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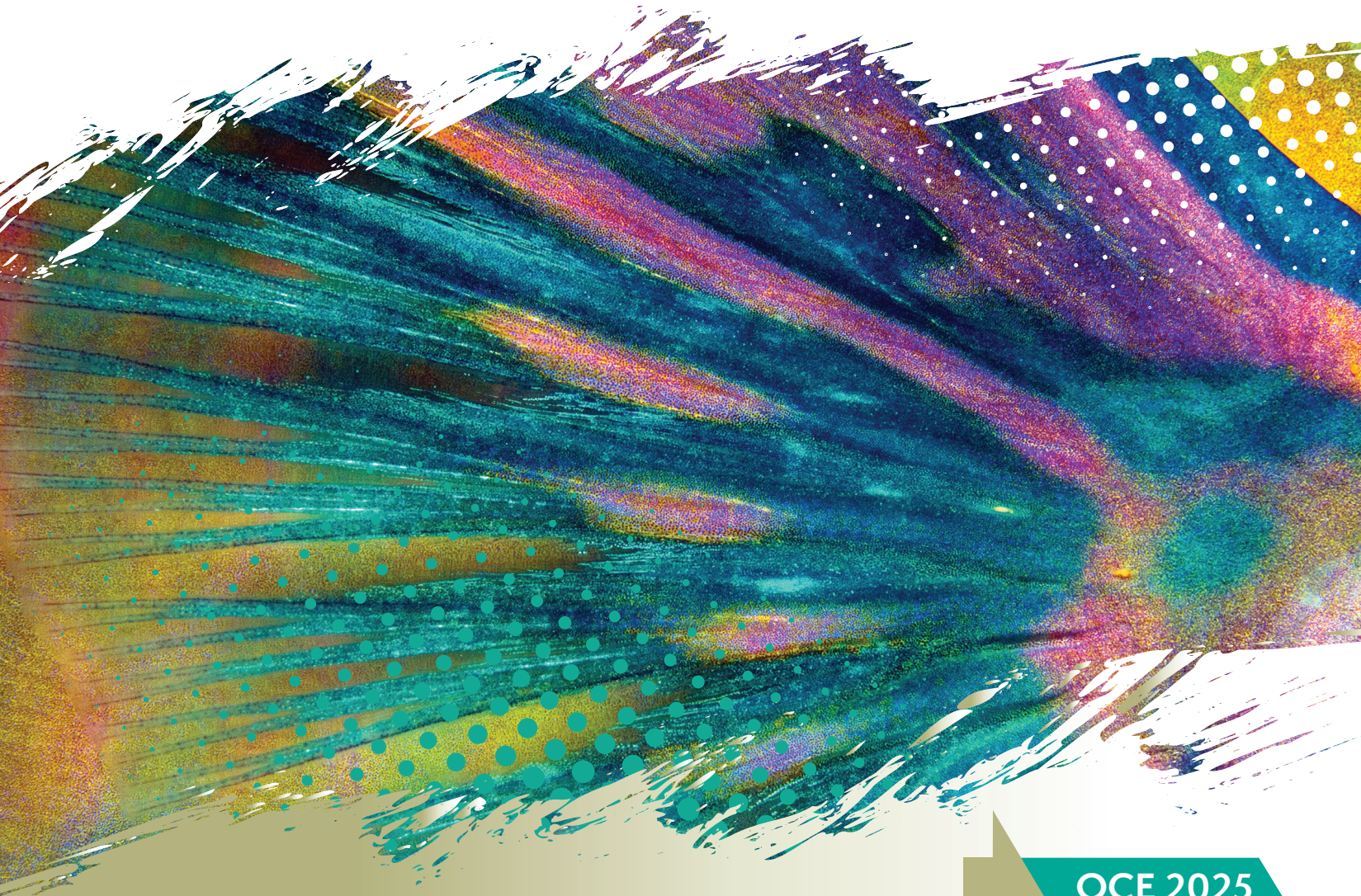


Student Book

QCE 2025
Biology
SYLLABUS

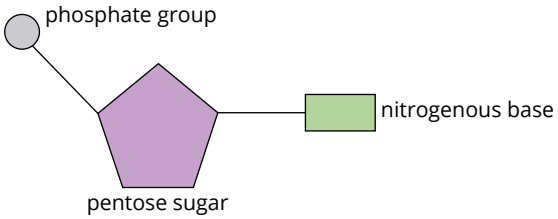
Chapter 5 DNA replication and protein synthesis

5.1 DNA structure and replication

5.1 KEY QUESTIONS

Describe

1 **a** nucleotides
b sugar, phosphate and nitrogenous base
c



2 **a** The primary structure of DNA is a single strand of polynucleotides, which consists of a specific sequence of nitrogenous bases (A, T, C and G). The secondary structure of the DNA forms the spiral, double-stranded helix structure often referred to simply as a double helix.
b The function of DNA is to carry the inheritable genetic code for the control of cell activities and protein synthesis.
c DNA strands are coiled around histones forming structures roughly 10 nm in diameter.

