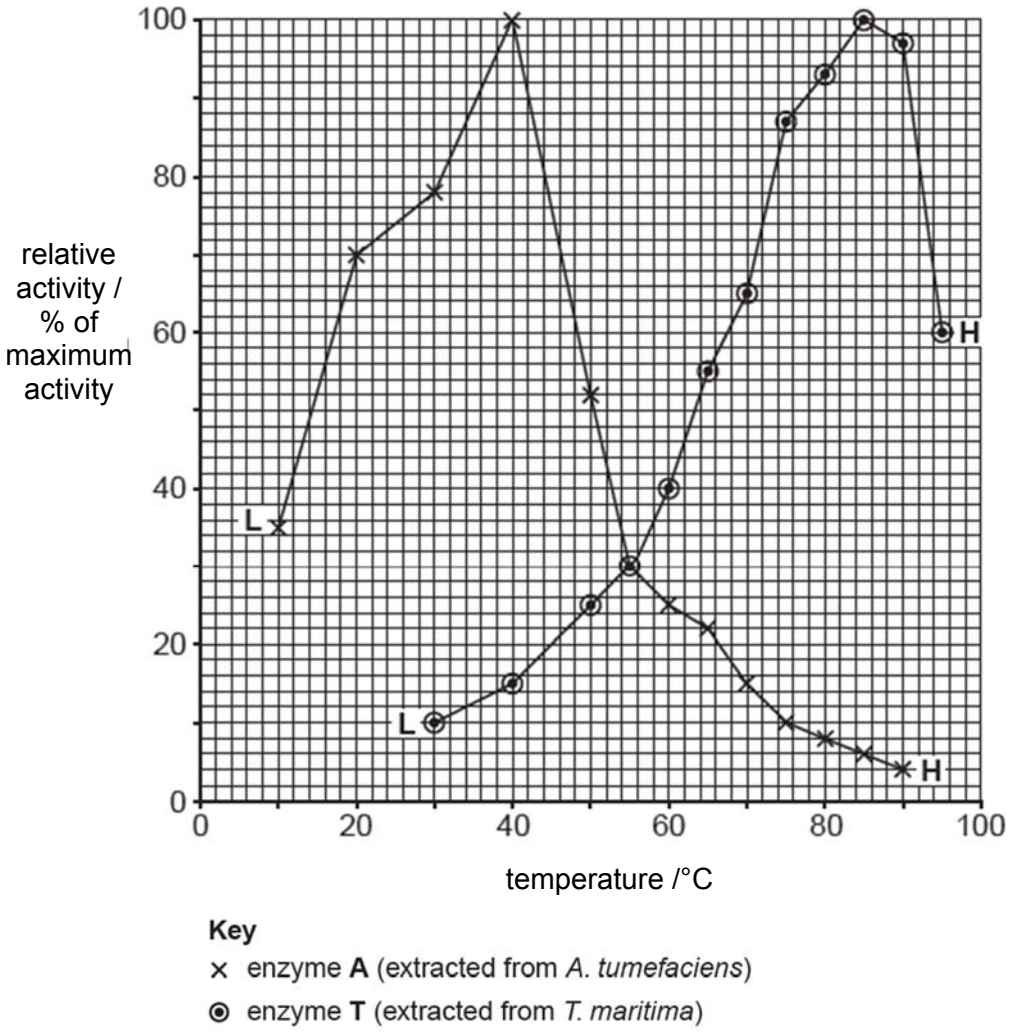


Fig. 1.1

(i) With reference to Fig. 1.1, describe the **differences** in the results for the two enzymes, **A** and **T**.

compare optimum temperatures
- optimum temperature, A lower (than T) / T higher (than A) / @maximum activity A is at a lower temperature +
- 40 °C(A) v 85° C(T) / A lower by 45 °C ;
- Difference in shape of curve before or after optimum ;
    - o e.g. after optimum, T does not have the less steep decrease after the initial steep decrease (unlike A)
    - o before optimum, steepest increase for A is at the lower temperatures, (unlike T)

compare activity below and above 55 °C
- below 55 °C, A has a higher activity / above 55 °C A has a lower activity, (than T) ;
- A has a higher activity at low(er) temperatures and a lower activity at high(er) temperatures +
- support;

compare temperature ranges of activity
- temperature range for activity is greater for A ;
- (A) spans 80 °C while (T) spans 65 °C / (A) 10–90 °C while (T) 30–95 °C

compare L for both
- A has a lower, L / lowest temperature for (detectable) activity
- L is 20 °C lower for A / 10 °C (A) VS 30 °C (T) ;
- (at L), A (relative) activity = 35%, which is higher than T = 10% ;

compare H for both
- T has a higher, H / highest temperature for detectable activity
- H is 5 °C higher for T / A 95° (T) VS 90°C (A) ;
- (at H) A (relative) activity = 4% which is much lower than T = 60% ;

[3]

(ii) Both enzyme A and enzyme T act on cellobiose. They have a similar, but not identical, primary structure.

Suggest how similarities **and** differences in the primary structure of the two enzymes could help to explain the results obtained in the investigation.

