Section A

1 (a) Suggest and explain three different hypotheses, other than those related to diet, that could account for any of the trends shown in Table 1.1.

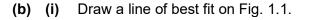
At least one of the hypotheses must refer to TB and at least one must refer to CVD. [6] Hypotheses about [quote data] tuberculosis death rate decreasing gradually over the years from 1900 to 2015, from 195 to 1 per 100 people per year respectively:

- 1. <u>Development of antibiotics</u> to treat infected TB patients since <u>TB is caused by</u> <u>Mycobacterium tuberculosis bacterial infections</u> which can be treated with <u>bacteriocidal and/or bacteriostatic antibiotics</u>;
- 2. <u>Vaccination programme</u> so that US citizens have <u>herd immunity</u> to prevent the spread of TB, reducing the number of deaths;
- 3. <u>Vaccination programme</u> to produce <u>memory B cells</u> in individuals so that there is a <u>faster</u>, <u>larger secondary immune response</u> which reduce the death rate;
- Increased awareness about the need to <u>isolate infected patients</u> as preventative measures so that the <u>Mycobacterium tuberculosis</u> bacterial infections which are <u>transmitted by airborne</u> means are limited in spread;

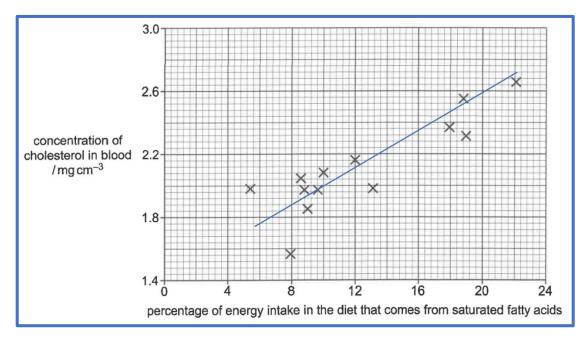
Hypotheses about [quote data] CVD death rate first increasing from 1900 to 1950, from 250 to 450 per 100 people per year respectively, and then decreasing from 1950 to 2015, from 450 to 220 per 100 people per year respectively:

- 5. <u>Increase in stress due to work</u> as US economy became more industrialised from 1990 to 1950, and an <u>improvement in emergency healthcare or drugs</u> from 1950 to 2015;
- 6. <u>Lack of awareness</u> about CVD being caused by a <u>sedentary lifestyle</u> from 1990 to 1950, and a <u>greater awareness of active lifestyle</u> from 1950 to 2015;

At least 1 from points 1-3 and 1 from points 5-6.



[1]



- (ii) Explain what is shown by the slope of the line of best fit you have drawn on Fig. 1.1. [1]
 - An increase in percentage of energy intake in the diet that comes from saturated fatty acids is <u>correlated to</u> (Reject: cause) a <u>proportional increase</u> in concentration of cholesterol in the blood;
 - [Quote Data] E.g. An increase from 6.6% to 20.2% of energy intake in diet that comes from saturated fatty acids is seen to correspond to an increase in 1.8 mg cm⁻³ to 2.6 mg cm⁻³ of cholesterol in blood;
- (iii) Distinguish between a triglyceride and a fatty acid. [2]
 - 1. A triglyceride is <u>hydrophobic</u> due to the <u>absence of carboxylic acid groups</u>, while a fatty acid is <u>hydrophilic</u> due to the presence of <u>carboxylic acid groups</u>;
 - 2. A triglyceride has a <u>glycerol joined to three fatty acids by three ester linkages</u>, while a fatty acid <u>does not have any ester linkage and no glycerol;</u>
- (iv) State two roles of cholesterol in cells. [2]
 - 1. Cholesterol provides <u>mechanical stability</u> as it forms <u>weak hydrophobic interactions</u> with <u>neighbouring hydrocarbon chains of phospholipids;</u>
 - Cholesterol <u>regulates membrane fluidity</u>* by preventing the membrane from being overly fluid at warmer temperatures as cholesterol's rigidity <u>restricts phospholipids</u>' <u>lateral movement</u>;

(Points 3 and 4 are further elaborations of point 2)

- 3. The membrane is <u>prevented from being overly firm at lower temperatures</u> as cholesterol <u>prevents close packing</u> of phospholipids and hence prevents its solidification/ crystallization;
- 4. Permeability increases when the membrane is overly fluid;
- (c) Complete Table 1.2 to show for each set of results:
 - which of the causal links of the Diet-Heart Hypothesis represented by the arrows in Fig. 1.2 was investigated (write A, B or C)
 - whether the results support the causal link shown by this arrow (write **yes** or **no**).