3 **a** DNA is the chemical that contains the genetic information of organisms and determines their inherited characteristics.
b The genome of an organism is the sum total of the organism's DNA, measured in the number of base pairs contained in a haploid (n) set of chromosomes.
c A gene is a segment of DNA that codes for a protein or cell activity that results in a particular characteristic in an organism.
d Alleles are different forms of a particular gene, distinguished at the molecular level by a different nucleotide sequence at the same gene locus.
e DNA replication is the process used by cells to make an exact copy of their DNA. DNA replication is essential for cell division as both daughter cells need a complete set of genetic information to function.
f A mutation is a change in the nucleotide sequence of an organism's DNA.

Apply

4 The complementary nitrogenous base pairing using hydrogen bonds that occurs in DNA gives the appearance of the rungs and steps of a ladder, while the repeating phosphates and pentose sugars form a 'backbone' that gives the appearance of the frame of a ladder.

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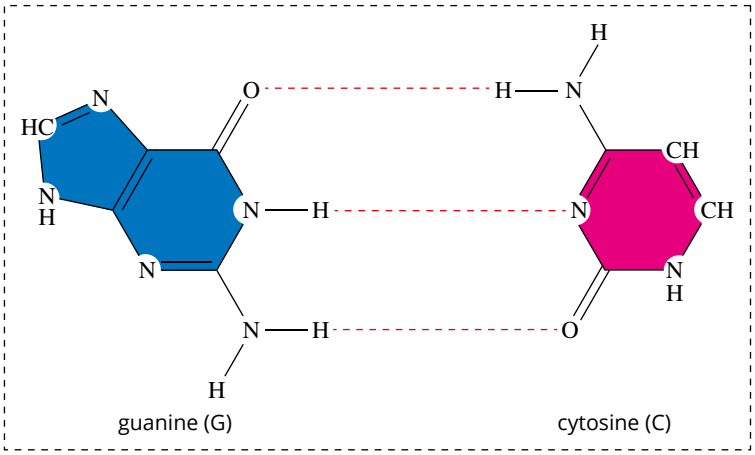
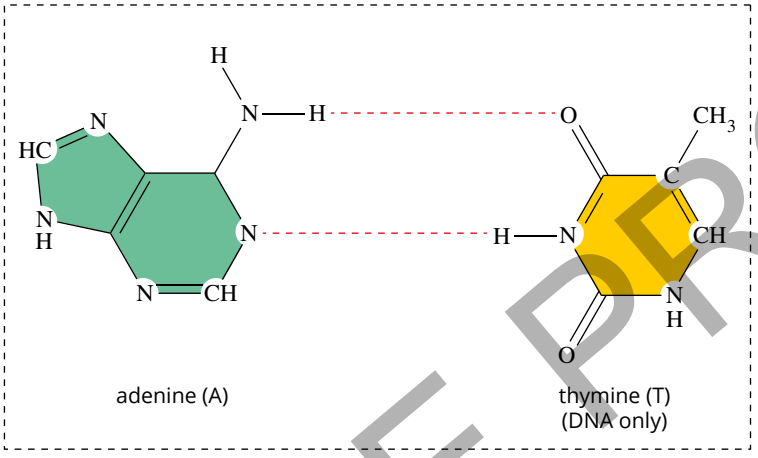
5 Complementary means matching or paired in that purines and pyrimidines bond together using the appropriate number of hydrogen bonds due to the structure of the nitrogen bases. The antiparallel structures physically complement each other to allow hydrogen bonding to occur, so that adenine (A) always bonds to thymine (T) with two weak hydrogen bonds, and cytosine (C) always bonds to guanine (G) with three weak hydrogen bonds.