- primary structure, dictates, **folding** of the polypeptide chain into the **specific/ unique three-dimensional / tertiary structure** ;
    - @ idea that differences in primary structure leads to differences in secondary / tertiary structure
    - @ in terms of folding to give the **active site**

Similarity

- same / (very) similar, (**shape** of) active site ;
- active site (shape) is **complementary** to / AW, substrate cellobiose ;
- @ ES complex forms

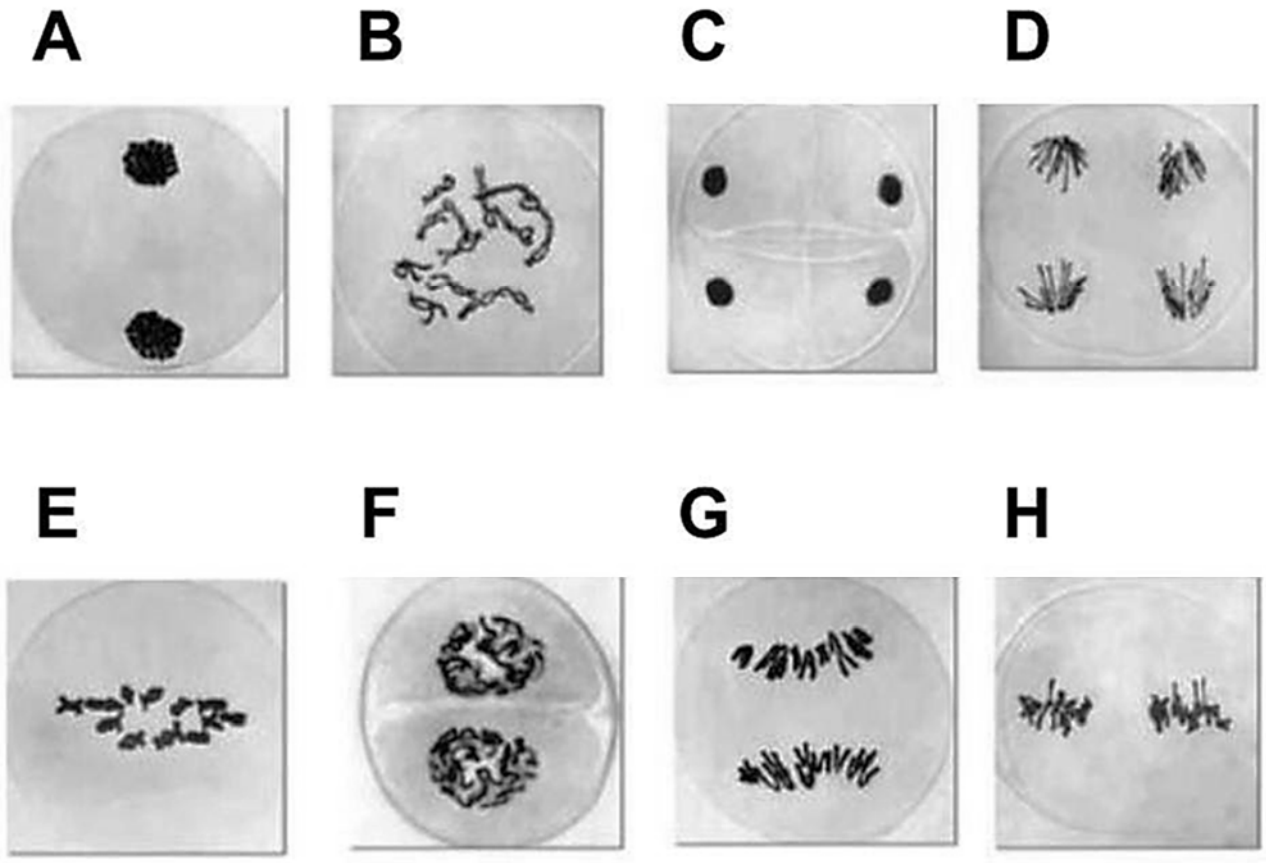
Differences

- differences in **side-chain / R-groups** due to slight differences in a.a. sequence;
- therefore differences in **numbers, types of bonds**, therefore differences in bonding to give different **stabilities**
  ® different bonds without further qualification
  ® peptide bond
- suggestion for **thermal stability** of T; e.g. **more** bonds / more of a named bond type
- suggestion of how active site may work in different ways

[3]

[Total: 7]

2 The micrographs below show nuclei of cells at different phases during meiosis in an animal.



(a) Micrograph B shows Prophase I. Arrange the letters shown on the micrographs to indicate the correct chronological sequence.

BEGAFHDC

[1]

(b) There are 50 units of DNA in the cell shown in micrograph B and the diploid number is 20.

(i) State the units of DNA in this cell during G1 phase prior to mitosis.

25 units

[1]

(ii) State the number of chromosomes in the mature sperm of this animal.

10 chromosomes

[1]

(c) Contrast the behaviour of chromosomes in mitosis and meiosis.

[3]

Meiosis	**Mitosis**
at anaphase 1, 2 homologous chrms separate & migrate to opp pole/cell ®: mention of chromosomes without homologous	no separation of 2 homologous chrm into different cells/ 2 homologous chrm migrate to the same pole
at anaphase 1, sister chromatids are joined & move to the same pole	sister chromatides separate and move to opposite poles
at prophase 1, synapsis where the 2 homologous chrms pair up/ crossing over/ formation of chiasma between non-sister chromatids of 2 homologous chrms ®: mention of chromosomes without homologous ®: Crossing over without non-sister chromatids ®: No double marks given	no synapsis/ formation of chiasma/ crossing over between two homologous chrms
at metaphase 1, centromeres of homologous chrms are at equidistance from metaphase plate	centromeres are aligned at the metaphase plate
at anaphase 1, no separation of centromere of chrms	separation of centromeres into 2
amt of DNA/ no. of chrms remained	halved the amt of DNA/ no. of chrms

A genetically modified tomato, known as Flavr Savr, is the first genetically modified food to be commercially sold for human consumption. This tomato is made more rot-resistant by adding an antisense gene (oligonucleotide - a short RNA or DNA molecule complementary to mRNA produced by a gene) to interfere with the production of the enzyme polygalacturonase (PG). The enzyme causes the softening of the fruit by degrading pectin and this result in the fruit being more susceptible to being damaged by fungal infection.

PG production during fruit ripening was measured in plants with one and with two antisense genes, and in normal plants. The results are shown in Fig. 2.2.

