2018 DNA Structure and Replication STQ MS

2018 / H2 / DHS PRELIM / P2 Q5

Question 1
(a)

- ref hydrogen bonds
- Adenine always base pair with Thymine and Cytosine always base pair with Guanine and vice versa / a pyrimidine on one strand always base-pairs with a purine on the other strand
- Thus width between the 2 sugar-phosphate backbones is constant / maintain 2nm

- Complementary DNA strands are antiparallel, thus A-T and G-C pairs would be able to maintain their hydrogen bonds/ antiparallel DNA is also more structurally stable than parallel DNA

- there is hydrophobic interactions between stacked bases

(b)(i)

- Peptidyl transferase
- catalyzes the formation of peptide bonds between amino acids via condensation reaction;

(b)(ii)

- RNA polynucleotide strands / molecules fold into compact 3D shape
- forming an active site with a specific shape
- The shape is maintained by hydrogen bonds between ribonucleotides ad interactions with ribosomal protein

(c)

- It prevents the translocation of ribosomes along the mRNA by binding to the empty “E” site, and so only dipeptides are formed

2018 / H2 / EJC PRELIM / P2 Q4

2 Fig. 4.1 shows part of a DNA molecule.

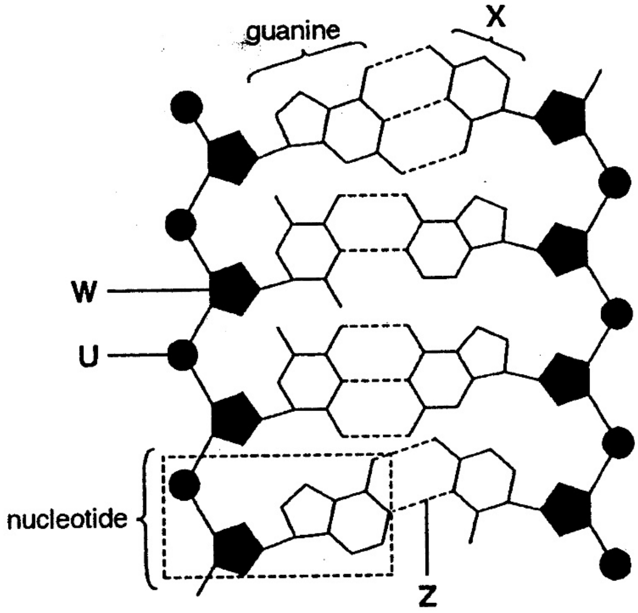

Fig. 4.1

(a) **(i)** Name **W** to **Z**. [2]

W ……………………………………………………………

U ……………………………………………………………

X ……………………………………………………………

Z ……………………………………………………………

1. **W = Deoxyribose (R: sugar, ribose, pentose)**
2. **U = Phosphate group (R: phosphate head)**
3. **X = Cytosine (R: nitrogenous base, pyrimidine)**
4. **Z = Hydrogen bond**

4 correct = 2 marks, 2-3 correct = 1 mark, less than 2 correct = 0 marks

(ii) Give **one** advantage of DNA having two strands.

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………[1]

1. **Collective/numerous hydrogen bonds between the complementary base pairs stabil the double helical structure/molecule;**
2. **One strand act as a template for repair during DNA replication;**

3. **<u>Protects / shields</u> the <u>hydrophobic nitrogenous bases</u> from the hydrophilic medium;**

(b) Fig. 4.2 shows a linear chromosome undergoing the first round of DNA replication.