6 TAAGGCAT

7

Base	Purine or pyrimidine structure	Complementary base	Complementary base purine or pyrimidine structure
adenine	purine	thymine	pyrimidine
guanine	purine	cytosine	pyrimidine
cytosine	pyrimidine	guanine	purine
thymine	pyrimidine	adenine	purine
uracil	pyrimidine	adenine	purine

8 DNA is made up of nucleotides. Each nucleotide consists of a phosphate group, a five-carbon deoxyribose sugar and one of four nitrogen-containing bases. The four bases are adenine (A), guanine (G), thymine (T) and cytosine (C). One nucleotide is joined to the next nucleotide by a covalent phosphodiester bond between the phosphate group on the 5′ carbon and the 3′ carbon of another nucleotide. When many nucleotides are joined together, a polynucleotide chain is formed. The bases in two polynucleotide chains form complementary base pairs (A pairs with T, C pairs with G) by hydrogen bonding. This hydrogen bonding between the base pairs stabilises the molecule so that it forms the shape of a double helix, similar to a twisted ladder. The antiparallel structure, with the 5′ to 3′ direction being opposite to the complementary strand, enables hydrogen bonds to form between the purines and pyrimidine base pairs according to the base-pairing rules. The sequence of bases on a template strand will determine the sequence of bases on the complementary strand. One end of each strand is called the 5′ end (where the phosphate group is attached). The other end of the strand has the 3′ carbon (without a phosphate group). The two polynucleotide chains of DNA are antiparallel, running in opposite directions, with one strand running from 5′ to 3′ and the other running from 3′ to 5′. The two polynucleotide strands need to run antiparallel to each other to allow complementary bases to form hydrogen bonds.

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9 **a** Autosomes are chromosomes that do not determine the biological sex of an individual. Allosomes are chromosomes that are involved in determining the biological sex of an individual.
b Homologous chromosomes are matching pairs of chromosomes that have the same genes found at the same loci. Non-homologous chromosomes differ from each other by having different genes at different loci.

10 The genetic code is described as universal because the same codons specify the same amino acids in almost all organisms on Earth, from bacteria to humans.

Analyse

11 There are consistently equivalent percentages of A to T and G to C in each species of organism. For example, in humans A:T is approximately 30% each, in salmon it is 29% each and in wheatgerm 28% each. For each species, the remaining percentage of nitrogenous bases is shared by C and G. Even in *E. coli*, where the percentages of all the nitrogenous bases are similar, C and G are within 0.3% and A and T are similar. This supports the theory that there are complementary base pairs.

12 **a** ethyl methanesulfonate > UV radiation > benzene > control
b The control group mutation rate of 0.3 mutations per million base pairs reflects the background rate of spontaneous mutations, which occur due to factors like DNA replication errors.
c Chemical mutagens directly alter the DNA bases or sugar–phosphate backbone, leading to changes in the DNA sequence. Their impact varies widely depending on the compound and what kind of changes it causes in the DNA.

13 **a** As UV exposure increases, the number of thymine dimers per 1000 base pairs rises steadily, indicating a direct relationship between exposure duration and DNA damage.
b Thymine dimers may impede DNA replication since they bond between nucleotides in a DNA strand. (Thymine dimers cause distortions in the DNA double helix, impeding normal replication. This can result in replication errors, leading to point mutations or stalled replication forks that may cause cell death if unrepaired.)

5.2 Protein synthesis and gene regulation

5.2 KEY QUESTIONS

Describe

1 **a** Start and stop codons are sequences in mRNA that signal where translation begins and ends, defining the protein-coding region of a gene.
b Promoter regions are upstream (i.e. before the start triplet) binding regions for the enzyme that is involved in the encoding process (RNA polymerase).
c Exons are DNA regions that are coding segments.
d Introns are DNA regions that are non-coding segments.

2 **a** A transcription factor is a protein that controls gene expression at the transcription stage. It binds to DNA sequences close to the promoter region of a gene or to the RNA polymerase to induce or repress the expression of specific genes.
b A regulatory gene is a gene that codes for transcription factors (which in turn controls gene expression at the transcription stage).
c A constitutive gene is a gene that is always switched on and is therefore transcribed continually.

3 **a** Hox genes are regulatory genes that control the spatial pattern of expression of other genes. They control genes that form particular tissues at specific times during embryonic development and influence the body plan of organisms.
b SRY genes produce proteins that direct the development of the gonads into the testes by turning on the relevant genes on the short arm of the Y chromosome. This sex determination process must occur at the correct time in embryonic development or the default ovary-forming pathway is activated.

Apply

4 Gene expression is the process by which the information stored in a gene is used to synthesise a functional gene product (protein or RNA). Gene regulation refers to the mechanisms and processes that control the timing, location and amount of gene expression.

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5 tRNA, or transfer RNA, transports amino acids to the ribosome and matches them to the codons on the mRNA using its anticodon. rRNA, or ribosomal RNA, is a structural part of the ribosome that helps catalyse peptide bond formation between amino acids during protein synthesis.