Table 1.2				
results	causal link investigated	do the results support the causal link?		
Fig. 1.3	С	No		
Fig. 1.4	С	No		
Fig. 1.5	В	Yes		
Fig. 1.6	А	Yes		
		[4		

(d) (i) Dietary fats, proteins and carbohydrates are digested by enzymes in the gut before being absorbed into the blood. These enzymes hydrolyse bonds in the food molecules that originally formed by condensation reactions.

List **three** types of covalent bonds broken by these digestive enzymes in the gut. [3]

1. Glycosidic bond

2. Peptide bond

3. Ester bond

- (ii) State the main roles in the body of the products of digestion of proteins and carbohydrates. [3]
 - Protein is digested to <u>amino acids</u>* while carbohydrates such as starch is digested to <u>glucose</u>*;
 - 2. Amino acids are needed for <u>synthesis of enzyme</u>, <u>proteins embedded in cell</u> <u>membrane such as receptors or transport proteins</u>, for synthesis of <u>signal</u> <u>molecules such as insulin;</u>
 - 3. Glucose is <u>main respiratory substrate</u> that upon oxidation by respiration produces ATP/ releases energy;
- (iii) Name the membrane system or organelle within the gut epithelial cells where each of these events may take place: [2] formation of triglyceride droplets smooth endoplasmic reticulum formation of exocytotic vesicles Golgi apparatus
- (iv) Suggest and explain why lipoprotein spheres are used to transport triglycerides in the blood. [2]
 - 1. Triglycerides have long <u>non-polar hydrocarbon chains</u> and are <u>hydrophobic*</u> and <u>insoluble*</u> in water of the blood plasma;
 - Lipoprotein sphere has <u>phosphate head</u> of phospholipid which is <u>charged</u> and <u>hydrophilic</u>* as well as the <u>hydrophilic regions</u> of embedded <u>proteins facing</u> <u>outwards</u> that can <u>interact with water</u> molecules;
 - 3. Triglycerides need to be <u>packaged within the lipoprotein spheres</u> in order to be transported in the blood as blood plasma is a hydrophilic environment;

(e)

Use this information and the data in Table 1.3 to discuss whether the dietary changes triggered by the Diet-Heart Hypothesis improved the health of people in the USA. [4]

- 1. Percentage prevalence of type 2 <u>diabetes increases slightly</u> by <u>1.5 %</u> over a period of 40 years from <u>1925 to 1975</u> but <u>increases significantly by 5.1%</u> over a shorter period of 50 years from <u>1975 to 2015</u>;
- 2. There is an <u>gradual increase</u> in <u>obesity</u> of <u>11%</u> from <u>1900 to 1975</u> and a <u>steep</u> <u>increase</u> of <u>22%</u> from <u>1975 to 2015</u>/ increase in obesity percentage from 1975 to 2015 is twice that of increase from 1900 to 1975;
- 3. Dietary change from fats to carbohydrate based on Diet-Heart Hypothesis <u>did not</u> <u>improve health</u> as percentage of people suffering from type 2 <u>diabetes and obesity</u> <u>increases more;</u>
- 4. However the data did not provide sufficient information such as the number of people involved, age and sex and whether their daily diets were monitored/ other factors such as regularity of exercise and adequacy of sleep were not taken into consideration;

[Total: 30]

- **2 (a)** Explain what can be learnt by comparing genomes of different species of fish such as seahorses and zebrafish. [3]
 - 1. Evaluating <u>molecular homologies</u> based on DNA of <u>cytochrome c gene</u> (any example) can determine <u>degree of nucleotide similarity;</u>
 - 2. The <u>more related they are</u>, the <u>greater similarity</u> there is in the sequence of their <u>homologous gene/DNA</u> allowing the <u>determination of ancestor-descendant</u> <u>relationships</u>;
 - 3. Understand the link between genotype and phenotype;
 - 4. Reveal structure of <u>genetic variation</u> between <u>different populations of the individual</u> <u>species;</u>
 - (b) Complete Table 2.1 by inserting the letters P, Q or R to show which type of genetic change is most likely to have occurred during the evolution of the seahorse from a zebrafish-like ancestor, for each of the phenotypic features listed. [2]

phenotypic feature	zebrafish	seahorse	type of genetic change
number of fin locations	5	3	R
male has pouch for	absent	present	Q
development of embryos		-	
number of teeth	22	0	Р