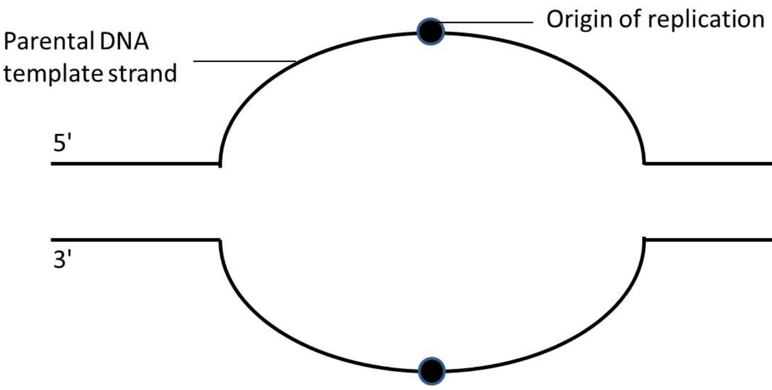
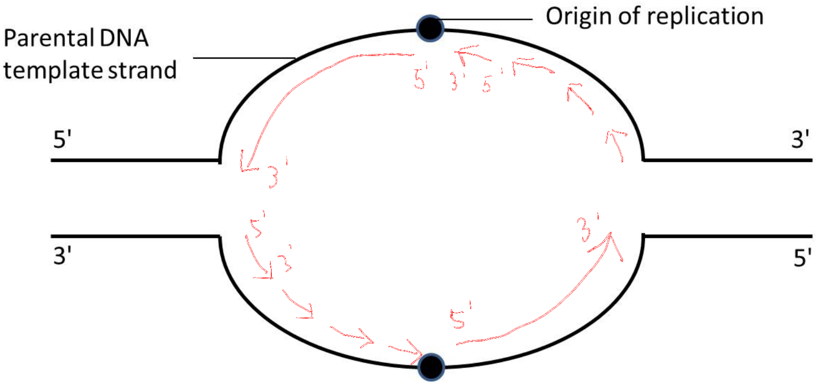


Fig. 4.2

(i) On Fig. 4.2, draw the direction of DNA synthesis for the leading strands using solid arrows (→) and for the lagging strands using dashed arrows (- - - >).

[1]



1. **All directions of leading and lagging strands (Okazaki fragments) correctly indicated;**
2. **Lagging strands must show several Okazaki fragments in correct directions;**

Points 1 and 2 must be present for full credit. Not marking for 5'/ 3' labels, but arrow he needed.

(ii) State **two** ways DNA replication is different from transcription.

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DNA Replication	Transcription
DNA polymerase used to polymerise nucleotides/synthesize new strands;	RNA polymerase used to polymerise nucleotides/synthesize new strands
Helicase used to unzip DNA strands;	RNA polymerase unzip DNA strands
Both parental strands used as templates;	Only one strand used as template
DNA strands produced;	mRNA/tRNA/rRNA strand produced
Deoyribonucleotide monomers;	Ribonucleotide monomers
Daughter DNA molecule double-stranded;	mRNA molecule single stranded
AVP;	AVP

(c) *Fig. 4.3 is an electronmicrograph showing the transcription of genes for ribosomal RNAs at adjac positions along the chromosome in a eukaryotic cell.*

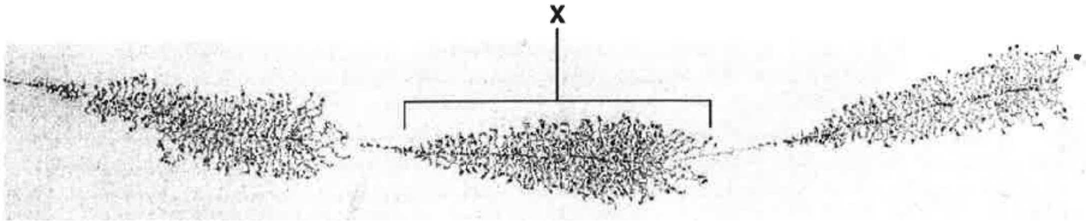

Fig. 4.3

(i) Describe and explain the pattern of transcription visible on the part of the DNA coding for riboso RNA, labelled **X** in Fig. 4.3.

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……………………………………………………………………………………………[2]

1. **The pattern shows shorter strands of rRNA emerging on the left and with longer strands**

rRNA seen on the right;

2. **This is because RNA polymerase transcribes DNA from 3’ to 5’ direction/ synthesi rRNA from 5’ to 3’ direction, hence the rRNA strands on the right (near 5’ end of D template) were the longest (transcription started earlier); (ora)**

(ii) Suggest possible roles for the non-transcribed DNA that is found between the ribosomal genes.

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……………………………………………………………………………………………[2]

[Total:10]

1. **The non-transcribed DNA may be enhancer sequences which are bound by activators which increase the transcription rate;**

2. **The non-transcribed DNA may be silencer sequences which are bound by repressors which decrease the transcription rate;**

3. **The non-transcribed DNA may be promoter sequences which are bound by general transcription factors and RNA polymerase bind to form transcription initiation complex to start transcription;**