6 **a** coding strand DNA: 5′-A T G T A T G C C A A T C G A-3′
b non-coding strand DNA: 3′-T A C A T A C G G T T A G C T-5′
c mRNA: 5′-A U G U A U G C C A A U C G A-3′
d anticodons on tRNA: 3′-U A C / A U A / C G G / U U A / G C U-5′

7 **a**

Stage of transcription	Transcription event
initiation	• Transcription factors combine with the region at the start of the gene, known as the promoter. • RNA polymerase attaches to the promoter, unwinding and unzipping the DNA molecule by breaking the weak hydrogen bonds between the two strands to expose the bases.
elongation	• RNA polymerase moves along the DNA molecule, producing a strand of mRNA. • RNA polymerase uses a strand of DNA as a template, attaching nucleotides (A, U, G, C) by complementary base pairing.
termination	• RNA polymerase reaches the termination site of the gene (stop codon) and translation ends. • The RNA polymerase detaches, releasing the mRNA and allowing the DNA molecule to re-form.

b

Stage of translation	Translation event
initiation	• A small ribosomal sub-unit attaches to the 5′ end of an mRNA strand. It then moves along the mRNA until it reaches a start codon (AUG). • A tRNA molecule with an anticodon (UAC) brings the amino acid methionine to the mRNA. The tRNA molecule joins to the mRNA start codon, attaching by complementary base pairing between the codon and anticodon.
elongation	• Following the attachment of the amino acid methionine, another tRNA, with a complementary anticodon to the next codon on the mRNA, attaches and adds its specific amino acid to the growing polypeptide chain. • The ribosome then releases the tRNA and moves further along the mRNA strand. At each codon a new tRNA binds and adds another amino acid.
termination	• The tRNA reaches a stop codon. • The polypeptide chain is released from the ribosome into the cytoplasm or the endoplasmic reticulum.

8 **a** Substitution mutations involve the substitution of one nucleotide for another in the DNA sequence. If a synonymous mutation results (where there is a difference in the mRNA processing but not in the overall amino acid sequence), a functional protein may still be produced but changes in post-transcription processing may impair the effectiveness of the protein's production and final function. If, however, the mutation results in a change in the amino acid sequence, then there may be structural and functional changes to the protein. The degree of harm caused by a non-synonymous mutation depends on which amino acid is substituted and how it will affect the protein shape. A frameshift mutation is the result of a deletion or insertion of a nucleotide that alters every triplet that follows the site of the mutation. In turn, this will alter the codons produced on the mRNA and the sequence of amino acids in the polypeptide formed from the mRNA strand. An alteration in the sequence of amino acids will change the folding of the polypeptide, and it will no longer be functional.

b The p53 protein prevents cancer by detecting DNA damage, halting the cell cycle to allow repair, or triggering apoptosis if the damage is irreparable. This ensures that damaged DNA is not passed to daughter cells.

9 Because prokaryotic cells do not have membrane-bound organelles, the DNA is present in the cytosol and all protein synthesis processes occur there. Therefore, transcription/translation is a continuous process and the ribosomes attach to the mRNA as it is being produced. Prokaryotic DNA does not contain introns, so RNA processing is not required. In eukaryotic cells, DNA is located in the membrane-bound nucleus, with several more steps in transcription and translation across multiple membrane-bound organelles. Each of these factors results in the rate of protein synthesis being faster in prokaryotic cells compared to eukaryotic cells.

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Analyse

10 The fourth codon codes for STOP, which will cease translation.

11 mature mRNA strand:

guanosine	AUG – CCU – AGA – UCU –	GCC – UUA – CGA	– UGU – GCC – CAU – UGU	AAAA

5' cap poly-A tail

amino acid sequence: Met-Pro-Arg-Ser-Ala-Leu-Arg-Cys-Ala-His-Cys

12 a The RNA polymerase will start transcription at the next start triplet after the TATA box.

G G G C T C T A T A A A G G G T A C C A C T T C A A T G C T

The mRNA strand will be 5′ AUG GUG AAG UUA CGA 3′ and the amino acid sequence will be Met–Val–Lys–Leu–Arg.

b As the TATA box is the binding site for RNA polymerase, it is likely that a mutation in the TATA box will stop the binding of RNA polymerase and hence transcription of the gene will not occur. This means the organism will lack the protein coded for by that particular gene. Whether this is a major problem for the organism will depend on the function of the protein.

13 a strand 1

b Given that the mRNA and the template strand are complementary, the complementary base pairing rule of A–U, G–C must apply. The percentage of A–U and G–C nucleotides must be similar in the template strand and the mRNA. Strand 1 is the mRNA because it contains the nucleotide U (21.1%) and has A (40.1%), G (28.9%) and C (9.9%). The DNA complementary strand should have approximately 21.1% A, 40.1% T, 28.9% C and 9.9% G. The strand that reflects this nucleotide ratio best is strand 2 and is therefore the template strand.

