VCE BIOLOGY UNIT 3 & 4
Australian Curriculum

WORKBOOK

Biology

TOPICS

UNIT 3: HOW DO CELLS MAINTAIN LIFE?

Area of Study 1: What is the role of nucleic acids and proteins in maintaining life?

Area of Study 2: How are biochemical pathways regulated?

UNIT 4: HOW DOES LIFE CHANGE AND RESPOND TO CHALLENGES?

Area of Study 1: How do organisms respond to pathogens?

Area of Study 2: How are species related over time?

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UNIT 3:
How do cells maintain life?

AREA OF STUDY 1: What is the role of nucleic acids and proteins in maintaining life?

3.1 The Relationship Between Nucleic Acids and Proteins

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3.1.1 Nucleic Acids

Nucleic acids are information molecules that encode instructions for the synthesis of proteins: the structure of DNA, the three main forms of RNA (mRNA, rRNA and tRNA) and a comparison of their respective nucleotides.

Living things rely on precise instructions to build and maintain the complex cellular structures and functions necessary for life. These instructions are encoded in **nucleic acids**, a class of macromolecules in cells that store, transmit, and regulate genetic information. Two key types of nucleic acids, **deoxyribonucleic acid (DNA)** and **ribonucleic acid (RNA)**, work together to direct the synthesis of proteins, which are essential for cellular structure and function.

Nucleic Acids

Nucleic acids are polymers known as **polynucleotides**, which consist of repeating subunits called **nucleotides** (Figure 3.01). A nucleotide is composed of three fundamental components: a **sugar**, a **nitrogenous base**, and a **phosphate group** (Figure 3.01). There are two main categories of nitrogenous bases: **pyrimidines** and **purines**. Pyrimidines have a single six-membered ring composed of carbon and nitrogen atoms. The three pyrimidine bases are **cytosine (C)**, **thymine (T)**, and **uracil (U)**. Purines, in contrast, are larger and consist of a six-membered ring fused to a five-membered ring. The two purines are **adenine (A)** and **guanine (G)**. Adenine, guanine, and cytosine are found in both DNA and RNA, while thymine is exclusive to DNA, and uracil is unique to RNA. The nitrogenous bases are covalently bonded to a sugar molecule. In DNA, the sugar is **deoxyribose**, whereas in RNA, it is **ribose** (Figure 3.01). The sugar contains five carbon atoms, numbered 1' to 5' (pronounced "one-prime" to "five-prime"). The 5' carbon is covalently bonded to a phosphate group within the same nucleotide. In contrast, the 3' carbon is covalently bonded with the phosphate group of the next nucleotide, creating the **sugar-phosphate backbone** of the polynucleotide strand.

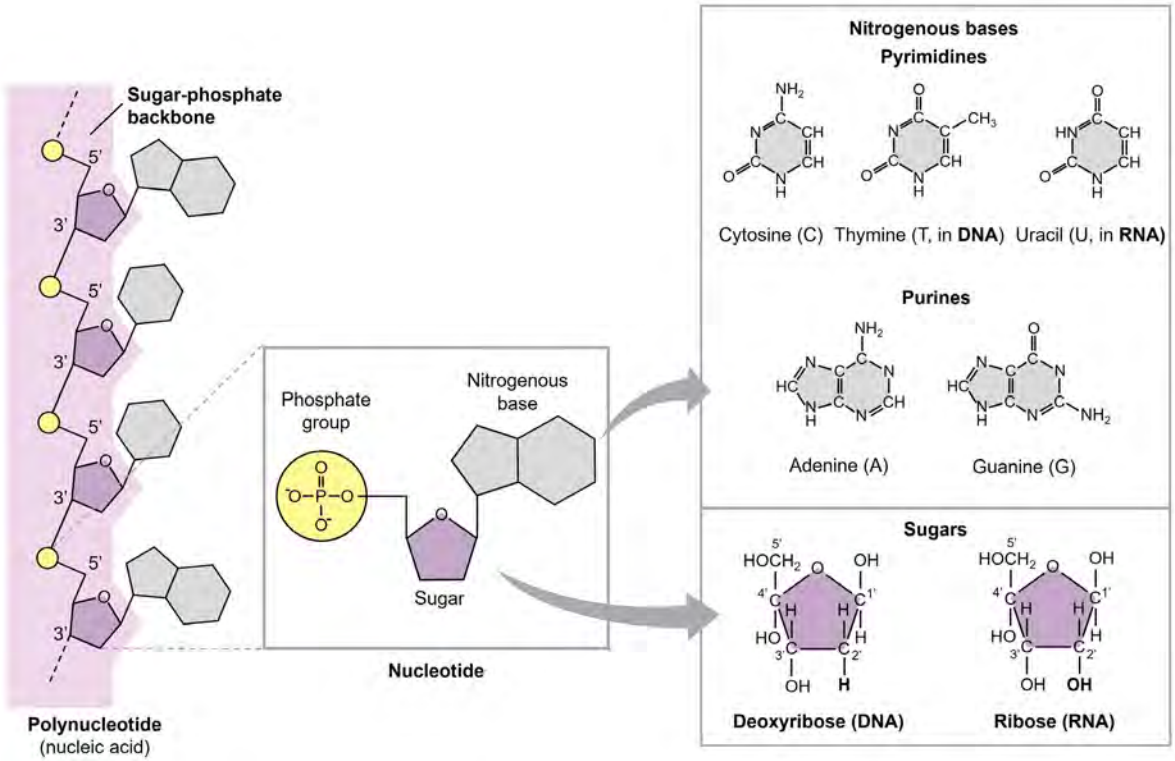


Figure 3.01: Components of Nucleic Acids

The Structures of DNA and RNA Molecules

A DNA molecule consists of two polynucleotide strands that coil around an imaginary axis, forming a double helix (**Figure 3.02**). The sugar-phosphate backbones of each strand run in opposite 5' → 3' directions, a structural arrangement known as **antiparallel**. In the double helix, the sugar-phosphate backbones are positioned on the outside, while the nitrogenous bases are aligned in the interior, where they pair through weak electrical forces of attraction called **hydrogen bonds** (**Figure 3.02**). Each DNA strand is complementary to the other due to specific base-pairing rules: adenine (A) always pairs with thymine (T), and guanine (G) pairs with cytosine (C). This complementarity ensures if one strand has the sequence 5'-AGGTCCG-3', the opposing strand must have the sequence 3'-TCCAGGC-5'. Because each strand serves as a template for its counterpart, DNA can be accurately replicated before cell division, ensuring that genetic information is transmitted to daughter cells. This structural feature is fundamental to DNA's role in heredity.

Unlike DNA, RNA molecules are usually comprised of a single polynucleotide strand. However, complementary base pairing can still occur, either between two RNA molecules or within different regions of the same molecule. This internal base pairing allows RNA to fold into complex three-dimensional structures, which are crucial for its function. For example, transfer RNA (tRNA), a type of RNA involved in protein synthesis, is about 80 nucleotides long and adopts a specific three-dimensional shape due to internal base pairing (**Figure 3.02**). Another key difference between RNA and DNA is in base pairing: adenine (A) pairs with uracil (U) in RNA, replacing thymine (T), which is exclusive to DNA. Furthermore, DNA molecules have a double helix structure, while RNA molecules are highly variable in structure.

RNA molecules play diverse and essential roles in cells, with **messenger RNA (mRNA)**, **transfer RNA (tRNA)**, and **ribosomal RNA (rRNA)** being the three main types involved in protein synthesis. mRNA serves as the intermediate between DNA and protein synthesis. It is transcribed from DNA and carries genetic instructions to the ribosome, where it directs the assembly of amino acids into a polypeptide chain. tRNA ensures the correct sequence of amino acids in the growing protein. rRNA is a key component of ribosomes, the cell's protein factories. It helps catalyse peptide bond formation and provides structural support to the ribosome. Together, these RNA types ensure the accurate synthesis of proteins, which are vital for cellular function and life.

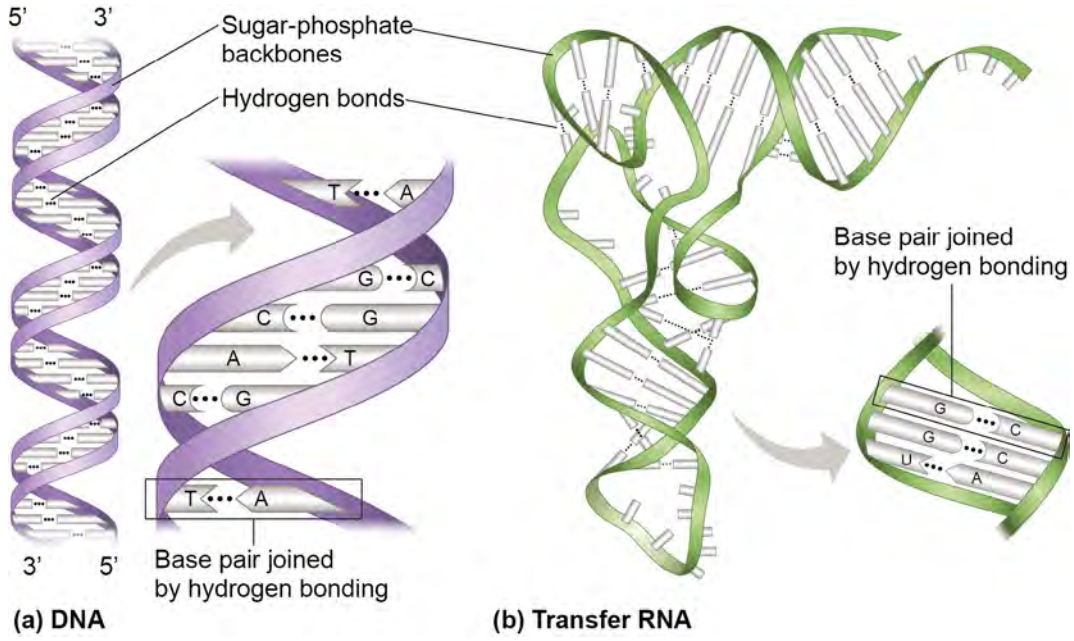


Figure 3.02: Hydrogen bonding in nucleic acids

Chromosomes

Most DNA molecules are very long, containing thousands or even millions of base pairs. For this reason, cells arrange DNA molecules into one or more **chromosomes**, highly condensed structures composed of a single DNA molecule and associated proteins. In eukaryotes, each cell contains two or more linear chromosomes housed in the cell nucleus. Each eukaryotic chromosome contains **chromatin**, a mixture containing one long DNA molecule bound to proteins (**Figure 3.03**). Among the proteins bound to DNA in eukaryotes are **histones** (**Figure 3.03**), small round proteins that help coil the DNA molecule, reducing its length and allowing it to fit into the nucleus. When a eukaryotic cell is not dividing, the chromatin is relaxed, and the chromosomes are observed under an optical microscope as a spread-out mass, indistinguishable from one another. However, as a cell prepares to divide, the chromatin condenses, and the chromosomes become thick enough to be distinguished from one another under an optical microscope. In addition, each eukaryotic species has a characteristic number of chromosomes. For example, a typical human body cell has 46 chromosomes in its nucleus, whereas a fruit fly body cell has only eight chromosomes.

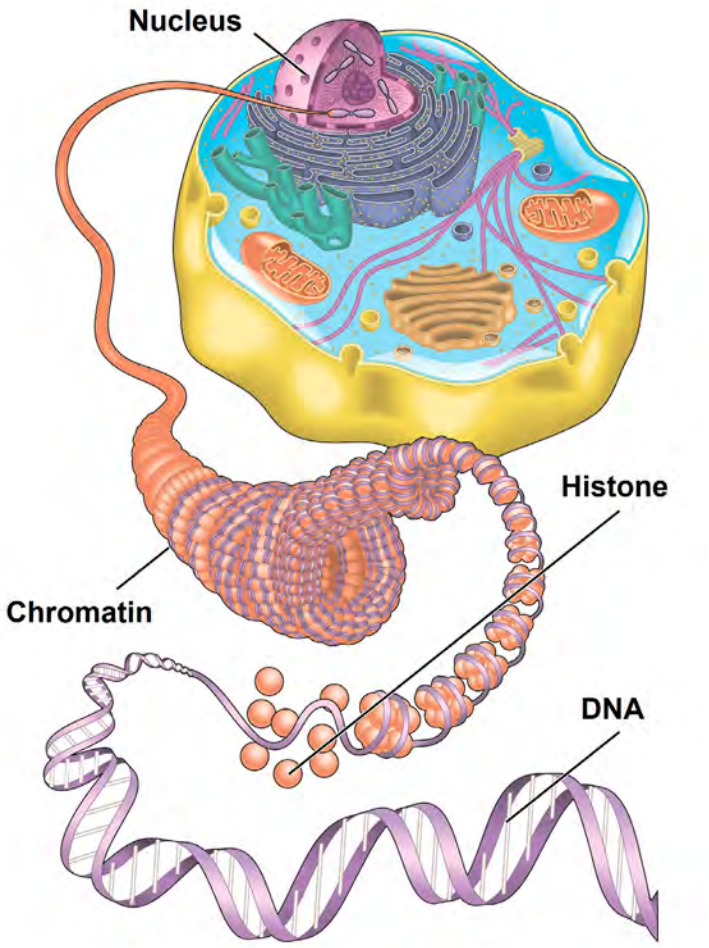


Figure 3.03: Chromosome structure eukaryotes

In contrast, prokaryotes each contain a single circular chromosome located in the **cytosol**, the fluid which fills the cell's cytoplasm. Prokaryotic chromosomes are composed of a single DNA molecule, but each is unbound and is not associated with proteins that regulate its length (**Figure 3.04**). In addition, the mitochondria and chloroplasts of eukaryotes also contain a single circular chromosome, a reflection of their evolutionary past as free-living prokaryotes.

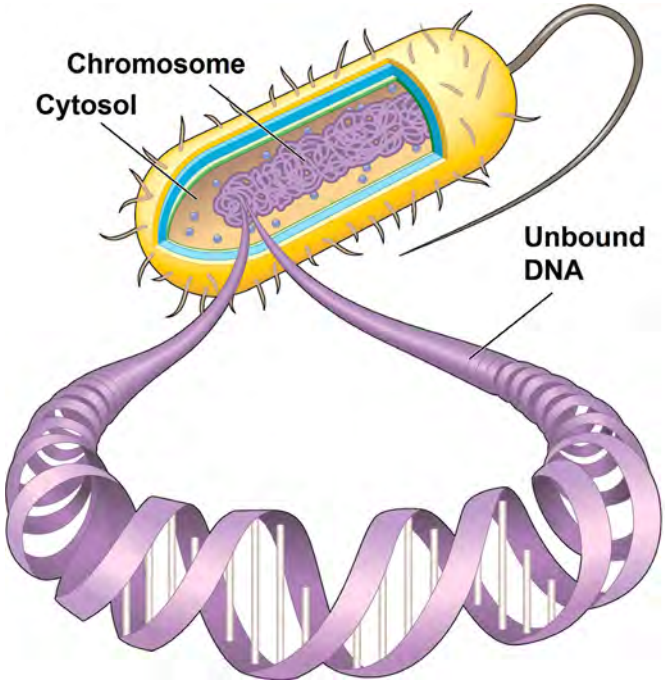


Figure 3.04: Chromosome structure prokaryotes

When a cell reproduces by dividing, its one or more chromosomes are copied and passed along from one generation of cells to the next, making them genetically identical. The transmission of genetic information from parent to daughter cells depends on the structure and replication of DNA.

