Nov 2014 H2 Bio Paper 2

N14P2Q1

(a) With reference to **Fig 1.1**, describe the curve between points A and B [2].

1. As temperature increases from 35^0C (pt **A**) to 50^0C, the rate of reaction of enzyme increases gradually from 0 to 8a.u.
2. However, from 50^0C to 65^0C (pt **B**), there is a steeper increase in rate of reaction of enzyme from 8a.u. to 65 a.u. This increase is about 7 times that of the increase in rate from 35^0C to 50^0C .

(b) Explain why the reaction rate changes from:

(i) A to B [3]

1. As temperature increase from 35^0C (at **A**) to 65^0C (at **B**), there is increase in kinetic energy of the enzyme and substrate molecule.
2. which increases ***frequency of effective collisions**** between substrate and enzyme thus rate of formation of ***enzyme-substrate complex**** increases ;
3. increasing temperature also increases the number of molecules having sufficient energy to overcome the ***activation energy**** barrier to form the products of reaction;

(ii) **C** to **D** [3]

1. At 75^0C (pt **C**), the ***optimum temperature**** of Taq polymerase, there is greatest number of molecular collisions and hence max rate of reaction
2. As temperature increase further to 85^0C (pt **D**), which is beyond optimum temperature, thermal agitation / vibration of enzyme molecule breaks hydrogen, ionic bonds and other weak interactions that stabilizes the 3D conformation resulting in ***denaturation****
3. The enzyme ***active site**** no longer ***complementary in shape**** and charge to the substrate and the rate of reaction decreases steeply from maximum rate of 95 a.u. to almost 0a.u.

(c) Suggest how the structural features of Taq polymerase make it thermostable [2]

1. More ***Cysteine**** residue may be present in the Taq polymerase allowing the formation of more ***disulphide linkages**** with another cysteine residue to maintain the 3D conformation
2. Disulphide linkages are strong covalent bonds difficult to be broken by high temperature
3. Hence the 3D conformation of active side maintained \

N14P2Q2

(a) Give the full name of the bond holding the two glucose molecules together in the way shown. [2]

1. α-1,4-glycosidic bond

(b) Describe how this bond may be broken to release two molecules of glucose. [2]

1. Addition of water in ***hydrolysis**** reaction
2. Enzymatic action of maltase
3. Acid hydrolysis by heating it with hydrochloric acid

(either 2. or 3.)

(c) (i) Describe the arrangement of phospholipids in cell membranes. [2]

1. 2 layers of phospholipid molecules in a bilayer
2. With the hydrocarbon tails facing the inside of the membrane and the phosphate heads facing the outside next to aqueous medium

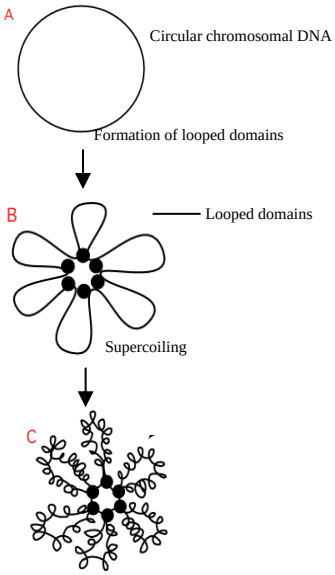
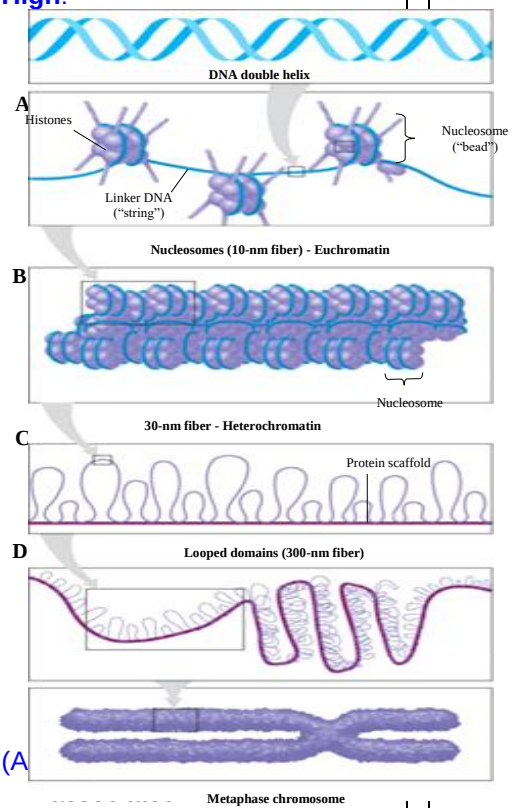
(ii) Explain how the structure of phospholipids is related to this arrangement in cell membranes. [3]