14

Feature	DNA	RNA
shape	• double helix • antiparallel strands	• typically single-stranded
repeating monomer unit	nucleotide consisting of: • deoxyribose • sugar–phosphate backbone • purine and pyrimidine bases	nucleotide consisting of: • ribose • sugar–phosphate backbone • purine and pyrimidine bases
nitrogen bases	adenine, guanine, cytosine, thymine	adenine, guanine, cytosine, uracil
bonding	• hydrogen bonding between matching base pairs holds the two strands together • covalent (phosphodiester bonds) connect the phosphate and deoxyribose sugars in the backbone	• covalent (phosphodiester bonds) connect the phosphate and ribose sugars in the backbone • hydrogen bonding is typically only present in double-stranded RNA because it is a single-stranded molecule (Note: hydrogen bonds can occur between the bases when single-stranded RNA like tRNA and rRNA folds back onto itself, creating secondary structures.)

15 The data suggests a strong link between higher p53 mutation rates and increased prevalence of each of the three cancers listed in the table. Lung cancer has the highest p53 mutation rate of 50% and the highest prevalence of 12%. The data also shows that the higher p53 mutation rate across the three types of cancer listed corresponds with an increasing population prevalence of any of these cancers. This indicates that p53 mutations may play a significant role in cancer development.

CHAPTER 5 REVIEW

Describe

1 A. Proteins are made of amino acids and do not form any part of a nucleotide.

2 B. Deoxyribose has 5 carbons. The building blocks of DNA are called nucleotides. DNA is a double-stranded helix.

3 D. Amino acids are the building blocks of polypeptides and ribosomes join them together using the information encoded in mRNA.

4 A. Stop codons do not code for an amino acid. Codons that code for amino acids do not do so exclusively: most amino acids are coded for by more than one codon. Any particular triplet (codon) can only code for one amino acid. There are 64 different codons.

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5 A. Exons are the part of the DNA that will be translated and are the parts left after RNA processing of the mRNA.

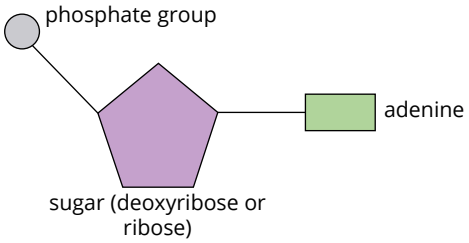
6 B. DNA polymerase is involved in DNA replication and does not involve the promoter. The repressor binds to the operator. The promoter is a part of the gene, not mRNA.

7 Eukaryotic cells contain double-stranded DNA bound to proteins in the chromosomes located in the nucleus, and unbound circular DNA in the mitochondria and chloroplasts. In prokaryotic cells, the DNA is located in the nucleoid region as large circular chromosomes and small circular molecules called plasmids.

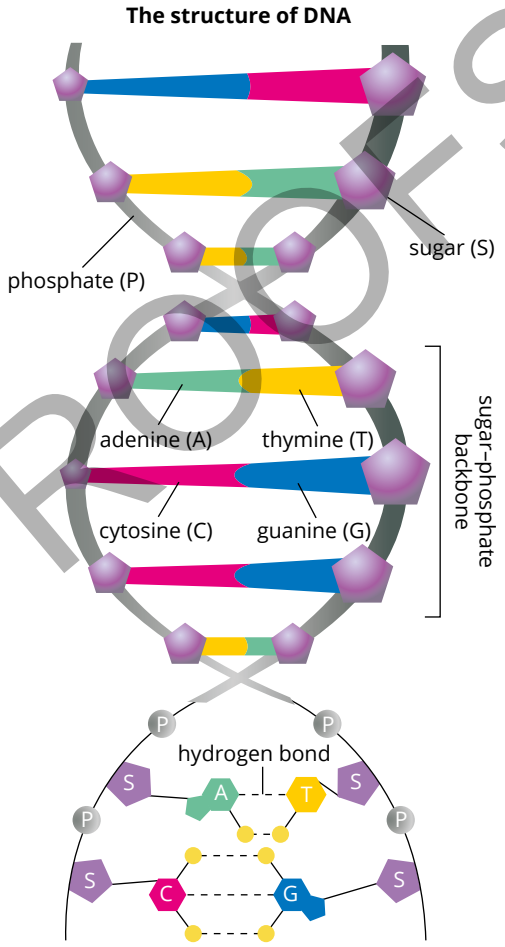
8 UAA is a STOP codon for translation and AUG is the START codon for translation.

9 The reading frame (codon sequence) of the mRNA is altered, and the wrong amino acids will be incorporated into the polypeptide chain for the remainder of the sequence, which is likely to result in a non-functional protein. This type of change is called a frameshift mutation.