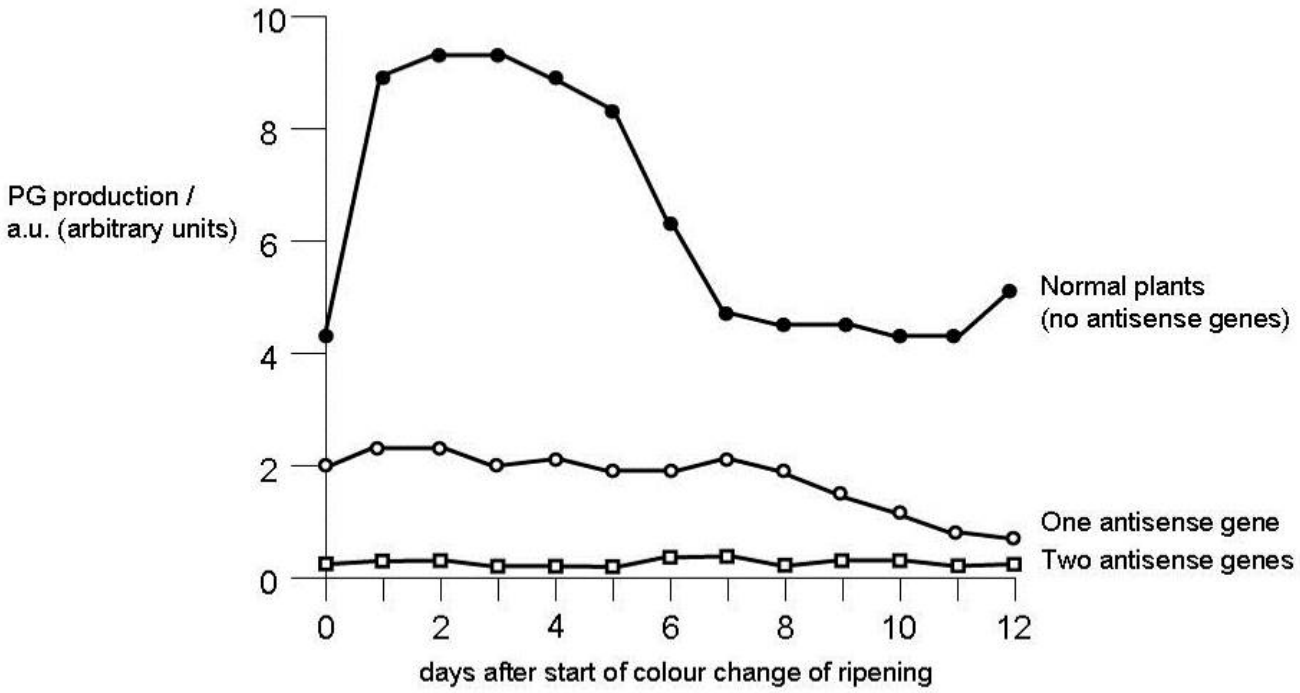


Fig. 2.2

(a) With reference to Fig. 2.2, describe and explain the difference in PG production between

(i) normal tomato plants and transformed plants with one antisense gene.

- *PG production in normal plants higher than plants with one antisense gene, min ~4 a.u./max~9 a.u. as compared to about 2 a.u.;*
- *antisense gene is being expressed in transformed plant cells, resulting in formation of duplex RNA;*
- *less translation initiation complex formation / decreased binding of ribosome to mRNA; resulting less translation of mRNA into PG proteins;*

[3]

(ii) transformed plants with one antisense gene and those with two antisense genes.

- *PG production in plants with one antisense gene is higher than PG production plants with two antisense genes, about 2 a.u. as compared to close to 0 a.u.; (accept reverse description);*

- *two antisense genes produce more anti-mRNA than one antisense gene, resulting in increased duplex RNA formation, increased inhibition of translation initiation complex formation, therefore much lower levels of translation of mRNA;*

[2]

[Total: 11]

3 A suspension of mitochondria was isolated from liver tissue and mixed with sucrose. A respiratory substrate was added. After which various substances were added to the suspension, at different time intervals and the amount of oxygen remaining in the preparation was monitored over some time. Fig. 3.1 shows the results as well as the times at which different substances were added.

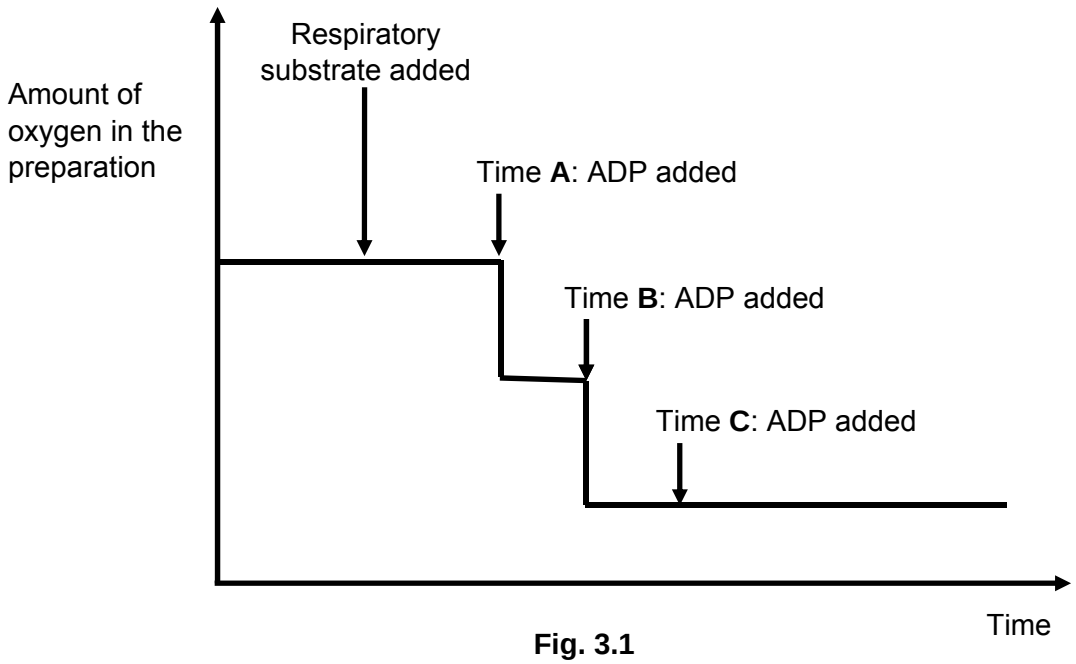


Fig. 3.1

(a) Explain why is there a need to add sucrose?