1. Phosphate heads are charged and hydrophilic and will form hydrogen with water
2. Hydrocarbon tails are non-polar and therefore hydrophobic and arranged away from aqueous medium
3. And forms hydrophobic interactions with the hydrocarbon tails of other phospholipid molecules to form a hydrophobic core in the bilayer structure

[Total : 9]

N14P2Q3

(a) Describe how bacterial chromosomes differ from eukaryotic chromosomes in terms of structure and organization. [4]

Feature	Prokaryotic genome	Eukaryotic genome
Size	10^5-10^7 base pairs	10^7-10^{11} base pairs
Appearance	Generally **a single, circular** molecule	**Multiple, linear** molecules
Molecule	Double Helix DNA	
Association with proteins	Yes – **relatively less** e.g. **histone-like proteins**	Yes – **large amounts** e.g. **histones**, scaffold proteins
Level of DNA packing/coiling	Relatively **low**: DNA double helix ↓ some looping around **histone-like proteins**  (A) Unfolded chromosome from *E. coli* has a diameter of 430µm. (B) DNA is folded into **chromosomal looped domains by protein-DNA associations**. Six domains are shown, but actual number is	**High**:  (A with proteins called **histones**. DNA molecules are negatively- charged, histone

	about 50. (C) **Supercoiling** cause further compaction, such that it fills an area of about 1 µm.	are **positively-charged**. DNA thus is held around histones by electrostatic interactions. Most of DNA is wound around octamers of 8 histone proteins to form **nucleosomes**, the 10 nm fibre. Remainder of DNA, called linker, joins adjacent nucleosomes. (B) The 10-nm fibre coils around itself to form a 30 nm chromatin fiber (or solenoid). (C) The 30-nm fibre forms loops called looped domains (a 300-nm fibre) when associated with scaffold proteins. (D) **Supercoiling** present. The loops further coil and fold to produce characteristic metaphase chromosome.
Location	**Nucleoid** region, not membrane-bound	**Nucleus** (surrounded by nuclear envelope)
Extrachromosomal DNA	Present – **plasmids** (much smaller rings of DNA compared with bacteria chromosome)	**No plasmids** (however mitochondria and chloroplast have their own DNA)
Number of genes	4,500	25,000
Non-coding regions (between and within genes)	**Not common** – typically less than 15%	**Common** – about 98%
i. introns	**None present** (rare; only in some genes)	**Many present**
ii. promoters	**Present**	
iii. enhancers/ silencers	**Rarely present**	**Present**
iv. repeated sequences	**Few**	**Many**
v. operons	**Many**	**Few known ones (e.g. in nematodes)**
Origin of replication (per chromosome)	**One**	**Many**

*__Genome__ refers to a complete set of genetic material in a particular cellular component.