DNA Replication

DNA is the genetic material that organisms inherit from their parents. When a cell reproduces, its one or more DNA molecules are copied and passed along from one generation of cells, called parent cells, to the next, called daughter cells, making them genetically identical. The transmission of genetic information from parent to daughter cells depends on the structure and replication of DNA.

Before a parent cell divides, its one or more chromosomes are copied, so the daughter cells each have a complete set of genetic information that programs a cell's activities. The process by which the chromosomes are copied is called **DNA replication**, a chemical reaction in which the two strands of a **parent DNA molecule** are separated, and free DNA nucleotides are used to construct complementary strands, forming two **daughter DNA molecules**, as in **Figure 3.05**. First, the two polynucleotide strands in the parent DNA molecule are separated, allowing each parent strand to serve as a template for synthesising one new strand. In living things, this separation is facilitated by the enzyme helicase, which breaks the weak hydrogen bonds between the base pairs in the parent strands. Next, the enzyme DNA polymerase binds free DNA nucleotides and attaches them to their complementary base pair on the exposed parent strands. Finally, DNA polymerase connects the nucleotides, forming the sugar-phosphate backbones of the daughter molecules.

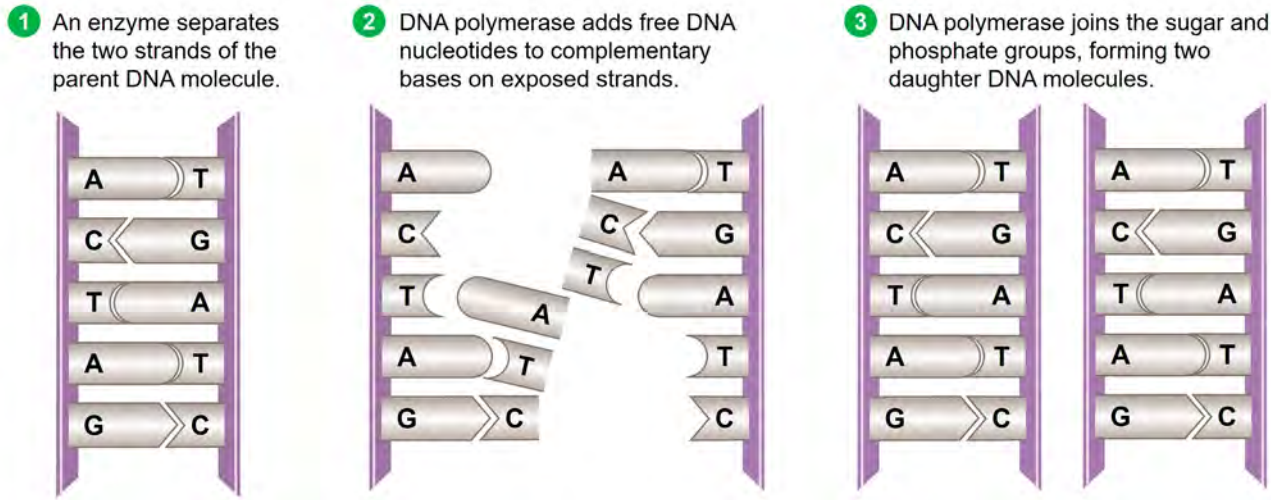


Figure 3.05: DNA replication process.

During DNA replication, the two strands of the parent molecule separate, and each functions as a template for synthesising a complementary strand. In this way, DNA replication is a **semi-conservative process**. When a double helix replicates, each of the daughter molecules has one old strand from the parent molecule and one new strand from DNA replication, as shown in **Figure 3.06**.

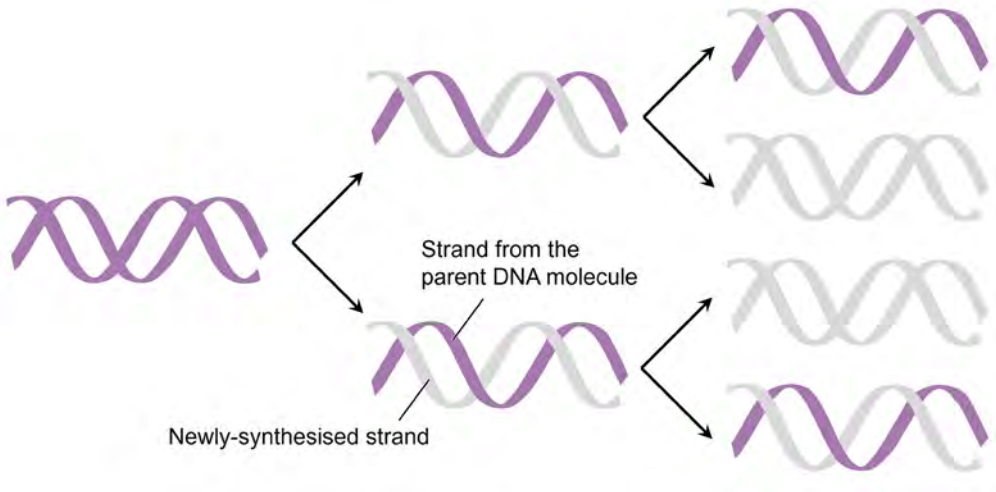


Figure 3.06: The semi-conservative model of DNA replication

DNA Replication and Inheritance

DNA replication ensures the faithful transmission of genetic information from a parent cell to its daughter cells, guaranteeing that each inherits a complete set of chromosomes. These chromosomes contain the genetic instructions necessary for cellular function, survival, and reproduction.

In eukaryotic cells, inheritance begins with DNA replication. Before replication, the cell contains **unduplicated chromosomes**, each a DNA molecule bound to histones in a highly condensed, linear structure. During replication, each chromosome is copied, resulting in a **duplicated chromosome**, where two identical DNA molecules—known as **sister chromatids**—are held together along their length by cohesin proteins, forming the characteristic X-shaped structure.

During cell division, the sister chromatids are separated, with each becoming an unduplicated chromosome that is distributed into a different daughter cell, as shown in **Figure 3.07**. In eukaryotes, DNA replication occurs during the S phase of the cell cycle, with its duration varying across species. In humans, the S phase lasts approximately 8 hours, during which 46 chromosomes are replicated.

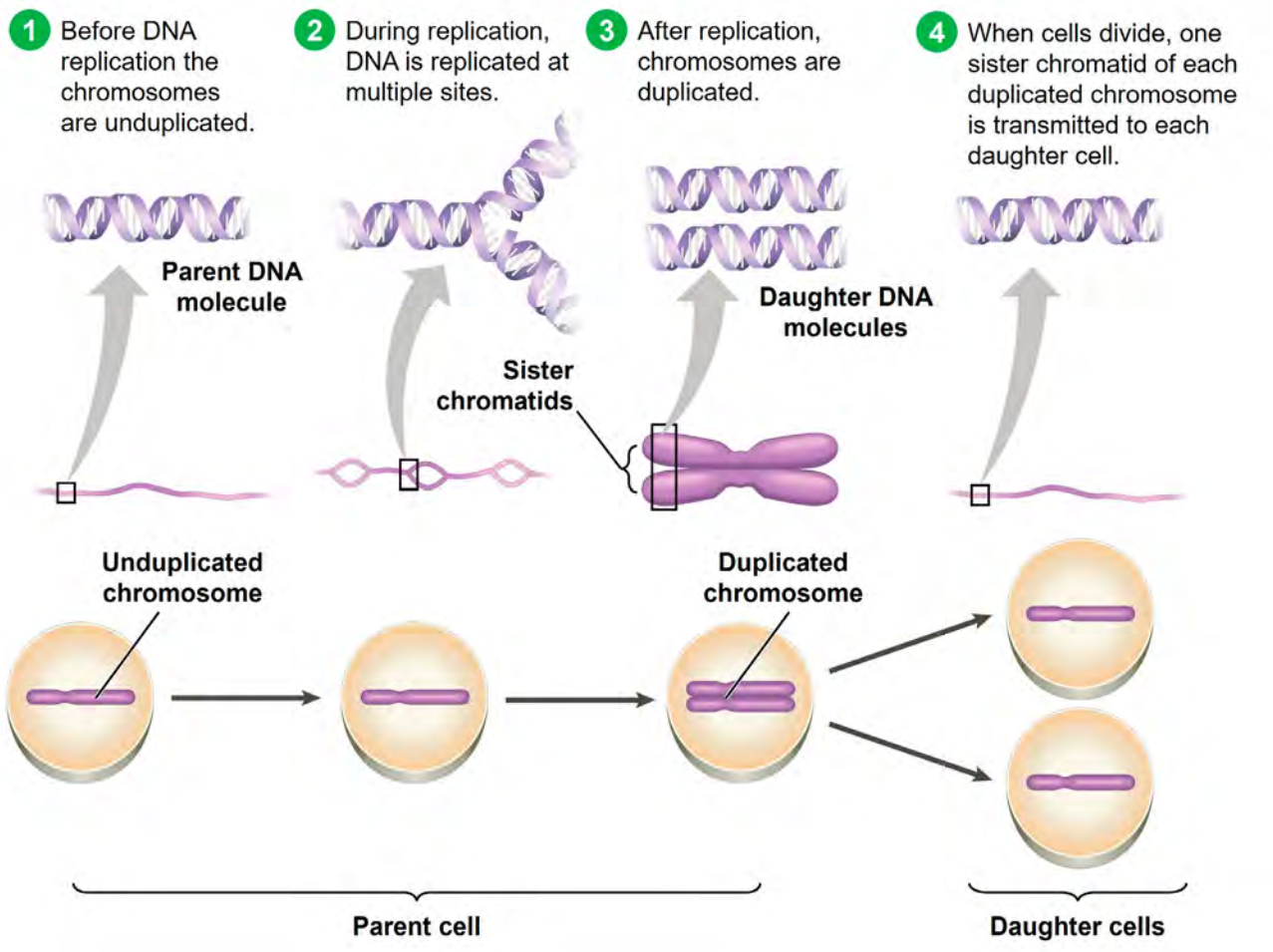
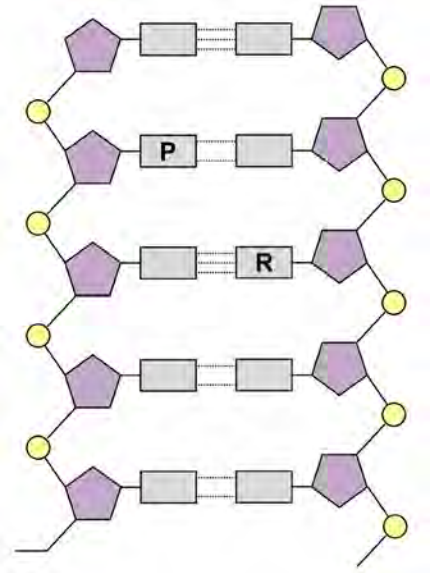


Figure 3.07: DNA replication and the transmission of genetic material.

In prokaryotes, DNA replication is more rapid as the single circular chromosome is much shorter in length than most eukaryotic chromosomes. In favourable environments, some bacteria can replicate their DNA in less than 15 minutes. Biologists have extensively studied the processes of DNA replication in prokaryotes and eukaryotes, concluding that most of these processes are fundamentally similar, indicating that DNA replication methods are universal.

Question 1

The diagram below shows part of a DNA double helix.



The double helix is 24% **P**. The percentage of **R** is

- A 24%
- B 48%
- C 26%
- D 52%

(1 mark)

Question 2

The production of proteins involves molecules of tRNA.

Which row in the table describes the structure of tRNA?

	Bases	*Number of strands*	*Type of sugar*
A	A, C, G, U	One	deoxyribose
B	A, C, G, U	One	ribose
C	A, C, G, T	Two	deoxyribose
D	A, C, G, T	Two	ribose

(1 mark)

Question 3

In DNA, the number of

- A phosphate groups equal the number of nitrogen bases.
- B guanine nucleotides equal the number of uracil nucleotides.
- C adenine nucleotides equal the number of cytosine nucleotides.
- D phosphate groups equals twice the number of sugar molecules.

(1 mark)

Question 4

The following nucleotide sequence forms part of a DNA strand.

TGGATGACA

Which base is present at the fourth position on the complementary DNA strand?

- ○ A C
- ○ B G
- ○ C T
- ○ D U

(1 mark)

Question 5

In a polynucleotide strand:

- ○ A The 5' carbon of the sugar bonds with the phosphate of the previous nucleotide.
- ○ B The 3' carbon of the sugar bonds with the base on the same nucleotide.
- ○ C The 5' carbon of the sugar bonds with the base on the next nucleotide.
- ○ D The 3' carbon on the sugar bonds with the phosphate group on the next nucleotide.

(1 mark)

Question 6

Cells in plant leaves have several organelles containing DNA.

Which one of the following combinations correctly identifies the location, shape, and number of chromosomes in a plant leaf cell?

	Location	*Shape*	*Number*
○ A	Nucleus	Linear	One
○ B	Nucleus	Circular	Multiple
○ C	Chloroplast	Linear	Multiple
○ D	Chloroplast	Circular	One

(1 mark)

Question 7

Which of the following statements about mRNA are correct?

I. mRNA contains four nitrogenous bases.
II. mRNA can form hydrogen bonds.
III. mRNA is single-stranded.

- ○ A I, II and III
- ○ B Only I and II
- ○ C Only II and III
- ○ D Only I and III

(1 mark)

Question 8

All living things contain DNA molecules, some of which are arranged into chromosomes.

Which of the following statements about DNA and chromosomes in living things is *incorrect*?

- ◯ A Eukaryotes contain multiple DNA molecules, each associated with proteins.
- ◯ B Prokaryotes have a single circular chromosome.
- ◯ C Eukaryotes and their organelles contain multiple linear chromosomes.
- ◯ D Prokaryotes have one DNA molecule that is not bound to proteins.

(1 mark)

Question 9

Which of the following statements is/are evidence that DNA replication is semi-conservative?

I. After one replication, the number of adenine nucleotides is equal to the number of guanine nucleotides.
II. After two replications, two DNA molecules have one original and one new strand, and two DNA molecules have two new strands.
III. After three replications, there are eight DNA molecules, only two of which have strands from the original DNA.

- ◯ A I, II and III
- ◯ B Only II and III
- ◯ C Only I and II
- ◯ D Only I

(1 mark)

Question 10

The table below refers to the shape and location of a chromosome in a non-dividing plant cell and whether or not it is bound to histone proteins.