to maintain the osmotic pressure of the solution such that water will not move into the mitochondria

resulting in the bursting of the mitochondria due to the hypotonic solution surrounding it

[2]

(b) Explain why glucose cannot be the respiratory substrate that was added.

Lack of enzymes involved in **glycolysis**, usually found in **cytosol** / **cytoplasm**, in the suspension to produce **pyruvate** ;

Which is required as a **substrate for Link reaction** / **Krebs cycle** in mitochondria

or

because **glucose cannot be broken down** / **utilized** by the mitochondria ;

[2]

(c) Explain the change in the amount of oxygen between Time A and Time B.

ADP is required as a **substrate** which is **phosphorylated** by the action of **ATP synthases** / **stalked particles**, synthesising ATP ;

Hence when ADP is added at Time A, **oxidative phosphorylation** is allowed to proceed ;

And more O_2 is used as the **final electron and proton acceptor** thus the decrease in amount of oxygen between Time A & B ;

[2]

(d) Account for the shape of the graph after Time C.

Respiratory substrates / inorganic phosphates / have been depleted ;

[1]

In aerobic respiration of the organelle, acetylcoenzyme A is broken down as shown in **Fig. 3.2**.

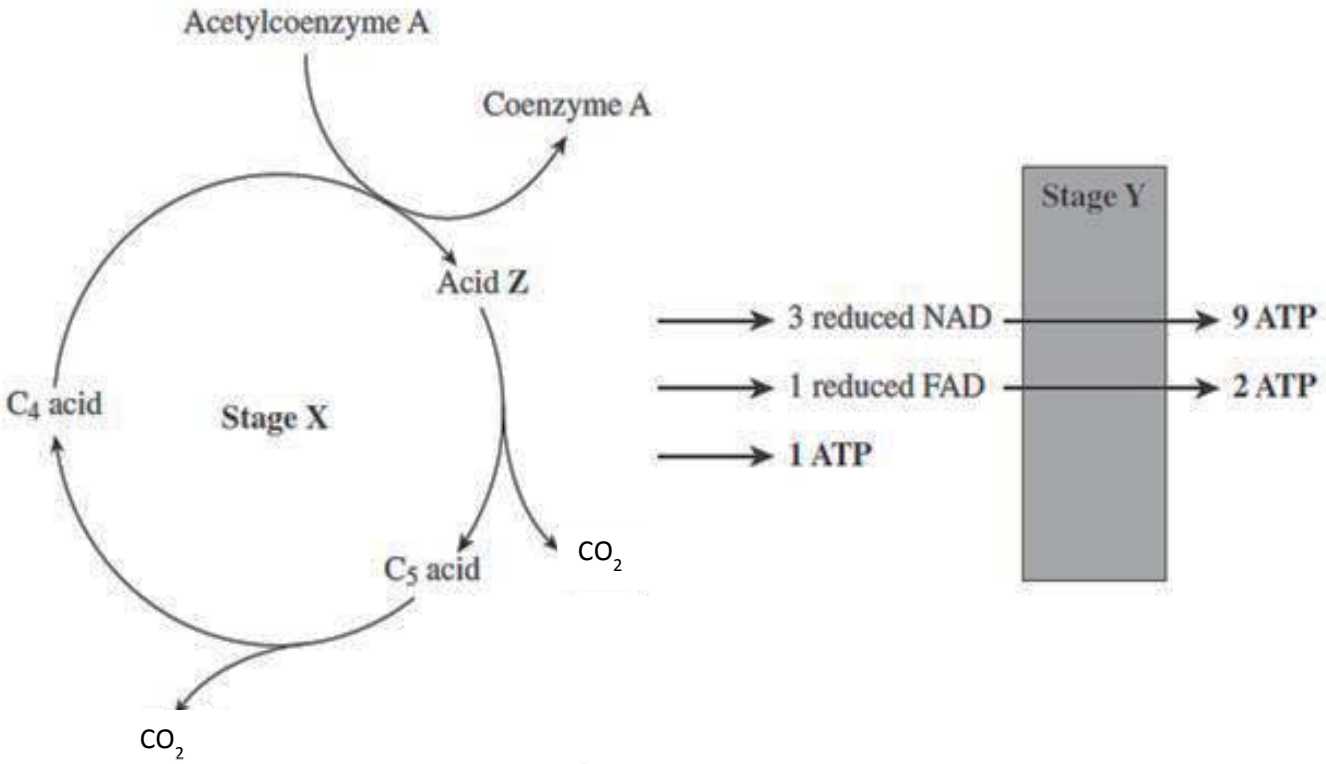


Fig. 3.2

Different fatty acids contain different numbers of carbon atoms. The first stages in the aerobic respiration of palmitic acid of stearic acid are given in equations 2 and 3

Equation 2

$$C_{15}H_{31}COOH + 8\ \text{Coenzyme A} \xrightarrow[2\ ATP]{7\ NAD,\ 7\ FAD} 8\ \text{Acetylcoenzyme A} + \underset{2\ ADP + 2Pi}{\underset{7\ \text{reduced FAD}}{7\ \text{reduced NAD}}}$$

Palmitic acid

Equation 3

$$C_{17}H_{35}COOH + 9\ \text{Coenzyme A} \xrightarrow[2\ ATP]{8\ NAD,\ 8\ FAD} 9\ \text{Acetylcoenzyme A} + \underset{2\ ADP + 2Pi}{\underset{8\ \text{reduced FAD}}{8\ \text{reduced NAD}}}$$

Stearic acid

(e) The greater the number of carbon atoms in a fatty acid, the greater the yield of ATP when the fatty acid molecule is respired aerobically. Use **Fig. 2.2** and equations 2 and 3 to explain why.