(b) Describe what occurs from the end of **stage 3** up to **stage 4**, as shown in Fig. 3.1. [4]

(i)

1. After contacting a recipient cell, the sex pilus retracts, pulling the two cells together.
2. the F^+ cell then forms a temporary cytoplasmic ***mating bridge**** with the F^- cell and transfers its F plasmid DNA to it.
3. one strand of the double-stranded F plasmid is nicked by a nuclease.
4. The free 3' end of the nick is extended by DNA polymerase for the synthesis of a new complementary strand using the intact strand as the template
5. The newly synthesized strand displaces the nicked strand which is transferred concurrently, via the 5' end, across the mating bridge into the recipient cell.
6. Upon completion of a unit length of the plasmid DNA (after 1 round), another nick occurs to release the original strand and end the replication of the newly synthesized strand;

(ii) Explain the role of F plasmid. [3]

1. F factor on F plasmid, codes for proteins necessary for the formation of sex pili and subsequent cytoplasmic mating bridge,
2. allowing for conjugation to occur between bacteria.
3. This allows for bacterial genes to be transferred between bacteria and hence increases genetic variation between bacteria.

[Total : 11]

N14P2Q4

(a) Suggest the reason for the peak in the rate of DNA synthesis shown in Fig. 4.1. [2]

1. Gene coding for ribosomal RNA was amplified;
2. To allow for an increase/high rate of ribosomal RNA synthesis during egg cell growth;

(b) Describe and explain the pattern of transcription visible on the part of the DNA coding for ribosomal RNA, labelled X in Fig. 4.2. [2]

1. Multiple ribosomal RNA transcripts are produced concurrently from transcription of a single gene,
2. and length of the ribosomal RNAs increase progressively from left to right of region X ;
3. This is because the direction of transcription takes place in a single direction/ribosomal RNA is produced in 5' to 3' direction;

c) Explain why such large amounts of ribosomal RNA are required in frog egg cells. [2]

1. Large amounts of ribosomal RNA are required for synthesis of large numbers of ribosomes in the frog egg cells;
2. This is required for high rate of protein synthesis following fertilisation of the egg cells;

d) Suggest possible roles for the non-transcribed DNA that is found between the ribosomal genes. [2]

1. the non-transcribed DNA contain ***promoter****;
2. which binds ***RNA polymerase**** and ***general transcription factors**** to form the ***transcription initiation complex**** for transcription to take place;

OR

3. the non-transcribed DNA may contain ***enhancer****;
4. which binds ***activators**** to promote the assembly of ***general transcription factors**** and ***RNA polymerase**** at the ***promoter**** of the ribosomal gene to form the ***transcription initiation complex****;

OR

5. the non-transcribed DNA may contain ***silencer****;
6. which binds ***repressors**** to prevent the assembly of ***general transcription factors**** and ***RNA polymerase**** at the ***promoter**** of the ribosomal gene to form the ***transcription initiation complex****;

e) Explain how operons allow for rapid response by bacteria to environmental change. [2]

1. multiple genes coding for products involved in the same biochemical pathway are under the control of a single ***promoter****;
2. these genes are therefore turned "on" or turned "off together, allowing the bacteria to respond rapidly to changes in the environment;

[Total : 10]

N14P2Q5

5(a) Draw a genetic diagram to explain both crosses. [5]

Use the following symbols to represent the different alleles involved:

R -red flowers r -white flowers A -axial flowers a -terminal flowers

Parental phenotype	Red, axial flowers	X	White, terminal flowers
Parental genotype	RRAA	X	rraa
Gametes	(RA)		(ra)

F1 phenotype RrAa [1]

F1 phenotype All red, axial flowers [1]

F1 selfing RrAa x RrAa

Gametes	(RA)	(Ra)	(rA)	(ra)
(RA)	RRAA **Red, axial**	RRAa **Red, axial**	RrAA **Red, axial**	RrAa **Red, axial**
(Ra)	RRAa **Red, axial**	RRaa **Red, terminal**	RrAa **Red, axial**	Rraa **Red, terminal**
(rA)	RrAA **Red, axial**	RrAa **Red, axial**	rrAA **white, axial**	rrAa **white, axial**
(ra)	RrAa **Red, axial**	Rraa **Red, terminal**	rrAa **white, axial**	rraa **White, terminal**

Offspring genotype	R_A_	R_aa	rrA_	rraa
Offspring phenotype	Red, axial flowers	Red, terminal flowers	White, axial flowers	White, terminal flowers
Phenotypic ratio	9.5	3.1	2.7	1
≈	9	3	3	1