	Shape	***Location***	***Bound to histone proteins***
A	linear	nucleus	yes
B	circular	nucleus	no
C	circular	cytosol	no
D	linear	cytosol	yes

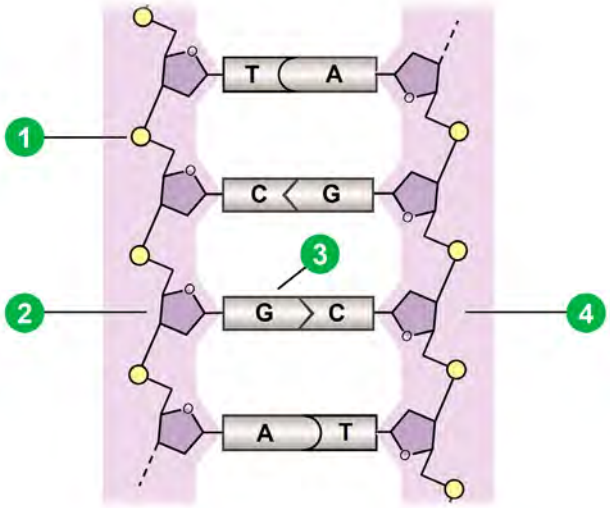
For a chromosome in a non-dividing plant cell, the combination in the table that correctly describes its shape, location, and whether or not it is bound to histone proteins is

- ◯ A
- ◯ B
- ◯ C
- ◯ D

(1 mark)

Question 11

The diagram below shows a short section of DNA



(a) Name the components **1**–**4**.

(4 marks)

(b) Describe the structure of a DNA molecule.

(3 marks)

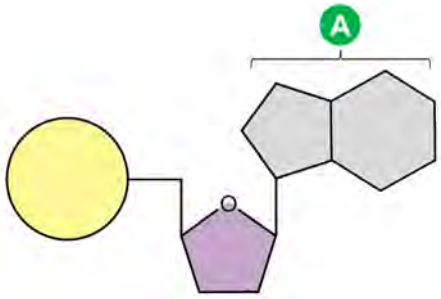
Question 12

DNA is a macromolecule in the cells of all living things.

(a) State the name of this type of macromolecule.

(1 mark)

(b) DNA molecules are composed of nucleotides, like the one shown below.



i. Name the component of the nucleotide labelled A in the diagram.

(1 mark)

ii. Describe how the nucleotides are arranged in DNA molecules.

(2 marks)

Question 13

The diagram opposite shows the DNA double helix.

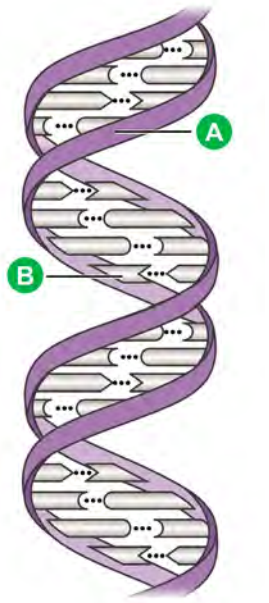
The double helix may be described as a coiled ladder.

(a) State the composition of the uprights of the ladder, labelled **A**.

(1 mark)

(b) The rungs of the ladder are made by pairing components labelled **B**.
Name the components and their specific pairs.

(2 marks)



Question 14

The diagram opposite is a coloured transmission electron micrograph (TEM) of the bacterium *Escherichia coli*.

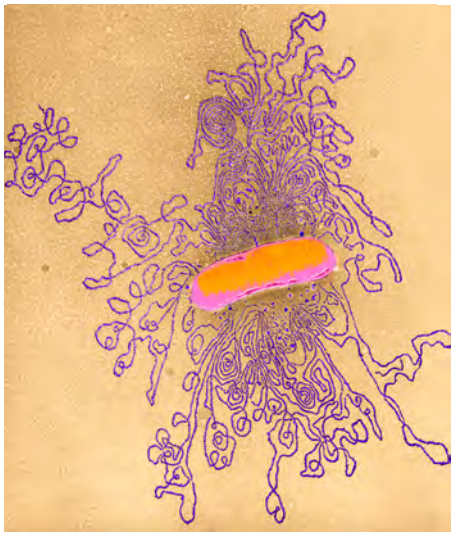
The cell has burst, and the chromosome has leaked out.

(a) Describe the structure and composition of the bacterial chromosome.

(2 marks)

(b) State the location of the chromosome before it leaked out of the cell.

(1 mark)

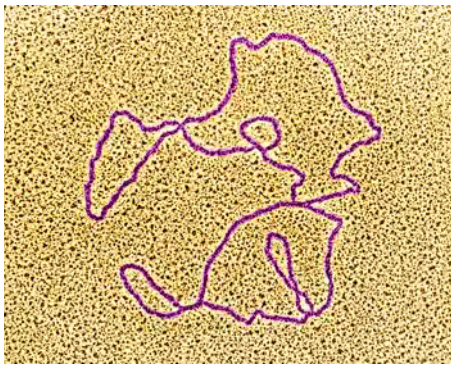


Question 15

The diagram opposite is a coloured TEM of mitochondrial DNA.

(a) Describe the structure of mitochondrial DNA using evidence from the diagram.

(2 marks)



(b) Mitochondrial DNA has a similar structure to DNA in prokaryotes.
Give one reason for this.

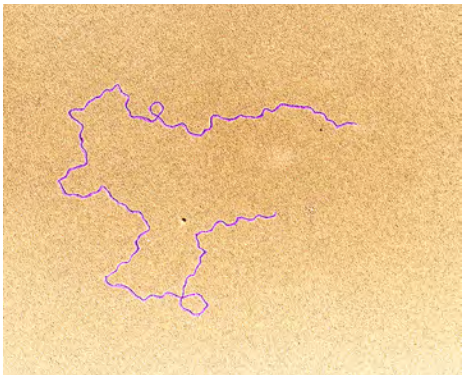
(1 mark)

(c) Mitochondria are one type of organelle containing DNA.
Name two other organelles that contain DNA.

(2 marks)

Question 16

The diagram below is a coloured TEM of a DNA molecule from the nucleus of a eukaryotic cell.



(a) State the evidence from the diagram showing this DNA molecule is from a eukaryotic cell.

(1 mark)

(b) The DNA molecule shown is one of twelve chromosomes in this cell.

Describe the structure of the twelve chromosomes in this eukaryotic cell.

(3 marks)

(c) The DNA molecule in the diagram is from the nucleus of a mesophyll cell in *Vicia faba*, the broad bean plant.

Mesophyll cells contain up to 60 chloroplasts, each containing DNA.

State two differences between the DNA in the nucleus and chloroplasts in *Vicia faba*.

(2 marks)

Question 17

The table below shows the relative percentages of the bases in DNA from various species.

Source cell	Percentage of each nucleotide			
	Adenine	Guanine	Thymine	Cytosine
Wheat	27.3	22.7	27.1	22.8
Sea urchin	32.8	17.7	32.1	17.3
Human	30.9	19.9	29.4	19.8

(a) DNA is a double-stranded molecule.

Explain how the data in the table supports the concept of complementary base-pairing.

(2 marks)

(b) Although sea urchins and humans are very different organisms, their DNA shows similar percentages of complementary bases.

Use your knowledge of DNA structure to explain how this is possible.

(2 marks)

Transcription

Transcription is the synthesis of an RNA molecule, including messenger RNA (mRNA), transfer RNA (tRNA) and ribosomal RNA (rRNA). This text will focus on the synthesis of mRNA, the carrier of information from the template DNA strand of a gene to the cell's protein-synthesising machinery. First, an **RNA polymerase** enzyme binds to the target gene at a specific nucleotide sequence called the **promoter**. The promoter provides a docking site, and a transcription start point for RNA polymerase. In addition, a group of proteins called **transcription factors** bind to the promoter and facilitate the attachment of RNA polymerase. Once bound, RNA polymerase pries the coding and template DNA strands apart and begins adding RNA nucleotides to the DNA template strand in accordance with base-pairing rules (U with A, A with T and G with C) (**Figure 3.09**). As the RNA polymerase moves along the gene, it unwinds the DNA double helix, exposing 10 and 20 nucleotides for pairing with complementary RNA nucleotides (**Figure 3.10**). The RNA polymerase enzyme reads the DNA molecule and adds RNA nucleotides in a 5' to 3' direction with respect to the DNA coding strand. As transcription proceeds, the newly synthesised RNA molecule peels away from the DNA template strand, and the DNA double helix re-forms. Transcription proceeds until the RNA polymerase reaches a nucleotide sequence that causes it to detach from the DNA and release the transcript. In bacteria, this sequence is called the **terminator**. Transcription progresses at about 40 nucleotides per second in eukaryotes, and a single gene is often transcribed simultaneously by several RNA polymerase molecules following each other. The congregation of many polymerase molecules simultaneously transcribing a single gene increases the amount of mRNA transcribed from it, which helps the cell synthesise large amounts of the encoded protein.

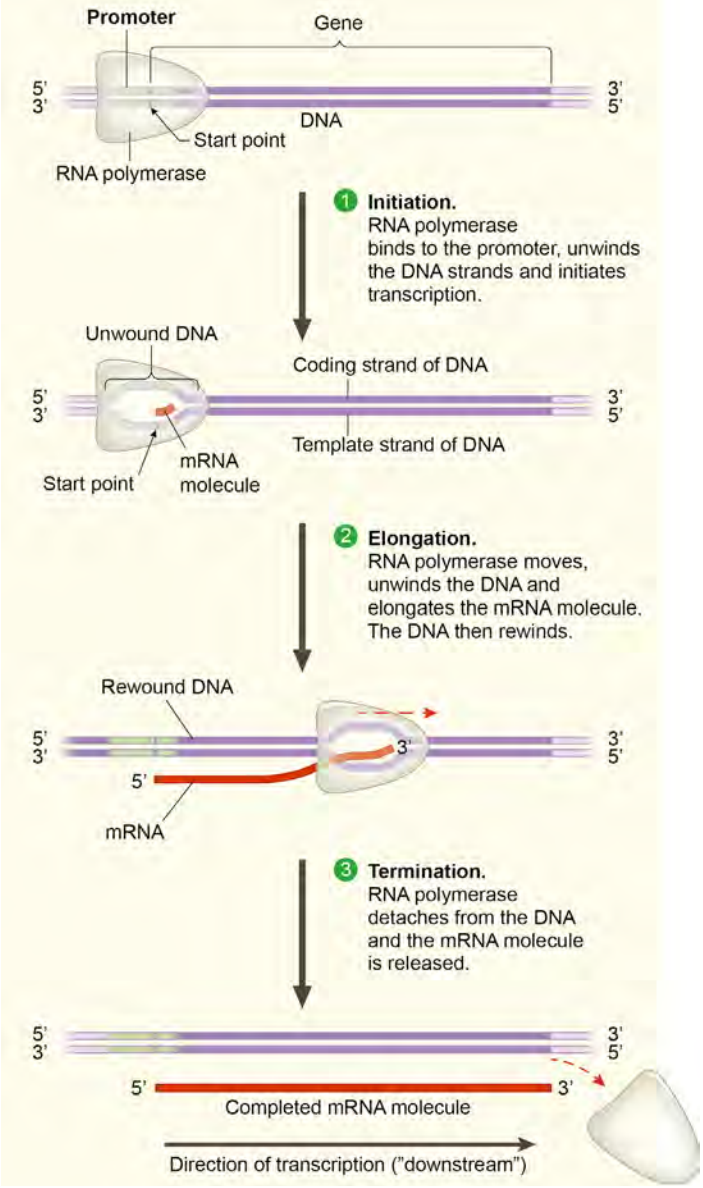


Figure 3.09: Transcription overview

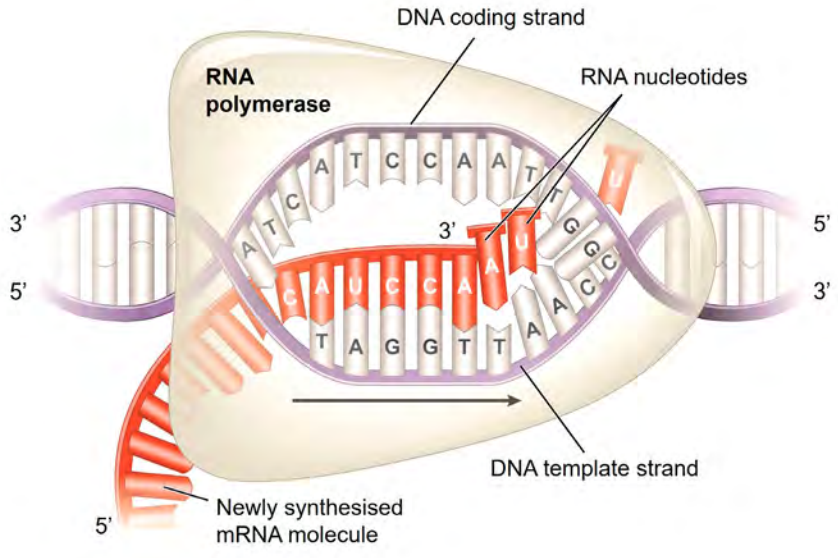


Figure 3.10: Transcription elongation

Translation

In translation, the genetic message on mRNA is translated from an RNA nucleotide sequence to an amino acid sequence. The message is a series of codons along an mRNA molecule, and the translator is called a transfer RNA (tRNA). The function of a tRNA is to transfer an amino acid from the cytoplasm to a growing polypeptide in a ribosome. A cell keeps its cytoplasm stocked with all 20 amino acids by synthesising them from other compounds or taking them up from the surrounding solution. The ribosome, a structure made of proteins and ribosomal RNA, adds each amino acid a tRNA brings to the growing end of a polypeptide chain (**Figure 3.14**).

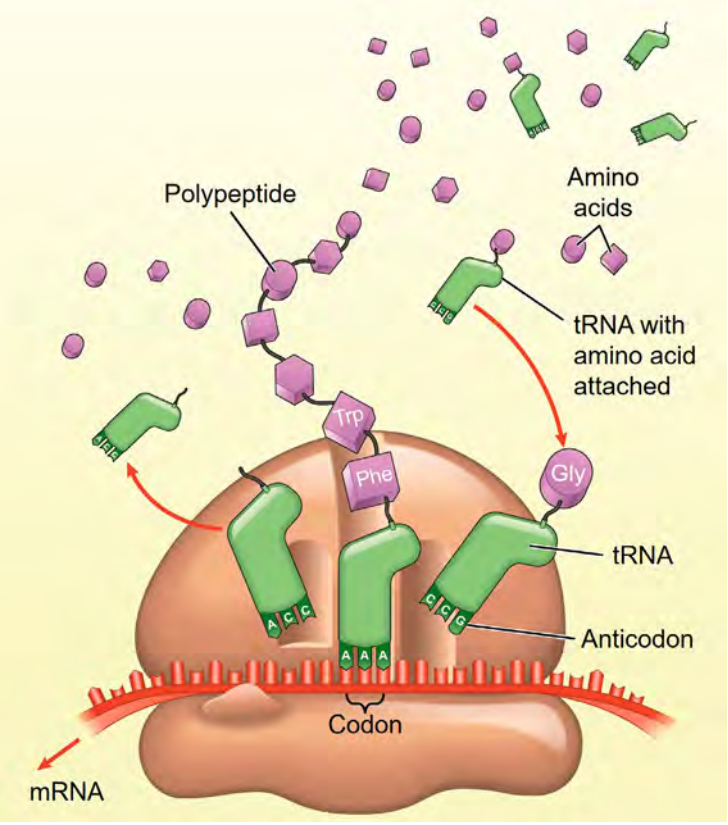


Figure 3.14: Translation

The key to translating a genetic message into a specific amino acid sequence is the transfer RNA (tRNA). A tRNA molecule has a specific amino acid binding site at one end of its structure and a nucleotide triplet called an **anticodon** that base-pairs with the complementary codon on mRNA at the other (**Figure 3.15**). As an example of how tRNAs work, consider the mRNA codon UUC, which is translated as the amino acid phenylalanine. The tRNA has AAG as its anticodon and carries phenylalanine at its other end. As an mRNA molecule is moved through a ribosome, phenylalanine is added to the polypeptide whenever the codon UUC is presented for translation. Codon by codon, the genetic message is translated as tRNAs position each amino acid in the order prescribed, and the ribosome adds that amino acid onto the growing polypeptide. The tRNA molecule is a translator as it reads a nucleic acid word (the mRNA codon) and interprets it as a protein word (the amino acid). In both bacterial and eukaryotic cells, each tRNA molecule is used repeatedly, picking up its designated amino acid in the cytosol, depositing this cargo onto a polypeptide chain at the ribosome, and then leaving the ribosome, ready to bind another of the same amino acid.