10 a



b



Apply

11

Type of RNA	Where it is produced	Where and how it functions in cells
messenger RNA (mRNA)	nucleus	carries instructions from the DNA in the nucleus to the ribosomes in the cytoplasm for the production of proteins
transfer RNA (tRNA)	nucleus	in the cytoplasm, brings amino acids to the ribosomes for attachment to the growing polypeptide chain
ribosomal RNA (rRNA)	nucleus	in the cytoplasm, combines with proteins to form the structure of the ribosome, which is the organelle that directs protein synthesis

12 A. The chain shows nucleotides so it must be either RNA or DNA. It contains uracil so it must be RNA.

13 E. According to base pairing, A and T join as do G and C. Thus, the number of As and Ts will be the same and the number of Gs and Cs will be the same in a strand of DNA so A + G = T + C.

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14 mRNA: 5′-A A G U C A G C A-3′
coding: 5′-A A G T C A G C A-3′
The coding strand and the mRNA nucleotide sequences are the same, except that there is U in the mRNA wherever there is T in the coding strand of DNA.

15 Normal DNA sequence
template strand: 3′-T A C T T G T C C G A T A T C-5′
mRNA strand: 5′-A U G A A C A G G C U A U A G-3′
amino acid sequence: Met–Asn–Arg–Leu–STOP
Mutated DNA sequence
template strand: 3′-T A C T T G T C C A A T A T C-5′
mRNA strand: 5-A U G A A C A G G U U A U A G-3′
amino acid sequence: Met–Asn–Arg–Leu–STOP
There is no effect on the amino acid sequence as both the normal and mutated amino acid sequences are the same, coding for Leu in the fourth codon irrespective of the point mutation that has occurred.

16 Both splicing and alternative splicing remove introns to form a mature mRNA molecule. Splicing sequentially removes the introns to form a mature mRNA to produce the typical functional protein. Alternative splicing removes the introns and some exons from the same genetic code, producing numerous alternatives of the mature mRNA and thus variations of the functional protein. This allows the synthesising of 75 000–100 000 different proteins from 20 000 genes.

17 Mutations that occur in somatic cells will not be passed onto offspring; only the organism with the mutation is affected. Germline mutations occur in the ova or sperm of the individual and therefore these mutations can be passed onto the organism's offspring and affect the next generation.

18 Sickle cell anaemia is a disease where there is a point mutation causing valine to be substituted for glycine. As a result the β-globin chain is non-functional and haemoglobin cannot be correctly synthesised.

19

Mutation	Characteristic	Implications of mutation
synonymous	a change in DNA sequence that does not result in a change in amino acid	There is no effect on the formation of the protein or its function; however, there may be significant impact on the rate of mRNA processing and protein synthesis.
non-synonymous	a base substitution that causes an amino acid substitution	This may affect the protein, depending upon the type of amino acid substituted and where it is on the gene. The resulting peptide may be less effective or non-functional, depending upon the type of amino acid substituted.
nonsense	a base substitution that causes a premature stop codon	The polypeptide formation is terminated early so the protein is non-functional.
frameshift	an insertion or deletion that results in changes of all amino acids after the point of mutation	The protein is likely to be non-functional, depending upon where in the sequence the deletion or insertion occurred.

20 Both spontaneous and induced mutations can cause similar changes in the DNA sequence. However, a spontaneous mutation occurs randomly during DNA synthesis, whereas an induced mutation is a genetic change that is produced by a mutagen such as exposure to UV radiation or chemical mutagens.

21 Homeotic genes are a group of master regulatory genes that control the expression of other genes during embryonic development. They ensure that the correct genes are expressed (turned on or off) at the correct time and in the correct cells. As a result, the different tissues of an organism, the body plan and specialised organs are arranged in the correct space in the embryo to ensure the organism grows and develops normally. For example, when the Hox genes are inhibited or mutated, the regulation of other genes is altered and tissues and organs are not developed or develop in organs that are not supposed to have that tissue.

22 **a** DNA helicase separates the DNA at the point of the replication fork.
b DNA polymerase adds nucleotides to the new DNA strand according to the rules of complementary base pairing (A pairs with T, C pairs with G).

23 Semi-conservative replication produces two DNA molecules, each with one original strand and one newly-synthesised strand. This process ensures accuracy by using the original strand as a template to be matched with complementary nucleotides.

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24 A stop codon signals the end of translation by prompting the ribosome to release the newly-synthesised polypeptide chain, terminating protein synthesis.

25 Transcription factors bind to specific DNA sequences, such as promoter or enhancer regions, to either activate or repress transcription.