More C atoms in the fatty acids result in more acetylcoenzyme A formed / Palmitic acid yield 8 acetylcoenzyme A and Stearic acid yields 9 acetylcoenzyme A

More ATP is formed in Stage X / Krebs Cycle by substrate level phosphorylation

More acetylcoenzyme A results in more reduced NAD and reduced FAD formation in Stage X / Krebs cycle

Thus more ATP is formed in Stage Y / oxidative phosphorylation

[2]

[Total: 9]

4 Factor VII is an essential blood clotting protein encoded by the gene *F8.* A deficiency of this protein in humans results in the failure of blood coagulation and hence, one suffers from the bleeding disorder haemophilia. Currently, *F8* can be artificially synthesized and inserted into the plasmid pGB119 to produce Factor VIII in bacteria. Factor VIII is then transfused into the blood of patients suffering from haemophilia. **Fig. 4.1** is a plasmid map of pGB119.

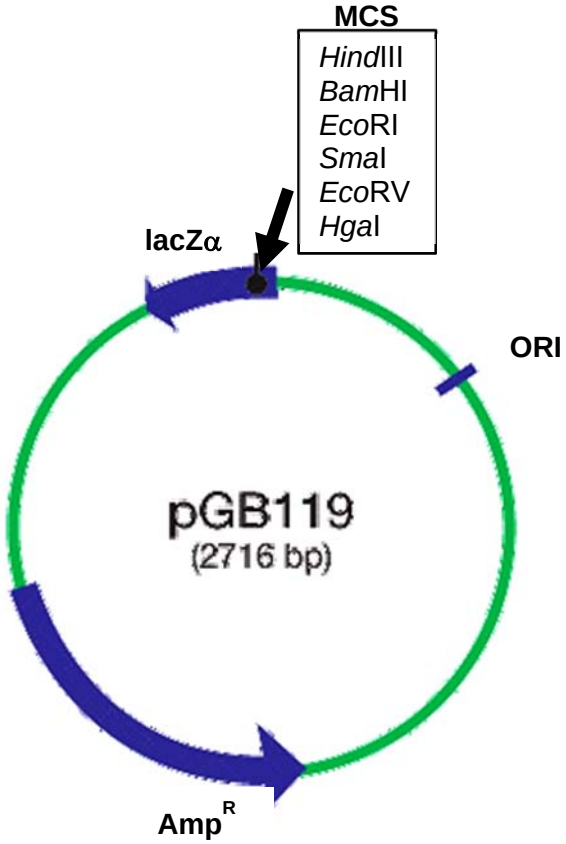


Fig. 4.1

The multiple cloning site (MCS) allows a large number of restriction enzymes to cut pGB119, producing sticky ends or blunt ends. The restriction enzyme *Bam*HI is used in the production of the recombinant plasmid with *F8,* which is then used to transform bacteria.

(a) (i) Compare the way in which sticky ends and blunt ends are produced.

Restriction enzymes recognise a specific restriction site and cleave phosphodiester bonds in the plasmid in a staggered manner to produce sticky ends,

Restriction enzymes that produce blunt ends will cleave phosphodiester bonds across both strands at a single point;

[2]

(b) The protein Factor VIII produced by the recombinant bacteria is identical to Factor VIII synthesized in humans. However, the engineered gene inserted into the plasmid may possess a nucleotide sequence that is different from that of a human gene.

Give reasons why this is so.

Different mRNA codons may code for the same amino acid sequence due to the degeneracy of the genetic code, hence a different nucleotide/ DNA sequence code be used for the same primary amino acid sequence;

The synthetic genes do not have introns;

Absence of eukaryotic promoter/ 5'UTR/ 3'UTR;

[2]

The plasmid Pgb119 is engineered to contain the marker gene *Hok* that codes for a protein found to be toxic to host bacteria, as it damages the cell membrane. Fig. 4.2 shows pGB119 with the MCS in the *Hok* gene.

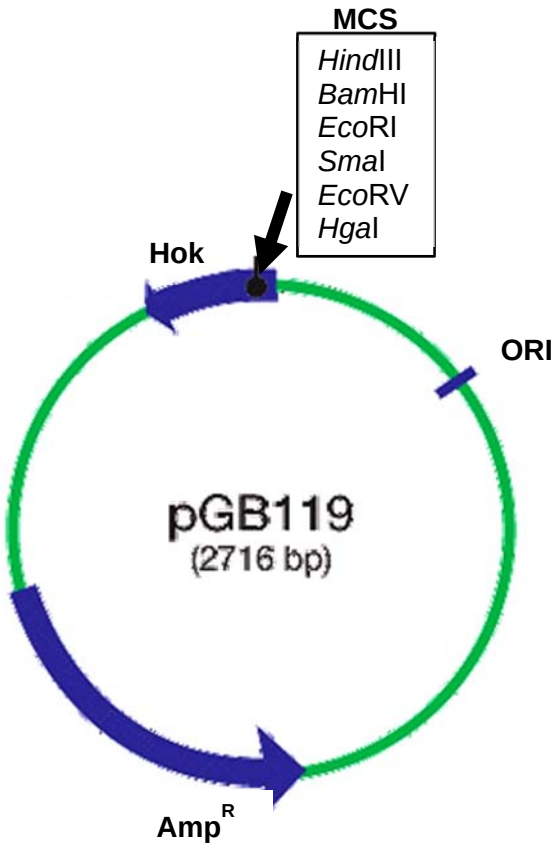


Fig. 4.2

(c) Bacteria transformed with either reannealed or recombinant pGB119 were plated onto a nutrient agar plate and left for a few days. Explain how the two types of bacteria can be distinguished from each other.