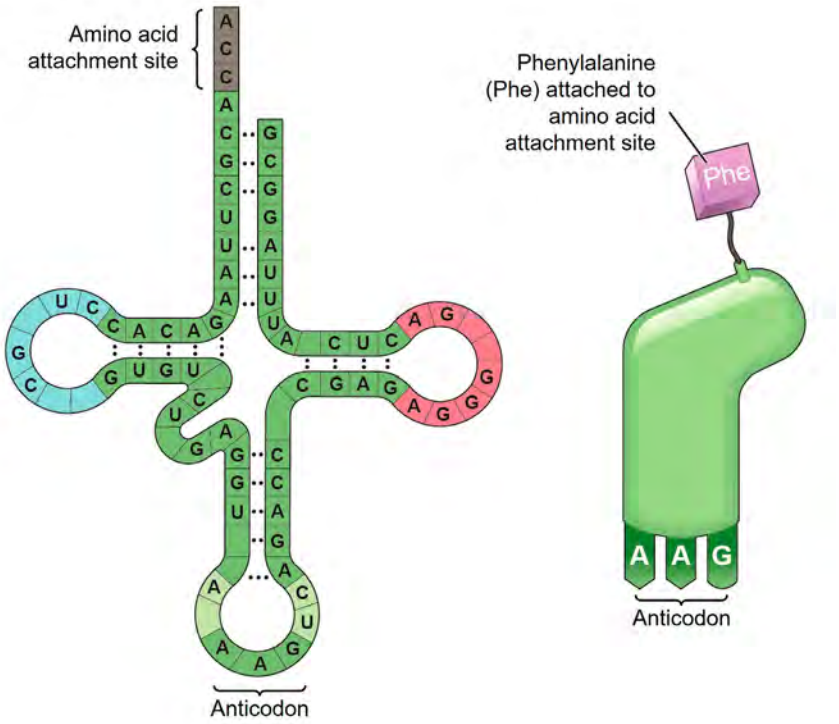


Figure 3.15: tRNA structure

The Structure of Genes

A gene is a specific DNA nucleotide sequence that contains the instructions for producing either a functional protein or an RNA molecule that aids in protein synthesis. Each gene is composed of both coding sequences, which determine the amino acid sequence of the resulting polypeptide, and **regulatory elements**, which control gene expression. The coding sequences are called **exons**, while the non-coding sequences are known as **introns**.

Genes also contain regulatory regions that mark where transcription begins and ends. The **promoter** is the DNA sequence where RNA polymerase binds to initiate transcription. It contains specific nucleotide motifs, such as the **TATA box** in eukaryotes or the **Pribnow box** in prokaryotes, which serve as recognition sites for RNA polymerase binding. For example, Figure 3.23 illustrates how transcription begins at a eukaryotic promoter. In eukaryotic cells, the coding strand of the promoter region includes a 5'-TATA-3' sequence, which serves as a binding site for transcription factors. These proteins recruit RNA polymerase, ensuring that it is correctly positioned and oriented for accurate transcription initiation.

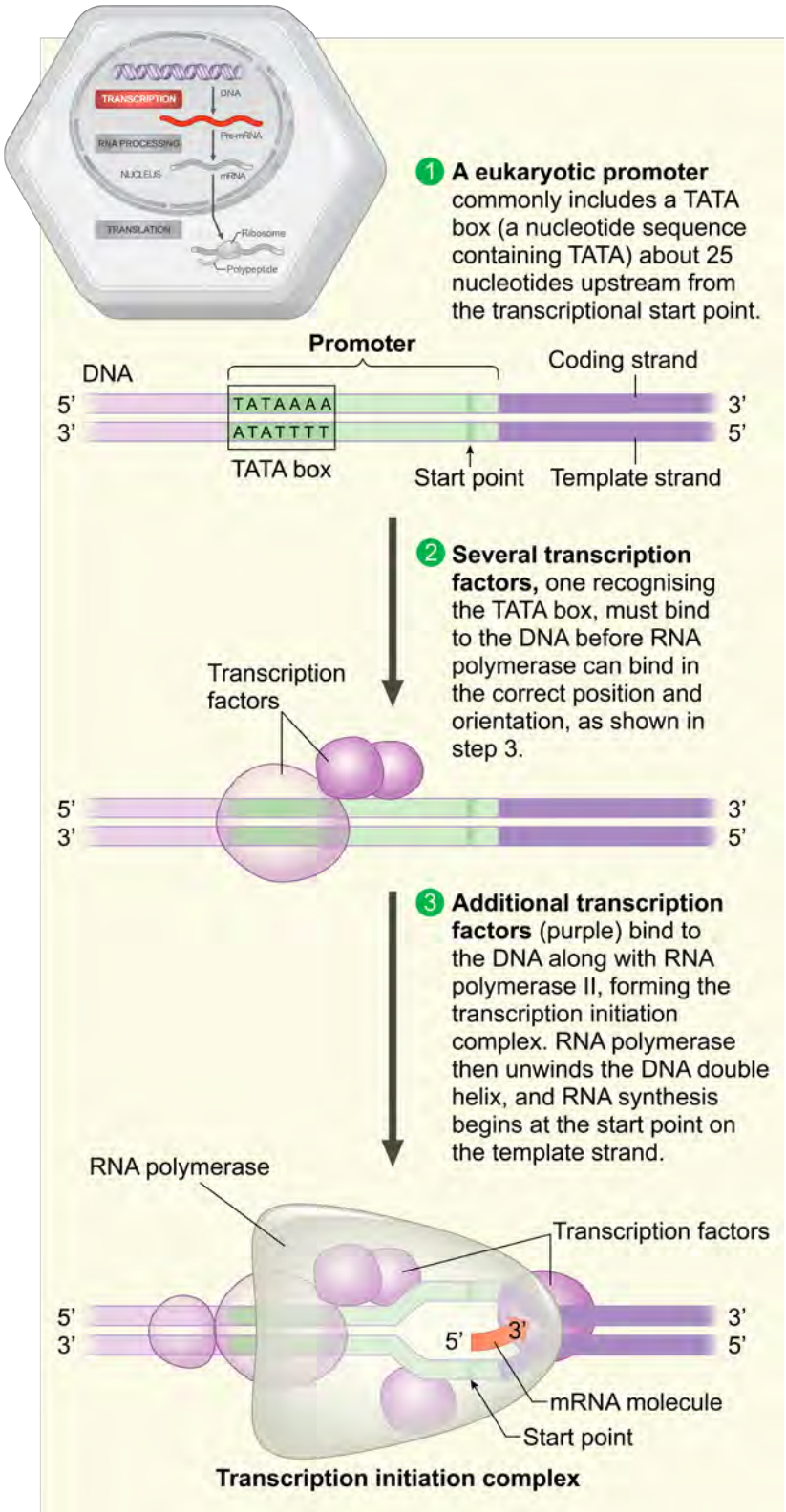


Figure 3.23: Initiation of transcription in eukaryotes

In prokaryotes, an additional regulatory element called the **operator** is present. This DNA sequence, located near or within the promoter, serves as a binding site for repressor proteins, which can block transcription in response to environmental changes, allowing the cell to regulate gene expression efficiently. Additionally, bacterial genes include a terminator sequence, which signals the end of transcription. Molecular biologists use the terms "upstream" and "downstream" to describe relative positions within a gene. The promoter is located upstream of the transcription start site, while the terminator is positioned downstream. The segment of DNA transcribed into RNA is referred to as the **transcription unit**.

3.1.4 Gene Regulation

Describe the basic elements of gene regulation: prokaryotic trp operon as a simplified example of a regulatory process.

The processes of transcription and translation use large quantities of energy and raw materials, including nucleotides and amino acids. Species comprised of cells that conserve resources and energy have a selective advantage over those that are unable to do so. Thus, evolution has favoured species that express only the genes whose products are needed by the cell. Consider *Escherichia coli* (*E. coli*), a bacterium living in the human large intestine. This single-celled organism obtains energy and raw materials from food ingested and digested by its host. Among the raw materials required by *E. coli* is the amino acid tryptophan. Suppose the host fails to ingest sufficient tryptophan, which the bacterium needs to survive. In that case, the cell responds by expressing genes coding enzymes that synthesise tryptophan from a precursor molecule in the three-step pathway shown in **Figure 3.24**. If the human host later eats a tryptophan-rich meal, the bacterial cell stops producing tryptophan to avoid wasting resources. The *E. coli* cell adjusts the concentrations of the enzymes, facilitating tryptophan synthesis by regulating the expression of specific genes that encode these enzymes. The five genes coding these enzymes are clustered together on the bacterial chromosome. A single promoter serves all five genes that are expressed at the same time. The on-off switch is a DNA nucleotide sequence positioned within a promoter called the operator. Together, the operator, the promoter, and the genes they control constitute an **operon**. The structure of the operon used in the tryptophan pathway, called the **trp operon**, is shown in **Figure 3.25**.

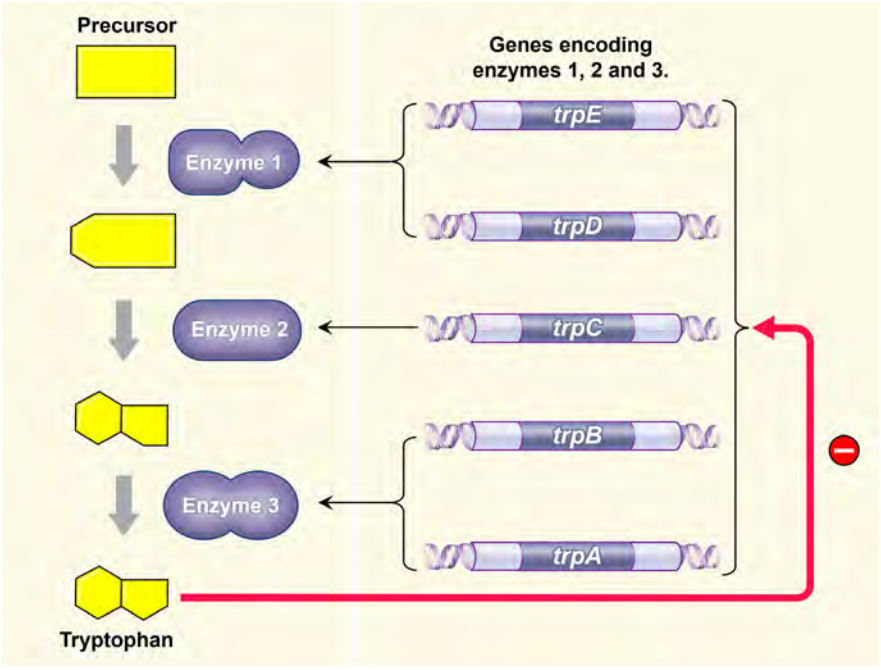


Figure 3.24: Regulation of tryptophan synthesis

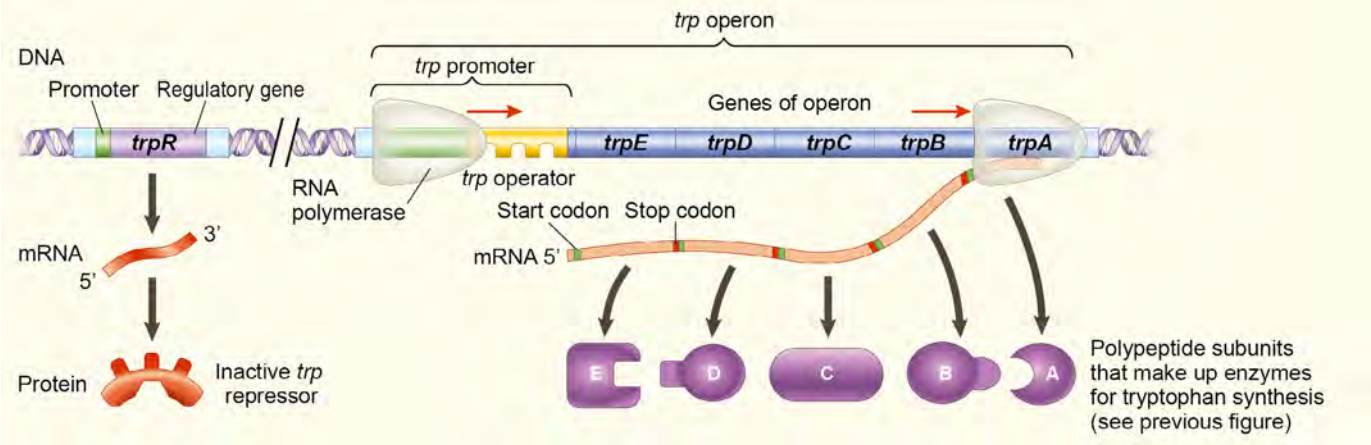


Figure 3.25: The trp operon

3.1.6 Protein Modification and Secretion

Describe the role of the rough endoplasmic reticulum, Golgi apparatus and associated vesicles in the export of proteins from a cell via the protein secretory pathway.

Ribosomes, the molecular machines responsible for polypeptide synthesis, are found in the cytosol of prokaryotic cells and in both the cytoplasm and rough endoplasmic reticulum of eukaryotic cells. Cells with high protein production rates contain large numbers of ribosomes and prominent nucleoli, which facilitate rapid ribosome assembly. For instance, pancreatic beta cells, which produce the hormone insulin, contain several million ribosomes, while plasma cells, responsible for antibody synthesis, can have up to ten million ribosomes. Ribosomes function in two distinct cytoplasmic regions. **Free ribosomes** remain suspended in the cytosol, while **bound ribosomes** attach to the outer surface of the rough endoplasmic reticulum (**Figure 3.40**), enabling the efficient synthesis of proteins destined for secretion or membrane integration.