- (c) Scientists carried out PCR (polymerase chain reaction) on the DNA of seahorses and zebrafish using a set of primers for a particular zebrafish gene. The scientists suspected that this gene was missing from seahorses.
 - Outline how the scientists could analyse the contents of the tubes containing the PCR products to determine whether this gene is missing from seahorses.
 - Describe the result that would confirm the absence of this gene from seahorses. [3]
 - <u>Separate PCR products</u> by performing <u>gel electrophoresis</u>* which separates the DNA fragments using current;
 - 2. <u>Meshwork</u> of agarose polysaccharides <u>impede movement of longer fragments more</u> than shorter fragments causing them to <u>migrate slower</u> than shorter fragments and end up <u>nearer to the well</u>;
 - A method of visualization is suggested stain gel with ethidium bromide followed by visualisation under UV light; or
 carry out a Southern Blot where a radioactive DNA probe complementary to

carry out a <u>Southern Blot</u> where a <u>radioactive DNA probe</u> complementary to the gene is used to bind to the gene and then detect the probe with <u>autoradiography using an</u> <u>X-Ray film</u>;

 If the <u>fragment that corresponds to the gene</u> is <u>not seen</u> as a band after visualisation, it means that <u>gene is absent</u> in seahorses; or
If the fragment that corresponds to the gene is seen as a band after visualisation, it

If the <u>fragment that corresponds to the gene is seen</u> as a band after visualisation, it means that <u>gene is present</u> in sea horses;

pt 1 & 4 are compulsory points

- (d) Scientists estimated the total number of genes in the seahorse genome using a combination of two methods:
 - searching published databases for gene sequences in other organisms that match sequences in the seahorse genome
 - searching the seahorse genome for sequences that match sequences of seahorse RNA.

Explain why combining both methods improves the accuracy of the estimate of the number of genes. [2]

- In method 1 looking for gene sequences in seahorses that match the known genes in other organisms would give a good estimate, even picking up those genes in the seahorse that are <u>present but switched off</u> (therefore not producing RNA);
- In method 2 looking for genome sequences that match RNA sequences would pick up <u>genes unique to the seahorses</u> that are <u>expressed</u>. These would be missed in method 1 since other organisms will not have these;

[Total: 10]

- **3** Trees remove carbon dioxide from the atmosphere and store this carbon in their biomass in the long term. This long-term storage of carbon is called carbon sequestration.
- (a) The carbon sequestered in a tree is not in the form of carbon dioxide.

Identify **three** biomolecules in which carbon may be sequestered in a tree. [3]

- 1. lignin
- 2. cellulose
- 3. starch
- (b) Show your working and give your answer in kilograms to three significant figures. [2] There are 26 226 trees in roads and 2356 in parks <u>Total number of trees = 28 582</u> <u>Rate of carbon sequestration for both road and park trees = 487+44 = 531</u> Mean mass of carbon sequestration by a single tree = <u>531/28582 = 0.0186 tonnes = 0.0186 x 1000 Kg = 18.6 kg</u>

mean mass of carbon sequestered =18.6......kg [2]

(c) (i) Use these data to calculate the percentage of the element carbon released into the atmosphere by cars in Singapore that is offset by the urban trees.

Show your working. [3] Total CO₂ emission by 600,000 cars = $4.04 \times 600\ 000 = 2\ 424\ 000$ tonnes of CO₂ 27% of 2 424 000 = mass of carbon = $654\ 480$ Urban trees sequester 3872 tonnes of carbon Total mass of carbon produced by cars = 654480Percentage offset by urban tree = $3872/654480 \times 100 = 0.59\%$

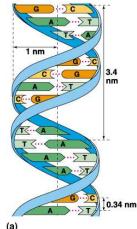
- (ii) Using your answer to (c) (i), comment on the benefits to the environment of planting urban trees in Singapore. [2]
 - 1. 0.59% of element carbon will be offset by urban trees;
 - 2. causing carbon sequestration resulting in less carbon in atmospheres;
 - 3. which will reduce the greenhouse gas effect and lessen the impacts of climate change;

[Total: 10]

Section B

4 (a) Describe the molecule structure of DNA.