Bacteria colonies which appear on the nutrient plate contain the recombinant plasmids/ Bacteria containing reannealed plasmids do not form colonies;

Due to intact *Hok* gene (in reannealed plasmids) + functional proteins/ toxins produced;

As gene of interest is inserted into *Hok* gene (in recombinant plasmids) ref. insertional inactivation, the gene is disrupted + non-functional proteins/ no proteins are produced;

(In reannealed plasmids) hence damaging the cell membrane, bacteria dies/ do not grow (in recombinant plasmids) Cell membrane of bacteria remains intact, bacteria survive/ growth;

[4]

Dogs have been used as animal models of haemophilia. Two populations of a dog species affected with haemophilia living in the wild were studied. One population was found to occupy the lowlands while the other population was found to occupy the highlands. While the dogs in the two populations were very similar, some phenotypic differences were observed to be present.

(e) Explain the presence of phenotypic differences between the dogs in the two populations.

1. **The different environmental conditions in (lowlands and highlands) act as different selection pressures;**
2. **Variations exist within populations;**
3. By **natural selection**, **different alleles selected for**, allow **better adapted** individuals which are **at selective advantage, survive better till reproductive age** and **passed on favourable alleles to offspring**;
4. leading to **increase in frequency** of the **alleles** for the **favourable phenotypes**

[3]

(f) To determine if a dog species and wolf species are related, an investigator studied DNA sequences which codes for an important protein that performs the same function in both species.

Sequence A (from dog species) and Sequence B (from wolf species) were identical except at two points.

Explain how Sequences A and B provide evidence to support the theory of evolution.

The two sequences are very similar and show **molecular homology/ are homologous sequences**;

Hence it is most likely that the similarities were inherited from a **common ancestor;**

This is evidence for **descent with modification** as the two sequences show a modification process from an ancestral sequence via **natural selection**.

[2]

[Total: 13]

Section B

Answer EITHER 5 OR 6.

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.

Either

5 **(a)** Discuss the importance of genetic variation in natural selection and evolution. [6]

(b) Outline the large scale production of human insulin using genetic engineering. [8]

(c) Discuss the ethical and social implications of genetically modified crop plants. [6]

[Total: 20]

Or

(a) Describe and explain the advantages of molecular (nucleotide and amino acid sequences) methods in classifying organisms. [6]

(b) Describe how information on mature mRNA is used to synthesise polypeptides in eukaryotes. [8]

(c) With reference to solving the demand for food in the world, explain, with a named example, the significance of genetically engineered crop plants to improve their yield. [6]

[Total: 20]

(a) Discuss the importance of genetic variation in natural selection and evolution. [6]

1. Genetic variation exist in the individuals present in the population, and this results in phenotypic variation;
2. (Phenotypic) variation is needed for **natural selection to act on**;
3. Variations may be caused by spontaneous mutations;
4. Which creates new alleles and increases the gene pool for natural selection to operate; / Individuals can only introduce new allele to the next generation through mutation during the formation of gametes
5. Different environment have different selection pressures;
6. selects for individuals with phenotype more suited to the existing environment / individuals who are well-adapted to the environment have a selective advantage over those who are not;
7. Resulting in the individual able to survive till reproductive age and reproduce successfully / differential reproductive success;
8. This leads to certain alleles being passed to the next generation;
9. Results in change in allele frequency in a population over time; (Evolution is the change in allelic frequency in a population over the generations/time.)
10. Variation results in differential survival and reproductive abilities of individuals in the population, the chance of having an allele in the gene pool that can confer selective advantage will increase,
11. In the absence of variation, selection pressure acts equally on all individuals

(b) Outline the large scale production of human insulin using genetic engineering. [8]

Synthesis of human insulin in bacteria, *Escherichia coli*

Using artificial DNA synthesis

1. Based on known amino acid sequences of the A and B chains, trinucleotides /triplet deoxyribonucleotides representing all the codons are synthesised and joined together in the order dictated by the amino acid sequences / DNA sequence of the polypeptide chains are artificially synthesised.

OR

Construction of ds DNA (Max 2 pts – 1 mark)

1. mRNA coding for insulin is isolated from β-cells of the islets of Langerhans in the pancreas.
2. Reverse transcriptase is used to make a single stranded complementary DNA (cDNA) using mRNA as a template and DNA polymerase is then used to synthesize the second DNA strand, using the first DNA strand as a template, forming a double stranded DNA;

Formation of recombinant plasmid (Max 6 pts – 3 marks)

3. Two recombinant bacteria plasmids are constructed, i.e. one carrying the artificial gene for the A chain and the other carrying the artificial gene for the B chain / two DNA fragments are cloned separately into two bacterial plasmids.
4. To form each of the recombinant plasmid, specific linker DNA (for e.g. EcoRI) is added to blunt ends of cDNA fragment. (followed by digest with EcoRI to obtain cDNA with sticky ends)

5. **DNA fragment and plasmids are then mixed together** and cleaved with the same restriction enzyme (e.g. EcoRI) **at the restriction sites** to produce complementary sticky ends. (can be separate steps)
6. Complementary base pairing between the sticky ends can form via hydrogen bonds (annealing) between i**nsulin gene fragment and plasmid**;
7. DNA ligase is added to seal the DNA fragment and plasmid via formation of phosphodiester bond, forming the recombinant plasmid.
8. Each artificial gene is placed under the control of ① the strong bacteria (*lac)* promoter, which is added at the 5' end for each of the DNA sequence of A and B chain

Transformation of bacteria cells (Max 2 pts – 1 mark)

9. Both recombinant plasmids containing the two artificial genes are transformed separately into *E. coli*
10. Method of transformation

Selection (Max 4 pts – 2 marks)

Successfully transformed bacterial colonies containing plasmids are selected using selection markers present.