26 Because DNA polymerase can only add nucleotides to the 3′ end of the growing strand, one strand is being replicated in the same direction as the replication fork, and the other is being replicated in the opposite direction. The lagging strand, which faces in the 'wrong' direction, must be built in discontinuous fragments (Okazaki fragments).

Analyse

27 The purpose of gene expression is to produce functional proteins or RNA. Both eukaryotic and prokaryotic cells transcribe and translate the genetic information in their DNA to make these products. Both types of cells will regulate the processes to ensure that only products required by the cell are produced as needed to conserve energy and materials. In prokaryotic cells, both transcription and translation processes occur in the cytoplasm because they do not contain membrane-bound organelles. The process is continuous, with the ribosomes attaching to the mRNA while it is being transcribed. There is no post-transcription processing. In eukaryotic cells, gene expression is completed in two separate stages. Transcription occurs in the nucleus of the cell. mRNA produced in this process is then modified as needed before it leaves the nucleus and migrates to the cytoplasm. The ribosomes in the cytoplasm will translate the mRNA strand to produce a fully functioning protein or gene product.

28 B. The template strand is complementary to the mRNA. In mRNA Phe is UUU so the DNA must be AAA. The template is DNA so does not contain uracil.

29 **a** The strand contains uracil so it is RNA. The protein is only four amino acids long but the RNA strand contains eight codons, so it must have been shortened before translation. Therefore, it must be pre-mRNA.

b Asn (asparagine)

30 Due to cell specialisation, not all genes are expressed in all cells. Only the necessary structural or functional proteins required for the cell to perform its specialised functions are produced by the cells.

31 A change to the TATA box due to mutation will prevent the RNA polymerase (which starts transcription) from binding to the DNA molecule. Therefore, transcription cannot begin, the mRNA sequence cannot be produced and the process of protein synthesis cannot proceed.

32 The *lac* operon is a constitutive gene, which means that it will always be turned on due to the repressor not being able to bind to the *lac* operator. Assuming the RNA polymerase can bind to the lac operator, β-galactosidase will continually be expressed. However, the mutation may also result in RNA polymerase being unable to bind to the lac operator and inhibiting β-galactosidase expression altogether.

33 **a** An operon like the *trp* operon is a section of DNA that consists of a series of genes that function as a single unit. It consists of a regulatory gene, followed by a promoter to which RNA polymerase attaches, an operator to which a transcriptional factor can attach, and then a series of structural genes that are either all transcribed or not. The repressor protein is always present in the cell because it is coded for by constitutive genes. As a result, the production of tryptophan can be stopped as soon as concentrations inside the cell are sufficiently high and energy is not wasted by the cell. The binding of the repressor to the operator means that RNA polymerase is blocked from moving along the DNA, so mRNA for the five tryptophan genes is not transcribed. Without the mRNA the necessary enzymes (A, B, C, D and E) are not produced, so tryptophan cannot be produced.

b In the case of the *lac* operon, inhibition of the repressor protein occurs as a result of high concentrations of the substrate of the biochemical pathway. In the case of the *trp* operon, high concentrations of the product of the biochemical pathway result in repression.

34 The amount of genetic information available to the organism present in the cell does not change significantly over time. It is the expression of particular genes in the DNA that provides for the cell requirements that are regulated. Gene expression is controlled by transcription factors acting on the genes to either induce or repress the production of mRNA needed for protein synthesis. For example, a particular enzyme or protein that is needed for survival may be synthesised at a greater rate as the rate of transcription and translation is increased. Alternatively, genes for substances that are not required under the changed conditions will no longer be expressed, in order to conserve resources and energy. Eukaryotic organisms, such as amoebae, will have related genes across a number of different chromosomes. The regulation of these genes is a complex process, involving any stage of the transcription, mRNA processing and translation phases. Gene transcription can be induced or repressed by transcription factors, which are regulated by the environmental conditions, and therefore amoebae are able to respond quickly to changes.

35 The data shows that the substitution mutation has resulted in a change in the codon, altering the resulting amino acid (methionine to valine) that is added to the growing polypeptide chain, which may affect the resulting protein structure. The nonsense mutation has converted an amino acid codon into a stop codon, truncating protein synthesis and likely producing a non-functional protein.

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36 In muscle cells, genes involved in contractile protein synthesis (e.g. myosin and actin) are located in euchromatin, allowing active expression. These same genes may be in heterochromatin in neurons, where they are not needed. Conversely, genes for neurotransmitter production are euchromatic in neurons and heterochromatic in muscle cells. These differences in chromatin state enable the distinct gene expression profiles necessary for cell specialisation.