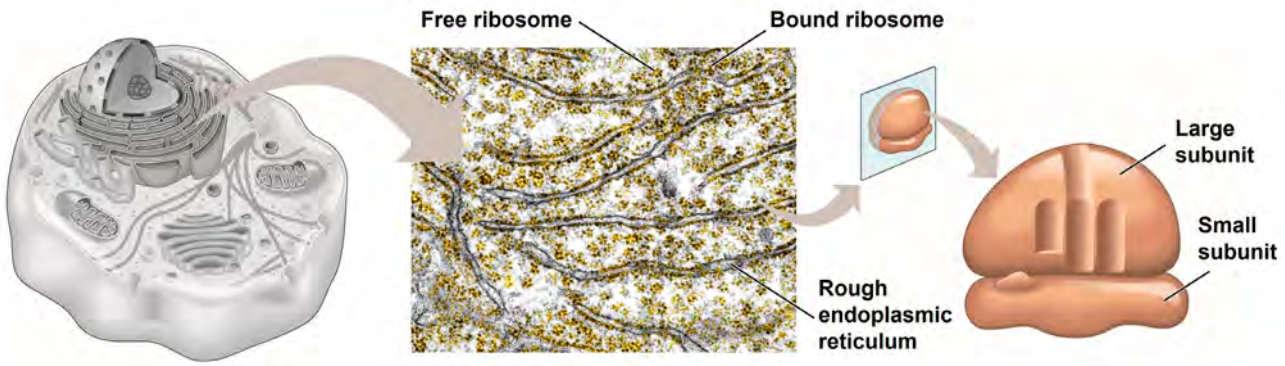


Figure 3.40: Ribosomes and their features.

Bound and free ribosomes are structurally identical, and ribosomes can play either role at different times. Most of the proteins made on free ribosomes function within the cytosol, such as the enzymes that catalyse the first steps of respiration. Bound ribosomes make proteins destined for insertion into membranes, packaging within specific organelles or secretion from the cell. Such polypeptides have a **signal peptide,** a short amino acid sequence recognised by a protein-RNA complex called a **signal-recognition particle** (SRP) that escorts the polypeptide and ribosome to the endoplasmic reticulum as in **Figure 3.41**.

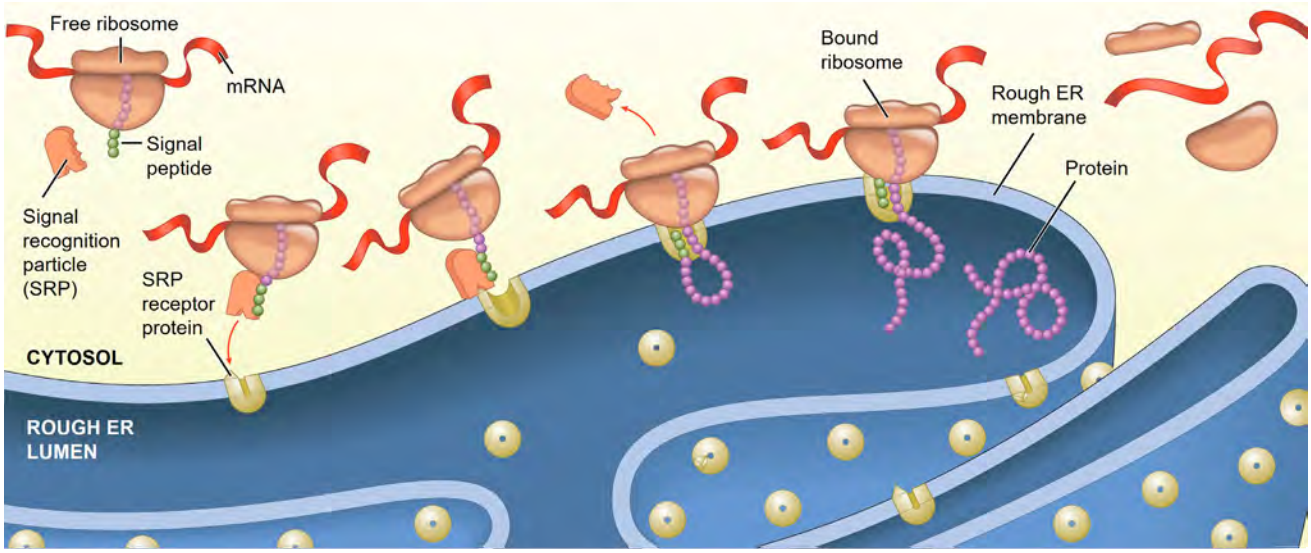


Figure 3.41: Bound ribosomes

processes, each of which has multiple steps. These two stages of photosynthesis are known as the **light-dependent** reactions and the **light-independent** reactions (see Figure 3.77).

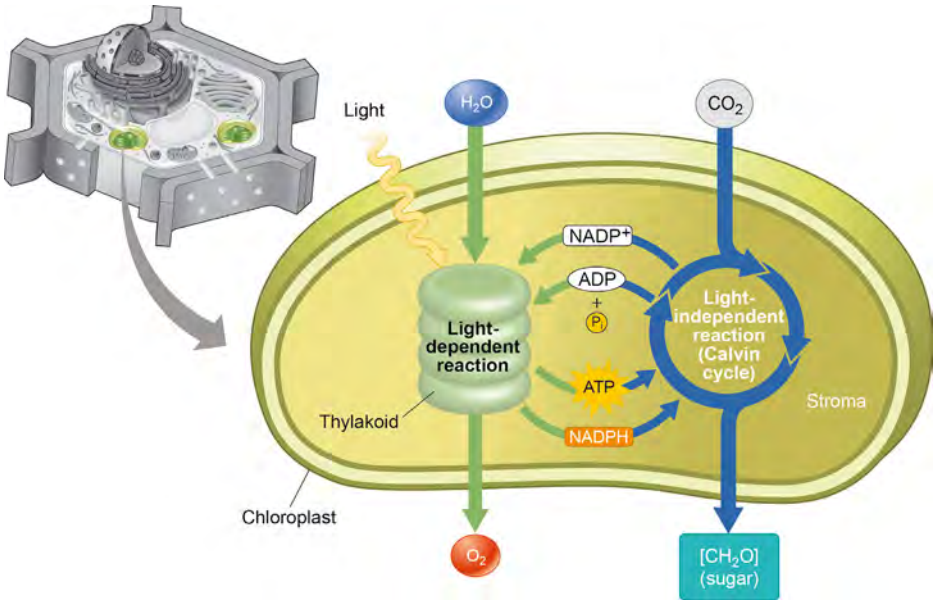


Figure 3.77: An overview of photosynthesis

The light-dependent stage takes place in the thylakoid membranes of chloroplasts. Light energy is absorbed by chlorophyll, which excites electrons that move through the electron transport chain. This process generates ATP and NADPH and splits water molecules to release oxygen as a by-product. The biochemical pathway is shown in Figure 3.78.

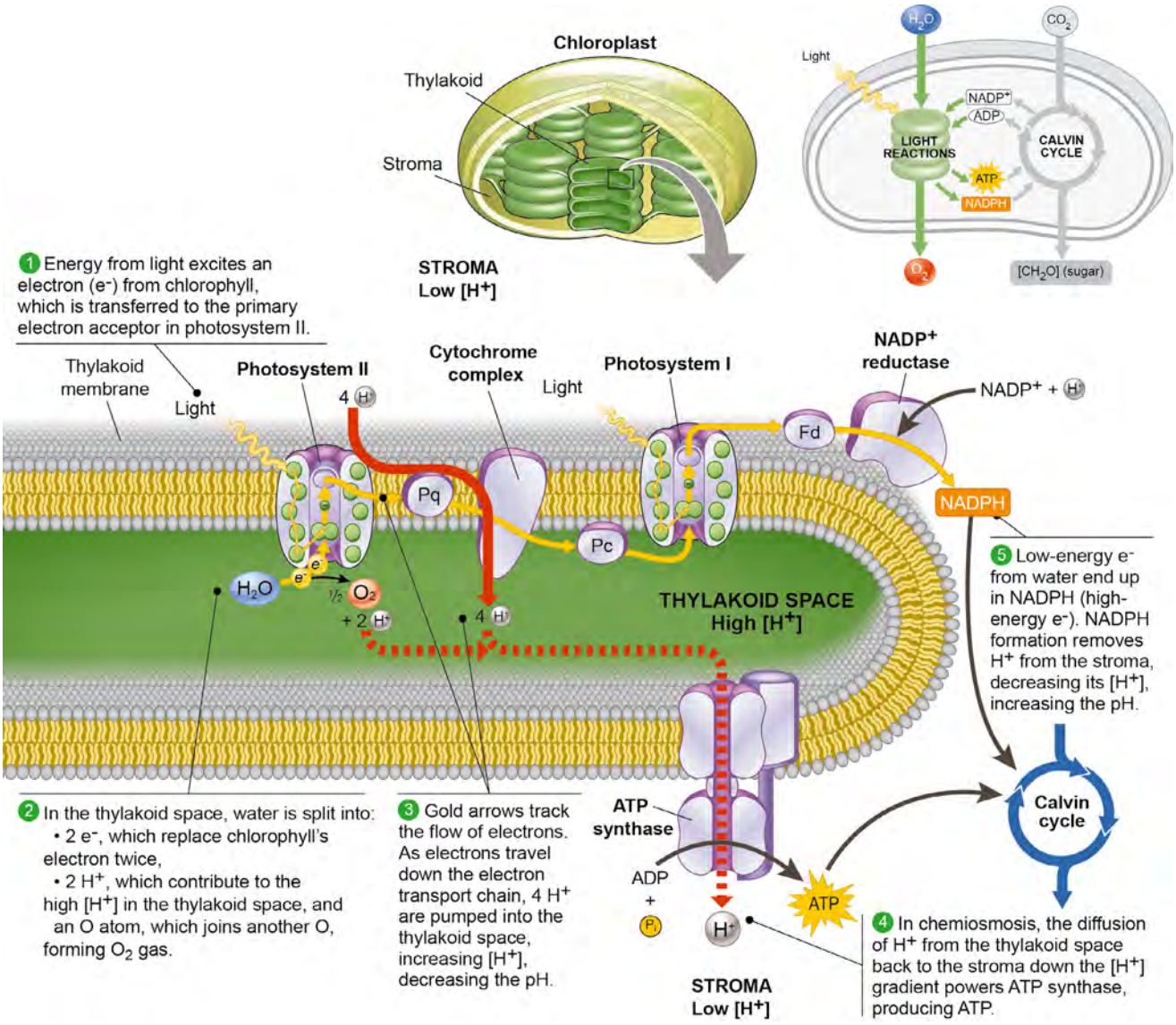


Figure 3.78: Light-dependent biochemical pathway in photosynthesis.

4.1 Responding to Antigens

4.1.1 Barrier Defences in Immunity

Explore physical, chemical and microbiota barriers as preventative mechanisms of pathogenic infection in animals and plants.

Health refers to the state in which an organism carries out all its vital functions effectively. A **disease** is any disturbance in this normal state that interferes with the organism's ability to function properly. Diseases can be broadly classified into two categories: infectious and non-infectious. **Non-infectious diseases** arise from factors such as genetic inheritance, environmental exposure, poor nutrition, or unhealthy lifestyle choices. In contrast, **infectious diseases** are caused by **pathogens**, including bacteria, viruses, fungi, protists, and helminths, as well as by their toxic products. These diseases are transmissible, meaning they can spread from an infected individual, called a **host**, to others.

To defend against infection, animals and plants rely on a variety of nonspecific preventative mechanisms that act as the **first line of defence**. These include physical, chemical, and microbiota (biological) barriers, which together create a robust and multilayered system that helps prevent the entry and establishment of pathogens. This section will explore the physical, chemical and microbiota barriers as preventive mechanisms of infection in animals and plants.

Physical Barriers

Physical barriers are structural features that form a mechanical shield against pathogens. In animals, the most important physical barrier is the skin, which acts as a tough, waterproof layer that prevents microbial entry. The outer layer of skin is composed of keratinised cells that are tightly packed and constantly shed, removing attached microbes. Mucous membranes lining the respiratory, gastrointestinal, and urogenital tracts also serve as physical barriers (see **Figure 4.01**). These membranes secrete mucus, which traps pathogens and are often lined with **cilia** that move microbes out of the body.

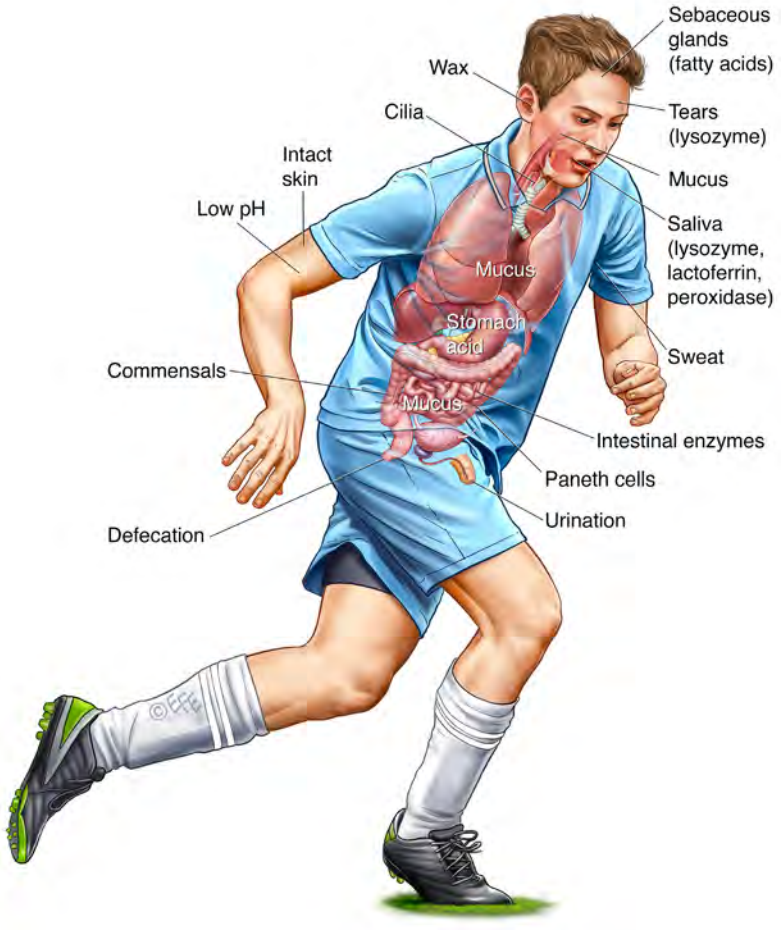


Figure 4.01: Barriers to infection in humans

In plants, the cell wall and waxy cuticle provide physical protection. The cell wall, primarily composed of cellulose, serves as a robust barrier to microbial invasion. Many plants also have a thick cuticle layer on leaves and stems that limits water loss and physically blocks pathogen entry. Stomata can close in response to the detection of microbes, reducing the risk of bacterial invasion through leaf openings.