Blue-white screening

11. Vector contains ampicillin-resistance gene as first selectable marker and lacZ gene as second selectable marker;;
12. Presence of ampicillin on the agar plate directly eliminates any bacterial cells that are not transformed;;
13. lacZ gene codes for the enzyme ß-galactosidase which breaks down colourless X-gal to yield a blue coloured product;;
14. If insulin cDNA is inserted at a restriction site in the lacZ gene, the gene will be insertionally inactivated and ß-galactosidase will not be synthesized;;
15. Transformed bacterial colonies containing recombinant plasmids will appear white on the agar medium;;

OR

16. Replica plating is carried out with master plate containing ampicillin and replica plate containing tetracycline;;
17. pBR322 ampicillin-**resistance gene** as first selectable marker and tetracycline **resistance gene** used as second selectable marker;;
18. Successfully transformed bacterial cells containing a (recombinant or non-recombinant) plasmid are able to survive and grow on nutrient agar with ampicillin;;
19. If insulin cDNA is inserted into restriction site within the tetracycline resistance gene, the gene will be insertional inactivated resulting in a non-functional gene product and transformed bacteria will not be able to survive and grow on agar plate containing tetracycline;;

Mass cloning of recombinant cells (Max 4 pts – 2 marks)

20. Pick up the white colonies and these **bacterial cells are cultured in fermenters** so that bacteria colonies are grown in large quantities and many copies of fusion bacterial-human polypeptide is synthesized by the bacterial cells.
21. The **polypeptide is harvested/extracted** from bacterial cells by lysing the bacterial cells. A and B chains are then **purified** from the lysate.
22. **Bacterial amino acids and N-formyl methionione are removed**.

23. The **purified chains are mixed together in equal portions** and **incubated under suitable conditions for formation of disulfide bonds** to form synthetic insulin.

OR

24. The two artificial genes are expressed independently as fusion proteins, consisting of the first few amino acids of β-galactosidase, followed by the A or B polypeptide

25. a. Each gene was designed such that its insulin and β-galactosidase segments were separated by a methionine residue
b. so that the insulin polypeptides could be cleaved from the β-galactosidase segments by treatment with cyanogen bromide
The purified A and B chains were mixed, reduced and reoxidized to form the disulfide bonds present in native insulin

c) Discuss the ethical and social **implications** of genetically modified crop plants. [6]

***BOTH POSITIVE AND NEGATIVE EFFECTS!**

I) POSITIVE – Benefits of growing GM crops

- Growth of pest-resistant plants means that lesser crops are lost due to insect damage / diseases spread by insect vectors, therefore resulting in higher yield.
- Lesser insecticide / pesticide is used, therefore the farmers can save more money, lesser ecological damage.
- Growth of herbicide-resistant plants means that farmers can spray herbicides to kill weeds without harming the crops. This results in reduction in competition from weeds, resulting in higher crop yield.
- Savings for famers translate into cheaper foods for consumers
- Enhanced quality of crop (e.g. Golden rice, expression of beta-carotene in endosperm in rice, which is converted into Vitamin A in the body when eaten) which helps to keep people healthy and to prevent malnutrition.

II) SAFETY OF GM CROPS: THE ENVIRONMENT – MAX 2

- There is a risk of transgene transfer to closely-related non-crop species. For e.g. for herbicide-resistant GM crops, the use of herbicides can lead to the rise of super-weeds that are resistant to herbicides as weeds are grown alongside herbicide-resistant GM crops, due to crossing with the closely related GM plant;
- Herbicide acts as a selection pressure when a grower continues to use only one particular herbicide without any other herbicide modes of action, or doesn't use any other cultural practices. The resistant weed type continues to survive, mature and produce seed. Subsequent populations of the resistant biotype will continue to increase, reducing crop yields.
- Farmers would then have to resort to heavy / excessive usage of herbicide, which persist in the environment (i.e. runoff of chemicals into waterways), affecting the ecosystem.
- Bt corn act as selection pressure, rapid evolution of corn rootworms / insects that are resistant to Bt corn (Rootworms that have alleles that allow them to survive

after eating Bt corn have selective advantage, more likely to breed, pass on resistance alleles to subsequent generations, increase in freq. of allele for resistance.

- As corn rootworms become more resistant, farmers will turn to insecticides, thus increasing their costs and losing the ecological benefits originally gained by using Bt corn.
- Effects on Non-target organisms e.g. Bt toxin affecting larvae of monarch butterflies → disruption of food chain / ecological balance;
- Reduction in biodiversity and changes in gene pool, when there is gene transfer of genetic material from GMO to other wild type / native population through e.g. pollination and dispersal.

III) SAFETY OF GM FOODS: HUMAN HEALTH – MAX 2

- Transfer of antibiotic resistance markers in GM crop (use of antibiotic resistance genes as selectable markers in vectors used for transforming plants) to pathogenic microorganisms (gut) which may result in increase in resistance to clinically important antibiotics;
- Probability of introducing novel allergens as GM foods may contain proteins introduced from sources people are allergic to;
- Long term unexpected/negative effect of transgenic food on human health with named examples;

- Monopolistic behaviour of biotechnology companies as terminator gene is likely to be inserted into many GMO seeds, causing second generation seeds to be sterile. Farmers have no choice but to purchase a new batch of GMO seeds;
- Companies seek patents and monopolize technology (e.g. make profits/protect results of research);;
  - Ref. to impact of patents (e.g. increase in price of seeds/ domination of world food production by few companies;;
- Increasing dependence of developing nations on industrialized nations
  - Ref. to advances being skewed to interests of developed countries/benefiting only rich countries;;
  - GM crops / seeds may be too expensive for the poor famers in developing countries;