Interpret

37 **a** A nucleotide-pair substitution may not have any noticeable effect on the structure of the protein if the substitution results in the same amino acid being coded for. This type of synonymous mutation results in the same protein being produced, but the rate and efficiency of protein synthesis may be affected, which could have some effect on the cell. If the substitution is non-synonymous, then the sequence of amino acids may be altered, and this may affect the folding and function of the protein.

b A deletion of three nucleotides removes a whole codon from the middle of the gene, meaning that one amino acid will not be present in the polypeptide chain. This may affect the protein structure if that amino acid was essential in the formation of the shape of the protein and therefore its function. This mutation may be significant, but only if it affects the folding of the protein.

c While introns are non-coding sections of DNA and typically do not directly affect protein synthesis, mutations in introns such as the deletion of a single nucleotide can have indirect effects. For example, the nucleotide deletion could disrupt splice sites, regulatory elements or other critical regions within the intron that affect proper mRNA splicing or gene expression. Since transcription involves continuous synthesis of the RNA strand, a single nucleotide deletion within an intron might result in a frameshift mutation in rare cases where splice sites are activated that would normally be non-functional.

d Deletion of a single nucleotide near the end of the coding sequence could cause a frameshift mutation. While such a mutation might not significantly disrupt most of the protein structure due to its proximity to the stop codon, there is a possibility of eliminating the stop codon itself. If the stop codon is disrupted, transcription and translation may continue until another stop codon is encountered downstream, leading to the production of an abnormally elongated, and likely non-functional, protein. This scenario could have significant biological consequences depending on the nature of the protein and its function in the organism.

e The single nucleotide insertion downstream of, and close to, the start of the coding sequence will have significant impact on the cell as it will result in a frameshift mutation at the start of the code. This will result in new and different codon sequences throughout the length of the genetic code, therefore producing different amino acid sequences and the protein will be non-functional. This will have serious implications for the cell as a protein will not be produced as required by the cell and this could be damaging to the cell depending on the role of the protein in the cell. Each protein has a particular function within the cell and, without the protein, the normal cell function will not be able to occur. This is the option that has the most impact on protein synthesis.

Data analysis

Question 1 (2 marks)

Identify the independent variables as temperature and nucleotide concentration. *(1 mark)*

Identify the dependent variables as replication time and protein production. *(1 mark)*

Sample answer: The independent variables are temperature and nucleotide concentration. The dependent variables are replication time and protein production.

Question 2 (3 marks)

Identify that replication time decreases from 10 min at 25°C to 5 min at 37°C. *(1 mark)*

Identify that replication time increases to 12 min at 45°C. *(1 mark)*

Explain that DNA replication is fastest at 37°C, likely due to optimal enzyme activity, and slows at higher or lower temperatures. *(1 mark)*

Sample answer: At 25°C, the replication time is 10 minutes, which decreases to 5 minutes at 37°C. At 45°C, the replication time increases to 12 minutes. This pattern suggests that DNA replication is fastest at 37°C, the optimal temperature for enzyme activity, while lower or higher temperatures slow replication.

Question 3 (3 marks)

Stating that protein production increases with higher nucleotide concentration. *(1 mark)*

Comparing protein production at 50% concentration (400 units/min) and 100% concentration (600 units/min). *(1 mark)*

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Explaining that higher nucleotide concentrations likely support faster replication, enabling increased transcription and translation rates. *(1 mark)*

Sample answer: At 37°C, protein production increases from 400 units/min at 50% nucleotide concentration to 600 units/min at 100% nucleotide concentration. This suggests that higher nucleotide concentrations support faster DNA replication, allowing for more efficient transcription and translation and resulting in higher protein production.

Question 4 (4 marks)

Predicting that replication time would likely increase. *(1 mark)*

Predicting that protein production would likely decrease. *(1 mark)*

Explaining that higher temperatures can denature enzymes involved in replication and protein synthesis. *(1 mark)*

Relating this prediction to the observed trend at 45°C. *(1 mark)*

Sample answer: At 50°C replication time would likely increase and protein production would likely decrease. This is because enzymes involved in DNA replication and protein synthesis may denature at higher temperatures, reducing their efficiency. This trend is consistent with the data at 45°C, where replication slows and protein production declines.

Question 5 (3 marks)

Stating that DNA replication is necessary to provide templates for transcription. *(1 mark)*

Explaining that transcription produces mRNA, which is essential for protein synthesis. *(1 mark)*

Connecting efficient replication with timely production of mRNA and proteins. *(1 mark)*

Sample answer: DNA replication provides the template for transcription and mRNA production. mRNA is essential for translation and protein synthesis. Efficient DNA replication ensures sufficient templates are available for transcription and subsequent protein production.

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