4.1.2 The Innate Immune Response

Describe the innate immune response, including the steps in an inflammatory response and the characteristics and roles of macrophages, neutrophils, dendritic cells, eosinophils, natural killer cells, mast cells, complement proteins and interferons.

The innate immune response is the body's **second line of defence** against invading pathogens such as bacteria, viruses, fungi, and parasites. Unlike the adaptive immune system, which is specific and develops over time (see **Chapter 4.2.2**), the innate immune system is non-specific, rapid, and present from birth. It recognises general patterns found on pathogens and initiates an immediate response to contain or eliminate them. Key components of the innate immune system include chemical defences, cellular defenders, proteins, and the inflammatory response. This section explores the innate immune response.

The Inflammatory Response

One of the features of the innate immune system is **inflammation**, which occurs in response to tissue injury or infection (see **Figure 4.03**). The primary goal of the inflammatory response is to contain the infection, recruit immune cells, and initiate the repair process. Inflammation is typically characterised by redness, heat, swelling, pain, and loss of function. The inflammatory response begins with the detection of pathogens or tissue damage, where receptors on the surfaces of immune cells recognise molecules on the surface of pathogens or released from damaged cells. In response, injured or infected cells release chemical signals, including histamine, prostaglandins, and cytokines. These mediators cause **vasodilation** (the widening of blood vessels) and increase the permeability of blood vessel walls, allowing immune cells and proteins to access the affected tissues. This change enables specialised immune cells known as **phagocytes** to exit the blood and move toward the infection site through a process called **chemotaxis**. Once at the site, neutrophils and macrophages engulf and destroy pathogens through a process known as **phagocytosis**. Once pathogens are eliminated, anti-inflammatory signals are released to suppress the immune response, allowing tissue repair to commence and the affected area to return to normal function gradually.

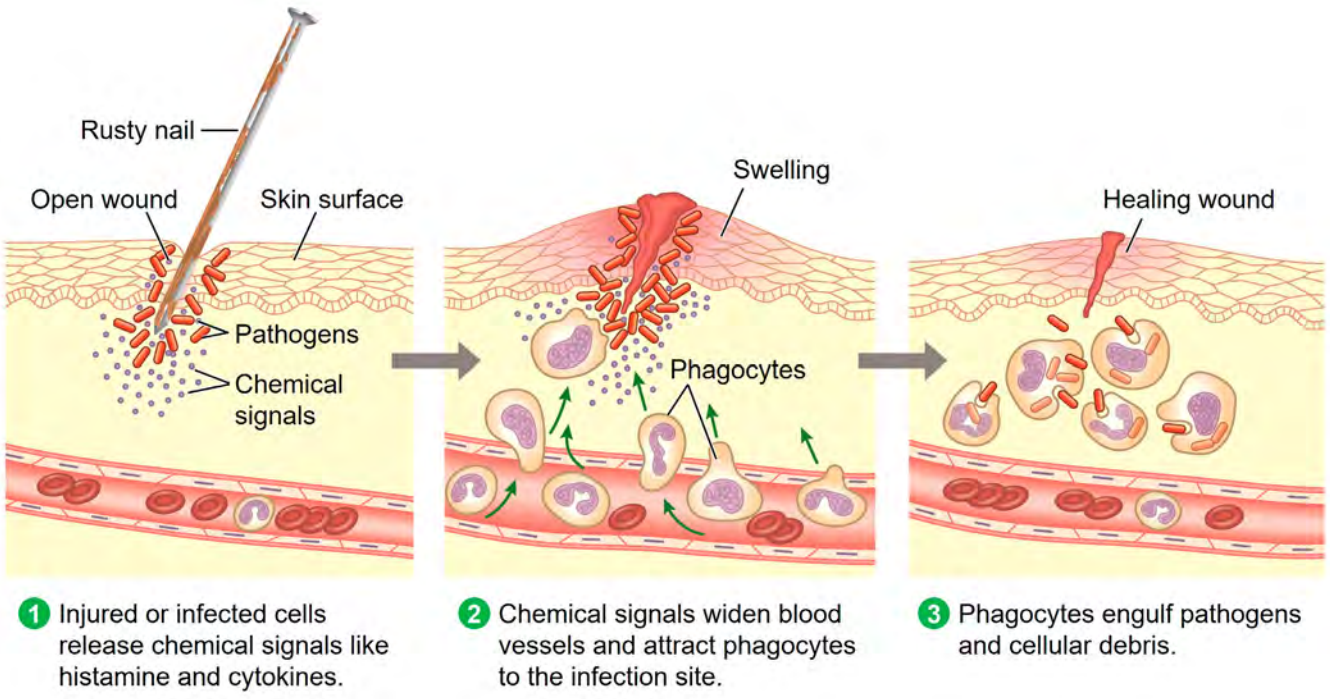


Figure 4.03: The inflammatory response

Cytokines

During the inflammatory response, phagocytes are recruited in large numbers to the site of infection. In addition to phagocytosis, these cells secrete **cytokines**, chemicals that enhance the innate immune response. Firstly, cytokines stimulate liver cells to secrete complement proteins. Secondly, cytokines increase the number of neutrophils and eosinophils circulating in the blood, which helps to fight infection. Finally, cytokines induce an increase in body temperature, known as **fever, which** slows the growth rate of pathogens. In adults, fever is an oral temperature above 37°C. **Figure 4.06** shows changes in oral temperature during fever in a person with measles.

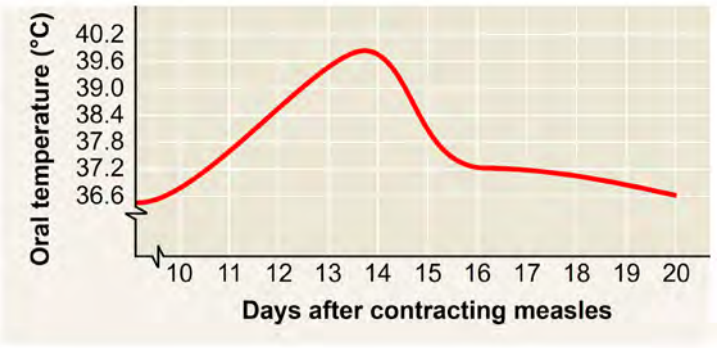


Figure 4.06: Fever during measles

Antimicrobial Proteins of the Innate Immune Response

In mammals, pathogen recognition triggers the production and release of various proteins that attack pathogens or prevent their reproduction. One class of proteins, called **interferons**, are cytokines produced by host cells in response to viral infections. Their primary role is to limit the spread of viruses. Interferons stimulate the synthesis of antiviral proteins that inhibit viral replication and enhance the ability of natural killer (NK) cells to recognise and eliminate infected cells.

The **complement system** comprises approximately 30 proteins that fight pathogens circulating in the blood. Complement proteins enhance the ability of immune cells to detect and eliminate pathogens. One key function is **opsonisation**, where complement proteins coat the surface of pathogens, making them easier for phagocytes to recognise and engulf. They also facilitate chemotaxis, attracting immune cells such as macrophages and neutrophils to the infection site. Additionally, complement proteins contribute to cell lysis through the formation of the **membrane attack complex (MAC)** (see **Figure 4.07**), which inserts into microbial membranes and creates pores, ultimately leading to the destruction of the pathogen.

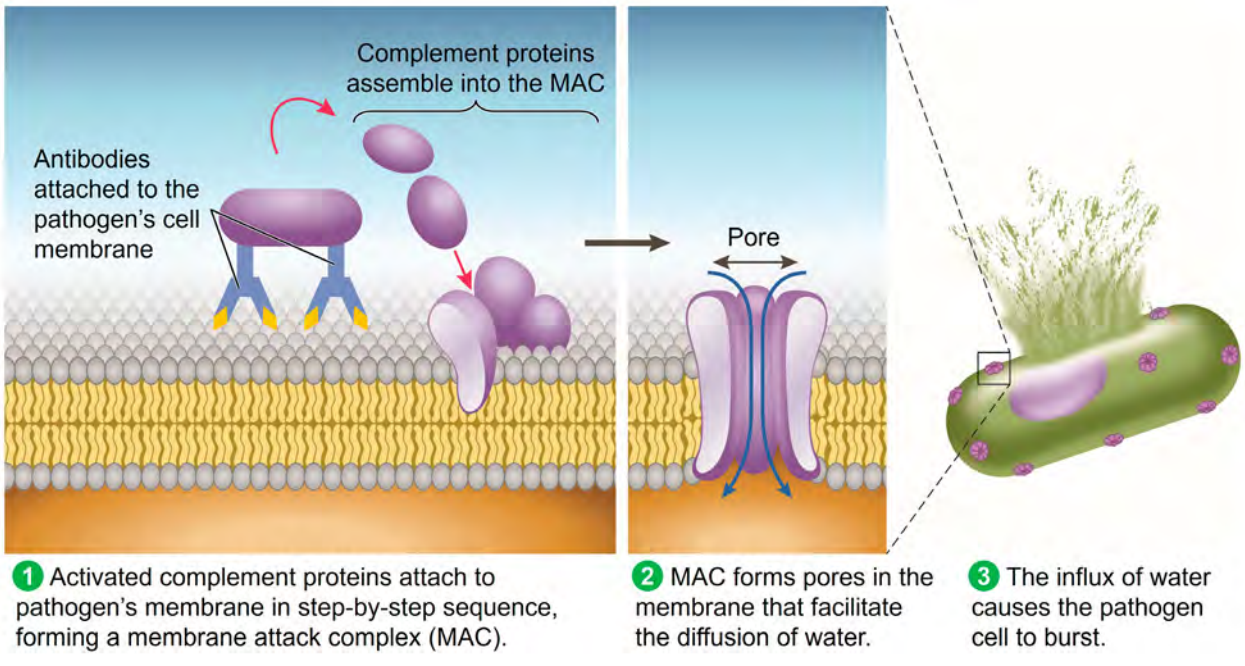


Figure 4.07: Membrane attack complex.

4.2 Acquiring immunity

4.2.1 Lymphatic System and Immune Response

Describe and explain the role of the lymphatic system in the immune response as a transport network and the role of lymph nodes as sites for antigen recognition by T and B lymphocytes.

The **lymphatic system** plays a crucial role in the immune response, serving as both a transport network for immune cells and proteins and as a surveillance system that detects and responds to infections. It consists of lymphatic vessels, lymph nodes, and specialised organs such as the spleen, thymus, and tonsils. Working together, these structures filter out pathogens, facilitate the movement of immune cells, and coordinate communication across different parts of the immune system. This section will examine how the lymphatic system supports immune responses.

Lymphatic System

One of the primary functions of the lymphatic system is to transport **lymph**, a clear fluid that surrounds tissue cells (see **Figure 4.19**). As blood circulates through capillaries, some plasma leaks into the surrounding tissues, forming **interstitial fluid**. If pathogens breach the body's physical barriers—such as the skin or mucous membranes—they can enter these tissues and accumulate in the interstitial fluid. Many pathogens use this fluid as a medium to move through the body and locate target cells. Upon reaching a host cell, pathogens may invade it to replicate, secrete toxins that damage nearby cells or multiply within the interstitial fluid before spreading deeper into tissues or entering the bloodstream. Tiny lymphatic capillaries absorb this fluid, which then becomes lymph once it is inside the vessels. Lymphatic vessels transport lymph to lymph nodes distributed throughout the body, where it is filtered and monitored for pathogens. After passing through the lymph nodes, the cleansed lymph is returned to the circulatory system.

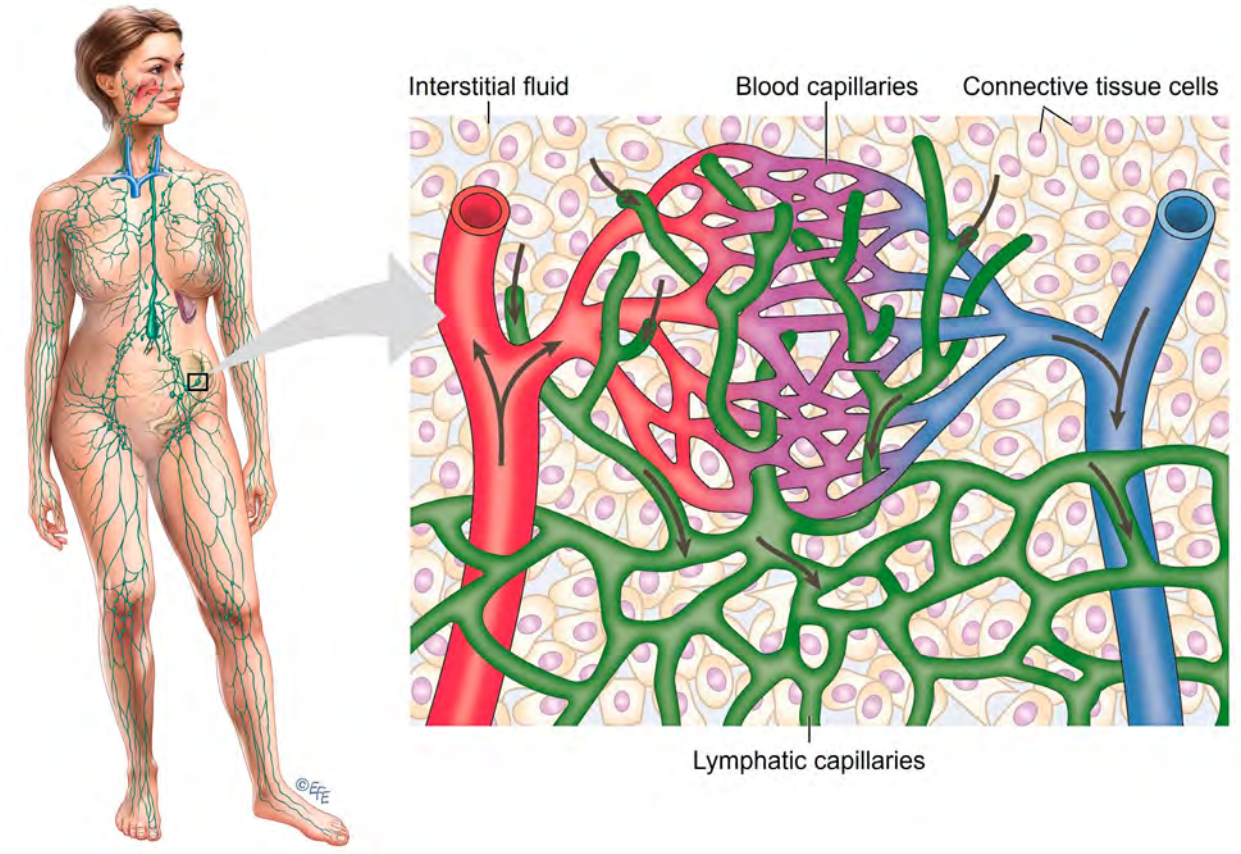


Figure 4.19: The lymphatic system and lymphatic capillaries

Antibodies

Antibodies, also known as immunoglobulins, are Y-shaped proteins produced by B lymphocytes. Each antibody consists of four polypeptide chains—two heavy and two light—held together by disulfide bonds (see **Figure 4.24**). The tips of the Y contain variable regions that form the antigen-binding sites. These regions are highly specific and complementary in shape to a particular antigen, allowing the antibody to bind with high precision. This binding enables the immune system to recognise and neutralise pathogens.