- 1. <u>Basic unit</u> of a DNA molecule is the <u>deoxyribonucleotide</u>*.
- 2. <u>Pentose sugar</u> of a DNA molecule is <u>deoxyribose</u>*.
- <u>Nitrogenous bases</u>* could be <u>adenine, thymine, guanine</u>* or <u>cytosine</u>* (A, T, G or C respectively).
- <u>Purines</u>* are nitrogenous bases with <u>2 rings</u> while <u>pyrimidines</u>* are nitrogenous bases with <u>1 ring</u>. <u>Purines</u> include <u>adenine and guanine</u> while <u>pyrimidines</u> include <u>thymine and cytosine</u>.
- 5. Nitrogenous base is joined to the <u>carbon 1</u> of <u>deoxyribose sugar</u> by <u>covalent</u> bond.
- 6. *Phosphate group** is derived from phosphoric acid and is joined to <u>carbon 5</u> of the deoxyribose sugar by <u>phosphoester bond</u>.
- 7. Phosphate groups are <u>negatively charged</u>, hence DNA is negatively charged molecule.
- 8. Covalent bond linking two adjacent nucleotides is called a phosphodiester bond*.
- 9. DNA molecule consists of <u>two polynucleotide chains/ strands</u> twisted around each other to form a <u>double helix</u>.
 - a. 2 strands have *complementary bases** to each other.
- 10. The two strands (or chains) run in opposite directions i.e. they are antiparallel.
 - a. One strand runs in the <u>5' to 3' direction</u> and the complementary strand runs in the <u>3' to 5' direction</u>
- 11. The <u>sugar-phosphate backbones of both strands lie on the outside</u> of the molecule, with the <u>nitrogen-containing bases on the interior</u>.
- 12. <u>Width between the 2 sugar phosphate backbones is</u> <u>constant (2.0 nm)</u> and equal to the <u>combined width of a</u> <u>purine and a pyrimidine</u>
- 13. The two strands are held together by <u>numerous weak</u> <u>hydrogen bonds</u> that form between the <u>nitrogenous bases</u> <u>of opposite strands</u>.
 - a. (purine) **A=T** (pyrimidine) base pair, forming **2** hydrogen bonds.
 - b. (purine) **GEC** (pyrimidine) base pair, forming **3 hydrogen bonds**.
- 14. Stacking one base pair on top of another, <u>one complete turn</u> of the double helix is seen to be made of <u>10 base pairs</u>, and spans a distance of <u>3.4 nm</u>.



15. The helix is right-handed

[15]

©1999 Addison Wesley Longman, Inc.

- (b) Outline the functions of non-coding DNA in eukaryotes and suggest how non-coding DNA may have a role in evolution. [10]
 - 1. Non-coding DNA includes <u>telomeres</u>, <u>centromeres</u>, <u>control elements such as</u> <u>promoter</u>, <u>enhancer</u>, <u>and silencer</u>, <u>and introns</u>.

Telomeres (max 2 marks)

- Telomeres are <u>non-coding</u>* <u>tandem repeat sequences</u> found at both <u>ends</u> of linear chromosomes;
- 3. <u>Each round of DNA replication</u> will result in the <u>shortening</u> of daughter molecules at <u>the telomeres</u> because DNA polymerase is unable to replace the RNA primers with DNA; (idea of end replication problem)
- 4. Since telomeres are non-coding, this ensures that <u>vital genetic information/genes</u> <u>are not lost / eroded</u> with each round of replication;
- 5. By forming a <u>loop</u> with 3' overhang, they <u>protect and stabilise terminal ends</u> of chromosome, hence <u>preventing fusion</u> of the ends with those of <u>other chromosomes</u>;
- 6. Prevent DNA repair machinery from recognising the ends of chromosomes as DNA breaks/damage, hence preventing <u>cell cycle arrest and/or apoptosis;</u>
- Either: The 3 overhang of the telomeres allow their own extension, by providing an attachment point for the correct positioning of the enzyme telomerase in certain cells, e.g. germ cells

OR:

They possess a 3' overhang which base pairs with the RNA template on telomerase, so ensures proper <u>alignment of telomerase</u> and allows extension of telomeric ends in certain cells e.g. germ cells.