[1] correct offspring genotypes in Punnett square

[1] relate genotype to phenotype

[1] correct phenotypic ratio of 9:3:3:1

(b) Explain how different characteristics can be inherited independently in dihybrid inheritance. [2]

1. 9: 3: 3: 1 offspring/F_2 phenotypic ratio indicates the alleles of each character are found on different chromosomes and inherited independently of one another;
2. The alleles of different genes ***assort independently**** of each other because homologous pairs of chromosome align randomly on either side of the metaphase plate/ because alignment of each homologous pair is independent of other homologous pairs/ because two alleles for flower colour segregate independently of the two alleles for flower position.

(c) Explain why heterozygous plants for this gene, Tt, have the same phenotype as homozygous dominant plants, TT. [3]

1. Allele T codes for a functional enzyme/is the functional copy of the gene involved in synthesis of gibberellic acid.
2. Allele t codes for the non-functional enzyme/ is the non-functional copy of the gene.
3. In a heterozygote, allele T masks the presence of allele t.
4. Presence of 1 T allele (in homozygous dominant or heterozygous individuals) causes T allele to be expressed, producing functional enzyme that causes plants to be grow tall. (Allele T is dominant over t)

[Total : 10]

N14P2Q6

(a) Name the structures labelled **A**, **B**, **C**, and **D** on **Fig. 6.1**. [4]

A Intergranal lamella
B Chloroplast envelope (R: inner membrane or outer membrane)
C Stroma
D Granum

b(i) Suggest **two** advantages of these large protein complexes being held in the membranes of structures **A** and **D** in Fig. 6.1. [2]

1. Maintains the sequential arrangement of the ***photosystems**** and ***electron carriers of electron transport chain**** for the flow of electrons;

2. Maintains proton gradient for ATP synthesis since the ***hydrophobic core**** of the membrane is impermeable to protons and this is essential for chemiosmosis
OR
The enclosed thylakoid space allows the build up of protons here by proton pumps found in the electron transport chain, enabling the establishment of a proton gradient across the thylakoid membrane for chemiosmosis.

3. Allows ATP synthase to be embedded in the correct orientation, where the active site faces the stroma / for protons to diffuse from thylakoid space to stroma.

4. Through compartmentalization, it improves the efficiency of the different reactions by bringing the large molecules involved in photophosphorylation closer together
5. The thylakoid membrane is highly folded, provides a large surface area to embed
Any of the elaboration:
many photosynthetic pigments / chlorophyll molecules in the photosystems for ***light absorption****
many electron carriers in the electron transport chain and ATP synthase for ATP production.

(ii) Outline the role of ATP synthase that is held in these membranes. [2]

1. Diffusion of protons from thylakoid space into the stroma, via ATP synthase
2. Leads to formation of ATP from ADP and inorganic phosphate via ***chemiosmosis****.

(c) Describe the role of NADP in linking the light dependent reactions to the Calvin cycle. [2]

1. NADP is the ***final electron acceptor**** at the end of the non-cyclic light dependent reaction, which is then reduced to NADPH.
2. Reduced NADP/NADPH is used to drive the reduction of glycerate phosphate (GP) to glyceraldehyde-3-phosphate (G3P), with the use of ATP in the Calvin cycle.

[Total : 10]

N14P2Q7

(a) Describe events occurring at A and B in Fig. 7.1. [4]

Stage A

1. ***Haemagglutinin**** binds to ***sialic acid receptors**** on host cell membrane
2. Virus then enters host cell by ***endocytosis**** where host cell membrane invaginates and pinches off, placing virus in an endocytic vesicle.