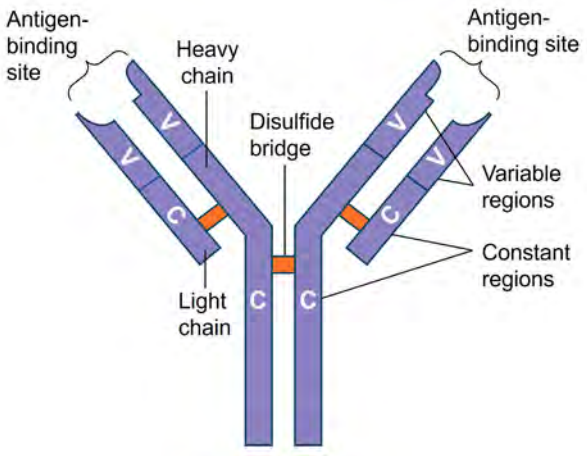


Figure 4.24: Antibody structure

Antibodies help the body neutralise and eliminate pathogens through several key mechanisms (see **Figure 4.25**). One such mechanism is **neutralisation**, in which antibodies bind directly to viruses or toxins, blocking them from attaching to and entering host cells. Another is **opsonisation**, where antibodies coat the surface of pathogens, marking them for easier recognition, uptake, and destruction by phagocytic immune cells such as macrophages. Additionally, antibodies facilitate **agglutination** by binding to multiple pathogens and **precipitation** by binding dissolved antigens, clumping them together and making them easier for the immune system to clear. Lastly, antibody-antigen complexes can initiate the assembly of complement proteins into a membrane attack complex (MAC), which punctures the pathogen's membrane, leading to its lysis. Through these coordinated actions, antibodies play a central role in neutralising, clearing, and destroying extracellular threats.

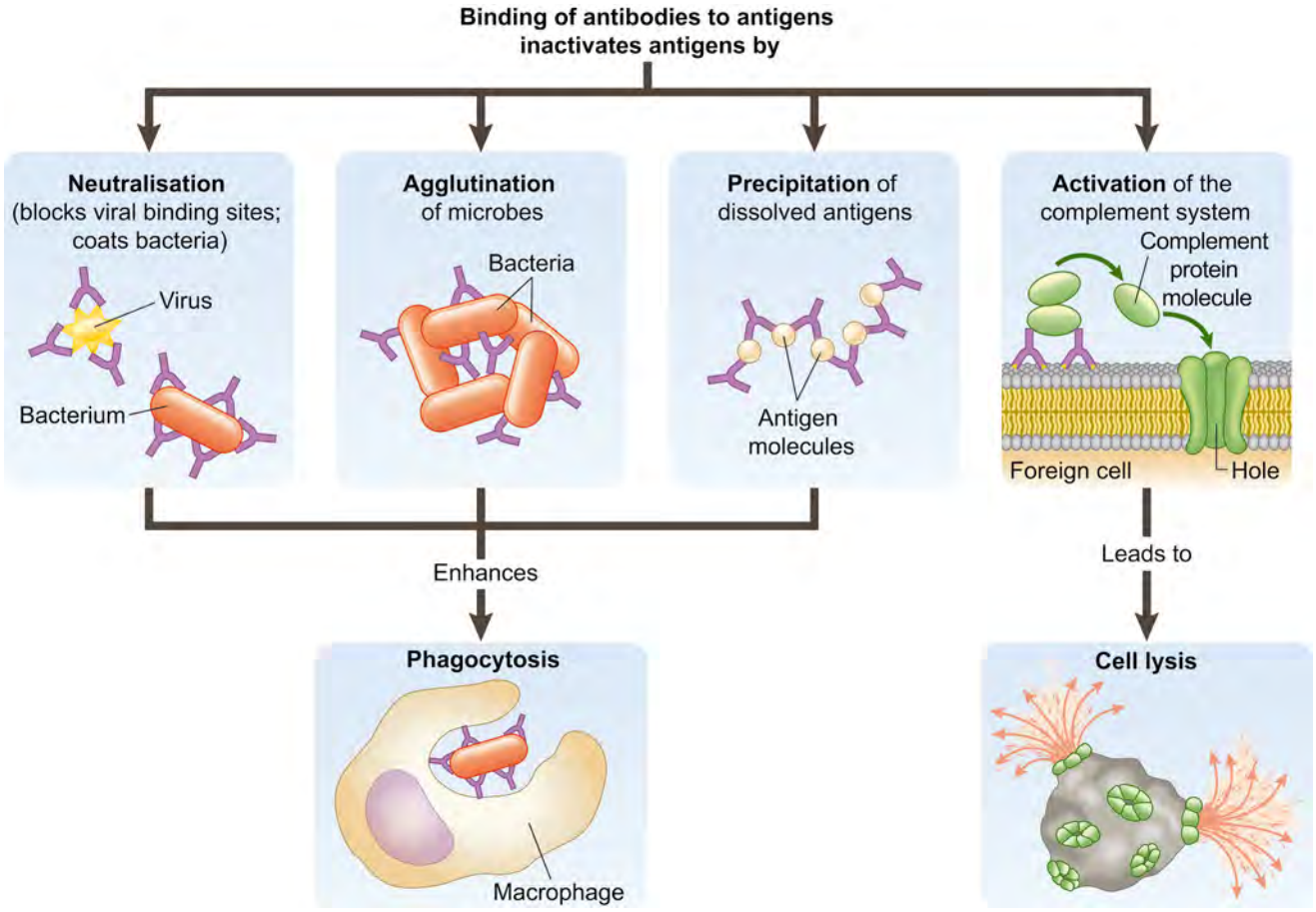


Figure 4.25: Actions of antibodies to pathogens and antigens

Selection Pressures

Environmental **selection pressures** play a major role in altering allele frequencies through the process of **natural selection**. When environmental conditions change, such as shifts in climate, changes in food availability, the presence of predators, or the introduction of diseases, certain traits become more or less advantageous for survival and reproduction. Individuals with beneficial alleles are more likely to survive and pass on their genes, increasing the frequency of those alleles in subsequent generations. For example, in a drought-affected environment, plants with alleles for deeper root systems are more likely to survive and reproduce, leading to an increased frequency of those alleles in the population over time.

This fundamental idea of traits being shaped by environmental pressures was central to Charles Darwin's theory of evolution. Between 1831 and 1836, during his voyage aboard the HMS Beagle (see **Figure 4.41**), Darwin observed numerous adaptations—heritable traits that improved an organism's chances of survival and reproduction in specific environments. Reflecting on these observations, he came to view adaptation and the formation of new species as interconnected processes. He proposed that new species arise from ancestral forms through the gradual accumulation of adaptations suited to different environments.

Figure 4.41: Voyage of the Beagle (1831 to 1836)

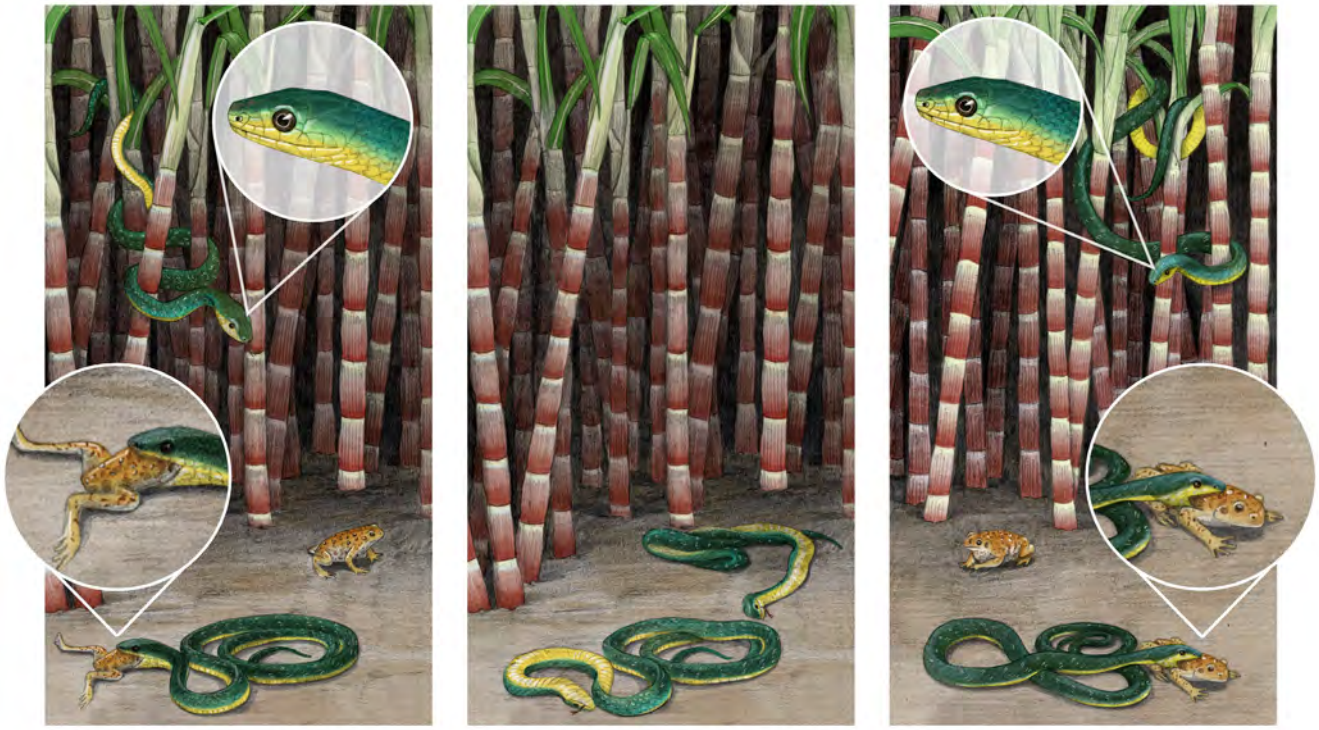
A key illustration of Darwin's theory emerged during his visit to the Galapagos Islands in 1835. There, he observed a diverse group of finches (see **Figure 4.42**), each exhibiting unique beak shapes and behaviours adapted to the specific food sources available on their islands. Darwin hypothesised that all these finches had descended from a single ancestral species that originally arrived from mainland South America. As separate groups of finches spread across the islands, they encountered a variety of habitats and selection pressures—such as differences in climate, food availability, competition, predation, and disease. Darwin concluded that natural selection was the driving force behind the diversification of these finch species. For example, finches with large, strong beaks were better equipped to crack hard seeds, giving them a competitive edge on islands where such food was prevalent. As these advantageous traits were passed down through generations, they became more common within the population, eventually leading to the development of new, specialised species.

Figure 4.42: Darwin finches

Question 334

A cane toad population was introduced to Australia in 1935 to control beetle populations that damaged sugar cane crops. Cane toads secrete venom from glands on each shoulder when threatened. The venom is often fatal if ingested as the toxins inhibit heart muscle function.

The diagram below describes one effect of the cane toad's introduction on the recent evolution of Australia's green tree snake population.



Before 1935, some green tree snakes had heads large enough to swallow cane toads.

These snakes were less likely to survive and reproduce.

Subsequent generations have smaller heads, incapable of swallowing cane toads.

(a) Identify the mechanism described in the diagram that decreases the frequency of alleles coding large heads in Australia's green tree snake population.

(1 mark)

(b) The cane toad is a selection pressure on Australia's green tree snake population.

i. Define a selection pressure using the cane toad as an example.

(2 marks)

ii. State one other selection pressure and describe its impacts on Australia's green tree snake population.

(2 marks)

Selective Breeding in Animals

In livestock, animals such as cattle, sheep, and chickens have been bred for faster growth, higher milk production, or specific physical features that improve meat quality. Similarly, in domestic animals like dogs and cats, selective breeding has created a wide range of breeds with distinct appearances and behaviours. Selective breeding in dogs has led to the development of a wide range of breeds, each with specific anatomical and behavioural traits suited to particular human needs (see **Figure 4.56**). This diversity is the result of targeted breeding over generations, where humans select dogs that exhibit desirable characteristics and use them to produce offspring with those same traits. For example, hunting dogs such as beagles were selectively bred to be smaller in size, allowing them to enter foxholes during hunts. Herding dogs, like sheepdogs, were bred for high intelligence, enabling them to understand and respond to complex herding commands. Racing dogs, such as greyhounds, were bred for speed and agility, resulting in sleek, lightweight bodies that are well-adapted for fast running. In contrast, toy dogs, including chihuahuas, were bred for their small size, making them suitable companions.

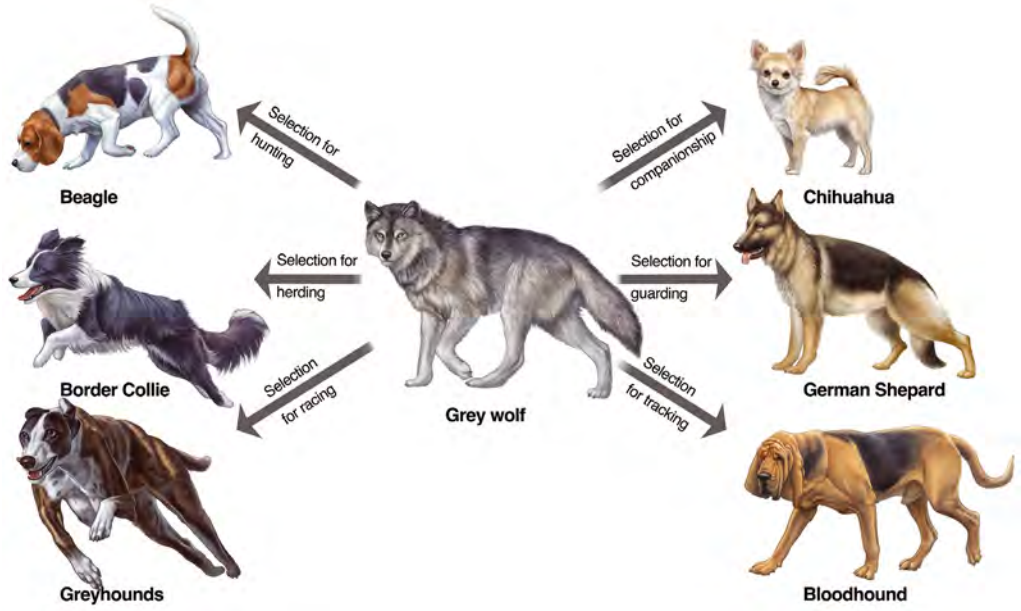


Figure 4.56: Selective breeding in *Canis Lupus*.

Horses have been selectively bred over many generations to develop traits suited to specific purposes. For example, racehorses have been bred for speed, resulting in animals that are typically leaner, lighter, taller, and faster. In contrast, draft horses have been selectively bred for strength and endurance, resulting in a stockier and more robust build that is well-suited for pulling heavy loads. Similarly, cattle have undergone selective breeding to enhance desirable traits. For many years, farmers have bred cows with higher milk yields to increase dairy production. Additionally, breeders have targeted a specific mutation in certain cattle that leads to increased muscle mass. This has led to the development of the Belgian Blue breed, which is renowned for its extreme muscularity and produces a higher proportion of lean, edible meat.