IV) ETHICAL IMPLICATIONS OF GENETIC ENGINEERING – MAX 2

1. Labelling of GM food is not mandatory in some countries (e.g. religious/medical/dietary concerns
2. Exploitation of animals for genetic engineering
   There is concern over the way animals are exploited for food and medical research.
3. Religious implications in food choices (ref. to animal genes in plants and response from religious groups/groups with dietary restrictions)

a) Describe and explain the advantages of molecular (nucleotide and amino acid sequences) methods in classifying organisms. [6]

Marking Point	Answer
1	Molecular evidences are quantifiable as compared to morphological evidence, which are qualitative because they involve visual observation of a phenotype;
2	For example, percentage homology in DNA and amino acid sequences between species as compared to shape of head;
3	Thus molecular evidences are unambiguous and objective while morphological evidences are subjective;
4	Molecular evidences are open to statistical analysis while it is very difficult to do so for morphological evidence as they are qualitative evidences;
5	Statistical analysis can include chi-square or t-test to determine goodness of fit or significant difference between samples;
6	Morphological evidence may be erroneous because morphological similarities between two species may be due to convergence evolution when the species are subjected to similar selective pressure but in fact they are from two different ancestral linages;
7	For example, sharks and dolphins both have streamlined bodies due to need to swim faster in the sea however, dolphins are mammals while sharks are fishes;

All forms of life use the same genetic language of DNA and RNA, and the genetic code is essentially universal;

Two species that show high molecular homology by comparing DNA / amino acid sequence probably have a common ancestor;

Evolutionary changes between species can be compared via similarities / differences in nucleotide / amino acid sequences even though they may differ vastly in terms of morphology;

Degree of divergence between different species can be **quantitatively** measured by comparison of nucleotide/ amino acid sequences;

- The less nucleotide differences between the gene, the more closely related they are, the more recent their common ancestor;

ref to idea of objectivity in methods;

allows us to classify species that are extinct as long as their DNA material is available.

Molecular comparisons transcend barriers among organisms whose relationships cannot be evaluated by traditional experimental techniques, e.g. selective breeding;

Evolutionary relationships of organisms which reproduce asexually can be established by carrying out molecular comparisons;

allows us to classify closely related organisms more accurately as they usually share very similar base sequences.

(b) Describe how information on mature mRNA is used to synthesise polypeptides in eukaryotes. [8]

Amino acid activation

1 attachment of an amino acid to its specific tRNA (amino acid activation)
2 catalysed by aminoacyl tRNA synthetases

Initiation (max 2.5)

3 initiator tRNA with anticodon UAC carrying methionine
4 associates with the small ribosomal subunit

5 (initiator tRNA-small ribosomal subunit) binds to the 5' cap of the mRNA
6 (small ribosomal subunit) then moves downstream along the mRNA until it reaches the start codon/AUG,
7 (initiator tRNA) binds with the start codon/AUG (through complementary base-pairing)
8 at P site of large ribosomal subunit

9 formation of translation initiation complex / assembly of ribosome + mRNA + translation initiation factors (TIFs)

Elongation (max 2.5)

10 ref. complementary base pairing between anti-codon of incoming aminoacyl-tRNA binds to codon on mRNA
11 at A site of large ribosomal subunit
12 peptide bonds formed between adjacent amino acids catalysed by peptidyl transferase;

13 ribosomes translocates one codon / 3 nucleotides along the mRNA in the 5' to 3' direction
14 movement expose codon at A site of ribosome to receive another aminoacyl-tRNA

15 initial tRNA is relocated to E site and ejected from ribosome
16 tRNA carrying the growing polypeptide chain is repositioned to P site

Termination

17 chain termination occurs when stop codon (UAG, UGA, UAA) in A site;
18 a protein called release factor binds directly to the stop codon in the 'A' site
19 addition of water instead of amino acid to release polypeptide chain;

(c) With reference to solving the demand for food in the world, explain, with an example, the significance of genetically engineered crop plants to improve their yield. [6]

1. Genetic engineering: process of changing the genetic make-up of a living organism or cell by introduction of gene from another species or mutation into a specific gene;
2. Problem: Pests such as the larvae of European corn borer and corn rootroom feed on the corn, resulting in lost crop yields and high spending in insecticides (which also causes env pollution)
3. **Genes** for Bt toxin can be isolated from **soil bacterium, *Bacillus thuringiensis*** and inserted into crops, for e.g. **corn**.
4. Transgenic plants containing the ***Bacillus thuringiensis* (Bt) gene** will produce the **Bt protoxin** which is **ingested** by the insect larvae;
5. Protoxin is cleaved in the insect gut and the **active Bt toxin** is released;
6. Protein binds to specific receptors on cell membranes of the gut wall and causes them to be permeable, causing gut **cells** of insect to **lyse,** eventually killing insects, thus less crops are eaten and yield is increased;;
7. Pest-resistant crops have reduced the need for pesticides, **improving quality and yield** of crop;
8. (opt) Bt crop is safe / harmless to other organisms and the environment due to its selectivity in action, as compared to broad-spectrum insecticides;

Marker's comments:

- Point (2): **® Bt toxin inserted / introduced.** The genes coding for Bt toxin is introduced, not the protein toxin itself!
- Bacteria is not inserted into plant!
- Point (3): Plant now produces the Bt protoxin (protein). The insect have to **feed** on the plant parts containing the protoxin for the Bt protoxin to enter the insect.
- Point (4): Bt protoxin **(inactive)** is converted to **active** Bt toxin in the insect's gut.
- Point (5): The gut / gut wall doesn't lyse. The gut **cells** lyse. (due to pores created in the gut epithelial cell membrane, allow free movement of ions across memb, disrupting natural ion gradients)