Centromeres (max 2 marks)

- 8. Centromeres are <u>non-coding DNA</u> consisting of <u>tandem repeat sequences</u> found at one location anywhere along the length of the chromosome;
- 9. They allow sister chromatids to adhere to each other;
- 10. They allow proteins called *kinetochores** to attach;
- 11. and subsequently <u>spindle fibres</u>, to attach to kinetochores so that <u>sister</u> <u>chromatids/homologous chromosomes can be separated</u> to opposite poles;

Promoter (max 2 marks)

- 12. serve as <u>recognition site</u> for the <u>binding of **general transcription factors**</u>* and <u>**RNA polymerase***</u> to <u>initiate</u> <u>transcription*</u>;
- 13. has critical elements, <u>TATA box*</u> that determines the precise location of transcription start site;
- 14. 14. has critical elements, <u>CAAT and GC boxes</u>* to <u>improve efficiency of</u> <u>promoter</u> by <u>recruiting</u> <u>general transcription factors</u>* and <u>RNA polymerase</u>* to promoter.

Enhancer (max 2 marks)

- 15. when <u>bound</u> with <u>specific transcription factors</u>* known as <u>activators</u>*, promotes assembly of <u>transcription initiation complex</u>*at promoter;
- 16. when <u>bound</u> with <u>specific transcription factors</u>* known as <u>activators</u>*, may <u>recruit</u> <u>histone acetyltransferase</u>* and <u>chromatin remodeling complexes</u>* to <u>decondense chromatin</u> (increase accessibility of promoter to general transcription factors and RNA polymerase)
- 17. increase frequency of transcription

Silencer (max 2 marks)

- 18. allow <u>binding</u> of <u>specific transcription factors</u>* called <u>repressors</u>* by <u>preventing</u> assembly of <u>transcription initiation complex</u>* at <u>promoter</u>
- 19. when <u>bound</u> with <u>specific transcription factors</u>* known as <u>repressors</u>*, may <u>recruit</u> <u>histone deacetylase</u>* and <u>chromatin remodeling complexes</u>* to <u>condense chromatin</u> (decrease accessibility of promoter to general transcription factors and RNA polymerase)
- 20. decreases the frequency of transcription;

Introns (max 2 marks)

- 21. <u>Splicing*</u> of pre-mRNA involves <u>cutting out introns and joining exons</u> to form a <u>mature mRNA*;</u>
- 22. <u>introns</u> are <u>excised</u> and hence non-coding, so the mature mRNA comprises of <u>exons</u> which <u>code for the sequence of amino acids</u> in a protein;
- 23. In <u>alternative RNA splicing</u>, <u>spliceosomes</u> are involved in <u>excision of introns</u> and some exons, and joining of remaining exons giving rise to different combinations of exons;
- 24. One gene produces *mature mRNA** with <u>different combinations of exons</u>, hence giving <u>different proteins/protein isoforms</u>;

Control elements' role in evolution (max 2 marks)

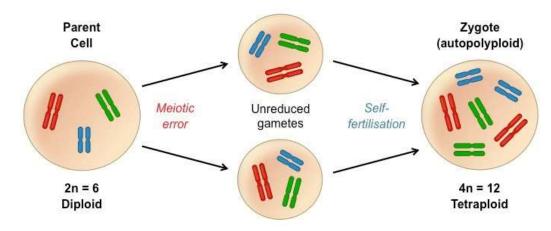
- 25. [compulsory point] <u>Mutations</u> to the <u>promoter</u>, <u>enhancer</u>, <u>or silencer</u> lead to <u>changes in transcription</u> of the gene they control
- 26. This affects the <u>amount of protein</u> coded, which in turn <u>affects the phenotype</u>, making the organism either <u>selected for</u> or <u>selected against</u>;
- 27. If the mutation to the control elements leads to <u>selective advantage</u>, then the <u>mutated control elements would be passed down to the offspring</u>.

Introns' role in evolution (max 2 marks)

- 28. [compulsory point] Mutations to the centromere result in non-disjunction;
- 29. Unequal separation of chromosomes due to <u>inability of spindle fibres</u> to attach to centromere may lead to <u>aneuploidy</u> or <u>polyploidy</u>.
- 30. Autopolyploidy and allopolyploidy would result in sympatric speciation.

QWC: must answer both functions AND role in evolution.