Stage B

3. Vesicle then fuses with a lysosome, and the resulting drop in pH stimulates fusion of viral envelope with vesicle membrane
4. Releasing nucleocapsid and eventually viral RNA into cytosol of host cell

(b) Explain why it is necessary for the viral RNA to enter the host cell nucleus. [3]

1. For ***transcription**** where the viral genome ***RNA**** is used as a **template*** to synthesise the ***mRNA**** strands catalyses by the viral ***RNA dependent RNA polymerase****
2. Which can be transported into cytosol as a ***template**** for ***translation*** of viral proteins
3. which in turn acts as a ***template**** for the replication of new viral RNA genome
4. Using the host cell's ribonucleotides (and ATP), which is abundant in nucleus, for its synthesis

(c) Suggest in outline how new strains of influenza virus may arise. [3]

1 New strains of viruses are formed as a result of mutation of the genome due to the change in the ribonucleotide sequence known as ***antigenic drift****

2 As a result of the lack of proof reading ability of RNA-dependent RNA polymerase in influenza / the fast/high rate of replication of the virus

3 gives rise to changes in the conformational of the glycoproteins

4 New viral strains are also formed when two or more strains of influenza viruses infect **a** common/same host cell where

5 Reassortment of the different RNA segments occur resulting in recombination of genetic material in a ***virion****, giving rise to ***antigenic shift****.

[Total : 10]

N14P2Q8

(a) Suggest why different species of picture-wing fly show different banding. [3] 6L

1. (Phenotypic differences/different wing patterns) distinguishes species in picture-wing flies;
2. Such differences are due to differences in DNA sequences/mutations in several gene loci;
3. These changes in DNA structure are reflected by the different staining of DNA / different banding patterns in the chromosomes;

(b) Suggest why different species of picture-wing fly evolved on different islands. [4] 8L

1. The islands were geographically isolated with the sea separating the islands/allopatric speciation (with mention of type of barrier);
2. This meant that the ***gene flow*** between populations of flies on the islands were ***disrupted****;
3. With the different environment with their ***different selection pressures****, e.g. predation, habitats, available food sources (name one example);
4. Allele frequencies change because of natural selection and ***genetic drift****;
5. The subpopulations evolve independently and accumulate different mutations and allele frequency changes, that over time led to reproductive isolation and formation of different species;

(c) Explain the differences between classification and phylogeny. [3]

Fig.8.3 was shown to direct you towards reasons related to the branching network of a phylogram. Any 3

1. Classification groups organisms based on overall/morphological similarities and does not take into account the evolutionary history of organisms while phylogeny traces the evolutionary history of organisms based on ancestor-descendent relationships;
2. Classification involves grouping organisms into a kingdom, phylum, class, order, family, genus and species using a ***hierarchical classification**** system but in phylogeny, organisms are arranged based on their evolutionary relationship with each other with each organism assigned a position on a branching tree relative to other organisms;
3. In classification, the organism is presented as a binomial nomenclature/name but in phylogeny, the organism is placed on a branch on a phylogenetic tree;
4. Classification does not allow inference of speciation events as it is just a naming system while phylogeny indicates speciation events as the node of the phylogenetic tree;
5. Classification does not allow inference of common ancestors while in phylogeny, descendants of a common ancestor are represented in the same branch;
6. You cannot infer of how closely related 2 species are especially since they are grouped together in the same hierarchy, e.g. “species” in classification. In phylogeny, how recently a branch point occurs indicates how closely related 2 species are;

[Total : 10]

N14P2Q9 (OUT OF SYLLABUS)

N14P2Q10

10 (a) Describe the structure and role of tRNA [8]

Structure:

1. Transfer RNA (tRNAs) are single-stranded RNA
2. It folds back upon itself and held in shape by hydrogen bonding between complementary base pairs at certain regions to form a 3D L-shaped structure
3. 3 bases form an ***anticodon****
4. 3’ end with CCA stem is attachment site for a specific amino acid that corresponds to anticodon.

Function:

5. ***Aminoacyl-tRNA synthetase**** catalyse formation of bond between specific amino acid and tRNA with specific anti-codon.
6. Different tRNA will have different ***specific conformation ~~and charges~~**** which are ***complementary**** to active site of corresponding aminoacyl-tRNA synthetase.
7. tRNA carries amino acid to the ribosome
8. Each tRNA has a specific ***anticodon**** that binds to a specific mRNA codon via ***complementary base-pairing****.

