Exam Papers Practice

7.1 DNA Structure & Replication

Mark Schemes

Course	DP IB Biology
Section	7. Nucleic Acids (HL Only)
Topic	7.1 DNA Structure & Replication
Difficulty	Medium

To be used by all students preparing for DP IB Biology HL
Students of other boards may also find this useful

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The correct answer is **B** because the nucleosome consists of a strand of DNA coiled around a core of eight histone proteins to form a bead-like structure. This helps to supercoil the DNA, resulting in a compact structure that saves space within the nucleus

- Option **A** is incorrect because although nucleosomes do contain histone proteins they also help supercoil DNA
- Option **C** is incorrect as prokaryotes such as bacteria do not possess nucleosomes, their DNA is referred to as 'naked DNA'
- Option **D** is incorrect as although nucleosomes are basic units that aggregate together to form chromatin, they don't specifically contain chromatin

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The correct answer is **D:** DNA polymerase forms a phosphodiester bond between the free **3' -OH group** of the pentose sugar of the existing nucleotide (at the end of the DNA chain) and the 5' phosphate group of the incoming (new) DNA nucleotide.

- Option **A** is incorrect as the nitrogenous base forms hydrogen bonds with a complementary base on the opposite DNA strand
- Option **B** is incorrect as there is no free 5' phosphate group on the last nucleotide as this has already bonded to the previous nucleotide
- Option **C** is incorrect as nitrogenous bases attach to the 1' carbon of the pentose sugar

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The correct answer is **D**: because DNA polymerase can only add new nucleotides in a 5' to 3' direction, the lagging strand needs to be replicated in short fragments as DNA polymerase can only move away from the replication fork. A new fragment is produced as more of the lagging strand is exposed.

- Option **A** is incorrect as the double helix is already unwound before Okazaki fragments are formed
- Option **B** is incorrect as Okazaki fragments only form on the lagging strand
- Option **C** is incorrect as the strands of DNA (leading and lagging) act as a template for DNA polymerase

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The correct answer is **B**: During DNA replication helicase unwinds the double helix but this creates strain ahead of the replication fork. DNA gyrase relieves this strain by removing any supercoils. DNA polymerase III can only add nucleotides to the 3' end of an existing DNA strand, it can't make DNA from 'scratch'. Therefore, DNA primase needs to synthesis a primer onto the template strand to act as a start point for DNA polymerase III which can then proceed to add nucleotides to the template strand. Finally, the RNA primers are replaced with DNA by the action of DNA polymerase I.

Answers **A**, **C** and **D** are incorrect as they refer to the events in the wrong order

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The correct answer is **D** because they are all associated with non-coding DNA.

Coding DNA contains genes that only code for a protein product. Functional RNA molecules such as transfer RNA (tRNA) and ribosomal RNA (rRNA) are coded by specific genes, but they are classed as non-coding DNA as the product is not protein. Some non-coding regions code for Promoter regions or other regulatory sequences that can enhance or suppress transcription. Eukaryotic protein-coding genes can contain many introns that are non-coding sequences. Different proteins can be produced depending on how the introns are removed. Telomeres are repeated nucleotide sequences found at the end of chromosomes, they help preserve the coding regions of the chromosome during cell-division.

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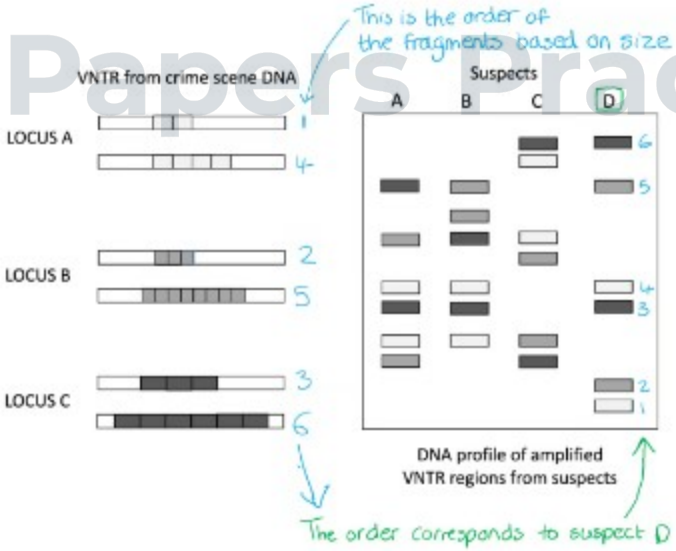
The correct answer is **D** because the separation of fragments corresponds to the length/size of the VNTR regions at each loci.



7

The correct answer is **C:** When DNA polymerase incorporates dideoxynucleotides into the growing DNA strand the lack of -OH group on the 3' carbon of the ribose means that an incoming deoxynucleotide cannot bond. Because DNA polymerase can't incorporate any new deoxynucleotides, it stops which **terminates** elongation of the DNA.

- Option **A** is incorrect as although dideoxynucleotides can be labelled it is not due to the lack of -OH group. Radioactive or fluorescent labels are usually attached to the nitrogenous base
- Option **B** is incorrect because as many parameters can influence the efficiency of the sequencing actions, not necessarily the lack of 3'-OH group
- Option **D** is incorrect, if a dideoxynucleotide is incorporated into the growing DNA strand it will prevent thymine from being incorporated but it will also prevent any other deoxynucleotide from being incorporated - therefore, it is not the most plausible answer

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The correct answer is **A:** Hershey and Chase took advantage of the chemical differences between DNA and proteins. DNA does not contain sulphur and protein does not contain phosphorus. As the virus inserts its DNA (and not protein) into the bacteria only bacteria containing the ^{32}P labelled was radioactive.

- Option **B** is incorrect because bacteria infected by the ^{32}P labelled virus were found in the pellet after centrifugation
- Option **C** is incorrect because only the protein coat of the virus contained ^{35}S and this was not inserted into the bacteria
- Option **D** is incorrect because prior to centrifugation, Hershey and Chase removed any viral protein coat (containing ^{35}S) from infected bacteria by agitation - this was detected in the supernatant

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The correct answer is **B**: it was Crick and Watson who determined how the nitrogenous bases were physically arranged on the sugar-phosphate backbone and how the base pairing of adenine to thymine and cytosine to guanine would fit between the two outer sugar-phosphate backbones. Their base-pairing hypothesis was supported by Franklin's X-ray diffraction results and Chargaff's data, whose research showed the amount of adenine and thymine was equal and the amount of cytosine and guanine.

The other answers are incorrect as they were the findings of Franklin.

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The correct answer is **B** because molecular visualisation software can be used for all of these activities and many more not listed.

C and **D** are incorrect as **IV** is not a true statement. BLAST (Basic Local Alignment Search Tool) is usually used to compare an unknown DNA sequence with all known gene sequences. Although some molecular visualisation software can now integrate with other software to identify unknown DNA sequences it is not its primary use.