Autopolyploid



Allopolyploid

Species A number not and the second s	ile hybric ypioid)
2020	
Normal gamete Normal gamete	and the second second

[Total: 25]

- **5 (a)** Describe the molecular structure and transport functions of haemoglobin. [15] Structure
 - 1. Haemoglobin molecule is a *globular** protein that has a <u>quaternary</u> structure with <u>4 polypeptide subunits</u>,
 - 2. namely <u>2 *α*-globin</u>* subunits and <u>2 β-globin</u>* subunits;
 - 3. Each polypeptide is made up of *a-helices**, which are its secondary structure;
 - 4. Each subunit is folded into a *globular** tertiary structure
 - Each subunit is arranged such that most of its amino acids with <u>hydrophilic R</u> <u>groups</u>* are on <u>external surface</u> while its amino acids with <u>hydrophobic R</u> <u>groups</u>* are <u>buried in interior</u>;
 - 6. makes it <u>soluble in water/aqueous environment</u>, so that it can be easily transported in blood;
 - The 4 subunits are held together by intermolecular interactions between R groups of amino acids. They are <u>ionic bonds*</u>, <u>hydrogen bonds*</u> and <u>hydrophobic</u> <u>interactions</u>*;
 - each subunit is made of <u>protein globin</u> and a prosthetic (non-protein) component called <u>haem group</u>*;
 - 9. each haem group consists of a *porphyrin ring** and an *iron ion (Fe*²⁺)*;

Function

- Haemoglobin is found in red blood cells of vertebrates, <u>transports oxygen</u>* in blood;
- 11. <u>Fe²⁺</u> of <u>haem group binds temporarily to oxygen molecule</u>,
- 12. so <u>1 Hb molecule can carry up to 4 oxygen molecules</u>, at a time forming oxyhaemoglobin; (ref. <u>transport oxygen</u> in blood)
- <u>4 subunits</u> held together by weak <u>intermolecular interactions formed</u> between R groups (hydrogen bonds, ionic bonds and hydrophobic interactions), allows movement that influences affinity for oxygen allowing for <u>cooperative binding</u>* of oxygen;
- As a result <u>binding of one oxygen molecule</u> to one haemoglobin subunit induces a <u>conformational</u>* <u>change</u> in remaining 3 subunits so that their <u>affinity for</u> <u>oxygen increases</u>;

- 15. At higher carbon dioxide concentration, due to a lot of respiration, haemoglobin can <u>bind to carbon dioxide</u> which causes a <u>conformational change in the haemoglobin;</u>
- 16. This <u>decreases</u> in hemoglobin's <u>affinity for oxygen</u> and facilitates the <u>release of oxygen</u>;

QWC: must answer both structure AND transport role.

- (b) In a blood transfusion, blood from a donor is transferred into the veins of a recipient patient. Before transfusion, blood is tested in various ways to ensure that it is:
 - safe for transfusion to any recipient.
 - safe for transfusion to the specific recipient.

Explain how physiological problems may develop in the recipient as a result of receiving blood that has not been tested in either of these ways. [10]

- 1. Blood needs to be tested to ensure safety for any recipient by checking that it is <u>does not contain microorganisms / pathogens,</u> such as bacteria and viruses;
- 2. Transfusion of blood containing bacteria or viruses to recipient would <u>cause</u> <u>infections</u> in the recipient;
- 3. Blood also needs to be tested as safe for the specific recipient by <u>matching the blood</u> <u>type</u>;
- 4. The ABO blood group in humans is controlled by a gene locus I with 3 alleles: I^A, I^B and I^o, resulting in 4 possible blood groups: A, B, AB and O;
- 5. Red blood cells can contain <u>antigen A</u> and/or <u>antigen B</u> based on the blood group of the individual;
- 6. Blood group A individuals express antigen A, blood group B individuals express antigen B, blood group AB individuals express both antigens A and B, and blood group O individuals do not express antigens A or B;
 - (description of each blood group and their respective antigens)
- 7. Individuals will produce antibodies against non-self antigens;
- Blood group A individuals produce antibodies against antigen B, blood group B individuals produce antibodies against antigen A, blood group AB individuals do not produce antibodies against antigens A and B, and blood group O individuals produce antibodies against both antigens A and B;
 (description of each blood group and the antibodies produced)

(description of each blood group and the antibodies produced)

- 9. If matching of blood group was not done, recipients could be given <u>incompatible</u> <u>blood</u>. The red blood cells in the transfused blood could be <u>recognised by the</u> <u>recipient's antibodies and destroyed/lysed</u>;
- 10. Recipient would hence not benefit from the blood transfused there is <u>still</u> insufficient red blood cells to transport oxygen in the recipient;
- 11. When an immune response is mounted against the transfused blood, <u>inflammatory</u> <u>responses</u> are also induced, contributing to <u>fever and pain</u> in the recipient;
- 12. AVP: ref to other antigens eg. rhesus factor;

QWC: must address both bullet points

[Total: 25]