9. Where adenine base pairs with uracil and cytosine base pairs with guanine, by forming ***hydrogen bonds****.
10. the sequence of bases on mRNA is translated into a specific sequence of amino acids in forming polypeptide chain.

(b) Describe how gene mutations may affect the protein coded for by a gene. [7]

1. A gene mutation is a change in the nucleotide /base sequence in ***DNA****;

2. **Substitution** mutation where a nucleotide/base is replaced by a different nucleotide
3. Consequence of mutation on RNA:
   Results in a change in sequence of the mRNA, and a change in ***codon****
4. Resulting in a different sequence of amino acid/primary structure of protein;
5. leads to different folding of polypeptide to tertiary structure / 3D conformation.
   OR
   same folding of the polypeptide to tertiary structure / 3D conformation occurs as the new amino acid coded for is chemically similar;

6. **Insertion or addition** – occurs when one or several nucleotides are inserted in a sequence
   OR
   Deletion – occurs when one or several nucleotides are removed from a sequence of base(s)
7. Consequence of mutation on RNA:
   Results in a frameshift mutation
8. Resulting in a different sequence of amino acid/primary structure of protein;
9. leads to different folding of polypeptide to tertiary structure / 3D conformation.
   OR
   truncated polypeptide hence non functional

10. **Inversion** – a segment of nucleotide sequences separates from the allele and rejoins at the original position but it is inverted;
11. Consequence of mutation on RNA:
    resulting in different ***codons**** on the mRNA
12. Resulting in a different sequence of amino acid/primary structure of protein;
13. leads to different folding of polypeptide to tertiary structure / 3D conformation.
    OR
    truncated polypeptide hence non functional

(c) For a named genetic disease, describe the causal mutation and outline its effect on the phenotype of an organism. [6]

Sickle cell anaemia

1) One genetic disease caused by mutation is ***sickle cell anaemia****
2) sickle cell anaemia is a result of a point substitution mutation / a single base substitution,
3) thymine is replaced by adenine in the gene coding for the β globin chain;

4) A change in a single base in the 6th triplet codon resulting in Valine replacing Glutamate amino acid;
5) Valine being non-polar compared with charged glutamate results in a change in properties of the polypeptide chain;
6) Causing changes in the 1°, 2°, and 3° structure resulting in change in 3D conformation and normal haemoglobin becomes sickle cell haemoglobin
7) When oxygen levels are low in the blood, the Hb S molecule undergoes an unusual conformation change that allows the Hb S to polymerise / crystallise to form rigid fibres.
8) This causes red blood cells to change from a circular biconcave shape to a sickle shape;
9) Sickle shaped RBC may obstruct blood vessels and interfere with blood circulation – organ failure/pain;
10) Sickled RBC more fragile and makes them susceptible to lysis and active destruction by spleen results in reduction in red blood cell numbers causing anaemia/shortness of breath/tiredness;
11) It is a recessive condition requiring both alleles of the β globin chains to be mutated in order for the symptoms to appear;

OR

Cystic fibrosis

1. One other genetic disease caused by mutation is ***cystic fibrosis****
2. Which is caused by of deletion mutation involving the deletion of 3 nucleotides on chromosome 7, resulting in loss of phenylalanine in the polypeptide.
3. This cause changes in the 1°, 2°, and 3° structure resulting in change in 3D conformation of the cystic fibrosis transmembrane conductance regulator (CFTR)
4. It is an autosomal recessive inheritance
5. This mutation results in either missing or defective CFTR
6. CFTR controls movement of Cl^- into or out of cells and influences Na^+ transport indirectly.
7. When Cl^- is not transported out of epithelial cells, Na^+ is also retained in the cell causing a high ion concentration, lowering water potential in cell
8. water cannot diffuse out of cells via osmosis, so water is retained in cells causing mucus in the lumen to be thick making it conducive for bacteria growth
9. thus causing severe breathing difficulty

[Total: 20]