While selective breeding can offer significant economic and practical benefits, it also raises important concerns about genetic diversity. Emphasising a narrow set of traits often reduces the gene pool, increasing the likelihood of inbreeding. This, in turn, can lead to the accumulation of harmful recessive alleles and a higher risk of health problems such as genetic disorders, physical deformities, and reduced fertility. In particular, some purebred dog breeds are known to suffer from inherited conditions—such as hip dysplasia, heart defects, or respiratory issues—due to generations of selective breeding within closed gene pools. Over time, this lack of genetic variation can also render populations more susceptible to environmental changes and disease outbreaks, thereby limiting their long-term viability and raising ethical concerns about animal welfare. To address these risks, responsible breeding programs now increasingly focus on maintaining genetic diversity while still selecting for desirable traits.

Antibiotic Resistance

Consider a population of *Staphylococcus aureus* bacteria (see **Figure 4.58**). The cells in this population have around 2,500 genes, with only minimal variation in their nucleotide sequences. Occasionally, a random mutation may occur during DNA replication in one of the cells. This mutation results in a change to a gene that enables the bacterium to produce an enzyme called β-lactamase that breaks down penicillin, rendering the antibiotic ineffective. As a result, the mutated bacterium becomes resistant to penicillin, while the rest of the population remains susceptible. This resistant cell gains a competitive advantage over its non-resistant counterparts. When exposed to penicillin, a selection pressure, the susceptible bacteria are destroyed, allowing the resistant cells to survive and replicate. Over time, it gives rise to a growing colony of antibiotic-resistant bacteria.

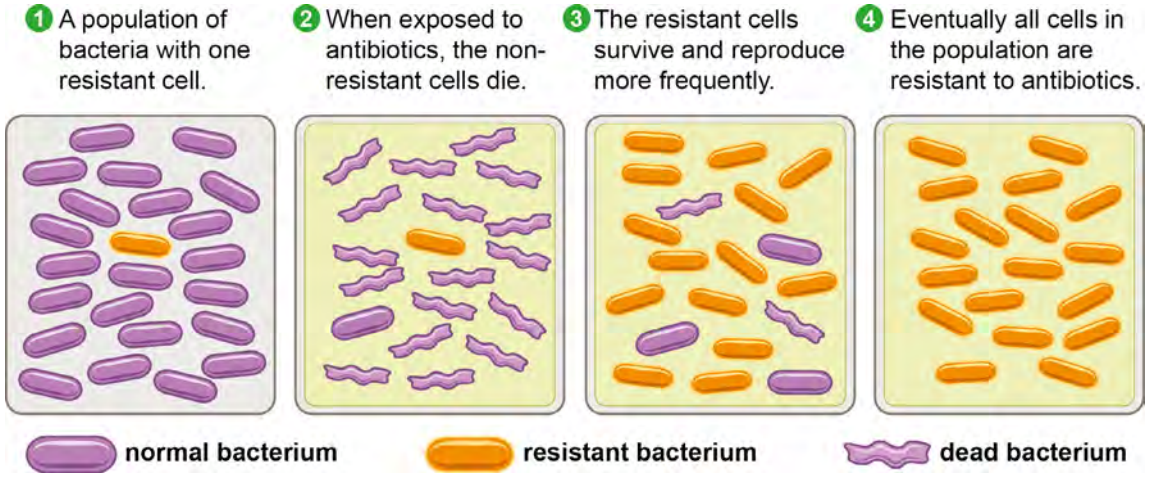


Figure 4.58: The Evolution of Antibiotic Resistance in Bacteria

Resistance is also spread between bacteria through **horizontal gene transfer**, a process in which plasmids carrying antibiotic-resistance genes are transferred from a donor cell to a recipient cell without the need for reproduction (see **Figure 4.59**). This allows the recipient to acquire new traits that improve their survival and adaptability. Horizontal gene transfer occurs both within and between bacterial populations, contributing to the rapid and widespread emergence of antibiotic resistance.

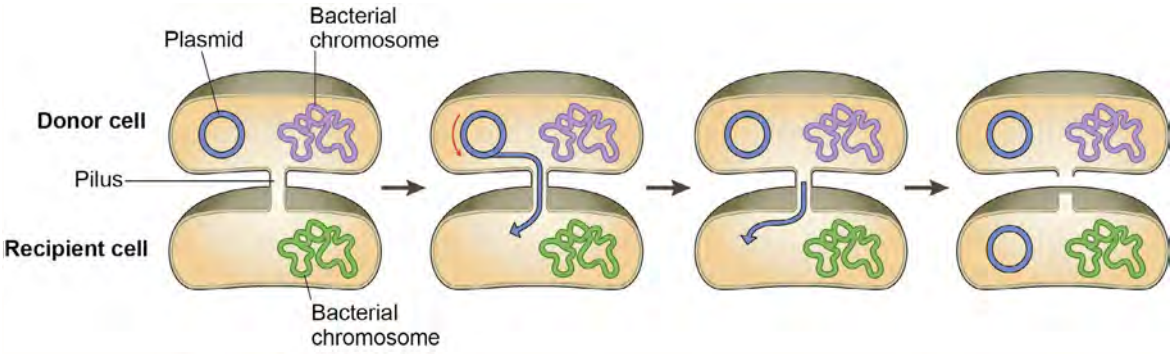


Figure 4.59: Horizontal gene transfer of resistance genes in bacteria

Antibiotic-resistant bacteria have become a major global health concern due to the increasing number of infections that are difficult to treat. Today, the World Health Organisation reports that over 50% of antibiotics in some countries are now ineffective against commonly encountered bacterial infections. Resistance to multiple antibiotics is increasing, with some strains exhibiting pan-resistance, meaning they are resistant to all known antibiotic treatments. The continued emergence of resistant bacteria highlights the urgent need for new antibiotics, better stewardship, and alternative treatment strategies.

Faunal Succession

Over time, natural processes such as erosion can wear away surface rock, gradually revealing deeper layers that were once buried. These exposed strata act as a vertical timeline, allowing scientists to study the chronological sequence of fossilised organisms. In general, deeper layers contain older and often more primitive life forms, while higher layers reveal more recent and typically more complex species. This observation underpins **stratigraphic analysis**, the study of rock layers and their arrangement to determine the relative ages and sequence of geological and fossil records.

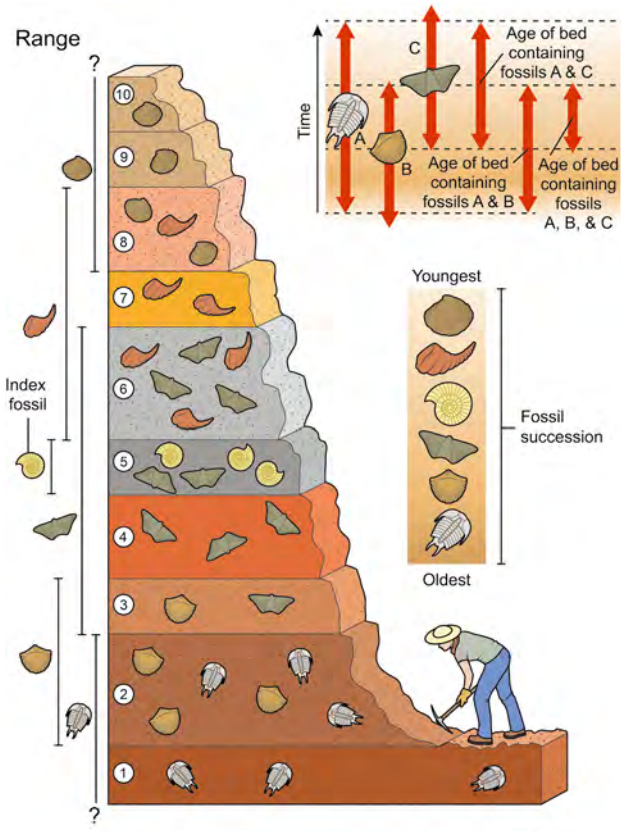


Figure 4.61: Faunal succession

A key concept in this analysis is **faunal succession** (see **Figure 4.61**), the principle that fossil organisms appear in a consistent and recognisable order within sedimentary rock layers. This allows scientists to use the presence or absence of specific fossils to compare and date rock layers across different regions. In doing so, they have observed consistent patterns in the fossil record, such as species disappearing between layers and new species appearing in more recent strata. These patterns reflect episodes of extinction and the rise of new species over time. Consequently, the fossil record provides strong evidence that life on Earth has undergone evolution over millions of years, occurring at times gradually and at other times more abruptly.

Index and Transitional Fossils

Transitional fossils are those displaying intermediate characteristics between ancestral organisms and their descendants. They are critical to our understanding of evolutionary change, as they provide direct evidence of how one group of organisms gradually evolved into another. These fossils often exhibit a blend of traits found in both earlier and more recent species. A well-known example is *Archaeopteryx* (**Figure 4.62**), which possesses both reptilian features, such as teeth and a long bony tail, and avian traits, including feathers and a wishbone, making it a transitional form between non-avian dinosaurs and modern birds.

Figure 4.62: *Archaeopteryx*

Similarly, the evolutionary history of cetaceans, such as whales, dolphins, and porpoises, provides a striking example of how transitional fossils illuminate major shifts in form and function. While scientists had long hypothesised that whales evolved from land-dwelling mammals, early fossil records lacked intermediate forms. That changed in recent decades with the discovery of a remarkable sequence of transitional fossils in places like Pakistan and Egypt. Fossils of early cetaceans, such as Pakicetus and Ambulocetus, reveal a gradual progression from terrestrial mammals to fully aquatic creatures, including adaptations like reduced hind limbs, the development of flippers, and the evolution of tail flukes. These forms closely resemble extinct even-toed ungulates, such as *Diacodexis*, supporting genetic evidence that cetaceans are closely related to deer and hippos (see **Figure 4.63**).

Polyploidy is a condition in which an error during cell division results in gametes containing an extra set of chromosomes. For instance, a mistake in cell division can double a cell's chromosome number from diploid (2*n*) to tetraploid (4*n*), as illustrated in **Figure 4.73**. An organism with this chromosomal duplication can reproduce successfully by self-fertilisation or by mating with another individual that has the same chromosome number. However, it becomes reproductively isolated from members of the original 2n population since mating between 4n and 2n individuals typically produces sterile offspring. Another form of polyploidy occurs when two different species interbreed, resulting in hybrid offspring. These hybrids are usually sterile because their chromosomes are not homologous and cannot pair properly during meiosis. This new polyploid is reproductively isolated from both parent species and cannot interbreed with them. Importantly, polyploidy leads to sympatric speciation, as the new species arises in the same geographic area as its parent population without physical isolation. Polyploidy has played a significant role in plant evolution, accounting for more than 80% of all living plant species today. Although less common in animals, it has also contributed to the evolution of some species, including certain salamanders, frogs, and leeches.

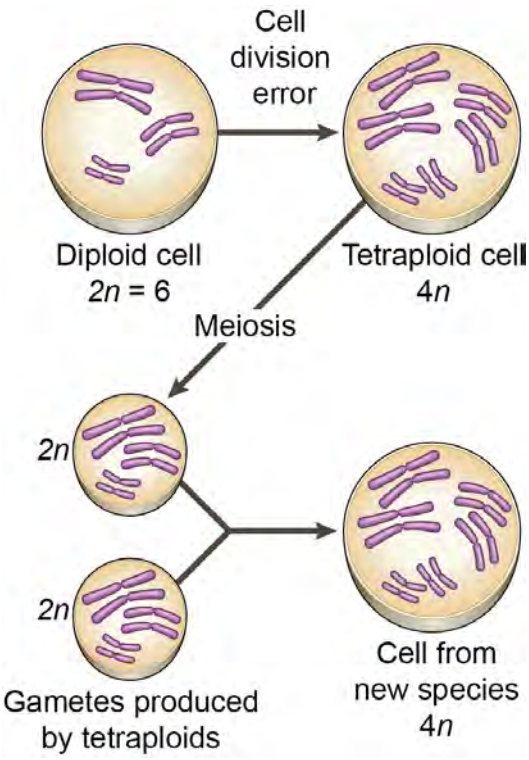


Figure 4.73: Polyploidy

Sympatric speciation can also occur through the emergence of new ecological niches. In East Africa's Lake Victoria, up to 600 cichlid species are thought to have evolved in the past 100,000 years from a small number of colonising species. As shown in **Figure 4.74**, four cichlid species descended from a common ancestor but adapted to different food sources. These ecological differences drove natural selection to favour different alleles in each group, gradually changing their genetic makeup. Over time, these changes led to reproductive isolation and the formation of new species, demonstrating sympatric speciation.

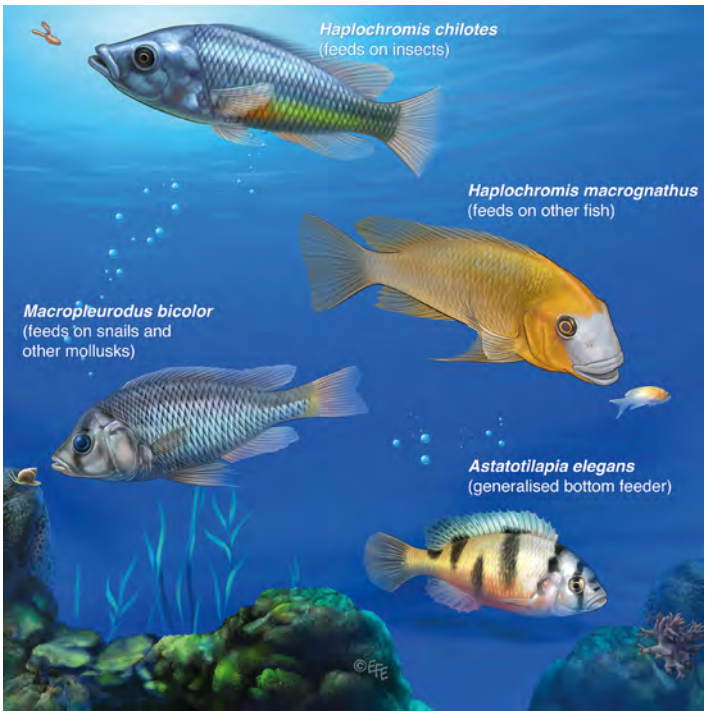


Figure 4.74: Sympatric speciation in cichlid species inhabiting Lake Victoria.

Sympatric speciation is also driven by **sexual selection**, in which females typically select males based on appearance. For example, researchers have studied two closely related sympatric species of cichlids in Lake Victoria that differ mainly in the colouration of breeding males. Cichlid species that inhabit shallow water are blue and prefer to mate with other blue-coloured fish, whereas cichlid species that live in deeper water are red and prefer to mate with red-coloured fish. This observation suggests that mate choice based on colouration can act as a reproductive barrier, keeping the gene pools of two species separate.